

Jin-Rong Xu

List of Publications by Year in descending order

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157
papers

16,096
citations

17405

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all docs

160
docs citations

160
times ranked

8577
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , 2005, 434, 980-986.	13.7	1,447
2	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
3	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	6.0	837
4	Comparative analysis of fungal genomes reveals different plant cell wall degrading capacity in fungi. <i>BMC Genomics</i> , 2013, 14, 274.	1.2	473
5	A Mitogen-Activated Protein Kinase Gene (MGV1) in <i>Fusarium graminearum</i> Is Required for Female Fertility, Heterokaryon Formation, and Plant Infection. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 1119-1127.	1.4	442
6	MAP Kinases in Fungal Pathogens. <i>Fungal Genetics and Biology</i> , 2000, 31, 137-152.	0.9	375
7	Mitogen-Activated Protein Kinase Pathways and Fungal Pathogenesis. <i>Eukaryotic Cell</i> , 2007, 6, 1701-1714.	3.4	344
8	Independent Signaling Pathways Regulate Cellular Turgor during Hyperosmotic Stress and Appressorium-Mediated Plant Infection by <i>Magnaporthe grisea</i> . <i>Plant Cell</i> , 1999, 11, 2045-2058.	3.1	334
9	Functional Analysis of the Kinome of the Wheat Scab Fungus <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002460.	2.1	309
10	Cellular Localization and Role of Kinase Activity of PMK1 in <i>Magnaporthe grisea</i> . <i>Eukaryotic Cell</i> , 2004, 3, 1525-1532.	3.4	280
11	A Mitogen-Activated Protein Kinase Cascade Regulating Infection-Related Morphogenesis in <i>Magnaporthe grisea</i> . <i>Plant Cell</i> , 2005, 17, 1317-1329.	3.1	241
12	Global gene regulation by <i>Fusarium</i> transcription factors <i>Tri6</i> and <i>Tri10</i> reveals adaptations for toxin biosynthesis. <i>Molecular Microbiology</i> , 2009, 72, 354-367.	1.2	241
13	The CPKA Gene of <i>Magnaporthe grisea</i> Is Essential for Appressorial Penetration. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 187-194.	1.4	239
14	The BMP1 Gene Is Essential for Pathogenicity in the Gray Mold Fungus <i>Botrytis cinerea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 724-732.	1.4	220
15	Osmoregulation and Fungicide Resistance: the <i>Neurospora crassa</i> <i>os-2</i> Gene Encodes a HOG1 Mitogen-Activated Protein Kinase Homologue. <i>Applied and Environmental Microbiology</i> , 2002, 68, 532-538.	1.4	220
16	One Fungus, One Name: Defining the Genus <i>Fusarium</i> in a Scientifically Robust Way That Preserves Longstanding Use. <i>Phytopathology</i> , 2013, 103, 400-408.	1.1	219
17	Multiple Plant Surface Signals are Sensed by Different Mechanisms in the Rice Blast Fungus for Appressorium Formation. <i>PLoS Pathogens</i> , 2011, 7, e1001261.	2.1	212
18	Specific adaptation of <i>Ustilaginoidea virens</i> in occupying host florets revealed by comparative and functional genomics. <i>Nature Communications</i> , 2014, 5, 3849.	5.8	202

