

# Zhenhui Zhong

## List of Publications by Year in descending order

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34  
papers

1,145  
citations

567281

15  
h-index

454955

30  
g-index

39  
all docs

39  
docs citations

39  
times ranked

1524  
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of ATXR6 expression in modulating genome stability and transposable element repression in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
2	A SYBR Gold-based Label-free in vitro Dicing Assay. Bio-protocol, 2022, 12, e4382.	0.4	1
3	<i>HAG</i> effector evolution in <i>Pyricularia</i> species and plant cell death suppression by <i>HAG4</i> . Molecular Plant-Microbe Interactions, 2022, , .	2.6	0
4	Genomic landscape of a relict fir-associated fungus reveals rapid convergent adaptation towards endophytism. ISME Journal, 2022, 16, 1294-1305.	9.8	3
5	Mutations in DNA polymerase $\beta$ subunit 1 co-segregate with CMD2-type resistance to Cassava Mosaic Geminiviruses. Nature Communications, 2022, 13, .	12.8	8
6	Bayogenin 3-O-acetylcellobioside confers non-cultivar-specific defence against the rice blast fungus <i>Pyricularia oryzae</i> . Plant Biotechnology Journal, 2021, 19, 589-601.	8.3	10
7	Carbon catabolite repressor MoCreA is required for the asexual development and pathogenicity of the rice blast fungus. Fungal Genetics and Biology, 2021, 146, 103496.	2.1	15
8	Evolution and Regulation of a Large Effector Family of <i>Pyricularia oryzae</i> . Molecular Plant-Microbe Interactions, 2021, 34, 255-269.	2.6	3
9	Ectopic targeting of CG DNA methylation in Arabidopsis with the bacterial SssI methyltransferase. Nature Communications, 2021, 12, 3130.	12.8	20
10	Divergence of a genomic island leads to the evolution of melanization in a halophyte root fungus. ISME Journal, 2021, 15, 3468-3479.	9.8	9
11	Arabidopsis MORC proteins function in the efficient establishment of RNA directed DNA methylation. Nature Communications, 2021, 12, 4292.	12.8	28
12	DNA methylation-linked chromatin accessibility affects genomic architecture in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	70
13	Mechanism of siRNA production by a plant Dicer-RNA complex in dicing-competent conformation. Science, 2021, 374, 1152-1157.	12.6	58
14	Efficient and accurate determination of genome-wide DNA methylation patterns in <i>Arabidopsis thaliana</i> with enzymatic methyl sequencing. Epigenetics and Chromatin, 2020, 13, 42.	3.9	60
15	The characterization of Mediator 12 and 13 as conditional positive gene regulators in Arabidopsis. Nature Communications, 2020, 11, 2798.	12.8	22
16	NAP1-RELATED PROTEIN1 and 2 negatively regulate H2A.Z abundance in chromatin in Arabidopsis. Nature Communications, 2020, 11, 2887.	12.8	25
17	Emergence of a hybrid PKS-NRPS secondary metabolite cluster in a clonal population of the rice blast fungus <i>Magnaporthe oryzae</i> . Environmental Microbiology, 2020, 22, 2709-2723.	3.8	6
18	Genetic Variation Bias toward Noncoding Regions and Secreted Proteins in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . MSystems, 2020, 5, .	3.8	7

#	ARTICLE	IF	CITATIONS
19	Genome Sequence Resource of <i>Magnaporthe oryzae</i> Laboratory Strain 2539. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1029-1031.	2.6	2
20	<i>Arabidopsis</i> SWR1-associated protein methyl-CpG-binding domain 9 is required for histone H2A.Z deposition. <i>Nature Communications</i> , 2019, 10, 3352.	12.8	60
21	Expression Divergence as an Evolutionary Alternative Mechanism Adopted by Two Rice Subspecies Against Rice Blast Infection. <i>Rice</i> , 2019, 12, 12.	4.0	9
22	RNA-directed DNA methylation involves co-transcriptional small-RNA-guided slicing of polymerase V transcripts in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2018, 4, 181-188.	9.3	106
23	Population genomic analysis of the rice blast fungus reveals specific events associated with expansion of three main clades. <i>ISME Journal</i> , 2018, 12, 1867-1878.	9.8	63
24	Evolutionary analysis of plant jacalin-related lectins (JRLs) family and expression of rice JRLs in response to <i>Magnaporthe oryzae</i> . <i>Journal of Integrative Agriculture</i> , 2018, 17, 1252-1266.	3.5	16
25	Comparative genomic analysis revealed rapid differentiation in the pathogenicity-related gene repertoires between <i>Pyricularia oryzae</i> and <i>Pyricularia penniseti</i> isolated from a <i>Pennisetum</i> grass. <i>BMC Genomics</i> , 2018, 19, 927.	2.8	14
26	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , 2018, 362, 1182-1186.	12.6	181
27	Whole genome and transcriptome analysis reveal adaptive strategies and pathogenesis of <i>Calonectria pseudoreteaudii</i> to <i>Eucalyptus</i> . <i>BMC Genomics</i> , 2018, 19, 358.	2.8	15
28	Mechanistic insights into plant SUVH family H3K9 methyltransferases and their binding to context-biased non-CG DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8793-E8802.	7.1	89
29	PacBio Sequencing Reveals Transposable Elements as a Key Contributor to Genomic Plasticity and Virulence Variation in <i>Magnaporthe oryzae</i> . <i>Molecular Plant</i> , 2017, 10, 1465-1468.	8.3	100
30	Methylmalonate- $\alpha$ -semialdehyde dehydrogenase mediated metabolite homeostasis essentially regulate conidiation, polarized germination and pathogenesis in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017, 19, 4256-4277.	3.8	23
31	Genome-wide analysis of RNA-interference pathway in <i>Brassica napus</i> , and the expression profile of BnAGOs in response to <i>Sclerotinia sclerotiorum</i> infection. <i>European Journal of Plant Pathology</i> , 2016, 146, 565-579.	1.7	10
32	Directional Selection from Host Plants Is a Major Force Driving Host Specificity in <i>Magnaporthe</i> Species. <i>Scientific Reports</i> , 2016, 6, 25591.	3.3	62
33	Two different subcellular-localized Acetoacetyl-CoA acetyltransferases differentiate diverse functions in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2015, 83, 58-67.	2.1	20
34	Putative RhoGAP proteins orchestrate vegetative growth, conidiogenesis and pathogenicity of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2014, 67, 37-50.	2.1	17