Zhengguang Zhang

List of Publications by Year
in descending order

118 papers	5,785 citations	71102 41 h-index	88630 70 g-index
125 all docs	125 docs citations	125 times ranked	4314 citing authors

#	Article	IF	Citations
1	Transcriptional Programming and Functional Interactions within the Phytophthora sojae RXLR Effector Repertoire Â Â. Plant Cell, 2011, 23, 2064-2086.	6.6	455
2	A Phytophthora sojae Glycoside Hydrolase 12 Protein Is a Major Virulence Factor during Soybean Infection and Is Recognized as a PAMP. Plant Cell, 2015, 27, 2057-2072.	6.6	335
3	The bZIP Transcription Factor MoAP1 Mediates the Oxidative Stress Response and Is Critical for Pathogenicity of the Rice Blast Fungus Magnaporthe oryzae. PLoS Pathogens, 2011, 7, e1001302.	4.7	266
4	The Magnaporthe oryzae Avirulence Gene AvrPiz-t Encodes a Predicted Secreted Protein That Triggers the Immunity in Rice Mediated by the Blast Resistance Gene Piz-t. Molecular Plant-Microbe Interactions, 2009, 22, 411-420.	2.6	240
5	The Basic Leucine Zipper Transcription Factor Moatf1 Mediates Oxidative Stress Responses and Is Necessary for Full Virulence of the Rice Blast Fungus Magnaporthe oryzae. Molecular Plant-Microbe Interactions, 2010, 23, 1053-1068.	2.6	156
6	Activation of ethylene signaling pathways enhances disease resistance by regulating <scp>ROS</scp> and phytoalexin production in rice. Plant Journal, 2017, 89, 338-353.	5.7	152
7	Global Genome and Transcriptome Analyses of Magnaporthe oryzae Epidemic Isolate 98-06 Uncover Novel Effectors and Pathogenicity-Related Genes, Revealing Gene Gain and Lose Dynamics in Genome Evolution. PLoS Pathogens, 2015, 11, e1004801.	4.7	148
8	Eight RGS and RGS-like Proteins Orchestrate Growth, Differentiation, and Pathogenicity of Magnaporthe oryzae. PLoS Pathogens, 2011, 7, e1002450.	4.7	131
9	MoSwi6, an APSES family transcription factor, interacts with MoMps1 and is required for hyphal and conidial morphogenesis, appressorial function and pathogenicity of Magnaporthe oryzae. Molecular Plant Pathology, 2012, 13, 677-689.	4.2	108
10	MgCRZ1, a transcription factor ofMagnaporthe grisea, controls growth, development and is involved in full virulence. FEMS Microbiology Letters, 2009, 293, 160-169.	1.8	102
11	A two-component histidine kinase, MoSLN1, is required for cell wall integrity and pathogenicity of the rice blast fungus, Magnaporthe oryzae. Current Genetics, 2010, 56, 517-528.	1.7	102
12	MoVam7, a Conserved SNARE Involved in Vacuole Assembly, Is Required for Growth, Endocytosis, ROS Accumulation, and Pathogenesis of Magnaporthe oryzae. PLoS ONE, 2011, 6, e16439.	2.5	101
13	The Magnaporthe grisea species complex and plant pathogenesis. Molecular Plant Pathology, 2016, 17, 796-804.	4.2	100
14	Systemâ€wide characterization of <scp>bZIP</scp> transcription factor proteins involved in infectionâ€related morphogenesis of <scp>M</scp>agnaporthe oryzae. Environmental Microbiology, 2015, 17, 1377-1396.	3.8	95
15	The role of respiratory burst oxidase homologues in elicitor-induced stomatal closure and hypersensitive response in Nicotiana benthamiana. Journal of Experimental Botany, 2009, 60, 3109-3122.	4.8	88
16	The syntaxin protein (MoSyn8) mediates intracellular trafficking to regulate conidiogenesis and pathogenicity of rice blast fungus. New Phytologist, 2016, 209, 1655-1667.	7.3	87
17	Consistent responses of the microbial community structure to organic farming along the middle and lower reaches of the Yangtze River. Scientific Reports, 2016, 6, 35046.	3.3	86
18	An oomycete plant pathogen reprograms host pre-mRNA splicing to subvert immunity. Nature Communications, 2017, 8, 2051.	12.8	84

