

Jin-Rong Xu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

154
papers

11,820
citations

57
h-index

107
g-index

160
ext. papers

14,615
ext. citations

6.5
avg, IF

6.11
L-index

#	Paper	IF	Citations
154	Deletion of all three MAP kinase genes results in severe defects in stress responses and pathogenesis in <i>Fusarium graminearum</i> . <i>Stress Biology</i> , 2022 , 2, 1		1
153	Mutations in FgPrp6 suppressive to the Fgprp4 mutant in <i>Fusarium graminearum</i> . <i>Journal of Integrative Agriculture</i> , 2022 , 21, 1375-1388	3.2	
152	Elucidation of ustilaginoidin biosynthesis reveals a previously unrecognised class of ene-reductases. <i>Chemical Science</i> , 2021 , 12, 14883-14892	9.4	1
151	Discovering RNA Editing Events in Fungi. <i>Methods in Molecular Biology</i> , 2021 , 2181, 35-50	1.4	0
150	FgBUD14 is important for ascosporeogenesis and involves both stage-specific alternative splicing and RNA editing during sexual reproduction. <i>Environmental Microbiology</i> , 2021 , 23, 5052-5068	5.2	1
149	Post-translational regulation of autophagy is involved in intra-microbiome suppression of fungal pathogens. <i>Microbiome</i> , 2021 , 9, 131	16.6	7
148	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	5.3	1
147	Fng1 is involved in crosstalk between histone acetylation and methylation. <i>Current Genetics</i> , 2021 , 67, 535-538	2.9	1
146	Stage-specific regulation of purine metabolism during infectious growth and sexual reproduction in <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2021 , 230, 757-773	9.8	1
145	Regulation of biotic interactions and responses to abiotic stresses by MAP kinase pathways in plant pathogenic fungi. <i>Stress Biology</i> , 2021 , 1, 1		7
144	High-Quality Genome Resource of Strain CanS41 by Oxford Nanopore Long-Read Sequencing. <i>Plant Disease</i> , 2021 , 105, 2231-2234	1.5	1
143	The SR-protein FgSrp2 regulates vegetative growth, sexual reproduction and pre-mRNA processing by interacting with FgSrp1 in <i>Fusarium graminearum</i> . <i>Current Genetics</i> , 2020 , 66, 607-619	2.9	3
142	Opposing functions of Fng1 and the Rpd3 HDAC complex in H4 acetylation in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2020 , 16, e1009185	6	9
141	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	5.7	9
140	FgPal1 regulates morphogenesis and pathogenesis in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2020 , 22, 5373-5386	5.2	2
139	An orphan protein of <i>Fusarium graminearum</i> modulates host immunity by mediating proteasomal degradation of TaSnRK1 β . <i>Nature Communications</i> , 2020 , 11, 4382	17.4	18
138	Coregulation of dimorphism and symbiosis by cyclic AMP signaling in the lichenized fungus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23847-23858 ^{11.5}		9

137	Shuffling effector genes through mini-chromosomes. <i>PLoS Genetics</i> , 2019 , 15, e1008345	6	5
136	Deletion of Is Suppressive to the Mutant by Stimulating Gpmk1 Activation and Avoiding Intracellular Turgor Elevation in. <i>Frontiers in Microbiology</i> , 2019 , 10, 1073	5.7	7
135	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	26.6	25
134	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	4.9	10
133	Stage-specific functional relationships between Tub1 and Tub2 beta-tubulins in the wheat scab fungus <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2019 , 132, 103251	3.9	8
132	Spontaneous mutations in FgSAD1 suppress the growth defect of the Fgprp4 mutant by affecting tri-snRNP stability and its docking in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2019 , 21, 4488-4503	5.2	4
131	The meiosis-specific APC activator FgAMA1 is dispensable for meiosis but important for ascosporeogenesis in <i>Fusarium graminearum</i> . <i>Molecular Microbiology</i> , 2019 , 111, 1245-1262	4.1	5
130	Independent losses and duplications of autophagy-related genes in fungal tree of life. <i>Environmental Microbiology</i> , 2019 , 21, 226-243	5.2	6
129	A-to-I mRNA editing in fungi: occurrence, function, and evolution. <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 329-340	10.3	16
128	Phosphorylation by Prp4 kinase releases the self-inhibition of FgPrp31 in <i>Fusarium graminearum</i> . <i>Current Genetics</i> , 2018 , 64, 1261-1274	2.9	8
127	MoCDC14 is important for septation during conidiation and appressorium formation in <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2018 , 19, 328-340	5.7	14
126	The cyclase-associated protein FgCap1 has both protein kinase A-dependent and -independent functions during deoxynivalenol production and plant infection in <i>Fusarium graminearum</i> . <i>Molecular Plant Pathology</i> , 2018 , 19, 552-563	5.7	21
125	The PKR 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	5.7	10
124	MFS Transporters and GABA Metabolism Are Involved in the Self-Defense Against DON in. <i>Frontiers in Plant Science</i> , 2018 , 9, 438	6.2	9
123	Targeted Deletion of the and Genes Efficiently in With the CRISPR-Cas9 System. <i>Frontiers in Plant Science</i> , 2018 , 9, 699	6.2	49
122	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	5.2	9
121	The fungal myosin I is essential for <i>Fusarium</i> toxosome formation. <i>PLoS Pathogens</i> , 2018 , 14, e1006827	7.6	54
120	Mitogen-activated protein kinase signaling in plant pathogenic fungi. <i>PLoS Pathogens</i> , 2018 , 14, e10068756	7.6	87

