

# Baoliang Zhou

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

3,605  
citations

430874

18  
h-index

289244

40  
g-index

42  
all docs

42  
docs citations

42  
times ranked

2537  
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	Genetic basis for glandular trichome formation in cotton. <i>Nature Communications</i> , 2016, 7, 10456.	12.8	130
5	Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 33.	8.8	128
6	Sequence-based ultra-dense genetic and physical maps reveal structural variations of allopolyploid cotton genomes. <i>Genome Biology</i> , 2015, 16, 108.	9.6	108
7	Cross-species transferability of <i>G. arboreum</i> -derived EST-SSRs in the diploid species of <i>Gossypium</i> . <i>Theoretical and Applied Genetics</i> , 2006, 112, 1573-1581.	3.6	75
8	Genome sequencing of the Australian wild diploid species <i>Gossypium australe</i> highlights disease resistance and delayed gland morphogenesis. <i>Plant Biotechnology Journal</i> , 2020, 18, 814-828.	8.3	61
9	LncRNAs in polyploid cotton interspecific hybrids are derived from transposon neofunctionalization. <i>Genome Biology</i> , 2018, 19, 195.	8.8	59
10	Characterization of conserved circular <i>scp</i> -RNA in polyploid <i>Gossypium</i> species and their ancestors. <i>FEBS Letters</i> , 2017, 591, 3660-3669.	2.8	51
11	Mutation of SELF-PRUNING homologs in cotton promotes short-branching plant architecture. <i>Journal of Experimental Botany</i> , 2018, 69, 2543-2553.	4.8	49
12	Reconstruction of the full-length transcriptome atlas using PacBio Iso-Seq provides insight into the alternative splicing in <i>Gossypium australe</i> . <i>BMC Plant Biology</i> , 2019, 19, 365.	3.6	43
13	Construction of a complete set of alien chromosome addition lines from <i>Gossypium australe</i> in <i>Gossypium hirsutum</i> : morphological, cytological, and genotypic characterization. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1105-1121.	3.6	34
14	Structure and size variations between 12A and 12D homoeologous chromosomes based on high-resolution cytogenetic map in allotetraploid cotton. <i>Chromosoma</i> , 2010, 119, 255-266.	2.2	32
15	A CC-NBS-LRR gene induces hybrid lethality in cotton. <i>Journal of Experimental Botany</i> , 2019, 70, 5145-5156.	4.8	32
16	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
17	Transcriptome Sequencing and Differential Gene Expression Analysis of Delayed Gland Morphogenesis in <i>Gossypium australe</i> during Seed Germination. <i>PLoS ONE</i> , 2013, 8, e75323.	2.5	26
18	Quantitative trait locus analysis of boll-related traits in an intraspecific population of <i>Gossypium hirsutum</i> . <i>Euphytica</i> , 2015, 203, 121-144.	1.2	24