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19	Two Phosphodiesterase Genes, PDEL and PDEH, Regulate Development and Pathogenicity by Modulating Intracellular Cyclic AMP Levels in Magnaporthe oryzae. PLoS ONE, 2011, 6, e17241.	2.5	83
20	MoEnd3 regulates appressorium formation and virulence through mediating endocytosis in rice blast fungus Magnaporthe oryzae. PLoS Pathogens, 2017, 13, e1006449.	4.7	81
21	R-SNARE Homolog MoSec22 Is Required for Conidiogenesis, Cell Wall Integrity, and Pathogenesis of Magnaporthe oryzae. PLoS ONE, 2010, 5, e13193.	2.5	78
22	The role of vacuolar processing enzyme (VPE) from Nicotiana benthamiana in the elicitor-triggered hypersensitive response and stomatal closure. Journal of Experimental Botany, 2010, 61, 3799-3812.	4.8	76
23	Sequencing of the Litchi Downy Blight Pathogen Reveals It Is a Phytophthora Species With Downy Mildew-Like Characteristics. Molecular Plant-Microbe Interactions, 2016, 29, 573-583.	2.6	73
24	Shedding light on autophagy coordinating with cell wall integrity signaling to govern pathogenicity of Magnaporthe oryzae. Autophagy, 2020, 16, 900-916.	9.1	72
25	Histone acetyltransferase MoHat1 acetylates autophagy-related proteins MoAtg3 and MoAtg9 to orchestrate functional appressorium formation and pathogenicity in Magnaporthe oryzae. Autophagy, 2019, 15, 1234-1257.	9.1	69
26	Phosphorylation-guarded light-harvesting complex II contributes to broad-spectrum blast resistance in rice. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17572-17577.	7.1	68
27	Abscisic Acid Inhibits Rice Protein Phosphatase PP45 via H₂O₂ and Relieves Repression of the Ca²⁺/CaM-Dependent Protein Kinase DMI3. Plant Cell, 2019, 31, 128-152.	6.6	64
28	MoDnm1 Dynamin Mediating Peroxisomal and Mitochondrial Fission in Complex with MoFis1 and MoMdv1 Is Important for Development of Functional Appressorium in Magnaporthe oryzae. PLoS Pathogens, 2016, 12, e1005823.	4.7	62
29	Phosphodiesterase <scp>MoPdeH</scp> targets <scp>MoM</scp>ck1 of the conserved mitogenâ€activated protein (<scp>MAP</scp>) kinase signalling pathway to regulate cell wall integrity in rice blast fungus <scp>M</scp>agnaporthe oryzae. Molecular Plant Pathology, 2016, 17, 654-668.	4.2	59
30	FgMon1, a guanine nucleotide exchange factor of FgRab7, is important for vacuole fusion, autophagy and plant infection in Fusarium graminearum. Scientific Reports, 2016, 5, 18101.	3.3	57
31	A novel outer membrane Î²-1,6-glucanase is deployed in the predation of fungi by myxobacteria. ISME Journal, 2019, 13, 2223-2235.	9.8	57
32	Pleiotropic Function of the Putative Zinc-Finger Protein MoMsn2 in Magnaporthe oryzae. Molecular Plant-Microbe Interactions, 2014, 27, 446-460.	2.6	56
33	Comparison of the Rhizosphere Bacterial Communities of Zigongdongdou Soybean and a High-Methionine Transgenic Line of This Cultivar. PLoS ONE, 2014, 9, e103343.	2.5	55
34	Acetolactate synthases <scp>Mollv2</scp> and <scp>Mollv6</scp> are required for infectionâ€related morphogenesis in <scp>M</scp>agnaporthe oryzae. Molecular Plant Pathology, 2013, 14, 870-884.	4.2	53
35	Repression of microRNA biogenesis by silencing of OsDCL1 activates the basal resistance to Magnaporthe oryzae in rice. Plant Science, 2015, 237, 24-32.	3.6	51
36	Distribution, Pathotypes, and Metalaxyl Sensitivity of Phytophthora sojae from Heilongjiang and Fujian Provinces in China. Plant Disease, 2010, 94, 881-884.	1.4	50

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37	The Putative Protein Phosphatase MoYvh1 Functions Upstream of MoPdeH to Regulate the Development and Pathogenicity in Magnaporthe oryzae. Molecular Plant-Microbe Interactions, 2016, 29, 496-507.	2.6	49
38	A self-balancing circuit centered on MoOsm1 kinase governs adaptive responses to host-derived ROS in Magnaporthe oryzae. ELife, 2020, 9, .	6.0	47