119	The tri-snRNP specific protein FgSnu66 is functionally related to FgPrp4 kinase in <i>Fusarium graminearum</i> . <i>Molecular Microbiology</i> , 2018 , 109, 494-508	4.1	4
118	Fungal Pathogenesis in the Rice Blast Fungus <i>Magnaporthe Grisea</i> 2018 , 138-165		1
117	Sexual specific functions of Tub1 beta-tubulins require stage-specific RNA processing and expression in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2018 , 20, 4009-4021	5.2	4
116	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	1.4	7
115	MST50 is involved in multiple MAP kinase signaling pathways in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017 , 19, 1959-1974	5.2	28
114	A Gin4-Like Protein Kinase GIL1 Involvement in Hyphal Growth, Asexual Development, and Pathogenesis in <i>Fusarium graminearum</i> . <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	2
113	A-to-I RNA editing is developmentally regulated and generally adaptive for sexual reproduction in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E7756-E7765	11.5	41
112	Expression of HopAI interferes with MAP kinase signalling in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017 , 19, 4190-4204	5.2	16
111	RNA editing of the AMD1 gene is important for ascus maturation and ascospore discharge in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2017 , 7, 4617	4.9	15
110	The FgSRP1 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	5.2	17
109	Characterization of the Two-Speed Subgenomes of Reveals the Fast-Speed Subgenome Specialized for Adaption and Infection. <i>Frontiers in Plant Science</i> , 2017 , 8, 140	6.2	32
108	PKA activity is essential for relieving the suppression of hyphal growth and appressorium formation by MoSfl1 in <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2017 , 13, e1006954	6	35
107	Distinct cell cycle regulation during saprophytic and pathogenic growth in fungal pathogens. <i>Current Genetics</i> , 2016 , 62, 185-9	2.9	6
106	A-to-I RNA editing independent of ADARs in filamentous fungi. <i>RNA Biology</i> , 2016 , 13, 940-945	4.8	17
105	Generic names in <i>Magnaporthales</i> . <i>IMA Fungus</i> , 2016 , 7, 155-9	6.8	66
104	<i>Peltaster fructicola</i> genome reveals evolution from an invasive phytopathogen to an ectophytic parasite. <i>Scientific Reports</i> , 2016 , 6, 22926	4.9	13
103	Compartmentalized gene regulatory network of the pathogenic fungus <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2016 , 211, 527-41	9.8	27
102	Genome-wide A-to-I RNA editing in fungi independent of ADAR enzymes. <i>Genome Research</i> , 2016 , 26, 499-509	9.7	74

