

Joe Win

List of Publications by Year in descending order

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76
papers

12,743
citations

41344

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74163

75
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all docs

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docs citations

89
times ranked

8874
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i> . Science Advances, 2022, 8, eabi5075.	10.3	9
2	Cleavage of a pathogen apoplastic protein by plant subtilases activates host immunity. New Phytologist, 2021, 229, 3424-3439.	7.3	24
3	Genomic rearrangements generate hypervariable mini-chromosomes in host-specific isolates of the blast fungus. PLoS Genetics, 2021, 17, e1009386.	3.5	46
4	Host-interactor screens of <i>Phytophthora infestans</i> RXLR proteins reveal vesicle trafficking as a major effector-targeted process. Plant Cell, 2021, 33, 1447-1471.	6.6	46
5	A single amino acid polymorphism in a conserved effector of the multihost blast fungus pathogen expands host-target binding spectrum. PLoS Pathogens, 2021, 17, e1009957.	4.7	32
6	Differential loss of effector genes in three recently expanded pandemic clonal lineages of the rice blast fungus. BMC Biology, 2020, 18, 88.	3.8	45
7	A Clone Resource of <i>Magnaporthe oryzae</i> Effectors That Share Sequence and Structural Similarities Across Host-Specific Lineages. Molecular Plant-Microbe Interactions, 2020, 33, 1032-1035.	2.6	20
8	Genome Sequences of Plant-Associated <i>Rhodococcus</i> sp. Isolates from Tunisia. Microbiology Resource Announcements, 2020, 9, .	0.6	2
9	Divergent Evolution of PcF/SCR74 Effectors in Oomycetes Is Associated with Distinct Recognition Patterns in Solanaceous Plants. MBio, 2020, 11, .	4.1	11
10	Extracellular proteolytic cascade in tomato activates immune protease Rcr3. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17409-17417.	7.1	55
11	Functional analysis of RXLR effectors from the New Zealand kauri dieback pathogen <i>Phytophthora agathidicida</i> . Molecular Plant Pathology, 2020, 21, 1131-1148.	4.2	13
12	A fungal substrate mimicking molecule suppresses plant immunity via an inter-kingdom conserved motif. Nature Communications, 2019, 10, 1576.	12.8	55
13	Cautionary Notes on Use of the MoT3 Diagnostic Assay for <i>Magnaporthe oryzae</i> Wheat and Rice Blast Isolates. Phytopathology, 2019, 109, 504-508.	2.2	23
14	An N-terminal motif in NLR immune receptors is functionally conserved across distantly related plant species. ELife, 2019, 8, .	6.0	162
15	A New Resistance Gene in Combination with <i>Rmg8</i> Confers Strong Resistance Against <i>Triticum</i> Isolates of <i>Pyricularia oryzae</i> in a Common Wheat Landrace. Phytopathology, 2018, 108, 1299-1306.	2.2	50
16	Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. Scientific Reports, 2017, 7, 482.	3.3	525
17	Protein-Protein Interaction Assays with Effector-GFP Fusions in <i>Nicotiana benthamiana</i> . Methods in Molecular Biology, 2017, 1659, 85-98.	0.9	8
18	Comparative secretome analysis of <i>Rhizoctonia solani</i> isolates with different host ranges reveals unique secretomes and cell death inducing effectors. Scientific Reports, 2017, 7, 10410.	3.3	62