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19	MST12 Regulates Infectious Growth But Not Appressorium Formation in the Rice Blast Fungus <i>Magnaporthe grisea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 183-192.	1.4	194
20	Mitogen-activated protein kinase signaling in plant pathogenic fungi. <i>PLoS Pathogens</i> , 2018, 14, e1006875.	2.1	181
21	Conidial germination in the filamentous fungus <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 389-399.	0.9	180
22	Different Chitin Synthase Genes Are Required for Various Developmental and Plant Infection Processes in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002526.	2.1	177
23	Random Insertional Mutagenesis Identifies Genes Associated with Virulence in the Wheat Scab Fungus <i>Fusarium graminearum</i> . <i>Phytopathology</i> , 2005, 95, 744-750.	1.1	170
24	Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002869.	1.5	167
25	Development of a <i>Fusarium graminearum</i> Affymetrix GeneChip for profiling fungal gene expression in vitro and in planta. <i>Fungal Genetics and Biology</i> , 2006, 43, 316-325.	0.9	164
26	Two Novel Fungal Virulence Genes Specifically Expressed in Appressoria of the Rice Blast Fungus. <i>Plant Cell</i> , 2002, 14, 2107-2119.	3.1	161
27	Genetic control of infection-related development in <i>Magnaporthe oryzae</i> . <i>Current Opinion in Microbiology</i> , 2012, 15, 678-684.	2.3	161
28	Genome sequence of <i>Valsa</i> canker pathogens uncovers a potential adaptation of colonization of woody bark. <i>New Phytologist</i> , 2015, 208, 1202-1216.	3.5	158
29	Multiple Upstream Signals Converge on the Adaptor Protein Mst50 in <i>Magnaporthe grisea</i> . <i>Plant Cell</i> , 2006, 18, 2822-2835.	3.1	147
30	Independent genetic mechanisms mediate turgor generation and penetration peg formation during plant infection in the rice blast fungus. <i>Molecular Microbiology</i> , 2004, 53, 1695-1707.	1.2	146
31	N-Glycosylation of Effector Proteins by an α -1,3-Mannosyltransferase Is Required for the Rice Blast Fungus to Evade Host Innate Immunity. <i>Plant Cell</i> , 2014, 26, 1360-1376.	3.1	146
32	The TOR signaling pathway regulates vegetative development and virulence in <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2014, 203, 219-232.	3.5	139
33	The Tig1 Histone Deacetylase Complex Regulates Infectious Growth in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2010, 22, 2495-2508.	3.1	138
34	Functional analysis of the <i>Fusarium graminearum</i> phosphatome. <i>New Phytologist</i> , 2015, 207, 119-134.	3.5	138
35	The FgHOG1 Pathway Regulates Hyphal Growth, Stress Responses, and Plant Infection in <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2012, 7, e49495.	1.1	138
36	A Novel Protein Com1 Is Required for Normal Conidium Morphology and Full Virulence in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 112-123.	1.4	135

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37	Two mitogen-activated protein kinase signalling cascades mediate basal resistance to antifungal plant defensins in <i>Fusarium graminearum</i> . <i>Cellular Microbiology</i> , 2007, 9, 1491-1506.	1.1	131
38	The G-beta subunit MGB1 is involved in regulating multiple steps of infection-related morphogenesis in <i>Magnaporthe grisea</i> . <i>Molecular Microbiology</i> , 2003, 50, 231-243.	1.2	129
39	Efficient Approaches for Generating GFP Fusion and Epitope-Tagging Constructs in Filamentous Fungi. <i>Methods in Molecular Biology</i> , 2011, 722, 199-212.	0.4	128
40	Analysis of expressed sequence tags from <i>Gibberella zeae</i> (anamorph <i>Fusarium graminearum</i>). <i>Fungal Genetics and Biology</i> , 2003, 38, 187-197.	0.9	120
41	Effectors and Effector Delivery in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2014, 10, e1003826.	2.1	114
42	The fungal myosin I is essential for <i>Fusarium toxiosome</i> formation. <i>PLoS Pathogens</i> , 2018, 14, e1006827.	2.1	113
43	Genome-wide A-to-I RNA editing in fungi independent of ADAR enzymes. <i>Genome Research</i> , 2016, 26, 499-509.	2.4	109
44	The Cyclase-Associated Protein Cap1 Is Important for Proper Regulation of Infection-Related Morphogenesis in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002911.	2.1	108
45	<i>TRI6</i> and <i>TRI10</i> play different roles in the regulation of deoxynivalenol (DON) production by cAMP signalling in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2016, 18, 3689-3701.	1.8	108
46	A MADS-box transcription factor MoMcm1 is required for male fertility, microconidium production and virulence in <i>Magnaporthe oryzae</i> . <i>Molecular Microbiology</i> , 2011, 80, 33-53.	1.2	105
47	Generic names in Magnaporthales. <i>IMA Fungus</i> , 2016, 7, 155-159.	1.7	98
48	MADS-Box Transcription Factor Mig1 Is Required for Infectious Growth in <i>Magnaporthe grisea</i> . <i>Eukaryotic Cell</i> , 2008, 7, 791-799.	3.4	97
49	The <i>HDF1</i> Histone Deacetylase Gene Is Important for Conidiation, Sexual Reproduction, and Pathogenesis in <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 487-496.	1.4	96
50	The Dawn of Fungal Pathogen Genomics. <i>Annual Review of Phytopathology</i> , 2006, 44, 337-366.	3.5	95
51	A highly conserved MAPK-docking site in Mst7 is essential for Pmk1 activation in <i>Magnaporthe grisea</i> . <i>Molecular Microbiology</i> , 2007, 63, 881-94.	1.2	92
52	Transducin Beta-Like Gene <i>FTL1</i> Is Essential for Pathogenesis in <i>Fusarium graminearum</i> . <i>Eukaryotic Cell</i> , 2009, 8, 867-876.	3.4	92
53	An orphan protein of <i>Fusarium graminearum</i> modulates host immunity by mediating proteasomal degradation of TaSnRK1 α . <i>Nature Communications</i> , 2020, 11, 4382.	5.8	92
54	A Homeobox Gene Is Essential for Conidiogenesis of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 366-375.	1.4	91