101	FgPrp4 Kinase Is Important for Spliceosome B-Complex Activation and Splicing Efficiency in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2016 , 12, e1005973	6	20
100	Evolution and Functional Insights of Different Ancestral Orthologous Clades of Chitin Synthase Genes in the Fungal Tree of Life. <i>Frontiers in Plant Science</i> , 2016 , 7, 37	6.2	11
99	TRI6 and TRI10 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	5.2	58
98	Thioredoxins are involved in the activation of the PMK1 MAP kinase pathway during appressorium penetration and invasive growth in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2016 , 18, 3768-3784	5.2	22
97	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	4.9	37
96	FgSsn3 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	4.9	13
95	Penetration Peg Formation and Invasive Hyphae Development Require Stage-Specific Activation of MoGT11 in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2016 , 29, 36-45	3.6	9
94	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>F. verticillioides</i> . <i>Molecular Plant Pathology</i> , 2016 , 17, 196-209	5.7	19
93	Fgk3 glycogen synthase kinase is important for development, pathogenesis, and stress responses in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2015 , 5, 8504	4.9	30
92	Activation of Mst11 and Feedback Inhibition of Germ Tube Growth in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2015 , 28, 881-91	3.6	15
91	The AreA transcription factor mediates the regulation of deoxynivalenol (DON) synthesis by ammonium and cyclic adenosine monophosphate (cAMP) signalling in <i>Fusarium graminearum</i> . <i>Molecular Plant Pathology</i> , 2015 , 16, 987-99	5.7	48
90	Functional analysis of the <i>Fusarium graminearum</i> phosphatome. <i>New Phytologist</i> , 2015 , 207, 119-134	9.8	63
89	Activation of the signalling mucin MoMsb2 and its functional relationship with Cbp1 in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2015 , 17, 2969-81	5.2	25
88	Genome sequence of <i>Valsa</i> canker pathogens uncovers a potential adaptation of colonization of woody bark. <i>New Phytologist</i> , 2015 , 208, 1202-16	9.8	74
87	FgCDC14 regulates cytokinesis, morphogenesis, and pathogenesis in <i>Fusarium graminearum</i> . <i>Molecular Microbiology</i> , 2015 , 98, 770-86	4.1	27
86	Two Cdc2 Kinase Genes with Distinct Functions in Vegetative and Infectious Hyphae in <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2015 , 11, e1004913	7.6	30
85	FgSKN7 and FgATF1 have overlapping functions in ascosporeogenesis, pathogenesis and stress responses in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2015 , 17, 1245-60	5.2	42
84	The MADS-box transcription factor FgMcm1 regulates cell identity and fungal development in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2015 , 17, 2762-76	5.2	23

83	Molecular evolution and functional divergence of tubulin superfamily in the fungal tree of life. <i>Scientific Reports</i> , 2014 , 4, 6746	4.9	47
82	The TOR signaling pathway regulates vegetative development and virulence in <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2014 , 203, 219-32	9.8	85
81	FgKin1 kinase localizes to the septal pore and plays a role in hyphal growth, ascospore germination, pathogenesis, and localization of Tub1 beta-tubulins in <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2014 , 204, 943-54	9.8	33
80	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, 557-66	3.6	57
79	Germination and infectivity of microconidia in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Nature Communications</i> , 2014 , 5, 4518	17.4	33
78	<i>Fusarium</i> Genetics and Pathogenicity 2014 , 607-621		1
77	Effectors and effector delivery in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2014 , 10, e1003826	7.6	76
76	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	3.6	29
75	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, 1360-76	11.6	94
74	Specific adaptation of <i>Ustilagoidea virens</i> in occupying host florets revealed by comparative and functional genomics. <i>Nature Communications</i> , 2014 , 5, 3849	17.4	122
73	Identification of a fungi-specific lineage of protein kinases closely related to tyrosine kinases. <i>PLoS ONE</i> , 2014 , 9, e89813	3.7	13
72	The Sch9 kinase regulates conidium size, stress responses, and pathogenesis in <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2014 , 9, e105811	3.7	23
71	Comparative analysis of fungal genomes reveals different plant cell wall degrading capacity in fungi. <i>BMC Genomics</i> , 2013 , 14, 274	4.5	288
70	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	3.9	54
69	One fungus, one name: defining the genus <i>Fusarium</i> in a scientifically robust way that preserves longstanding use. <i>Phytopathology</i> , 2013 , 103, 400-8	3.8	155
68	The MAT locus genes play different roles in sexual reproduction and pathogenesis in <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2013 , 8, e66980	3.7	48
67	Genetic control of infection-related development in <i>Magnaporthe oryzae</i> . <i>Current Opinion in Microbiology</i> , 2012 , 15, 678-84	7.9	122
66	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	3.7	30