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19	New <sc>QTL</sc>s for lint percentage and boll weight mined in introgression lines from two feral landraces into <i>Gossypium hirsutum</i> acc <sc>TM</sc>. <i>Plant Breeding</i> , 2016, 135, 90-101.	1.9	19
20	Molecular Evolution and Phylogenetic Analysis of Eight COL Superfamily Genes in Group I Related to Photoperiodic Regulation of Flowering Time in Wild and Domesticated Cotton ( <i>Gossypium</i> ) Species. <i>PLoS ONE</i> , 2015, 10, e0118669.	2.5	18
21	Evaluation of Cotton Leaf Curl Virus Resistance in BC1, BC2, and BC3 Progenies from an Interspecific Cross between <i>Gossypium arboreum</i> and <i>Gossypium hirsutum</i> . <i>PLoS ONE</i> , 2014, 9, e111861.	2.5	16
22	A New Synthetic Amphiploid (AADDAA) between <i>Gossypium hirsutum</i> and <i>G. arboreum</i> Lays the Foundation for Transferring Resistances to <i>Verticillium</i> and Drought. <i>PLoS ONE</i> , 2015, 10, e0128981.	2.5	16
23	A New Synthetic Allotetraploid (A1A1G2G2) between <i>Gossypium herbaceum</i> and <i>G. australe</i> : Bridging for Simultaneously Transferring Favorable Genes from These Two Diploid Species into Upland Cotton. <i>PLoS ONE</i> , 2015, 10, e0123209.	2.5	16
24	Identification of centromeric regions on the linkage map of cotton using centromere-related repeats. <i>Genomics</i> , 2014, 104, 587-593.	2.9	15
25	QTL analysis for yield and fibre quality traits using three sets of introgression lines developed from three <i>Gossypium hirsutum</i> race stocks. <i>Molecular Genetics and Genomics</i> , 2019, 294, 789-810.	2.1	14
26	Construction of microsatellite-based linkage map and mapping of nectarilessness and hairiness genes in <i>Gossypium tomentosum</i> . <i>Journal of Genetics</i> , 2013, 92, 445-459.	0.7	13
27	A and D genomes spatial separation at somatic metaphase in tetraploid cotton: evidence for genomic disposition in a polyploid plant. <i>Plant Journal</i> , 2015, 84, 1167-1177.	5.7	13
28	Localization of high level of sequence conservation and divergence regions in cotton. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1173-1182.	3.6	11
29	Characterization of eleven monosomic alien addition lines added from <i>Gossypium anomalum</i> to <i>Gossypium hirsutum</i> using improved GISH and SSR markers. <i>BMC Plant Biology</i> , 2016, 16, 218.	3.6	11
30	Fine-mapping and candidate gene analysis of qFS-Chr. D02, a QTL for fibre strength introgressed from a semi-wild cotton into <i>Gossypium hirsutum</i> . <i>Plant Science</i> , 2020, 297, 110524.	3.6	10
31	Inducement and identification of chromosome introgression and translocation of <i>Gossypium australe</i> on <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2018, 19, 15.	2.8	8
32	Overcoming obstacles to interspecific hybridization between <i>Gossypium hirsutum</i> and <i>G. turneri</i> . <i>Euphytica</i> , 2018, 214, 1.	1.2	6
33	Mapping of genes for flower-related traits and QTLs for flowering time in an interspecific population of <i>Gossypium hirsutum</i> × <i>G. darwinii</i> . <i>Journal of Genetics</i> , 2016, 95, 197-201.	0.7	5
34	Genome-Wide Identification and Expression Profile Analysis of the PHT1 Gene Family in <i>Gossypium hirsutum</i> and Its Two Close Relatives of Subgenome Donor Species. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4905.	4.1	5
35	Role of phasiRNAs from two distinct phasing frames of ChMYB2 loci in cis- gene regulation in the cotton genome. <i>BMC Plant Biology</i> , 2020, 20, 219.	3.6	5
36	Ten alien chromosome additions of <i>Gossypium hirsutum</i> from <i>Gossypium bickii</i> developed by integrative uses of GISH and species-specific SSR markers. <i>Molecular Genetics and Genomics</i> , 2018, 293, 945-955.	2.1	4

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37	Genome-Wide Introgression and Quantitative Trait Locus Mapping Reveals the Potential of Asian Cotton ( <i>Gossypium arboreum</i> ) in Improving Upland Cotton ( <i>Gossypium hirsutum</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 719371.	3.6	4
38	Characterization of a sterile dwarf mutant and the cloning of zeaxanthin epoxidase in Asian cotton ( <i>Gossypium arboreum</i> L.). <i>Plant Growth Regulation</i> , 2018, 85, 57-72.	3.4	2
39	Chromosome duplication causing geneâ€dosageâ€based effects on the gene expression level in <i>Gossypium hirsutum</i> â€ <i>Gossypium australe</i> addition lines. <i>Plant Direct</i> , 2020, 4, e00247.	1.9	1
40	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1
41	TIP41L, a putative candidate gene conferring both seed size and boll weight, was fine-mapped in an introgression line of <i>Gossypium hirsutum</i> - <i>Gossypium arboreum</i> . <i>Plant Science</i> , 2022, 317, 111197.	3.6	1