

Qian-Hao Zhu

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

5,308
citations

101543

36
h-index

91884

69
g-index

105
all docs

105
docs citations

105
times ranked

5739
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Widespread noncoding circular <i>scRNA</i> s in plants. <i>New Phytologist</i> , 2015, 208, 88-95. | 7.3 | 374 |
| 2 | Regulation of flowering time and floral patterning by miR172. <i>Journal of Experimental Botany</i> , 2011, 62, 487-495. | 4.8 | 341 |
| 3 | A diverse set of microRNAs and microRNA-like small RNAs in developing rice grains. <i>Genome Research</i> , 2008, 18, 1456-1465. | 5.5 | 332 |
| 4 | DNA demethylases target promoter transposable elements to positively regulate stress responsive genes in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2014, 15, 458. | 8.8 | 243 |
| 5 | Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1187-1209. | 1.8 | 226 |
| 6 | Over-expression of miR172 causes loss of spikelet determinacy and floral organ abnormalities in rice (<i>Oryza sativa</i>). <i>BMC Plant Biology</i> , 2009, 9, 149. | 3.6 | 210 |
| 7 | Long noncoding <i>scRNA</i> s responsive to <i>Fusarium oxysporum</i> infection in <i>Azadirachta indica</i> . <i>New Phytologist</i> , 2014, 201, 574-584. | 7.3 | 188 |
| 8 | miR482 Regulation of NBS-LRR Defense Genes during Fungal Pathogen Infection in Cotton. <i>PLoS ONE</i> , 2013, 8, e84390. | 2.5 | 163 |
| 9 | The ANTH1 INDEHISCENCE1 Gene Encoding a Single MYB Domain Protein Is Involved in Anther Development in Rice. <i>Plant Physiology</i> , 2004, 135, 1514-1525. | 4.8 | 152 |
| 10 | Molecular Functions of Long Non-Coding RNAs in Plants. <i>Genes</i> , 2012, 3, 176-190. | 2.4 | 139 |
| 11 | PlantcircBase: A Database for Plant Circular RNAs. <i>Molecular Plant</i> , 2017, 10, 1126-1128. | 8.3 | 131 |
| 12 | Twenty years of plant genome sequencing: achievements and challenges. <i>Trends in Plant Science</i> , 2022, 27, 391-401. | 8.8 | 125 |
| 13 | Characterization of the defense transcriptome responsive to <i>Fusarium oxysporum</i> -infection in <i>Arabidopsis</i> using RNA-seq. <i>Gene</i> , 2013, 512, 259-266. | 2.2 | 120 |
| 14 | Full-length sequence assembly reveals circular RNAs with diverse non-GT/AG splicing signals in rice. <i>RNA Biology</i> , 2017, 14, 1055-1063. | 3.1 | 113 |
| 15 | Regulation of Nicotine Biosynthesis by an Endogenous Target Mimicry of MicroRNA in Tobacco. <i>Plant Physiology</i> , 2015, 169, 1062-1071. | 4.8 | 96 |
| 16 | Analysis of transcriptional and epigenetic changes in hybrid vigor of allopolyploid <i>Brassica napus</i> uncovers key roles for small <i>scRNA</i> s. <i>Plant Journal</i> , 2017, 91, 874-893. | 5.7 | 95 |
| 17 | Fine-tuning the amylose content of rice by precise base editing of the <i>Wx</i> gene. <i>Plant Biotechnology Journal</i> , 2021, 19, 11-13. | 8.3 | 95 |
| 18 | Epigenetic Mechanisms: An Emerging Player in Plant-Microbe Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 187-196. | 2.6 | 72 |