65	The Cyclase-associated protein Cap1 is important for proper regulation of infection-related morphogenesis in Magnaporthe oryzae. <i>PLoS Pathogens</i> , 2012 , 8, e1002911	7.6	72
64	Comparative analysis of the genomes of two field isolates of the rice blast fungus Magnaporthe oryzae. <i>PLoS Genetics</i> , 2012 , 8, e1002869	6	125
63	Different chitin synthase genes are required for various developmental and plant infection processes in the rice blast fungus Magnaporthe oryzae. <i>PLoS Pathogens</i> , 2012 , 8, e1002526	7.6	128
62	The FgHOG1 pathway regulates hyphal growth, stress responses, and plant infection in Fusarium graminearum. <i>PLoS ONE</i> , 2012 , 7, e49495	3.7	97
61	TaDAD2, 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	3.6	27
60	Efficient approaches for generating GFP fusion and epitope-tagging constructs in filamentous fungi. <i>Methods in Molecular Biology</i> , 2011 , 722, 199-212	1.4	89
59	The FvMK1 mitogen-activated protein kinase gene regulates conidiation, pathogenesis, and fumonisin production in Fusarium verticillioides. <i>Fungal Genetics and Biology</i> , 2011 , 48, 71-9	3.9	42
58	The HDF1 histone deacetylase gene is important for conidiation, sexual reproduction, and pathogenesis in Fusarium graminearum. <i>Molecular Plant-Microbe Interactions</i> , 2011 , 24, 487-96	3.6	62
57	A novel transcriptional factor important for pathogenesis and ascosporeogenesis in Fusarium graminearum. <i>Molecular Plant-Microbe Interactions</i> , 2011 , 24, 118-28	3.6	49
56	A MADS-box transcription factor MoMcm1 is required for male fertility, microconidium production and virulence in Magnaporthe oryzae. <i>Molecular Microbiology</i> , 2011 , 80, 33-53	4.1	74
55	Histological and molecular studies of the non-host interaction between wheat and Uromyces fabae. <i>Planta</i> , 2011 , 234, 979-91	4.7	26
54	Identification of wheat proteins with altered expression levels in leaves infected by the stripe rust pathogen. <i>Acta Physiologiae Plantarum</i> , 2011 , 33, 2423-2435	2.6	6
53	A Pmk1-interacting gene is involved in appressorium differentiation and plant infection in Magnaporthe oryzae. <i>Eukaryotic Cell</i> , 2011 , 10, 1062-70		25
52	Multiple plant surface signals are sensed by different mechanisms in the rice blast fungus for appressorium formation. <i>PLoS Pathogens</i> , 2011 , 7, e1001261	7.6	156
51	Functional analysis of the kinome of the wheat scab fungus Fusarium graminearum. <i>PLoS Pathogens</i> , 2011 , 7, e1002460	7.6	202
50	MoSfl1 is important for virulence and heat tolerance in Magnaporthe oryzae. <i>PLoS ONE</i> , 2011 , 6, e199513	3.7	37
49	Molecular characterization of a Fus3/Kss1 type MAPK from Puccinia striiformis f. sp. tritici, PsMAPK1. <i>PLoS ONE</i> , 2011 , 6, e21895	3.7	29
48	Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium. <i>Nature</i> , 2010 , 464, 367-73	5.4	1085

47	The <i>tig1</i> histone deacetylase complex regulates infectious growth in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2010 , 22, 2495-508	11.6	98
46	The <i>CID1</i> cyclin C-like gene is important for plant infection in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2010 , 47, 143-51	3.9	60
45	A homeobox gene is essential for conidiogenesis of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010 , 23, 366-75	3.6	65
44	A novel protein <i>Com1</i> is required for normal conidium morphology and full virulence in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010 , 23, 112-23	3.6	87
43	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, 522-336	3.6	63
42	The PMK1 MAP Kinase Pathway and Infection-Related Morphogenesis 2009 , 13-21		3
41	Protein Chips and Chromatin Immunoprecipitation Emerging Technologies to Study Macromolecule Interactions in <i>M. grisea</i> 2009 , 73-82		1
40	Transducin beta-like gene <i>FTL1</i> is essential for pathogenesis in <i>Fusarium graminearum</i> . <i>Eukaryotic Cell</i> , 2009 , 8, 867-76		72
39	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, 354-67	4.1	191
38	The cAMP Signaling and MAP Kinase Pathways in Plant Pathogenic Fungi 2009 , 157-172		7
37	Conidial germination in the filamentous fungus <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2008 , 45, 389-99	3.9	136
36	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, 1098-108		23
35	MADS-box transcription factor <i>mig1</i> is required for infectious growth in <i>Magnaporthe grisea</i> . <i>Eukaryotic Cell</i> , 2008 , 7, 791-9		72
34	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, 1491-506	3.9	112
33	A highly conserved MAPK-docking site in <i>Mst7</i> is essential for <i>Pmk1</i> activation in <i>Magnaporthe grisea</i> . <i>Molecular Microbiology</i> , 2007 , 63, 881-94	4.1	80
32	Mitogen-activated protein kinase pathways and fungal pathogenesis. <i>Eukaryotic Cell</i> , 2007 , 6, 1701-14		270
31	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	3.3	45
30	<i>Mirl</i> is highly upregulated and localized to nuclei during infectious hyphal growth in the rice blast fungus. <i>Molecular Plant-Microbe Interactions</i> , 2007 , 20, 448-58	3.6	23