39	The actinâ€regulating kinase homologue <scp>MoArk1</scp> plays a pleiotropic function in <scp>M</scp>agnaporthe oryzae. Molecular Plant Pathology, 2013, 14, 470-482.	4.2	46
40	MoCAP proteins regulated by MoArk1-mediated phosphorylation coordinate endocytosis and actin dynamics to govern development and virulence of Magnaporthe oryzae. PLoS Genetics, 2017, 13, e1006814.	3.5	46
41	SNARE protein FgVam7 controls growth, asexual and sexual development, and plant infection in Fusarium graminearum. Molecular Plant Pathology, 2016, 17, 108-119.	4.2	45
42	The Nicotiana benthamiana Mitogen-Activated Protein Kinase Cascade and WRKY Transcription Factor Participate in Nep1_{Mo}-Triggered Plant Responses. Molecular Plant-Microbe Interactions, 2012, 25, 1639-1653.	2.6	43
43	Pleiotropic roles of O-mannosyltransferase MoPmt4 in development and pathogenicity of Magnaporthe oryzae. Current Genetics, 2019, 65, 223-239.	1.7	43
44	The role of G-proteins in plant immunity. Plant Signaling and Behavior, 2012, 7, 1284-1288.	2.4	42
45	Heat-Shock Proteins MoSsb1, MoSsz1, and MoZuo1 Attenuate MoMkk1-Mediated Cell-Wall Integrity Signaling and Are Important for Growth and Pathogenicity of Magnaporthe oryzae. Molecular Plant-Microbe Interactions, 2018, 31, 1211-1221.	2.6	42
46	MADS1, a novel MADS-box protein, is involved in the response ofNicotiana benthamianato bacterial harpin_{Xoo}. Journal of Experimental Botany, 2016, 67, 131-141.	4.8	41
47	The FgVps39-FgVam7-FgSso1 Complex Mediates Vesicle Trafficking and Is Important for the Development and Virulence of Fusarium graminearum. Molecular Plant-Microbe Interactions, 2017, 30, 410-422.	2.6	38
48	Comparative genome-wide analysis of extracellular small RNAs from the mucormycosis pathogen Rhizopus delemar. Scientific Reports, 2018, 8, 5243.	3.3	38
49	Magnaporthe oryzae Auxiliary Activity Protein MoAa91 Functions as Chitin-Binding Protein To Induce Appressorium Formation on Artificial Inductive Surfaces and Suppress Plant Immunity. MBio, 2020, 11, .	4.1	38
50	The thioredoxin MoTrx2 protein mediates reactive oxygen species (ROS) balance and controls pathogenicity as a target of the transcription factor MoAP1 in Magnaporthe oryzae. Molecular Plant Pathology, 2017, 18, 1199-1209.	4.2	37
51	Silencing of G proteins uncovers diversified plant responses when challenged by three elicitors in Nicotiana benthamiana. Plant, Cell and Environment, 2012, 35, 72-85.	5.7	36
52	Shared and distinct functions of two <scp>G</scp>ti1/<scp>P</scp>ac2 family proteins in growth, morphogenesis and pathogenicity of <scp>M</scp>agnaporthe oryzae. Environmental Microbiology, 2014, 16, 788-801.	3.8	36
53	MoLys2 is necessary for growth, conidiogenesis, lysine biosynthesis, and pathogenicity in Magnaporthe oryzae. Fungal Genetics and Biology, 2014, 67, 51-57.	2.1	36
54	The adenylate cyclase UvAc1 and phosphodiesterase UvPdeH control the intracellular cAMP level, development, and pathogenicity of the rice false smut fungus Ustilaginoidea virens. Fungal Genetics and Biology, 2019, 129, 65-73.	2.1	36

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55	MoPpe1 partners with MoSap1 to mediate TOR and cell wall integrity signalling in growth and pathogenicity of the rice blast fungus Magnaporthe oryzae. Environmental Microbiology, 2018, 20, 3964-3979.	3.8	35
56	Pore Structure Characteristics of Coal and Their Geological Controlling Factors in Eastern Yunnan and Western Guizhou, China. ACS Omega, 2020, 5, 19565-19578.	3.5	34
57	Auxilinâ€like protein MoSwa2 promotes effector secretion and virulence as a clathrin uncoating factor in the rice blast fungus Magnaporthe oryzae. New Phytologist, 2021, 230, 720-736.	7.3	33
58	The LCB₂ subunit of the sphingolip biosynthesis enzyme serine palmitoyltransferase can function as an attenuator of the hypersensitive response and Baxâ€induced cell death. New Phytologist, 2009, 181, 127-146.	7.3	32