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|----|--|-----|-----------|
| 19 | Identification of wounding and topping responsive small RNAs in tobacco (<i>Nicotiana tabacum</i>). <i>BMC Plant Biology</i> , 2012, 12, 28. | 3.6 | 68 |
| 20 | Ds tagging of BRANCHED FLORETLESS 1 (BFL1) that mediates the transition from spikelet to floret meristem in rice (<i>Oryza sativa</i> L). <i>BMC Plant Biology</i> , 2003, 3, 6. | 3.6 | 67 |
| 21 | An iAc/Ds gene and enhancer trapping system for insertional mutagenesis in rice. <i>Functional Plant Biology</i> , 2002, 29, 547. | 2.1 | 65 |
| 22 | Isolation and characterization of a Ds-tagged rice (<i>Oryza sativa</i> L.) GA-responsive dwarf mutant defective in an early step of the gibberellin biosynthesis pathway. <i>Plant Cell Reports</i> , 2005, 23, 819-833. | 5.6 | 61 |
| 23 | Long non-coding RNAs in plants: emerging modulators of gene activity in development and stress responses. <i>Planta</i> , 2020, 252, 92. | 3.2 | 57 |
| 24 | Diversity analysis of cotton (<i>Gossypium hirsutum</i> L.) germplasm using the CottonSNP63K Array. <i>BMC Plant Biology</i> , 2017, 17, 37. | 3.6 | 56 |
| 25 | Diverse genetic mechanisms underlie worldwide convergent rice feralization. <i>Genome Biology</i> , 2020, 21, 70. | 8.8 | 55 |
| 26 | Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. <i>Plant Biotechnology Journal</i> , 2019, 17, 1998-2010. | 8.3 | 54 |
| 27 | Genome-wide identification of non-coding RNAs interacted with microRNAs in soybean. <i>Frontiers in Plant Science</i> , 2014, 5, 743. | 3.6 | 53 |
| 28 | Dissociation (Ds) constructs, mapped Ds launch pads and a transiently-expressed transposase system suitable for localized insertional mutagenesis in rice. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1326-1341. | 3.6 | 51 |
| 29 | Selection and mutation on microRNA target sequences during rice evolution. <i>BMC Genomics</i> , 2008, 9, 454. | 2.8 | 45 |
| 30 | Identification, evolution, and expression partitioning of miRNAs in allopolyploid <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 7241-7253. | 4.8 | 44 |
| 31 | Polyamine and Its Metabolite H ₂ O ₂ Play a Key Role in the Conversion of Embryogenic Callus into Somatic Embryos in Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1063. | 3.6 | 43 |
| 32 | Integrated mapping and characterization of the gene underlying the okra leaf trait in <i>Gossypium hirsutum</i> L. <i>Journal of Experimental Botany</i> , 2016, 67, 763-774. | 4.8 | 43 |
| 33 | Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. <i>Euphytica</i> , 2017, 213, 1. | 1.2 | 42 |
| 34 | Long non-coding RNA-mediated mechanisms independent of the RNAi pathway in animals and plants. <i>RNA Biology</i> , 2011, 8, 404-414. | 3.1 | 41 |
| 35 | Characterization of the Ch4CL gene family reveals a role of Ch4CL7 in drought tolerance. <i>BMC Plant Biology</i> , 2020, 20, 125. | 3.6 | 40 |
| 36 | Identification of phasiRNAs in wild rice (<i>Oryza rufipogon</i>). <i>Plant Signaling and Behavior</i> , 2013, 8, e25079. | 2.4 | 38 |

