## Zhikun Li

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Genome Wide Association Study Revealed Key Single Nucleotide Polymorphisms/Genes Associated With Seed Germination in Gossypium hirsutum L. Frontiers in Plant Science, 2022, 13, 844946.	3.6	3
2	Development and Utilization of Functional Kompetitive Allele-Specific PCR Markers for Key Genes Underpinning Fiber Length and Strength in Gossypium hirsutum L Frontiers in Plant Science, 2022, 13, 853827.	3.6	4
3	Dynamic characteristics and functional analysis provide new insights into long non-coding RNA responsive to Verticillium dahliae infection in Gossypium hirsutum. BMC Plant Biology, 2021, 21, 68.	3.6	19
4	Evolution, expression and functional analysis of cultivated allotetraploid cotton DIR genes. BMC Plant Biology, 2021, 21, 89.	3.6	13
5	Cotton <i>GhSSI2</i> isoforms from the stearoyl acyl carrier protein fatty acid desaturase family regulate Verticillium wilt resistance. Molecular Plant Pathology, 2021, 22, 1041-1056.	4.2	16
6	Tissueâ€specific expression of <i>GhnsLTPs</i> identified via GWAS sophisticatedly coordinates disease and insect resistance by regulating metabolic flux redirection in cotton. Plant Journal, 2021, 107, 831-846.	5.7	22
7	A largeâ€scale genomic association analysis identifies a fragment in Dt11 chromosome conferring cotton Verticillium wilt resistance. Plant Biotechnology Journal, 2021, 19, 2126-2138.	8.3	21
8	High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement. Nature Genetics, 2021, 53, 1385-1391.	21.4	76
9	Proteomic analyses on xylem sap provides insights into the defense response of Gossypium hirsutum against Verticillium dahliae. Journal of Proteomics, 2020, 213, 103599.	2.4	15
10	Genomeâ€wide dissection of hybridization for fiber quality―and yieldâ€related traits in upland cotton. Plant Journal, 2020, 104, 1285-1300.	5.7	9
11	Genetic variation associated with the shoot biomass of upland cotton seedlings under contrasting phosphate supplies. Molecular Breeding, 2020, 40, 1.	2.1	2
12	A high-density genetic map and multiple environmental tests reveal novel quantitative trait loci and candidate genes for fibre quality and yield in cotton. Theoretical and Applied Genetics, 2020, 133, 3395-3408.	3.6	24
13	Evaluation of the genetic diversity of fibre quality traits in upland cotton (Gossypium hirsutum L.) inferred from phenotypic variations. Journal of Cotton Research, 2019, 2, .	2.5	1
14	The cotton laccase gene <i>GhLAC15 </i> enhances Verticillium wilt resistance via an increase in defenceâ€induced lignification and lignin components in the cell walls of plants. Molecular Plant Pathology, 2019, 20, 309-322.	4.2	111
15	HyPRP1 performs a role in negatively regulating cotton resistance to V. dahliae via the thickening of cell walls and ROS accumulation. BMC Plant Biology, 2018, 18, 339.	3.6	41
16	Identification of SNPs and Candidate Genes Associated With Salt Tolerance at the Seedling Stage in Cotton (Gossypium hirsutum L.). Frontiers in Plant Science, 2018, 9, 1011.	3.6	50
17	Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield. Nature Genetics, 2018, 50, 803-813.	21.4	368
18	A genome-wide association study uncovers novel genomic regions and candidate genes of yield-related traits in upland cotton. Theoretical and Applied Genetics, 2018, 131, 2413-2425.	3.6	31

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19	Genomeâ€wide association study discovered genetic variation and candidate genes of fibre quality traits in <i>Gossypium hirsutum</i> L Plant Biotechnology Journal, 2017, 15, 982-996.	8.3	199
20	Histochemical Analyses Reveal That Stronger Intrinsic Defenses in Gossypium barbadense Than in G. hirsutum Are Associated With Resistance to Verticillium dahliae. Molecular Plant-Microbe Interactions, 2017, 30, 984-996.	2.6	65
21	Mapping QTL for cotton fiber quality traits using simple sequence repeat markers, conserved intron-scanning primers, and transcript-derived fragments. Euphytica, 2015, 201, 215-230.	1.2	40