

# Qian-Hao Zhu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5509052/publications.pdf>

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	Recent origination of circular RNAs in plants. <i>New Phytologist</i> , 2022, 233, 515-525.	7.3	14
2	Twenty years of plant genome sequencing: achievements and challenges. <i>Trends in Plant Science</i> , 2022, 27, 391-401.	8.8	125
3	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
4	Transcriptome Analysis Reveals Differences in Anthocyanin Accumulation in Cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT/Overlock <sub>10</sub> Tf 50 6	3.6	7
5	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
6	Genomic prediction of cotton fibre quality and yield traits using Bayesian regression methods. <i>Heredity</i> , 2022, 129, 103-112.	2.6	3
7	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
8	Cotton Breeding in Australia: Meeting the Challenges of the 21st Century. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	7
9	PlantcircBase 7.0: Full-length transcripts and conservation of plant circRNAs. <i>Plant Communications</i> , 2022, 3, 100343.	7.7	8
10	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
11	Lateral transfers lead to the birth of momilactone biosynthetic gene clusters in grass. <i>Plant Journal</i> , 2022, 111, 1354-1367.	5.7	8
12	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
13	Creating a novel herbicide-tolerance <i>OsALS</i> allele using CRISPR/Cas9-mediated gene editing. <i>Crop Journal</i> , 2021, 9, 305-312.	5.2	36
14	GhAlaRP, a cotton alanine rich protein gene, involves in fiber elongation process. <i>Crop Journal</i> , 2021, 9, 313-324.	5.2	5
15	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
16	Explore the gene network regulating the composition of fatty acids in cottonseed. <i>BMC Plant Biology</i> , 2021, 21, 177.	3.6	7
17	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
18	Breeding Next-Generation Naturally Colored Cotton. <i>Trends in Plant Science</i> , 2021, 26, 539-542.	8.8	24

#	ARTICLE	IF	CITATIONS
19	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
20	Rice bioinformatics in the genomic era: Status and perspectives. <i>Crop Journal</i> , 2021, 9, 609-621.	5.2	9
21	Heterodimer formed by ROC8 and ROC5 modulates leaf rolling in rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 2662-2672.	8.3	9
22	Effects of Sample Size on Plant Single-Cell RNA Profiling. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1685-1697.	2.4	4
23	Efficient Breeding of Early-Maturing Rice Cultivar by Editing PHYC via CRISPR/Cas9. <i>Rice</i> , 2021, 14, 86.	4.0	11
24	Genetic mapping and transcriptomic characterization of a new fuzzless-tufted cottonseed mutant. G3: Genes, Genomes, Genetics, 2021, 11, 1-14.	1.8	7
25	Intron-targeted gene insertion in rice using CRISPR/Cas9: A case study of the Pi-ta gene. <i>Crop Journal</i> , 2020, 8, 424-431.	5.2	14
26	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
27	Diverse genetic mechanisms underlie worldwide convergent rice feralization. <i>Genome Biology</i> , 2020, 21, 70.	8.8	55
28	Characterization of the Gh4CL gene family reveals a role of Gh4CL7 in drought tolerance. <i>BMC Plant Biology</i> , 2020, 20, 125.	3.6	40
29	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
30	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
31	Characterization and transcriptome analysis of a dominant genic male sterile cotton mutant. <i>BMC Plant Biology</i> , 2020, 20, 312.	3.6	12
32	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
33	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
34	CRISPR/Cas9-targeted mutagenesis of the OsROS1 gene induces pollen and embryo sac defects in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 1999-2001.	8.3	18
35	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
36	Characterization and evolution of gene clusters for terpenoid phytoalexin biosynthesis in tobacco. <i>Planta</i> , 2019, 250, 1687-1702.	3.2	11

#	ARTICLE	IF	CITATIONS
37	RiceRelativesGD: a genomic database of rice relatives for rice research. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	13
38	GhFAD2-3 is required for anther development in <i>Gossypium hirsutum</i> . BMC Plant Biology, 2019, 19, 393.	3.6	12
39	Transcriptome Sequencing and Metabolome Analysis Reveal Genes Involved in Pigmentation of Green-Colored Cotton Fibers. International Journal of Molecular Sciences, 2019, 20, 4838.	4.1	33
40	Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. Plant Biotechnology Journal, 2019, 17, 1998-2010.	8.3	54
41	A transcriptomic profile of topping responsive non-coding RNAs in tobacco roots ( <i>Nicotiana glauca</i> ). Frontiers in Plant Science, 2018, 9, 1078.	2.8	22
42	Historical Datasets Support Genomic Selection Models for the Prediction of Cotton Fiber Quality Phenotypes Across Multiple Environments. G3: Genes, Genomes, Genetics, 2018, 8, 1721-1732.	1.8	30
43	Genetic dissection of the fuzzless seed trait in <i>Gossypium barbadense</i> . Journal of Experimental Botany, 2018, 69, 997-1009.	4.8	34
44	iTRAQ-based comparative proteomic analysis provides insights into somatic embryogenesis in <i>Gossypium hirsutum</i> L.. Plant Molecular Biology, 2018, 96, 89-102.	3.9	36
45	Characteristics of plant circular RNAs. Briefings in Bioinformatics, 2018, , .	6.5	37
46	Highly Efficient Targeted Gene Editing in Upland Cotton Using the CRISPR/Cas9 System. International Journal of Molecular Sciences, 2018, 19, 3000.	4.1	27
47	Genome-wide identification of oil biosynthesis-related long non-coding RNAs in allopolyploid <i>Brassica napus</i> . BMC Genomics, 2018, 19, 745.	2.8	38
48	Identification and Functional Characterization of a Microtubule-Associated Protein, GhCLASP2, From Upland Cotton ( <i>Gossypium hirsutum</i> L.). Frontiers in Plant Science, 2018, 9, 882.	3.6	28
49	Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. Euphytica, 2017, 213, 1.	1.2	42
50	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> . Plant Journal, 2017, 90, 383-395.	5.7	34
51	Analysis of transcriptional and epigenetic changes in hybrid vigor of allopolyploid <i>Brassica napus</i> uncovers key roles for small RNAs. Plant Journal, 2017, 91, 874-893.	5.7	95
52	PlantcircBase: A Database for Plant Circular RNAs. Molecular Plant, 2017, 10, 1126-1128.	8.3	131
53	Molecular analysis of caffeoyl residues related to pigmentation in green cotton fibers. Journal of Experimental Botany, 2017, 68, 4559-4569.	4.8	15
54	Simultaneous silencing of GhFAD2-1 and GhFATB enhances the quality of cottonseed oil with high oleic acid. Journal of Plant Physiology, 2017, 215, 132-139.	3.5	31

