

# Zhenhui Zhong

## List of Publications by Year in descending order

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Version: 2024-02-01

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	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , 2018, 362, 1182-1186.	12.6	181
2	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
3	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
4	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
5	DNA methylation-linked chromatin accessibility affects genomic architecture in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	70
6	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
7	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
8	<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
9	Efficient and accurate determination of genome-wide DNA methylation patterns in <i>Arabidopsis thaliana</i> with enzymatic methyl sequencing. <i>Epigenetics and Chromatin</i> , 2020, 13, 42.	3.9	60
10	Mechanism of siRNA production by a plant Dicer-RNA complex in dicing-competent conformation. <i>Science</i> , 2021, 374, 1152-1157.	12.6	58
11	<i>Arabidopsis</i> MORC proteins function in the efficient establishment of RNA directed DNA methylation. <i>Nature Communications</i> , 2021, 12, 4292.	12.8	28
12	NAP1-RELATED PROTEIN1 and 2 negatively regulate H2A.Z abundance in chromatin in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2020, 11, 2887.	12.8	25
13	Methylmalonate 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
14	The characterization of Mediator 12 and 13 as conditional positive gene regulators in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2020, 11, 2798.	12.8	22
15	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
16	Ectopic targeting of CG DNA methylation in <i>Arabidopsis</i> with the bacterial Sss1 methyltransferase. <i>Nature Communications</i> , 2021, 12, 3130.	12.8	20
17	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
18	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

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19	Whole genome and transcriptome analysis reveal adaptive strategies and pathogenesis of <i>Calonectria pseudoreteauidii</i> to <i>Eucalyptus</i> . <i>BMC Genomics</i> , 2018, 19, 358.	2.8	15
20	Carbon catabolite repressor MoCreA is required for the asexual development and pathogenicity of the rice blast fungus. <i>Fungal Genetics and Biology</i> , 2021, 146, 103496.	2.1	15
21	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
22	The role of ATXR6 expression in modulating genome stability and transposable element repression in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
23	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
24	Bayogenin 3-O-acetylcellobioside confers non-cultivar-specific defence against the rice blast fungus <i>Pyricularia oryzae</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 589-601.	8.3	10
25	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
26	Divergence of a genomic island leads to the evolution of melanization in a halophyte root fungus. <i>ISME Journal</i> , 2021, 15, 3468-3479.	9.8	9
27	Mutations in DNA polymerase $\epsilon$ subunit 1 co-segregate with CMD2-type resistance to Cassava Mosaic Geminiviruses. <i>Nature Communications</i> , 2022, 13, .	12.8	8
28	Genetic Variation Bias toward Noncoding Regions and Secreted Proteins in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>MSystems</i> , 2020, 5, .	3.8	7
29	Emergence of a hybrid PKS-NRPS secondary metabolite cluster in a clonal population of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2020, 22, 2709-2723.	3.8	6
30	Evolution and Regulation of a Large Effector Family of <i>Pyricularia oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 255-269.	2.6	3
31	Genomic landscape of a relict fir-associated fungus reveals rapid convergent adaptation towards endophytism. <i>ISME Journal</i> , 2022, 16, 1294-1305.	9.8	3
32	Genome Sequence Resource of <i>Magnaporthe oryzae</i> Laboratory Strain 2539. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1029-1031.	2.6	2
33	A SYBR Gold-based Label-free in vitro Dicing Assay. <i>Bio-protocol</i> , 2022, 12, e4382.	0.4	1
34	<i>HAG</i> effector evolution in <i>Pyricularia</i> species and plant cell death suppression by <i>HAG4</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, , .	2.6	0