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19	Genome analysis of the foxtail millet pathogen <i>Sclerospora graminicola</i> reveals the complex effector repertoire of gramincolous downy mildews. <i>BMC Genomics</i> , 2017, 18, 897.	2.8	27
20	An effector of the Irish potato famine pathogen antagonizes a host autophagy cargo receptor. <i>ELife</i> , 2016, 5, .	6.0	189
21	Heterologous Expression Screens in <i>Nicotiana benthamiana</i> Identify a Candidate Effector of the Wheat Yellow Rust Pathogen that Associates with Processing Bodies. <i>PLoS ONE</i> , 2016, 11, e0149035.	2.5	99
22	Rust fungal effectors mimic host transit peptides to translocate into chloroplasts. <i>Cellular Microbiology</i> , 2016, 18, 453-465.	2.1	90
23	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.	3.8	355
24	Genome analyses of the sunflower pathogen <i>Plasmopara halstedii</i> provide insights into effector evolution in downy mildews and <i>Phytophthora</i> . <i>BMC Genomics</i> , 2015, 16, 741.	2.8	135
25	A Recent Expansion of the RXLR Effector Gene <i>Avrblb2</i> Is Maintained in Global Populations of <i>Phytophthora infestans</i> Indicating Different Contributions to Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 901-912.	2.6	44
26	Candidate Effector Proteins of the Rust Pathogen <i>Melampsora larici-populina</i> Target Diverse Plant Cell Compartments. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 689-700.	2.6	172
27	<i>Phytophthora infestans</i> RXLR Effector PexRD2 Interacts with Host MAPKK μ to Suppress Plant Immune Signaling. <i>Plant Cell</i> , 2014, 26, 1345-1359.	6.6	188
28	Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. <i>PLoS Genetics</i> , 2014, 10, e1004078.	3.5	238
29	Antagonistic Regulation of Growth and Immunity by the Arabidopsis Basic Helix-Loop-Helix Transcription Factor HOMOLOG OF BRASSINOSTEROID ENHANCED EXPRESSION2 INTERACTING WITH INCREASED LEAF INCLINATION1 BINDING bHLH1. <i>Plant Physiology</i> , 2014, 164, 1443-1455.	4.8	117
30	The genome sequence and effector complement of the flax rust pathogen <i>Melampsora lini</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 98.	3.6	126
31	Effector Specialization in a Lineage of the Irish Potato Famine Pathogen. <i>Science</i> , 2014, 343, 552-555.	12.6	179
32	Two-Dimensional Data Binning for the Analysis of Genome Architecture in Filamentous Plant Pathogens and Other Eukaryotes. <i>Methods in Molecular Biology</i> , 2014, 1127, 29-51.	0.9	44
33	From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. <i>Genome Biology</i> , 2013, 14, 211.	8.8	64
34	Regulation of Transcription of Nucleotide-Binding Leucine-Rich Repeat-Encoding Genes SNC1 and RPP4 via H3K4 Trimethylation. <i>Plant Physiology</i> , 2013, 162, 1694-1705.	4.8	93
35	Large-Scale Gene Disruption in <i>Magnaporthe oryzae</i> Identifies MC69, a Secreted Protein Required for Infection by Monocot and Dicot Fungal Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002711.	4.7	150
36	Sequence Divergent RXLR Effectors Share a Structural Fold Conserved across Plant Pathogenic Oomycete Species. <i>PLoS Pathogens</i> , 2012, 8, e1002400.	4.7	153

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37	Host Protein BSL1 Associates with <i>Phytophthora infestans</i> RXLR Effector AVR2 and the <i>Solanum demissum</i> Immune Receptor R2 to Mediate Disease Resistance. <i>Plant Cell</i> , 2012, 24, 3420-3434.	6.6	130
38	Effector Biology of Plant-Associated Organisms: Concepts and Perspectives. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2012, 77, 235-247.	1.1	355
39	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	2.6	264
40	Using Hierarchical Clustering of Secreted Protein Families to Classify and Rank Candidate Effectors of Rust Fungi. <i>PLoS ONE</i> , 2012, 7, e29847.	2.5	235
41	Purification of Effector-Target Protein Complexes via Transient Expression in <i>Nicotiana benthamiana</i> . <i>Methods in Molecular Biology</i> , 2011, 712, 181-194.	0.9	90
42	<i>Phytophthora infestans</i> effector AVRblb2 prevents secretion of a plant immune protease at the haustorial interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20832-20837.	7.1	285
43	454 Genome Sequencing of <i>Pseudoperonospora cubensis</i> Reveals Effector Proteins with a QXLR Translocation Motif. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 543-553.	2.6	110
44	Structures of <i>Phytophthora</i> RXLR Effector Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 35834-35842.	3.4	178
45	Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of <i>Phytophthora infestans</i> . <i>BMC Genomics</i> , 2010, 11, 637.	2.8	188
46	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.	2.1	108
47	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 1015-1015.	2.1	11
48	An Effector-Targeted Protease Contributes to Defense against <i>Phytophthora infestans</i> and Is under Diversifying Selection in Natural Hosts. <i>Plant Physiology</i> , 2010, 154, 1794-1804.	4.8	166
49	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.	12.6	492
50	A Functional Genomics Approach Identifies Candidate Effectors from the Aphid Species <i>Myzus persicae</i> (Green Peach Aphid). <i>PLoS Genetics</i> , 2010, 6, e1001216.	3.5	397
51	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	9.6	391
52	Association Genetics Reveals Three Novel Avirulence Genes from the Rice Blast Fungal Pathogen <i>Magnaporthe oryzae</i> . <i>Plant Cell</i> , 2009, 21, 1573-1591.	6.6	410
53	In Planta Expression Screens of <i>Phytophthora infestans</i> RXLR Effectors Reveal Diverse Phenotypes, Including Activation of the <i>Solanum bulbocastanum</i> Disease Resistance Protein Rpi-blb2. <i>Plant Cell</i> , 2009, 21, 2928-2947.	6.6	376
54	Candidate effector gene identification in the ascomycete fungal phytopathogen <i>Venturia inaequalis</i> by expressed sequence tag analysis. <i>Molecular Plant Pathology</i> , 2009, 10, 431-448.	4.2	33