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|----|--|-----|-----------|
| 37 | Genome-wide identification of oil biosynthesis-related long non-coding RNAs in allopolyploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2018, 19, 745. | 2.8 | 38 |
| 38 | Molecular evolution and selection of a gene encoding two tandem microRNAs in rice. <i>FEBS Letters</i> , 2007, 581, 4789-4793. | 2.8 | 37 |
| 39 | De novo transcriptome analysis reveals insights into dynamic homeostasis regulation of somatic embryogenesis in upland cotton (<i>G. hirsutum</i> L.). <i>Plant Molecular Biology</i> , 2016, 92, 279-292. | 3.9 | 37 |
| 40 | Characteristics of plant circular RNAs. <i>Briefings in Bioinformatics</i> , 2018, , . | 6.5 | 37 |
| 41 | iTRAQ-based comparative proteomic analysis provides insights into somatic embryogenesis in <i>Gossypium hirsutum</i> L.. <i>Plant Molecular Biology</i> , 2018, 96, 89-102. | 3.9 | 36 |
| 42 | Creating a novel herbicide-tolerance OsALS allele using CRISPR/Cas9-mediated gene editing. <i>Crop Journal</i> , 2021, 9, 305-312. | 5.2 | 36 |
| 43 | GhWRKY70D13 Regulates Resistance to <i>Verticillium dahliae</i> in Cotton Through the Ethylene and Jasmonic Acid Signaling Pathways. <i>Frontiers in Plant Science</i> , 2020, 11, 69. | 3.6 | 35 |
| 44 | Transgene structures suggest that multiple mechanisms are involved in T-DNA integration in plants. <i>Plant Science</i> , 2006, 171, 308-322. | 3.6 | 34 |
| 45 | Mutants in the imprinted <i>PICKLE RELATED 2</i> gene suppress seed abortion of fertilization independent seed class mutants and paternal excess interploidy crosses in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2017, 90, 383-395. | 5.7 | 34 |
| 46 | Genetic dissection of the fuzzless seed trait in <i>Gossypium barbadense</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 997-1009. | 4.8 | 34 |
| 47 | Genomic dissection of small RNAs in wild rice (<i>Oryza rufipogon</i>): lessons for rice domestication. <i>New Phytologist</i> , 2012, 196, 914-925. | 7.3 | 33 |
| 48 | Transcriptome Sequencing and Metabolome Analysis Reveal Genes Involved in Pigmentation of Green-Colored Cotton Fibers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4838. | 4.1 | 33 |
| 49 | Sequence variation and selection of small RNAs in domesticated rice. <i>BMC Evolutionary Biology</i> , 2010, 10, 119. | 3.2 | 32 |
| 50 | High-Throughput Sequencing and De Novo Assembly of the <i>Isatis indigotica</i> Transcriptome. <i>PLoS ONE</i> , 2014, 9, e102963. | 2.5 | 32 |
| 51 | Comparative profiling of miRNA expression in developing seeds of high linoleic and high oleic safflower (<i>Carthamus tinctorius</i> L.) plants. <i>Frontiers in Plant Science</i> , 2013, 4, 489. | 3.6 | 31 |
| 52 | Simultaneous silencing of GhFAD2-1 and GhFATB enhances the quality of cottonseed oil with high oleic acid. <i>Journal of Plant Physiology</i> , 2017, 215, 132-139. | 3.5 | 31 |
| 53 | Historical Datasets Support Genomic Selection Models for the Prediction of Cotton Fiber Quality Phenotypes Across Multiple Environments. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1721-1732. | 1.8 | 30 |
| 54 | Identification and Functional Characterization of a Microtubule-Associated Protein, GhCLASP2, From Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 882. | 3.6 | 28 |

