

# Nick Talbot

## List of Publications by Year in descending order

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197  
papers

30,992  
citations

9775

73  
h-index

4641

170  
g-index

219  
all docs

219  
docs citations

219  
times ranked

33828  
citing authors

#	ARTICLE	IF	CITATIONS
1	Foliar Diseases and the Associated Fungi in Rice Cultivated in Kenya. <i>Plants</i> , 2022, 11, 1264.	1.6	2
2	The Biology of Invasive Growth by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Methods in Molecular Biology</i> , 2021, 2356, 19-40.	0.4	7
3	Protein glycosylation during infection by plant pathogenic fungi. <i>New Phytologist</i> , 2021, 230, 1329-1335.	3.5	18
4	Chitosan inhibits septin-mediated plant infection by the rice blast fungus <i>Magnaporthe oryzae</i> in a protein kinase C and Nox1 NADPH oxidase-dependent manner. <i>New Phytologist</i> , 2021, 230, 1578-1593.	3.5	21
5	Investigating the cell and developmental biology of plant infection by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2021, 154, 103562.	0.9	40
6	A putative PKA phosphorylation site S227 in MoSom1 is essential for infection-related morphogenesis and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Cellular Microbiology</i> , 2021, 23, e13370.	1.1	2
7	Integrated Strategies for Durable Rice Blast Resistance in Sub-Saharan Africa. <i>Plant Disease</i> , 2021, 105, 2749-2770.	0.7	15
8	From appressorium to transpressorium—Defining the morphogenetic basis of host cell invasion by the rice blast fungus. <i>PLoS Pathogens</i> , 2021, 17, e1009779.	2.1	28
9	Appressorium-mediated plant infection by <i>Magnaporthe oryzae</i> is regulated by a Pmk1-dependent hierarchical transcriptional network. <i>Nature Microbiology</i> , 2021, 6, 1383-1397.	5.9	44
10	Leucine biosynthesis is required for infection-related morphogenesis and pathogenicity in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Current Genetics</i> , 2020, 66, 155-171.	0.8	22
11	Getting a grip on blast. <i>Nature Microbiology</i> , 2020, 5, 1457-1458.	5.9	2
12	Discovery of broad-spectrum fungicides that block septin-dependent infection processes of pathogenic fungi. <i>Nature Microbiology</i> , 2020, 5, 1565-1575.	5.9	44
13	The sorting nexin FgAtg20 is involved in the Cvt pathway, non-selective macroautophagy, pexophagy and pathogenesis in <i>Fusarium graminearum</i> . <i>Cellular Microbiology</i> , 2020, 22, e13208.	1.1	11
14	A sensor kinase controls turgor-driven plant infection by the rice blast fungus. <i>Nature</i> , 2019, 574, 423-427.	13.7	87
15	Plant health emergencies demand open science: Tackling a cereal killer on the run. <i>PLoS Biology</i> , 2019, 17, e3000302.	2.6	28
16	Appressoria. <i>Current Biology</i> , 2019, 29, R144-R146.	1.8	43
17	Environment-dependent fitness gains can be driven by horizontal gene transfer of transporter-encoding genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5613-5622.	3.3	37
18	Conidial Morphogenesis and Septin-Mediated Plant Infection Require Smo1, a Ras GTPase-Activating Protein in <i>Magnaporthe oryzae</i> . <i>Genetics</i> , 2019, 211, 151-167.	1.2	23