59	MoYvh1 subverts rice defense through functions of ribosomal protein MoMrt4 in Magnaporthe oryzae. PLoS Pathogens, 2018, 14, e1007016.	4.7	32
60	Evaluation of Coal Body Structures and Their Distributions by Geophysical Logging Methods: Case Study in the Laochang Block, Eastern Yunnan, China. Natural Resources Research, 2021, 30, 2225-2239.	4.7	32
61	MoTup1 is required for growth, conidiogenesis and pathogenicity of <scp>M</scp>agnaporthe oryzae. Molecular Plant Pathology, 2015, 16, 799-810.	4.2	30
62	MoErv29 promotes apoplastic effector secretion contributing to virulence of the rice blast fungus Magnaporthe oryzae. New Phytologist, 2022, 233, 1289-1302.	7.3	29
63	The seven transmembrane domain protein MoRgs7 functions in surface perception and undergoes coronin MoCrn1-dependent endocytosis in complex with GÎ± subunit MoMagA to promote cAMP signaling and appressorium formation in Magnaporthe oryzae. PLoS Pathogens, 2019, 15, e1007382.	4.7	28
64	Threonine deaminase Mollv1 is important for conidiogenesis and pathogenesis in the rice blast fungus Magnaporthe oryzae. Fungal Genetics and Biology, 2014, 73, 53-60.	2.1	27
65	Antifungal potential of Corallococcus sp. strain EGB against plant pathogenic fungi. Biological Control, 2017, 110, 10-17.	3.0	27
66	The N-terminus of an Ustilaginoidea virens Ser-Thr-rich glycosylphosphatidylinositol-anchored protein elicits plant immunity as a MAMP. Nature Communications, 2021, 12, 2451.	12.8	25
67	Balancing of the mitotic exit network and cell wall integrity signaling governs the development and pathogenicity in Magnaporthe oryzae. PLoS Pathogens, 2021, 17, e1009080.	4.7	24
68	ALY proteins participate in multifaceted Nep1Mo-triggered responses in Nicotiana benthamiana and Arabidopsis thaliana. Journal of Experimental Botany, 2014, 65, 2483-2494.	4.8	23
69	Comparative proteomic analyses reveal that the regulators of G-protein signaling proteins regulate amino acid metabolism of the rice blast fungusMagnaporthe oryzae. Proteomics, 2014, 14, 2508-2522.	2.2	23
70	A subunit of the HOPS endocytic tethering complex, FgVps41, is important for fungal development and plant infection in Fusarium graminearum. Environmental Microbiology, 2018, 20, 1436-1451.	3.8	22
71	The rice blast fungus MoRgs1 functioning in cAMP signaling and pathogenicity is regulated by casein kinase MoCk2 phosphorylation and modulated by membrane protein MoEmc2. PLoS Pathogens, 2021, 17, e1009657.	4.7	22
72	A doubleâ€edged sword: reactive oxygen species (ROS) during the rice blast fungus and host interaction. FEBS Journal, 2022, 289, 5505-5515.	4.7	22

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73	MoMyb1 is required for asexual development and tissue-specific infection in the rice blast fungus Magnaporthe oryzae. BMC Microbiology, 2015, 15, 37.	3.3	21
74	A class-II myosin is required for growth, conidiation, cell wall integrity and pathogenicity ofMagnaporthe oryzae. Virulence, 2017, 8, 1335-1354.	4.4	21
75	Glycoside Hydrolase MoGls2 Controls Asexual/Sexual Development, Cell Wall Integrity and Infectious Growth in the Rice Blast Fungus. PLoS ONE, 2016, 11, e0162243.	2.5	21
76	The putative GÎ³ subunit gene MGG1 is required for conidiation, appressorium formation, mating and pathogenicity in Magnaporthe oryzae. Current Genetics, 2015, 61, 641-651.	1.7	20
77	The role of vacuolar processing enzymes in plant immunity. Plant Signaling and Behavior, 2010, 5, 1565-1567.	2.4	19
78	A Ric8/Synembryn Homolog Promotes Gpa1 and Gpa2 Activation To Respectively Regulate Cyclic AMP and Pheromone Signaling in Cryptococcus neoformans. Eukaryotic Cell, 2014, 13, 1290-1299.	3.4	19