29	A systematic analysis of T-DNA insertion events in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2007 , 44, 1050-64	3.9	52
28	Development of a high throughput transformation system for insertional mutagenesis in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2007 , 44, 1035-49	3.9	66
27	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization. <i>Science</i> , 2007 , 317, 1400-2	33.3	668
26	Multiple upstream signals converge on the adaptor protein Mst50 in <i>Magnaporthe grisea</i> . <i>Plant Cell</i> , 2006 , 18, 2822-35	11.6	121
25	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	2.9	44
24	The dawn of fungal pathogen genomics. <i>Annual Review of Phytopathology</i> , 2006 , 44, 337-66	10.8	86
23	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	3.9	34
22	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, 316-25	3.9	150
21	MGOS: A resource for studying <i>Magnaporthe grisea</i> and <i>Oryza sativa</i> interactions. <i>Molecular Plant-Microbe Interactions</i> , 2006 , 19, 1055-61	3.6	24
20	Random Insertional Mutagenesis Identifies Genes Associated with Virulence in the Wheat Scab Fungus <i>Fusarium graminearum</i> . <i>Phytopathology</i> , 2005 , 95, 744-50	3.8	124
19	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , 2005 , 434, 980-6	50.4	1202
18	A mitogen-activated protein kinase cascade regulating infection-related morphogenesis in <i>Magnaporthe grisea</i> . <i>Plant Cell</i> , 2005 , 17, 1317-29	11.6	203
17	Cellular localization and role of kinase activity of PMK1 in <i>Magnaporthe grisea</i> . <i>Eukaryotic Cell</i> , 2004 , 3, 1525-32		204
16	Independent genetic mechanisms mediate turgor generation and penetration peg formation during plant infection in the rice blast fungus. <i>Molecular Microbiology</i> , 2004 , 53, 1695-707	4.1	130
15	Two PAK kinase genes, CHM1 and MST20, have distinct functions in <i>Magnaporthe grisea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004 , 17, 547-56	3.6	81
14	A Ligation-PCR Approach for Generating Gene Replacement Constructs in <i>Magnaporthe grisea</i> . <i>Fungal Genetics Reports</i> , 2004 , 51, 17-18	0	18
13	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, 231-43	4.1	123
12	Analysis of expressed sequence tags from <i>Gibberella zeae</i> (anamorph <i>Fusarium graminearum</i>). <i>Fungal Genetics and Biology</i> , 2003 , 38, 187-97	3.9	111

11	Time for a blast: genomics of <i>Magnaporthe grisea</i> . <i>Molecular Plant Pathology</i> , 2002 , 3, 173-6	5.7	10
10	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, 1119-27	3.6	342
9	Two novel fungal virulence genes specifically expressed in appressoria of the rice blast fungus. <i>Plant Cell</i> , 2002 , 14, 2107-19	11.6	143
8	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, 532-8	4.8	193
7	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, 183-92	3.6	164
6	Map kinases in fungal pathogens. <i>Fungal Genetics and Biology</i> , 2000 , 31, 137-52	3.9	343
5	The BMP1 gene is essential for pathogenicity in the gray mold fungus <i>Botrytis cinerea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2000 , 13, 724-32	3.6	181
4	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, 2045-58	11.6	280
3	The CPKA Gene of <i>Magnaporthe grisea</i> Is Essential for Appressorial Penetration. <i>Molecular Plant-Microbe Interactions</i> , 1997 , 10, 187-194	3.6	212
2	A Genetic Map of <i>Gibberella fujikuroi</i> Mating Population A (<i>Fusarium moniliforme</i>). <i>Genetics</i> , 1996 , 143, 175-189	4	40
1	Sensitivity of Field Strains of <i>Gibberella Fujikuroi</i> (<i>Fusarium</i> Section <i>Liseola</i>) to Benomyl and Hygromycin B. <i>Mycologia</i> , 1993 , 85, 206-213	2.4	28