#	ARTICLE	IF	CITATIONS
55	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
56	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
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	Epigenetic Mechanisms: An Emerging Player in Plant-Microbe Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 187-196.	2.6	72
59	Molecular mapping of bunchy top disease resistance in <i>Gossypium hirsutum</i> L.. <i>Euphytica</i> , 2016, 210, 135-142.	1.2	17
60	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
61	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
62	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
63	Widespread noncoding circular <i>scp</i> RNA <i>s</i> in plants. <i>New Phytologist</i> , 2015, 208, 88-95.	7.3	374
64	Polyamine and Its Metabolite H <sub>2</sub> O <sub>2</sub> 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
65	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
66	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
67	Regulation of Nicotine Biosynthesis by an Endogenous Target Mimicry of MicroRNA in Tobacco. <i>Plant Physiology</i> , 2015, 169, 1062-1071.	4.8	96
68	High-Throughput Sequencing and De Novo Assembly of the <i>Isatis indigotica</i> Transcriptome. <i>PLoS ONE</i> , 2014, 9, e102963.	2.5	32
69	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
70	Genome-wide identification of non-coding RNAs interacted with microRNAs in soybean. <i>Frontiers in Plant Science</i> , 2014, 5, 743.	3.6	53
71	Long noncoding <i>scp</i> RNA <i>s</i> responsive to <i>Fusarium oxysporum</i> infection in <i>Azadirachta indica</i> . <i>New Phytologist</i> , 2014, 201, 574-584.	7.3	188
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	miR482 Regulation of NBS-LRR Defense Genes during Fungal Pathogen Infection in Cotton. <i>PLoS ONE</i> , 2013, 8, e84390.	2.5	163
75	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
76	Identification of phasiRNAs in wild rice ( <i>Oryza rufipogon</i> ). <i>Plant Signaling and Behavior</i> , 2013, 8, e25079.	2.4	38
77	Molecular Functions of Long Non-Coding RNAs in Plants. <i>Genes</i> , 2012, 3, 176-190.	2.4	139
78	Genomic dissection of small RNA in wild rice ( <i>Oryza rufipogon</i> ): lessons for rice domestication. <i>New Phytologist</i> , 2012, 196, 914-925.	7.3	33
79	Generation of Plant Small RNA cDNA Libraries for High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2012, 894, 123-137.	0.9	1
80	Functions of miRNAs in Rice. <i>Signaling and Communication in Plants</i> , 2012, , 149-176.	0.7	4
81	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
82	Identification of lncRNAs Using Computational and Experimental Approaches. , 2012, , 319-340.		0
83	Regulation of flowering time and floral patterning by miR172. <i>Journal of Experimental Botany</i> , 2011, 62, 487-495.	4.8	341
84	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
85	Transposon Insertional Mutagenesis in Rice. <i>Methods in Molecular Biology</i> , 2011, 678, 147-177.	0.9	8
86	Sequence variation and selection of small RNAs in domesticated rice. <i>BMC Evolutionary Biology</i> , 2010, 10, 119.	3.2	32
87	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
88	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
89	RGMIMS: a web-based Laboratory Information Management System for plant functional genomics research. <i>Molecular Breeding</i> , 2008, 22, 151-157.	2.1	4
90	Selection and mutation on microRNA target sequences during rice evolution. <i>BMC Genomics</i> , 2008, 9, 454.	2.8	45

#	ARTICLE	IF	CITATIONS
91	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
92	Molecular evolution and selection of a gene encoding two tandem microRNAs in rice. <i>FEBS Letters</i> , 2007, 581, 4789-4793.	2.8	37
93	Transposon Insertional Mutants: A Resource for Rice Functional Genomics. , 2007, , 223-271.		12
94	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
95	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
96	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
97	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
98	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
99	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
100	Rice Gene Machine: A Vehicle for Finding Functions of Cereal Genes. <i>Asia Pacific Biotech News</i> , 2002, 06, 936-942.	0.0	4
101	An iAc/Ds gene and enhancer trapping system for insertional mutagenesis in rice. <i>Functional Plant Biology</i> , 2002, 29, 547.	2.1	65
102	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