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19	<i>Pyricularia graminis</i> <i>tritici</i> is not the correct species name for the wheat blast fungus: response to Ceresini <i>et al.</i> (MPP 20:2). <i>Molecular Plant Pathology</i> , 2019, 20, 173-179.	2.0	42
20	Cycling in synchrony. <i>ELife</i> , 2019, 8, .	2.8	0
21	Gene Flow between Divergent Cereal- and Grass-Specific Lineages of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>MBio</i> , 2018, 9, .	1.8	163
22	A single fungal MAP kinase controls plant cell-to-cell invasion by the rice blast fungus. <i>Science</i> , 2018, 359, 1399-1403.	6.0	164
23	CRISPR-Cas9 ribonucleoprotein-mediated co-editing and counterselection in the rice blast fungus. <i>Scientific Reports</i> , 2018, 8, 14355.	1.6	136
24	Osmotrophy. <i>Current Biology</i> , 2018, 28, R1179-R1180.	1.8	29
25	An Immune-Responsive Cytoskeletal-Plasma Membrane Feedback Loop in Plants. <i>Current Biology</i> , 2018, 28, 2136-2144.e7.	1.8	32
26	MoSnt2-dependent deacetylation of histone H3 mediates MoTor-dependent autophagy and plant infection by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Autophagy</i> , 2018, 14, 1543-1561.	4.3	89
27	The role of glycerol in the pathogenic lifestyle of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017, 19, 1008-1016.	1.8	84
28	The glycogen synthase kinase MoGsk1, regulated by Mps1 MAP kinase, is required for fungal development and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2017, 7, 945.	1.6	18
29	The cyclin dependent kinase subunit Cks1 is required for infection-associated development of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017, 19, 3959-3981.	1.8	13
30	Two independent S-phase checkpoints regulate appressorium-mediated plant infection by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E237-E244.	3.3	57
31	Cell cycle-dependent regulation of plant infection by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Communicative and Integrative Biology</i> , 2017, 10, e1372067.	0.6	21
32	Genome-wide functional analysis reveals that autophagy is necessary for growth, sporulation, deoxynivalenol production and virulence in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2017, 7, 11062.	1.6	69
33	Genotyping-by-Sequencing-Based Genetic Analysis of African Rice Cultivars and Association Mapping of Blast Resistance Genes Against <i>Magnaporthe oryzae</i> Populations in Africa. <i>Phytopathology</i> , 2017, 107, 1039-1046.	1.1	14
34	Fungal pathogenesis: Combatting the oxidative burst. <i>Nature Microbiology</i> , 2017, 2, 17095.	5.9	12
35	The Î²-1,3-glucanosyltransferases (Gels) affect the structure of the rice blast fungal cell wall during appressorium-mediated plant infection. <i>Cellular Microbiology</i> , 2017, 19, e12659.	1.1	51
36	Septins Focus Cellular Growth for Host Infection by Pathogenic Fungi. <i>Frontiers in Cell and Developmental Biology</i> , 2017, 5, 33.	1.8	31

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37	Tpc1 is an important Zn(II)2Cys6 transcriptional regulator required for polarized growth and virulence in the rice blast fungus. <i>PLoS Pathogens</i> , 2017, 13, e1006516.	2.1	56
38	Genome-Wide Association Mapping of Rice Resistance Genes Against <i>Magnaporthe oryzae</i> Isolates from Four African Countries. <i>Phytopathology</i> , 2016, 106, 1359-1365.	1.1	25
39	Nick Talbot. <i>Current Biology</i> , 2016, 26, R1122-R1124.	1.8	0
40	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
41	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i> . <i>BMC Biology</i> , 2016, 14, 84.	1.7	355
42	<i>ZNF1</i> Encodes a Putative C2H2 Zinc-Finger Protein Essential for Appressorium Differentiation by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 22-35.	1.4	38
43	Generic names in Magnaporthales. <i>IMA Fungus</i> , 2016, 7, 155-159.	1.7	98
44	Investigating the cell biology of plant infection by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Current Opinion in Microbiology</i> , 2016, 34, 147-153.	2.3	117
45	4 Septation and Cytokinesis in Pathogenic Fungi. , 2016, , 67-79.		3
46	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	4.3	4,701
47	Investigating the biology of plant infection by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2016, 90, 61-68.	0.9	76
48	New and Improved Techniques for the Study of Pathogenic Fungi. <i>Trends in Microbiology</i> , 2016, 24, 35-50.	3.5	39
49	Harbouring public good mutants within a pathogen population can increase both fitness and virulence. <i>ELife</i> , 2016, 5, .	2.8	21
50	Protein kinase <i>C</i> is essential for viability of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Microbiology</i> , 2015, 98, 403-419.	1.2	35
51	Regulation of appressorium development in pathogenic fungi. <i>Current Opinion in Plant Biology</i> , 2015, 26, 8-13.	3.5	179
52	Taming a wild beast: Developing molecular tools and new methods to understand the biology of <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 193-195.	0.9	5
53	Plant Immunity: A Little Help from Fungal Friends. <i>Current Biology</i> , 2015, 25, R1074-R1076.	1.8	15
54	Septin-Dependent Assembly of the Exocyst Is Essential for Plant Infection by <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2015, 27, 3277-3289.	3.1	79