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55	Two PAK Kinase Genes, CHM1 and MST20, Have Distinct Functions in <i>Magnaporthe grisea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 547-556.	1.4	89
56	Targeted Deletion of the USTA and UvSLT2 Genes Efficiently in <i>Ustilaginoidea virens</i> With the CRISPR-Cas9 System. <i>Frontiers in Plant Science</i> , 2018, 9, 699.	1.7	87
57	Development of a high throughput transformation system for insertional mutagenesis in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 1035-1049.	0.9	81
58	The cAMP Signaling Pathway in <i>Fusarium verticillioides</i> Is Important for Conidiation, Plant Infection, and Stress Responses but Not Fumonisin Production. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 522-533.	1.4	79
59	Molecular evolution and functional divergence of tubulin superfamily in the fungal tree of life. <i>Scientific Reports</i> , 2014, 4, 6746.	1.6	79
60	The MAT Locus Genes Play Different Roles in Sexual Reproduction and Pathogenesis in <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2013, 8, e66980.	1.1	73
61	The cAMP-PKA Pathway Regulates Growth, Sexual and Asexual Differentiation, and Pathogenesis in <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 557-566.	1.4	73
62	A-to-I RNA editing is developmentally regulated and generally adaptive for sexual reproduction in <i>Neurospora crassa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7756-E7765.	3.3	73
63	The CID1 cyclin C-like gene is important for plant infection in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2010, 47, 143-151.	0.9	69
64	Differences between appressoria formed by germ tubes and appressorium-like structures developed by hyphal tips in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2013, 56, 33-41.	0.9	68
65	UvHOG1 is important for hyphal growth and stress responses in the rice false smut fungus <i>Ustilaginoidea virens</i> . <i>Scientific Reports</i> , 2016, 6, 24824.	1.6	64
66	A systematic analysis of T-DNA insertion events in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 1050-1064.	0.9	61
67	The <i>AreA</i> transcription factor mediates the regulation of deoxynivalenol (<i>DON</i>) synthesis by ammonium and cyclic adenosine monophosphate (<i>cAMP</i>) signalling in <i>Fusarium graminearum</i> . <i>Molecular Plant Pathology</i> , 2015, 16, 987-999.	2.0	60
68	An expanded subfamily of G-protein-coupled receptor genes in <i>Fusarium graminearum</i> required for wheat infection. <i>Nature Microbiology</i> , 2019, 4, 1582-1591.	5.9	60
69	Characterization of the Two-Speed Subgenomes of <i>Fusarium graminearum</i> Reveals the Fast-Speed Subgenome Specialized for Adaption and Infection. <i>Frontiers in Plant Science</i> , 2017, 8, 140.	1.7	56
70	<i>FgSKN7</i> and <i>FgATF1</i> have overlapping functions in ascosporeogenesis, pathogenesis and stress responses in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2015, 17, 1245-1260.	1.8	55
71	The <i>MADS</i> transcription factor <i>FgMcm1</i> regulates cell identity and fungal development in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2015, 17, 2762-2776.	1.8	55
72	The <i>FvMK1</i> mitogen-activated protein kinase gene regulates conidiation, pathogenesis, and fumonisin production in <i>Fusarium verticillioides</i> . <i>Fungal Genetics and Biology</i> , 2011, 48, 71-79.	0.9	54