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55	Ten things to know about oomycete effectors. <i>Molecular Plant Pathology</i> , 2009, 10, 795-803.	4.2	185
56	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
57	Apoplastic effectors secreted by two unrelated eukaryotic plant pathogens target the tomato defense protease Rcr3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1654-1659.	7.1	260
58	Analysis of the <i>Pythium ultimum</i> transcriptome using Sanger and Pyrosequencing approaches. <i>BMC Genomics</i> , 2008, 9, 542.	2.8	78
59	Adaptive evolution has targeted the C-terminal domain of the RXLR effectors of plant pathogenic oomycetes. <i>Plant Signaling and Behavior</i> , 2008, 3, 251-253.	2.4	12
60	Structure of the Glucanase Inhibitor Protein (GIP) Family from <i>Phytophthora</i> Species Suggests Coevolution with Plant Endo- β -1,3-Glucanases. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 820-830.	2.6	101
61	Structure and Function of RXLR Effectors of Plant Pathogenic Oomycetes. , 2008, , 161-171.		1
62	A <i>Phytophthora infestans</i> Cystatin-Like Protein Targets a Novel Tomato Papain-Like Apoplastic Protease. <i>Plant Physiology</i> , 2007, 143, 364-377.	4.8	277
63	Adaptive Evolution Has Targeted the C-Terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes. <i>Plant Cell</i> , 2007, 19, 2349-2369.	6.6	315
64	A functional genetic assay for nuclear trafficking in plants. <i>Plant Journal</i> , 2007, 50, 149-158.	5.7	70
65	Oomycete genomics: new insights and future directions. <i>FEMS Microbiology Letters</i> , 2007, 274, 1-8.	1.8	79
66	<i>Phytophthora</i> Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.	12.6	1,059
67	Computational and comparative analyses of 150 full-length cDNA sequences from the oomycete plant pathogen <i>Phytophthora infestans</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 20-33.	2.1	65
68	The C-terminal half of <i>Phytophthora infestans</i> RXLR effector AVR3a is sufficient to trigger R3a-mediated hypersensitivity and suppress INF1-induced cell death in <i>Nicotiana benthamiana</i> . <i>Plant Journal</i> , 2006, 48, 165-176.	5.7	402
69	<i>Phytophthora</i> functional genomics database (PFGD): functional genomics of phytophthora-plant interactions. <i>Nucleic Acids Research</i> , 2006, 34, D465-D470.	14.5	20
70	The Malarial Host-Targeting Signal Is Conserved in the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2006, 2, e50.	4.7	189
71	Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene Family of <i>Phytophthora infestans</i> . <i>Molecular Biology and Evolution</i> , 2005, 22, 659-672.	8.9	140
72	Linking sequence to phenotype in <i>Phytophthora</i> -plant interactions. <i>Trends in Microbiology</i> , 2004, 12, 193-200.	7.7	65

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73	Characterisation of a protein from <i>Venturia inaequalis</i> that induces necrosis in <i>Malus</i> carrying the <i>Vm</i> resistance gene. <i>Physiological and Molecular Plant Pathology</i> , 2003, 62, 193-202.	2.5	32
74	Effects of cyanide and hypoxia on membrane currents in neurones acutely dissociated from the rostral ventrolateral medulla of the rat. <i>Brain Research</i> , 1999, 830, 246-257.	2.2	38
75	Detection of mRNA species in bulbospinal neurons isolated from the rostral ventrolateral medulla using single-cell RT-PCR. <i>Brain Research Protocols</i> , 1999, 4, 367-377.	1.6	27
76	O ₂ -sensitive K ⁺ current in undifferentiated and NGF-treated PC12 cell variants. <i>NeuroReport</i> , 1997, 8, 1369-1373.	1.2	3