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55	Exploitation of sulfonylurea resistance marker and non-homologous end joining mutants for functional analysis in <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 102-109.	0.9	20
56	A gene locus for targeted ectopic gene integration in <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 118-124.	0.9	35
57	FgRIC8 is involved in regulating vegetative growth, conidiation, deoxynivalenol production and virulence in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2015, 83, 92-102.	0.9	4
58	Construction and high-throughput phenotypic screening of <i>Zymoseptoria tritici</i> over-expression strains. <i>Fungal Genetics and Biology</i> , 2015, 79, 110-117.	0.9	9
59	A codon-optimized green fluorescent protein for live cell imaging in <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 125-131.	0.9	37
60	Characterisation of Four LIM Protein-Encoding Genes Involved in Infection-Related Development and Pathogenicity by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2014, 9, e88246.	1.1	20
61	Hook is an adapter that coordinates kinesin-3 and dynein cargo attachment on early endosomes. <i>Journal of Cell Biology</i> , 2014, 204, 989-1007.	2.3	135
62	$\alpha$ -Glycosylation of Effector Proteins by an $\alpha$ -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
63	Long-distance endosome trafficking drives fungal effector production during plant infection. <i>Nature Communications</i> , 2014, 5, 5097.	5.8	86
64	Fungal model systems and the elucidation of pathogenicity determinants. <i>Fungal Genetics and Biology</i> , 2014, 70, 42-67.	0.9	133
65	FAR1 and FAR2 Regulate the Expression of Genes Associated with Lipid Metabolism in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2014, 9, e99760.	1.1	26
66	NADPH oxidases regulate septin-mediated cytoskeletal remodeling during plant infection by the rice blast fungus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3179-3184.	3.3	168
67	Horizontal gene transfer in osmotrophs: playing with public goods. <i>Nature Reviews Microbiology</i> , 2013, 11, 720-727.	13.6	85
68	Two distinct secretion systems facilitate tissue invasion by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Nature Communications</i> , 2013, 4, 1996.	5.8	321
69	Glycogen Metabolic Genes Are Involved in Trehalose-6-Phosphate Synthase-Mediated Regulation of Pathogenicity by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003604.	2.1	54
70	The MET13 Methylene-tetrahydrofolate Reductase Gene Is Essential for Infection-Related Morphogenesis in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2013, 8, e76914.	1.1	43
71	Genome-wide Transcriptional Profiling of Appressorium Development by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002514.	2.1	162
72	Saprotrophic competitiveness and biocontrol fitness of a genetically modified strain of the plant-growth-promoting fungus <i>Trichoderma hamatum</i> GD12. <i>Microbiology (United Kingdom)</i> , 2012, 158, 84-97.	0.7	29