79	Distribution Characteristics of In Situ Stress Field and Vertical Development Unit Division of CBM in Western Guizhou, China. Natural Resources Research, 2021, 30, 3659-3671.	4.7	19
80	Noncanonical GÎ² Gib2 Is a Scaffolding Protein Promoting cAMP Signaling through Functions of Ras1 and Cac1 Proteins in Cryptococcus neoformans. Journal of Biological Chemistry, 2014, 289, 12202-12216.	3.4	18
81	Carbamoyl Phosphate Synthetase Subunit MoCpa2 Affects Development and Pathogenicity by Modulating Arginine Biosynthesis in Magnaporthe oryzae. Frontiers in Microbiology, 2016, 7, 2023.	3.5	18
82	The ArfGAP protein MoGlo3 regulates the development and pathogenicity of Magnaporthe oryzae. Environmental Microbiology, 2017, 19, 3982-3996.	3.8	18
83	Phosphataseâ€associated protein <scp>MoTip41</scp> interacts with the phosphatase <scp>MoPpe1</scp> to mediate crosstalk between <scp>TOR</scp> and cell wall integrity signalling during infection by the rice blast fungus Magnaporthe oryzae. Environmental Microbiology, 2021, 23, 791-809.	3.8	18
84	Community Structure of Arbuscular Mycorrhizal Fungi in Rhizospheric Soil of a Transgenic High-Methionine Soybean and a Near Isogenic Variety. PLoS ONE, 2015, 10, e0145001.	2.5	18
85	Co-evolved plant and blast fungus ascorbate oxidases orchestrate the redox state of host apoplast to modulate rice immunity. Molecular Plant, 2022, 15, 1347-1366.	8.3	17
86	MoMip11, a MoRgs7â€interacting protein, functions as a scaffolding protein to regulate cAMP signaling and pathogenicity in the rice blast fungus Magnaporthe oryzae. Environmental Microbiology, 2018, 20, 3168-3185.	3.8	16
87	The Function of MoGlk1 in Integration of Glucose and Ammonium Utilization in Magnaporthe oryzae. PLoS ONE, 2011, 6, e22809.	2.5	16
88	System-Wide Characterization of MoArf GTPase Family Proteins and Adaptor Protein MoGga1 Involved in the Development and Pathogenicity of Magnaporthe oryzae. MBio, 2019, 10, .	4.1	14
89	MoVrp1, a putative verprolin protein, is required for asexual development and infection in the rice blast fungus Magnaporthe oryzae. Scientific Reports, 2017, 7, 41148.	3.3	13
90	MoYcp4 is required for growth, conidiogenesis and pathogenicity in Magnaporthe oryzae. Molecular Plant Pathology, 2017, 18, 1001-1011.	4.2	13

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91	Disruption of actin motor function due to MoMyo5 mutation impairs host penetration and pathogenicity in Magnaporthe oryzae. Molecular Plant Pathology, 2018, 19, 689-699.	4.2	13
92	Transcriptomic Analysis of Extracellular RNA Governed by the Endocytic Adaptor Protein Cin1 of Cryptococcus deneoformans. Frontiers in Cellular and Infection Microbiology, 2020, 10, 256.	3.9	12
93	Mammalian pro-apoptotic bax gene enhances tobacco resistance to pathogens. Plant Cell Reports, 2008, 27, 1559-1569.	5.6	11
94	The Atypical Guanylate Kinase MoGuk2 Plays Important Roles in Asexual/Sexual Development, Conidial Septation, and Pathogenicity in the Rice Blast Fungus. Frontiers in Microbiology, 2017, 8, 2467.	3.5	11
95	MoImd4 mediates crosstalk between MoPdeHâ€cAMP signalling and purine metabolism to govern growth and pathogenicity in Magnaporthe oryzae. Molecular Plant Pathology, 2019, 20, 500-518.	4.2	11
96	Magnaporthe oryzae Abp1, a MoArk1 Kinase-Interacting Actin Binding Protein, Links Actin Cytoskeleton Regulation to Growth, Endocytosis, and Pathogenesis. Molecular Plant-Microbe Interactions, 2019, 32, 437-451.	2.6	11
97	MicroRNA-like milR236, regulated by transcription factor MoMsn2, targets histone acetyltransferase MoHat1 to play a role in appressorium formation and virulence of the rice blast fungus Magnaporthe oryzae. Fungal Genetics and Biology, 2020, 137, 103349.	2.1	11
98	Phytophthora elicitor PB90 induced apoptosis in suspension cultures of tobacco. Science Bulletin, 2005, 50, 435-439.	1.7	10