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73	A Novel Transcriptional Factor Important for Pathogenesis and Ascospore Germination in <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 118-128.	1.4	54
74	MoSf1 Is Important for Virulence and Heat Tolerance in <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2011, 6, e19951.	1.1	54
75	<i>MST50</i> is involved in multiple MAP kinase signaling pathways in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017, 19, 1959-1974.	1.8	50
76	A Genetic Map of <i>Gibberella fujikuroi</i> Mating Population A (<i>Fusarium moniliforme</i>). <i>Genetics</i> , 1996, 143, 175-189.	1.2	50
77	PKA activity is essential for relieving the suppression of hyphal growth and appressorium formation by MoSf1 in <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2017, 13, e1006954.	1.5	50
78	Compartmentalized gene regulatory network of the pathogenic fungus <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2016, 211, 527-541.	3.5	48
79	From Genes to Genomes: A New Paradigm for Studying Fungal Pathogenesis in <i>Magnaporthe oryzae</i> . <i>Advances in Genetics</i> , 2007, 57, 175-218.	0.8	47
80	A-to-I mRNA editing in fungi: occurrence, function, and evolution. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 329-340.	2.4	47
81	<i>FgCDC14</i> regulates cytokinesis, morphogenesis, and pathogenesis in <i>Fusarium graminearum</i> . <i>Molecular Microbiology</i> , 2015, 98, 770-786.	1.2	45
82	Genomic analysis of host-pathogen interaction between <i>Fusarium graminearum</i> and wheat during early stages of disease development. <i>Microbiology (United Kingdom)</i> , 2006, 152, 1877-1890.	0.7	44
83	Germination and infectivity of microconidia in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Nature Communications</i> , 2014, 5, 4518.	5.8	44
84	The AMT1 Arginine Methyltransferase Gene Is Important for Plant Infection and Normal Hyphal Growth in <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2012, 7, e38324.	1.1	43
85	Two Cdc2 Kinase Genes with Distinct Functions in Vegetative and Infectious Hyphae in <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2015, 11, e1004913.	2.1	42
86	<i>Fgk3</i> glycogen synthase kinase is important for development, pathogenesis and stress responses in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2015, 5, 8504.	1.6	42
87	Bypassing Both Surface Attachment and Surface Recognition Requirements for Appressorium Formation by Overactive Ras Signaling in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 996-1004.	1.4	41
88	Molecular Characterization of a Fus3/Kss1 Type MAPK from <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , PsMAPK1. <i>PLoS ONE</i> , 2011, 6, e21895.	1.1	41
89	<i>FgK11</i> kinase localizes to the septal pore and plays a role in hyphal growth, ascospore germination, pathogenesis, and localization of β -tubulins in <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2014, 204, 943-954.	3.5	40
90	Thioredoxins are involved in the activation of the <i>PMK1</i> MAP kinase pathway during appressorium penetration and invasive growth in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2016, 18, 3768-3784.	1.8	38