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73	Effector-Mediated Suppression of Chitin-Triggered Immunity by <i>Magnaporthe oryzae</i> Is Necessary for Rice Blast Disease. <i>Plant Cell</i> , 2012, 24, 322-335.	3.1	493
74	Guidelines for the use and interpretation of assays for monitoring autophagy. <i>Autophagy</i> , 2012, 8, 445-544.	4.3	3,122
75	Regulating morphogenetic transitions during development and pathogenesis of microbial eukaryotes. <i>Current Opinion in Microbiology</i> , 2012, 15, 633-636.	2.3	1
76	Septin-Mediated Plant Cell Invasion by the Rice Blast Fungus, <i>Magnaporthe oryzae</i> . <i>Science</i> , 2012, 336, 1590-1595.	6.0	311
77	<i>Magnaporthe oryzae</i> Populations Adapted to Finger Millet and Rice Exhibit Distinctive Patterns of Genetic Diversity, Sexuality and Host Interaction. <i>Molecular Biotechnology</i> , 2012, 50, 145-158.	1.3	72
78	Infection-Associated Nuclear Degeneration in the Rice Blast Fungus <i>Magnaporthe oryzae</i> Requires Non-Selective Macro-Autophagy. <i>PLoS ONE</i> , 2012, 7, e33270.	1.1	33
79	RNA Interference of Endochitinases in the Sugarcane Endophyte <i>Trichoderma virens</i> 223 Reduces Its Fitness as a Biocontrol Agent of Pineapple Disease. <i>PLoS ONE</i> , 2012, 7, e47888.	1.1	36
80	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	1.5	902
81	A sterol 14 $\alpha$ -demethylase is required for conidiation, virulence and for mediating sensitivity to sterol demethylation inhibitors by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2011, 48, 144-153.	0.9	59
82	Structure-Function Analysis of a CVNH-LysM Lectin Expressed during Plant Infection by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Structure</i> , 2011, 19, 662-674.	1.6	47
83	Gene transfer into the fungi. <i>Fungal Biology Reviews</i> , 2011, 25, 98-110.	1.9	127
84	The biology of blast: Understanding how <i>Magnaporthe oryzae</i> invades rice plants. <i>Fungal Biology Reviews</i> , 2011, 25, 61-67.	1.9	26
85	Horizontal gene transfer facilitated the evolution of plant parasitic mechanisms in the oomycetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15258-15263.	3.3	225
86	Two Novel Transcriptional Regulators Are Essential for Infection-related Morphogenesis and Pathogenicity of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002385.	2.1	68
87	Anti-Apoptotic Machinery Protects the Necrotrophic Fungus <i>Botrytis cinerea</i> from Host-Induced Apoptotic-Like Cell Death during Plant Infection. <i>PLoS Pathogens</i> , 2011, 7, e1002185.	2.1	147
88	Characterization of <i>MoLDB1</i> Required for Vegetative Growth, Infection-Related Morphogenesis, and Pathogenicity in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1260-1274.	1.4	35
89	<i>MoRic8</i> Is a Novel Component of G-Protein Signaling During Plant Infection by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 317-331.	1.4	42
90	Raiding the sweet shop. <i>Nature</i> , 2010, 468, 510-511.	13.7	12