99	Functional analysis of MoSnf7 in Magnaporthe oryzae. Fungal Genetics and Biology, 2018, 121, 29-45.	2.1	10
100	A 2-year field trial reveals no significant effects of GM high-methionine soybean on the rhizosphere bacterial communities. World Journal of Microbiology and Biotechnology, 2018, 34, 113.	3.6	10
101	Orotate phosphoribosyl transferase MoPyr5 is involved in uridine 5â€²-phosphate synthesis and pathogenesis of Magnaporthe oryzae. Applied Microbiology and Biotechnology, 2016, 100, 3655-3666.	3.6	9
102	Genome plasticity in filamentous plant pathogens contributes to the emergence of novel effectors and their cellular processes in the host. Current Genetics, 2016, 62, 47-51.	1.7	9
103	Segmentation of multi-coal seam pore structure in single well profile and its sedimentary control: a case study of Well Y1 in Panguan syncline, western Guizhou, China. Arabian Journal of Geosciences, 2019, 12, 1.	1.3	9
104	Transcription factor <scp>MoMsn2</scp> targets the putative <scp>3â€methylglutaconylâ€CoA</scp> hydrataseâ€encoding gene <scp>MoAUH1</scp> to govern infectious growth via mitochondrial fusion/fission balance in Magnaporthe oryzae. Environmental Microbiology, 2021, 23, 774-790.	3.8	9
105	Gene deletion and constitutive expression of the pectate lyase gene 1 (MoPL1) lead to diminished virulence of Magnaporthe oryzae. Journal of Microbiology, 2022, 60, 79-88.	2.8	9
106	New findings on phosphodiesterases, MoPdeH and MoPdeL, in Magnaporthe oryzae revealed by structural analysis. Molecular Plant Pathology, 2018, 19, 1061-1074.	4.2	8
107	The inhibitor of apoptosis protein MoBir1 is involved in the suppression of hydrogen peroxide-induced fungal cell death, reactive oxygen species generation, and pathogenicity of rice blast fungus. Applied Microbiology and Biotechnology, 2019, 103, 6617-6627.	3.6	8
108	Transcription factor UvMsn2 is important for vegetative growth, conidiogenesis, stress response, mitochondrial morphology and pathogenicity in the rice false smut fungus Ustilaginoidea virens. Phytopathology Research, 2021, 3, .	2.4	8

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109	Comparative proteomic analysis of Gib2 validating its adaptor function in Cryptococcus neoformans. PLoS ONE, 2017, 12, e0180243.	2.5	7
110	Molug4 is a novel secreted effector promoting rice blast by counteracting host OsAHL1â€regulated ethylene gene transcription. New Phytologist, 2022, 235, 1163-1178.	7.3	7
111	The Peroxisomal-CoA Synthetase MoPcs60 Is Important for Fatty Acid Metabolism and Infectious Growth of the Rice Blast Fungus. Frontiers in Plant Science, 2021, 12, 811041.	3.6	6
112	Characterization of the Papain-Like Protease p29 of the Hypovirus CHV1-CN280 in Its Natural Host Fungus Cryphonectria parasitica and Nonhost Fungus Magnaporthe oryzae. Phytopathology, 2019, 109, 736-747.	2.2	5
113	Homeostasis of cell wall integrity pathway phosphorylation is required for the growth and pathogenicity of Magnaporthe oryzae. Molecular Plant Pathology, 2022, 23, 1214-1225.	4.2	5
114	FgRIC8 is involved in regulating vegetative growth, conidiation, deoxynivalenol production and virulence in Fusarium graminearum. Fungal Genetics and Biology, 2015, 83, 92-102.	2.1	4
115	Cloning of genes encoding nonhost hypersensitive response-inducing elicitors from Phytophthora boehmeriae. Science Bulletin, 2007, 52, 231-237.	1.7	2
116	Pyricularia sp. jiangsuensis , a new cryptic rice panicle blast pathogen from rice fields in Jiangsu Province, China. Environmental Microbiology, 2021, 23, 5463-5480.	3.8	1
117	Chitin Extraction and Content Measurement in Magnaporthe oryzae. Bio-protocol, 2017, 7, e2164.	0.4	1
118	Endocytosis Detection in Magnaporthe oryzae. Bio-protocol, 2019, 9, e3322.	0.4	0