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91	<i>TaDAD2</i> , a Negative Regulator of Programmed Cell Death, Is Important for the Interaction Between Wheat and the Stripe Rust Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 79-90.	1.4	37
92	Cryptic promoter activity in the coding region of the HMG-CoA reductase gene in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 34-41.	0.9	36
93	Post-translational regulation of autophagy is involved in intra-microbiome suppression of fungal pathogens. <i>Microbiome</i> , 2021, 9, 131.	4.9	36
94	Regulation of biotic interactions and responses to abiotic stresses by MAP kinase pathways in plant pathogenic fungi. <i>Stress Biology</i> , 2021, 1, 1.	1.5	36
95	A Ligation-PCR Approach for Generating Gene Replacement Constructs in <i>Magnaporthe grisea</i> . <i>Fungal Genetics Reports</i> , 2004, 51, 17-18.	0.6	35
96	Activation of the signalling mucin <i>MoMsb2</i> and its functional relationship with <i>Cbp1</i> in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2015, 17, 2969-2981.	1.8	33
97	RNA editing of the <i>AMD1</i> gene is important for ascus maturation and ascospore discharge in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2017, 7, 4617.	1.6	33
98	The <i>Sch9</i> Kinase Regulates <i>Conidium</i> Size, Stress Responses, and Pathogenesis in <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2014, 9, e105811.	1.1	33
99	A <i>Pmk1</i> -Interacting Gene Is Involved in Appressorium Differentiation and Plant Infection in <i>Magnaporthe oryzae</i> . <i>Eukaryotic Cell</i> , 2011, 10, 1062-1070.	3.4	31
100	<i>MoCDC14</i> is important for septation during conidiation and appressorium formation in <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 328-340.	2.0	31
101	Functional Characterization of <i>CgCTR2</i> , a Putative Vacuole Copper Transporter That Is Involved in Germination and Pathogenicity in <i>Colletotrichum gloeosporioides</i> . <i>Eukaryotic Cell</i> , 2008, 7, 1098-1108.	3.4	30
102	Histological and molecular studies of the non-host interaction between wheat and <i>Uromyces fabae</i> . <i>Planta</i> , 2011, 234, 979-991.	1.6	29
103	The cyclase-associated protein <i>FgCap1</i> has both protein kinase A-dependent and A-independent functions during deoxynivalenol production and plant infection in <i>Fusarium graminearum</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 552-563.	2.0	29
104	Sensitivity of Field Strains of <i>Gibberella fujikuroi</i> (<i>Fusarium section Liseola</i>) to Benomyl and Hygromycin B. <i>Mycologia</i> , 1993, 85, 206-213.	0.8	28
105	Stage-specific functional relationships between <i>Tub1</i> and <i>Tub2</i> beta-tubulins in the wheat scab fungus <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2019, 132, 103251.	0.9	28
106	<i>FgPrp4</i> Kinase Is Important for Spliceosome B-Complex Activation and Splicing Efficiency in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2016, 12, e1005973.	1.5	27
107	<i>FgSsn3</i> kinase, a component of the mediator complex, is important for sexual reproduction and pathogenesis in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2016, 6, 22333.	1.6	27
108	Expression of <i>HopAl</i> interferes with MAP kinase signalling in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017, 19, 4190-4204.	1.8	26