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|----|---|------|-----------|
| 55 | GhGSTF12, a glutathione S-transferase gene, is essential for anthocyanin accumulation in cotton (<i>Gossypium hirsutum</i> L.). <i>Plant Science</i> , 2021, 305, 110827. | 3.6 | 28 |
| 56 | Highly Efficient Targeted Gene Editing in Upland Cotton Using the CRISPR/Cas9 System. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3000. | 4.1 | 27 |
| 57 | Hairpin RNA Targeting Multiple Viral Genes Confers Strong Resistance to Rice Black-Streaked Dwarf Virus. <i>International Journal of Molecular Sciences</i> , 2016, 17, 705. | 4.1 | 26 |
| 58 | Genomic insights into the evolution of <i>Echinochloa</i> species as weed and orphan crop. <i>Nature Communications</i> , 2022, 13, 689. | 12.8 | 26 |
| 59 | Breeding Next-Generation Naturally Colored Cotton. <i>Trends in Plant Science</i> , 2021, 26, 539-542. | 8.8 | 24 |
| 60 | Transcriptome and Complexity-Reduced, DNA-Based Identification of Intraspecies Single-Nucleotide Polymorphisms in the Polyploid <i>Gossypium hirsutum</i> L.. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1893-1905. | 1.8 | 22 |
| 61 | A transcriptomic profile of topping responsive non-coding RNAs in tobacco roots (<i>Nicotiana glauca</i>). <i>Plant Biotechnology Journal</i> , 2018, 16, 1077-1088. | 2.8 | 22 |
| 62 | Genetic Identification and Transcriptome Analysis of Lintless and Fuzzless Traits in <i>Gossypium arboreum</i> L.. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1675. | 4.1 | 19 |
| 63 | Molecular phylogeny of miR390-guided trans-acting siRNA genes (TAS3) in the grass family. <i>Plant Systematics and Evolution</i> , 2009, 283, 125-132. | 0.9 | 18 |
| 64 | CRISPR/Cas9-targeted mutagenesis of the <i>OsROS1</i> gene induces pollen and embryo sac defects in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 1999-2001. | 8.3 | 18 |
| 65 | Molecular mapping of bunchy top disease resistance in <i>Gossypium hirsutum</i> L.. <i>Euphytica</i> , 2016, 210, 135-142. | 1.2 | 17 |
| 66 | Molecular analysis of caffeoyl residues related to pigmentation in green cotton fibers. <i>Journal of Experimental Botany</i> , 2017, 68, 4559-4569. | 4.8 | 15 |
| 67 | Expansion of <i>MIR482/2118</i> by a class II transposable element in cotton. <i>Plant Journal</i> , 2020, 103, 2084-2099. | 5.7 | 15 |
| 68 | Transcriptome Analysis and RNA Interference Reveal GhGDH2 Regulating Cotton Resistance to Verticillium Wilt by JA and SA Signaling Pathways. <i>Frontiers in Plant Science</i> , 2021, 12, 654676. | 3.6 | 15 |
| 69 | Intron-targeted gene insertion in rice using CRISPR/Cas9: A case study of the <i>Pi-ta</i> gene. <i>Crop Journal</i> , 2020, 8, 424-431. | 5.2 | 14 |
| 70 | Recent origination of circular RNAs in plants. <i>New Phytologist</i> , 2022, 233, 515-525. | 7.3 | 14 |
| 71 | CRISPR/Cas9-mediated saturated mutagenesis of the cotton <i>MIR482</i> family for dissecting the functionality of individual members in disease response. <i>Plant Direct</i> , 2022, 6, . | 1.9 | 14 |
| 72 | RiceRelativesGD: a genomic database of rice relatives for rice research. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, . | 3.0 | 13 |

