Richard A Wilson

List of Publications by Year
in descending order

45 papers	3,712 citations	201674 27 h-index	243625 44 g-index
49 all docs	49 docs citations	49 times ranked	4142 citing authors

#	Article	IF	Citations
1	Two <i>Magnaporthe</i> appressoriaâ€specific (MAS) proteins, MoMas3 and MoMas5, are required for suppressing host innate immunity and promoting biotrophic growth in rice cells. Molecular Plant Pathology, 2022, , .	4.2	4
2	Recent advances in understanding of fungal and oomycete effectors. Current Opinion in Plant Biology, 2022, 68, 102228.	7.1	15
3	Identification of antiâ€inflammatory vesicleâ€like nanoparticles in honey. Journal of Extracellular Vesicles, 2021, 10, e12069.	12.2	47
4	Mimicking the surface mechanical properties of rice (Oryzae sativa) leaf using PDMS soft lithography. JMST Advances, 2021, 3, 11-17.	1.9	1
5	Plant killers make the cut. Nature Microbiology, 2021, 6, 975-976.	13.3	1
6	Magnaporthe oryzae. Trends in Microbiology, 2021, 29, 663-664.	7.7	23
7	Specimen Preparation and Observations of Appressorial Cells Under Electron. Methods in Molecular Biology, 2021, 2356, 79-85.	0.9	0
8	Tandem Affinity Purification (TAP) of Low-Abundance Protein Complexes in Filamentous Fungi Demonstrated Using Magnaporthe oryzae. Methods in Molecular Biology, 2021, 2356, 97-108.	0.9	2
9	Terminating rice innate immunity induction requires a network of antagonistic and redoxâ€responsive E3 ubiquitin ligases targeting a fungal sirtuin. New Phytologist, 2020, 226, 523-540.	7.3	22
10	Spermine-mediated tight sealing of the Magnaporthe oryzae appressorial poreâ€"rice leaf surface interface. Nature Microbiology, 2020, 5, 1472-1480.	13.3	41
11	<i>Magnaporthe oryzae</i> nucleoside diphosphate kinase is required for metabolic homeostasis and redoxâ€mediated host innate immunity suppression. Molecular Microbiology, 2020, 114, 789-807.	2.5	7
12	Nutritional factors modulating plant and fruit susceptibility to pathogens: BARD workshop, Haifa, Israel, February 25â€"26, 2018. Phytoparasitica, 2020, 48, 317-333.	1.2	0
13	Essential, deadly, enigmatic: Polyamine metabolism and roles in fungal cells. Fungal Biology Reviews, 2019, 33, 47-57.	4.7	44
14	A Feed-Forward Subnetwork Emerging from Integrated TOR- and cAMP/PKA-Signaling Architecture Reinforces <i>Magnaporthe oryzae</i> Appressorium Morphogenesis. Molecular Plant-Microbe Interactions, 2019, 32, 593-607.	2.6	18
15	Genetic evidence for Magnaporthe oryzae vitamin B3 acquisition from rice cells. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Ov	1.8	2
16	Reactive oxygen species metabolism and plant-fungal interactions. Fungal Genetics and Biology, 2018, 110, 1-9.	2.1	138
17	TOR-autophagy branch signaling via Imp1 dictates plant-microbe biotrophic interface longevity. PLoS Genetics, 2018, 14, e1007814.	3.5	45
18	Does increased nutritional carbon availability in fruit and foliar hosts contribute to modulation of pathogen colonization?. Postharvest Biology and Technology, 2018, 145, 27-32.	6.0	11