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109	A-to-I RNA editing independent of ADARs in filamentous fungi. <i>RNA Biology</i> , 2016, 13, 940-945.	1.5	25
110	MGOS: A Resource for Studying <i>Magnaporthe grisea</i> and <i>Oryza sativa</i> Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1055-1061.	1.4	24
111	MFS Transporters and GABA Metabolism Are Involved in the Self-Defense Against DON in <i>Fusarium graminearum</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 438.	1.7	24
112	Opposing functions of Fng1 and the Rpd3 HDAC complex in H4 acetylation in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2020, 16, e1009185.	1.5	24
113	Mir1 is Highly Upregulated and Localized to Nuclei During Infectious Hyphal Growth in the Rice Blast Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 448-458.	1.4	23
114	Conservation and divergence of the cyclic adenosine monophosphate-protein kinase A (cAMP-PKA) pathway in two plant pathogenic fungi: <i>Fusarium graminearum</i> and <i>Fusarium verticillioides</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 196-209.	2.0	23
115	The <i>FgSRP1</i> SR-protein gene is important for plant infection and pre-mRNA processing in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2017, 19, 4065-4079.	1.8	23
116	Activation of Mst11 and Feedback Inhibition of Germ Tube Growth in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 881-891.	1.4	22
117	Extensive chromosomal rearrangements and rapid evolution of novel effector superfamilies contribute to host adaptation and speciation in the basal ascomycetous fungi. <i>Molecular Plant Pathology</i> , 2020, 21, 330-348.	2.0	22
118	Identification of a Fungi-Specific Lineage of Protein Kinases Closely Related to Tyrosine Kinases. <i>PLoS ONE</i> , 2014, 9, e89813.	1.1	22
119	<i>Peltaster fructicola</i> genome reveals evolution from an invasive phytopathogen to an ectophytic parasite. <i>Scientific Reports</i> , 2016, 6, 22926.	1.6	21
120	Landscape and regulation of alternative splicing and alternative polyadenylation in a plant pathogenic fungus. <i>New Phytologist</i> , 2022, 235, 674-689.	3.5	21
121	The <i>PKR</i> regulatory subunit of protein kinase A (PKA) is involved in the regulation of growth, sexual and asexual development, and pathogenesis in <i>Fusarium graminearum</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 909-921.	2.0	20
122	Assays for MAP Kinase Activation in <i>Magnaporthe oryzae</i> and Other Plant Pathogenic Fungi. <i>Methods in Molecular Biology</i> , 2018, 1848, 93-101.	0.4	20
123	Coregulation of dimorphism and symbiosis by cyclic AMP signaling in the lichenized fungus <i>Umbilicaria muhlenbergii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23847-23858.	3.3	19
124	Srk1 kinase, a SR protein-specific kinase, is important for sexual reproduction, plant infection and pre-mRNA processing in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2018, 20, 3261-3277.	1.8	17
125	Determination of the absolute configurations of the stereogenic centers of ustilaginoidins by studying the biosynthetic monomers from a gene knockout mutant of <i>Villosiclava virens</i> . <i>Scientific Reports</i> , 2019, 9, 1855.	1.6	17
126	Penetration Peg Formation and Invasive Hyphae Development Require Stage-Specific Activation of <i>MoGT11</i> in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 36-45.	1.4	16

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131	The Fng3 <i>ING</i> protein regulates <i>H3</i> acetylation and <i>H4</i> deacetylation by interacting with two distinct histone-modifying complexes. <i>New Phytologist</i> , 2022, 235, 2350-2364.	3.5	13
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143	Shuffling effector genes through mini-chromosomes. <i>PLoS Genetics</i> , 2019, 15, e1008345.	1.5	8
144	<i>FgBUD14</i> is important for ascosporeogenesis and involves both stage-specific alternative splicing and <i>RNA</i> editing during sexual reproduction. <i>Environmental Microbiology</i> , 2021, 23, 5052-5068.	1.8	8

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146	The triâ€snRNP specific protein FgSnu66 is functionally related to FgPrp4 kinase in <i>Fusarium graminearum</i> . <i>Molecular Microbiology</i> , 2018, 109, 494-508.	1.2	7
147	Distinct cell cycle regulation during saprophytic and pathogenic growth in fungal pathogens. <i>Current Genetics</i> , 2016, 62, 185-189.	0.8	6
148	The PMK1 MAP Kinase Pathway and Infection-Related Morphogenesis. , 2009, , 13-21.		5
149	Comparative transcriptome analysis reveals distinct gene expression profiles in <i>Brachypodium distachyon</i> infected by two fungal pathogens. <i>BMC Plant Biology</i> , 2021, 21, 304.	1.6	5
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