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91	Comparative Genome Analysis Reveals an Absence of Leucine-Rich Repeat Pattern-Recognition Receptor Proteins in the Kingdom Fungi. PLoS ONE, 2010, 5, e12725.	1.1	31
92	Cell Cycle-Mediated Regulation of Plant Infection by the Rice Blast Fungus. Plant Cell, 2010, 22, 497-507.	3.1	144
93	An NADPH-dependent genetic switch regulates plant infection by the rice blast fungus. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21902-21907.	3.3	130
94	Spatial Uncoupling of Mitosis and Cytokinesis during Appressorium-Mediated Plant Infection by the Rice Blast Fungus <i>Magnaporthe oryzae</i> . Plant Cell, 2010, 22, 2417-2428.	3.1	100
95	Living the Sweet Life: How Does a Plant Pathogenic Fungus Acquire Sugar from Plants?. PLoS Biology, 2010, 8, e1000308.	2.6	52
96	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. Science, 2010, 330, 1543-1546.	6.0	725
97	Genome-wide functional analysis reveals that infection-associated fungal autophagy is necessary for rice blast disease. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15967-15972.	3.3	270
98	Phylogenomic Analysis Demonstrates a Pattern of Rare and Ancient Horizontal Gene Transfer between Plants and Fungi. Plant Cell, 2009, 21, 1897-1911.	3.1	162
99	The emerging role of autophagy in plant pathogen attack and host defence. Current Opinion in Plant Biology, 2009, 12, 444-450.	3.5	43
100	Metabolomic analysis reveals a common pattern of metabolic reprogramming during invasion of three host plant species by <i>Magnaporthe grisea</i> . Plant Journal, 2009, 59, 723-737.	2.8	209
101	Under pressure: investigating the biology of plant infection by <i>Magnaporthe oryzae</i> . Nature Reviews Microbiology, 2009, 7, 185-195.	13.6	809
102	Real-time PCR quantification and live-cell imaging of endophytic colonization of barley ( <i>Hordeum</i> ) by <i>Tilletia horrida</i> . Fungal Genetics and Biology, 2009, 46, 213-228.	3.5	112
103	Fungal physiology – a future perspective. Microbiology (United Kingdom), 2009, 155, 3810-3815.	0.7	37
104	Comparative genomics of MAP kinase and calcium-calmodulin-dependent protein kinase signalling components in plant and human pathogenic fungi. Fungal Genetics and Biology, 2009, 46, 287-298.	0.9	302
105	Rice blast infection of <i>Brachypodium distachyon</i> as a model system to study dynamic host/pathogen interactions. Nature Protocols, 2008, 3, 435-445.	5.5	95
106	Unwrapping the <i>Laccaria</i> genome. New Phytologist, 2008, 180, 259-260.	3.5	0
107	Silencing the crowd: high-throughput functional genomics in <i>Magnaporthe oryzae</i> . Molecular Microbiology, 2008, 68, 1341-1344.	1.2	8
108	Genomes, free radicals and plant cell invasion: recent developments in plant pathogenic fungi. Current Opinion in Plant Biology, 2008, 11, 367-372.	3.5	15

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109	Moving targets: rapid evolution of oomycete effectors. Trends in Microbiology, 2008, 16, 507-510.	3.5	15
110	Guidelines for the use and interpretation of assays for monitoring autophagy in higher eukaryotes. Autophagy, 2008, 4, 151-175.	4.3	2,064
111	Comparative Genome Analysis of Filamentous Fungi Reveals Gene Family Expansions Associated with Fungal Pathogenesis. PLoS ONE, 2008, 3, e2300.	1.1	169
112	Comparative genome analysis across a kingdom of eukaryotic organisms: Specialization and diversification in the Fungi. Genome Research, 2007, 17, 1809-1822.	2.4	94
113	Autophagic Cell Death and its Importance for Fungal Developmental Biology and Pathogenesis. Autophagy, 2007, 3, 126-127.	4.3	23
114	Plant Parasitic Oomycetes Such as <i>Phytophthora</i> Species Contain Genes Derived from Three Eukaryotic Lineages. Plant Signaling and Behavior, 2007, 2, 112-114.	1.2	17
115	Insights from Sequencing Fungal and Oomycete Genomes: What Can We Learn about Plant Disease and the Evolution of Pathogenicity?. Plant Cell, 2007, 19, 3318-3326.	3.1	110
116	Generation of reactive oxygen species by fungal NADPH oxidases is required for rice blast disease. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11772-11777.	3.3	367
117	Functional Analysis of Lipid Metabolism in <i>Magnaporthe grisea</i> Reveals a Requirement for Peroxisomal Fatty Acid $\beta$ -Oxidation During Appressorium-Mediated Plant Infection. Molecular Plant-Microbe Interactions, 2007, 20, 475-491.	1.4	183
118	A Methodology for Comparative Functional Genomics. Journal of Integrative Bioinformatics, 2007, 4, 112-122.	1.0	1
119	Cellular differentiation and host invasion by the rice blast fungus <i>Magnaporthe grisea</i> . Current Opinion in Microbiology, 2007, 10, 339-345.	2.3	62
120	Deadly special deliveries. Nature, 2007, 450, 41-43.	13.7	7
121	Fungal genomics goes industrial. Nature Biotechnology, 2007, 25, 542-543.	9.4	13
122	Tps1 regulates the pentose phosphate pathway, nitrogen metabolism and fungal virulence. EMBO Journal, 2007, 26, 3673-3685.	3.5	165
123	e-Fungi: a data resource for comparative analysis of fungal genomes. BMC Genomics, 2007, 8, 426.	1.2	32
124	Autophagic Fungal Cell Death Is Necessary for Infection by the Rice Blast Fungus. Science, 2006, 312, 580-583.	6.0	457
125	Peroxisomal carnitine acetyl transferase is required for elaboration of penetration hyphae during plant infection by <i>Magnaporthe grisea</i> . Molecular Microbiology, 2006, 61, 46-60.	1.2	97
126	Comparative genomic analysis of phytopathogenic fungi using expressed sequence tag (EST) collections. Molecular Plant Pathology, 2006, 7, 61-70.	2.0	36