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19	Metabolic constraints on Magnaporthe biotrophy: loss of de novo asparagine biosynthesis aborts invasive hyphal growth in the first infected rice cell. Microbiology (United Kingdom), 2018, 164, 1541-1546.	1.8	8
20	The Magnaporthe oryzae nitrooxidative stress response suppresses rice innate immunity during blast disease. Nature Microbiology, 2017, 2, 17054.	13.3	75
21	Glucose-ABL1-TOR Signaling Modulates Cell Cycle Tuning to Control Terminal Appressorial Cell Differentiation. PLoS Genetics, 2017, 13, e1006557.	3.5	58
22	GATA-Dependent Glutaminolysis Drives Appressorium Formation in Magnaporthe oryzae by Suppressing TOR Inhibition of cAMP/PKA Signaling. PLoS Pathogens, 2015, 11, e1004851.	4.7	95
23	Chromatin Immunoprecipitation (ChIP) Assay for Detecting Direct and Indirect Protein ï¿½ DNA Interactions in Magnaporthe oryzae. Bio-protocol, 2015, 5, .	0.4	5
24	Characterizing Roles for the Glutathione Reductase, Thioredoxin Reductase and Thioredoxin Peroxidase-Encoding Genes of Magnaporthe oryzae during Rice Blast Disease. PLoS ONE, 2014, 9, e87300.	2.5	61
25	Evidence for a Transketolase-Mediated Metabolic Checkpoint Governing Biotrophic Growth in Rice Cells by the Blast Fungus Magnaporthe oryzae. PLoS Pathogens, 2014, 10, e1004354.	4.7	57
26	Plant defence suppression is mediated by a fungal sirtuin during rice infection by <scp><i>M</i></scp><i>agnaporthe oryzae</i>. Molecular Microbiology, 2014, 94, 70-88.	2.5	59
27	Redox and rice blast: new tools for dissecting molecular fungalâ€"plant interactions. New Phytologist, 2014, 201, 367-369.	7.3	7
28	Mechanisms of Nutrient Acquisition and Utilization During Fungal Infections of Leaves. Annual Review of Phytopathology, 2014, 52, 155-174.	7.8	54
29	Cells in cells: morphogenetic and metabolic strategies conditioning rice infection by the blast fungus Magnaporthe oryzae. Protoplasma, 2014, 251, 37-47.	2.1	32
30	Glycogen Metabolic Genes Are Involved in Trehalose-6-Phosphate Synthase-Mediated Regulation of Pathogenicity by the Rice Blast Fungus Magnaporthe oryzae. PLoS Pathogens, 2013, 9, e1003604.	4.7	54
31	Growth in rice cells requires de novo purine biosynthesis by the blast fungus Magnaporthe oryzae. Scientific Reports, 2013, 3, 2398.	3.3	52
32	Principles of Carbon Catabolite Repression in the Rice Blast Fungus: Tps1, Nmr1-3, and a MATEâ€"Family Pump Regulate Glucose Metabolism during Infection. PLoS Genetics, 2012, 8, e1002673.	3.5	112
33	Towards Defining Nutrient Conditions Encountered by the Rice Blast Fungus during Host Infection. PLoS ONE, 2012, 7, e47392.	2.5	56
34	The sugar sensor, trehalose-6-phosphate synthase (Tps1), regulates primary and secondary metabolism during infection by the rice blast fungus: Will<i>Magnaporthe oryzae's</i>â€œsweet toothâ€•become its â€œAchillesâ€™ heelâ€?. Mycology, 2011, 2, 46-53.	4.4	25
35	Fungal Virulence and Development Is Regulated by Alternative Pre-mRNA 3â€²End Processing in Magnaporthe oryzae. PLoS Pathogens, 2011, 7, e1002441.	4.7	45
36	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.	7.1	130

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37	Under pressure: investigating the biology of plant infection by Magnaporthe oryzae. Nature Reviews Microbiology, 2009, 7, 185-195.	28.6	809
38	Fungal physiology â€“ a future perspective. Microbiology (United Kingdom), 2009, 155, 3810-3815.	1.8	37
39	Oxygenase Coordination Is Required for Morphological Transition and the Hostâ€“Fungus Interaction of<i>Aspergillus flavus</i>. Molecular Plant-Microbe Interactions, 2009, 22, 882-894.	2.6	84
40	Tps1 regulates the pentose phosphate pathway, nitrogen metabolism and fungal virulence. EMBO Journal, 2007, 26, 3673-3685.	7.8	165
41	Fundamental Contribution of Î²-Oxidation to Polyketide Mycotoxin Production In Planta. Molecular Plant-Microbe Interactions, 2005, 18, 783-793.	2.6	115
42	Two Î”9-stearic acid desaturases are required for Aspergillus nidulans growth and development. Fungal Genetics and Biology, 2004, 41, 501-509.	2.1	29
43	Relationship between Secondary Metabolism and Fungal Development. Microbiology and Molecular Biology Reviews, 2002, 66, 447-459.	6.6	865
44	Cultivar-Dependent Expression of a Maize Lipoxygenase Responsive to Seed Infesting Fungi. Molecular Plant-Microbe Interactions, 2001, 14, 980-987.	2.6	89
45	Mutational Analysis of AREA, a Transcriptional Activator Mediating Nitrogen Metabolite Repression in <i>Aspergillus nidulans</i> and a Member of the â€œStreetwiseâ€•GATA Family of Transcription Factors. Microbiology and Molecular Biology Reviews, 1998, 62, 586-596.	6.6	109