

# Joe Win

## List of Publications by Year in descending order

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76  
papers

12,743  
citations

41344

49  
h-index

74163

75  
g-index

89  
all docs

89  
docs citations

89  
times ranked

8874  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | 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     |
| 2  | <i>Phytophthora</i> Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.   | 12.6 | 1,059     |
| 3  | Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. <i>Scientific Reports</i> , 2017, 7, 482.   | 3.3  | 525       |
| 4  | Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. <i>Science</i> , 2010, 330, 1549-1551.   | 12.6 | 492       |
| 5  | 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       |
| 6  | 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       |
| 7  | 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       |
| 8  | 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       |
| 9  | 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       |
| 10 | 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       |
| 11 | 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       |
| 12 | 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       |
| 13 | <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       |
| 14 | 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       |
| 15 | 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       |
| 16 | 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       |
| 17 | Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. <i>PLoS Genetics</i> , 2014, 10, e1004078.   | 3.5  | 238       |
| 18 | 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       |

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|----|--|------|-----------|
| 19 | The Malarial Host-Targeting Signal Is Conserved in the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2006, 2, e50.   | 4.7  | 189       |
| 20 | An effector of the Irish potato famine pathogen antagonizes a host autophagy cargo receptor. <i>ELife</i> , 2016, 5, .   | 6.0  | 189       |
| 21 | 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       |
| 22 | <i>Phytophthora infestans</i> RXLR Effector PexRD2 Interacts with Host MAPKKK1 to Suppress Plant Immune Signaling. <i>Plant Cell</i> , 2014, 26, 1345-1359.  | 6.6  | 188       |
| 23 | Ten things to know about oomycete effectors. <i>Molecular Plant Pathology</i> , 2009, 10, 795-803.   | 4.2  | 185       |
| 24 | Effector Specialization in a Lineage of the Irish Potato Famine Pathogen. <i>Science</i> , 2014, 343, 552-555.   | 12.6 | 179       |
| 25 | Structures of <i>Phytophthora</i> RXLR Effector Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 35834-35842.   | 3.4  | 178       |
| 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 | 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       |
| 28 | An N-terminal motif in NLR immune receptors is functionally conserved across distantly related plant species. <i>ELife</i> , 2019, 8, .  | 6.0  | 162       |
| 29 | Sequence Divergent RXLR Effectors Share a Structural Fold Conserved across Plant Pathogenic Oomycete Species. <i>PLoS Pathogens</i> , 2012, 8, e1002400.   | 4.7  | 153       |
| 30 | 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       |
| 31 | 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       |
| 32 | 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       |
| 33 | 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       |
| 34 | 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       |
| 35 | Antagonistic Regulation of Growth and Immunity by the <i>Arabidopsis</i> 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       |
| 36 | 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       |

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|----|--|------|-----------|
| 37 | Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.  | 2.1  | 108       |
| 38 | Structure of the Glucanase Inhibitor Protein (GIP) Family from <i>Phytophthora</i> Species Suggests Coevolution with Plant Endo- $\beta$ -1,3-Glucanases. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 820-830. | 2.6  | 101       |
| 39 | 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        |
| 40 | 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        |
| 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 | Rust fungal effectors mimic host transit peptides to translocate into chloroplasts. <i>Cellular Microbiology</i> , 2016, 18, 453-465.  | 2.1  | 90        |
| 43 | Oomycete genomics: new insights and future directions. <i>FEMS Microbiology Letters</i> , 2007, 274, 1-8.  | 1.8  | 79        |
| 44 | Analysis of the <i>Pythium ultimum</i> transcriptome using Sanger and Pyrosequencing approaches. <i>BMC Genomics</i> , 2008, 9, 542.   | 2.8  | 78        |
| 45 | A functional genetic assay for nuclear trafficking in plants. <i>Plant Journal</i> , 2007, 50, 149-158.  | 5.7  | 70        |
| 46 | Linking sequence to phenotype in <i>Phytophthora</i> plant interactions. <i>Trends in Microbiology</i> , 2004, 12, 193-200.  | 7.7  | 65        |
| 47 | 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        |
| 48 | From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. <i>Genome Biology</i> , 2013, 14, 211.  | 8.8  | 64        |
| 49 | Comparative secretome analysis of <i>Rhizoctonia solani</i> isolates with different host ranges reveals unique secretomes and cell death inducing effectors. <i>Scientific Reports</i> , 2017, 7, 10410.                   | 3.3  | 62        |
| 50 | A fungal substrate mimicking molecule suppresses plant immunity via an inter-kingdom conserved motif. <i>Nature Communications</i> , 2019, 10, 1576.   | 12.8 | 55        |
| 51 | Extracellular proteolytic cascade in tomato activates immune protease Rcr3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17409-17417.                               | 7.1  | 55        |
| 52 | 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. <i>Phytopathology</i> , 2018, 108, 1299-1306.    | 2.2  | 50        |
| 53 | Genomic rearrangements generate hypervariable mini-chromosomes in host-specific isolates of the blast fungus. <i>PLoS Genetics</i> , 2021, 17, e1009386.   | 3.5  | 46        |
| 54 | Host-interactor screens of <i>Phytophthora infestans</i> RXLR proteins reveal vesicle trafficking as a major effector-targeted process. <i>Plant Cell</i> , 2021, 33, 1447-1471.   | 6.6  | 46        |