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127	A P-type ATPase required for rice blast disease and induction of host resistance. <i>Nature</i> , 2006, 440, 535-539.	13.7	96
128	Evolution of Filamentous Plant Pathogens: Gene Exchange across Eukaryotic Kingdoms. <i>Current Biology</i> , 2006, 16, 1857-1864.	1.8	197
129	Immunofluorescence microscopy and immunogold EM for investigating fungal infection of plants. <i>Nature Protocols</i> , 2006, 1, 2506-2511.	5.5	15
130	The molecular biology of appressorium turgor generation by the rice blast fungus <i>Magnaporthe grisea</i> . <i>Biochemical Society Transactions</i> , 2005, 33, 384-388.	1.6	95
131	Four conserved intramolecular disulphide linkages are required for secretion and cell wall localization of a hydrophobin during fungal morphogenesis. <i>Molecular Microbiology</i> , 2005, 56, 117-125.	1.2	44
132	A bioinformatic tool for analysis of EST transcript abundance during infection-related development by <i>Magnaporthe grisea</i> . <i>Molecular Plant Pathology</i> , 2005, 6, 503-512.	2.0	19
133	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , 2005, 434, 980-986.	13.7	1,447
134	Moving Toward a Systems Biology Approach to the Study of Fungal Pathogenesis in the Rice Blast Fungus <i>Magnaporthe grisea</i> . <i>Advances in Applied Microbiology</i> , 2005, 57, 177-215.	1.3	18
135	Use of a Substrate/Alliinase Combination To Generate Antifungal Activity in Situ. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 574-580.	2.4	41
136	A Fungal Metallothionein Is Required for Pathogenicity of <i>Magnaporthe grisea</i> . <i>Plant Cell</i> , 2004, 16, 1575-1588.	3.1	91
137	<i>Magnaporthe grisea</i> interactions with the model grass <i>Brachypodium distachyon</i> closely resemble those with rice ( <i>Oryza sativa</i> ). <i>Molecular Plant Pathology</i> , 2004, 5, 253-265.	2.0	72
138	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
139	Let there be blight: functional analysis of virulence in <i>Phytophthora infestans</i> . <i>Molecular Microbiology</i> , 2004, 51, 913-915.	1.2	1
140	Stage-specific cellular localisation of two hydrophobins during plant infection by the pathogenic fungus <i>Cladosporium fulvum</i> . <i>Fungal Genetics and Biology</i> , 2004, 41, 624-634.	0.9	24
141	The influence of genotypic variation on metabolite diversity in populations of two endophytic fungal species. <i>Fungal Genetics and Biology</i> , 2004, 41, 721-734.	0.9	22
142	Building filaments in the air: aerial morphogenesis in bacteria and fungi. <i>Current Opinion in Microbiology</i> , 2004, 7, 594-601.	2.3	91
143	Functional Genomic Analysis of the Rice Blast Fungus <i>Magnaporthe grisea</i> . <i>Applied Mycology and Biotechnology</i> , 2004, , 331-352.	0.3	3
144	Molecular Interactions of Phytopathogens and Hosts. , 2004, , 385-403.		0

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145	Trehalose synthesis and metabolism are required at different stages of plant infection by <i>Magnaporthe grisea</i> . <i>EMBO Journal</i> , 2003, 22, 225-235.	3.5	202
146	Aerial Morphogenesis: Enter the Chaplins. <i>Current Biology</i> , 2003, 13, R696-R698.	1.8	27
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