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|----|---|-----|-----------|
| 73 | Transposon Insertional Mutants: A Resource for Rice Functional Genomics. , 2007, , 223-271. | | 12 |
| 74 | compact shoot and leafy head 1, a mutation affects leaf initiation and developmental transition in rice (<i>Oryza sativa</i> L.). <i>Plant Cell Reports</i> , 2007, 26, 421-427. | 5.6 | 12 |
| 75 | ChFAD2 ³ is required for anther development in <i>Gossypium hirsutum</i> . <i>BMC Plant Biology</i> , 2019, 19, 393. | 3.6 | 12 |
| 76 | Characterization and transcriptome analysis of a dominant genic male sterile cotton mutant. <i>BMC Plant Biology</i> , 2020, 20, 312. | 3.6 | 12 |
| 77 | Transcriptomic analysis of gene expression of <i>Verticillium dahliae</i> upon treatment of the cotton root exudates. <i>BMC Genomics</i> , 2020, 21, 155. | 2.8 | 12 |
| 78 | Characterization and evolution of gene clusters for terpenoid phytoalexin biosynthesis in tobacco. <i>Planta</i> , 2019, 250, 1687-1702. | 3.2 | 11 |
| 79 | Efficient Breeding of Early-Maturing Rice Cultivar by Editing PHYC via CRISPR/Cas9. <i>Rice</i> , 2021, 14, 86. | 4.0 | 11 |
| 80 | Gene Modules Co-regulated with Biosynthetic Gene Clusters for Allelopathy between Rice and Barnyardgrass. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3846. | 4.1 | 9 |
| 81 | Characterization and Genetic Mapping of Black Root Rot Resistance in <i>Gossypium arboreum</i> L.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2642. | 4.1 | 9 |
| 82 | Rice bioinformatics in the genomic era: Status and perspectives. <i>Crop Journal</i> , 2021, 9, 609-621. | 5.2 | 9 |
| 83 | Heterodimer formed by ROC8 and ROC5 modulates leaf rolling in rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 2662-2672. | 8.3 | 9 |
| 84 | Transposon Insertional Mutagenesis in Rice. <i>Methods in Molecular Biology</i> , 2011, 678, 147-177. | 0.9 | 8 |
| 85 | PlantcircBase 7.0: Full-length transcripts and conservation of plant circRNAs. <i>Plant Communications</i> , 2022, 3, 100343. | 7.7 | 8 |
| 86 | Lateral transfers lead to the birth of momilactone biosynthetic gene clusters in grass. <i>Plant Journal</i> , 2022, 111, 1354-1367. | 5.7 | 8 |
| 87 | Explore the gene network regulating the composition of fatty acids in cottonseed. <i>BMC Plant Biology</i> , 2021, 21, 177. | 3.6 | 7 |
| 88 | Genetic mapping and transcriptomic characterization of a new fuzzless-tufted cottonseed mutant. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-14. | 1.8 | 7 |
| 89 | Transcriptome Analysis Reveals Differences in Anthocyanin Accumulation in Cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11 | 3.6 | 7 |
| 90 | Cotton Breeding in Australia: Meeting the Challenges of the 21st Century. <i>Frontiers in Plant Science</i> , 2022, 13, . | 3.6 | 7 |

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|-----|--|-----|-----------|
| 91 | GhAlaRP, a cotton alanine rich protein gene, involves in fiber elongation process. <i>Crop Journal</i> , 2021, 9, 313-324. | 5.2 | 5 |
| 92 | Mapping-by-sequencing enabled fast forward genetics in crops with complex genomes.. <i>CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources</i> , 0, , 1-12. | 1.0 | 5 |
| 93 | Identification and Characterization of Cinnamyl Alcohol Dehydrogenase Encoding Genes Involved in Lignin Biosynthesis and Resistance to <i>Verticillium dahliae</i> in Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 840397. | 3.6 | 5 |
| 94 | Rice Gene Machine: A Vehicle for Finding Functions of Cereal Genes. <i>Asia Pacific Biotech News</i> , 2002, 06, 936-942. | 0.0 | 4 |
| 95 | RGMIMS: a web-based Laboratory Information Management System for plant functional genomics research. <i>Molecular Breeding</i> , 2008, 22, 151-157. | 2.1 | 4 |
| 96 | Functions of miRNAs in Rice. <i>Signaling and Communication in Plants</i> , 2012, , 149-176. | 0.7 | 4 |
| 97 | Genome-wide identification and characterization of the homeodomain-leucine zipper I family of genes in cotton (<i>Gossypium</i> spp.). <i>Plant Gene</i> , 2016, 7, 50-61. | 2.3 | 4 |
| 98 | Effects of Sample Size on Plant Single-Cell RNA Profiling. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1685-1697. | 2.4 | 4 |
| 99 | Genomic prediction of cotton fibre quality and yield traits using Bayesian regression methods. <i>Heredity</i> , 2022, 129, 103-112. | 2.6 | 3 |
| 100 | Transcriptome Profiling Provides New Insights into the Molecular Mechanism Underlying the Sensitivity of Cotton Varieties to Mepiquat Chloride. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5043. | 4.1 | 2 |
| 101 | Generation of Plant Small RNA cDNA Libraries for High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2012, 894, 123-137. | 0.9 | 1 |
| 102 | Identification of lncRNAs Using Computational and Experimental Approaches. , 2012, , 319-340. | | 0 |