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|----|--|------|-----------|
| 55 | Differential loss of effector genes in three recently expanded pandemic clonal lineages of the rice blast fungus. <i>BMC Biology</i> , 2020, 18, 88.   | 3.8  | 45        |
| 56 | 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        |
| 57 | 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        |
| 58 | Effects of cyanide and hypoxia on membrane currents in neurons acutely dissociated from the rostral ventrolateral medulla of the rat. <i>Brain Research</i> , 1999, 830, 246-257.  | 2.2  | 38        |
| 59 | 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        |
| 60 | 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        |
| 61 | A single amino acid polymorphism in a conserved effector of the multihost blast fungus pathogen expands host-target binding spectrum. <i>PLoS Pathogens</i> , 2021, 17, e1009957.  | 4.7  | 32        |
| 62 | Detection of mRNA species in bulbospinal neurons isolated from the rostral ventrolateral medulla using single-cell RT-qPCR. <i>Brain Research Protocols</i> , 1999, 4, 367-377.  | 1.6  | 27        |
| 63 | Genome analysis of the foxtail millet pathogen <i>Sclerospora graminicola</i> reveals the complex effector repertoire of graminicolous downy mildews. <i>BMC Genomics</i> , 2017, 18, 897.   | 2.8  | 27        |
| 64 | Cleavage of a pathogen apoplastic protein by plant subtilases activates host immunity. <i>New Phytologist</i> , 2021, 229, 3424-3439.  | 7.3  | 24        |
| 65 | Cautionary Notes on Use of the MoT3 Diagnostic Assay for <i>Magnaporthe oryzae</i> Wheat and Rice Blast Isolates. <i>Phytopathology</i> , 2019, 109, 504-508.  | 2.2  | 23        |
| 66 | <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        |
| 67 | A Clone Resource of <i>Magnaporthe oryzae</i> Effectors That Share Sequence and Structural Similarities Across Host-Specific Lineages. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1032-1035.  | 2.6  | 20        |
| 68 | Functional analysis of RXLR effectors from the New Zealand kauri dieback pathogen <i>Phytophthora agathidicida</i> . <i>Molecular Plant Pathology</i> , 2020, 21, 1131-1148.   | 4.2  | 13        |
| 69 | 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        |
| 70 | Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 1015-1015.  | 2.1  | 11        |
| 71 | Divergent Evolution of PcF/SCR74 Effectors in Oomycetes Is Associated with Distinct Recognition Patterns in Solanaceous Plants. <i>MBio</i> , 2020, 11, .  | 4.1  | 11        |
| 72 | Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i> . <i>Science Advances</i> , 2022, 8, eabi5075.   | 10.3 | 9         |

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| 73 | Protein-Protein Interaction Assays with Effector-GFP Fusions in <i>Nicotiana benthamiana</i> . <i>Methods in Molecular Biology</i> , 2017, 1659, 85-98. | 0.9 | 8         |
| 74 | O <sub>2</sub> -sensitive K <sup>+</sup> current in undifferentiated and NGF-treated PC12 cell variants. <i>NeuroReport</i> , 1997, 8, 1369-1373.       | 1.2 | 3         |
| 75 | Genome Sequences of Plant-Associated <i>Rhodococcus</i> sp. Isolates from Tunisia. <i>Microbiology Resource Announcements</i> , 2020, 9, .              | 0.6 | 2         |
| 76 | Structure and Function of RXLR Effectors of Plant Pathogenic Oomycetes. , 2008, , 161-171.  |     | 1         |