Richard P Oliver

List of Publications by Year
in descending order

81 papers	6,787 citations	81900 39 h-index	66911 78 g-index
84 all docs	84 docs citations	84 times ranked	4881 citing authors

#	Article	IF	Citations
1	Emergence of a new disease as a result of interspecific virulence gene transfer. Nature Genetics, 2006, 38, 953-956.	21.4	667
2	Effector diversification within compartments of the Leptosphaeria maculans genome affected by Repeat-Induced Point mutations. Nature Communications, 2011, 2, 202.	12.8	481
3	A unique wheat disease resistance-like gene governs effector-triggered susceptibility to necrotrophic pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13544-13549.	7.1	450
4	Effectors as Tools in Disease Resistance Breeding Against Biotrophic, Hemibiotrophic, and Necrotrophic Plant Pathogens. Molecular Plant-Microbe Interactions, 2014, 27, 196-206.	2.6	363
5	Host-specific toxins: effectors of necrotrophic pathogenicity. Cellular Microbiology, 2008, 10, 1421-1428.	2.1	275
6	Arabidopsis pathology breathes new life into the necrotrophs-vs.-biotrophs classification of fungal pathogens. Molecular Plant Pathology, 2004, 5, 347-352.	4.2	238
7	Dothideomyceteâ€"Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i>. Plant Cell, 2007, 19, 3347-3368.	6.6	235
8	The Cysteine Rich Necrotrophic Effector SnTox1 Produced by Stagonospora nodorum Triggers Susceptibility of Wheat Lines Harboring Snn1. PLoS Pathogens, 2012, 8, e1002467.	4.7	233
9	The Complete Genome Sequence of the Phytopathogenic Fungus Sclerotinia sclerotiorum Reveals Insights into the Genome Architecture of Broad Host Range Pathogens. Genome Biology and Evolution, 2017, 9, 593-618.	2.5	187
10	SnTox3 Acts in Effector Triggered Susceptibility to Induce Disease on Wheat Carrying the Snn3 Gene. PLoS Pathogens, 2009, 5, e1000581.	4.7	175
11	Comparative Genomics of a Plant-Pathogenic Fungus,<i>Pyrenophora tritici-repentis</i>, Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. G3: Genes, Genomes, Genetics, 2013, 3, 41-63.	1.8	167
12	Evolution of Linked Avirulence Effectors in Leptosphaeria maculans Is Affected by Genomic Environment and Exposure to Resistance Genes in Host Plants. PLoS Pathogens, 2010, 6, e1001180.	4.7	158
13	CodingQuarry: highly accurate hidden Markov model gene prediction in fungal genomes using RNA-seq transcripts. BMC Genomics, 2015, 16, 170.	2.8	158
14	RIPCAL: a tool for alignment-based analysis of repeat-induced point mutations in fungal genomic sequences. BMC Bioinformatics, 2008, 9, 478.	2.6	151
15	Governing Principles Can Guide Fungicide-Resistance Management Tactics. Annual Review of Phytopathology, 2014, 52, 175-195.	7.8	150
16	Characterization of the Interaction of a Novel <i>Stagonospora nodorum</i> Host-Selective Toxin with a Wheat Susceptibility Gene. Plant Physiology, 2008, 146, 323-324.	4.8	149
17	OcculterCut: A Comprehensive Survey of AT-Rich Regions in Fungal Genomes. Genome Biology and Evolution, 2016, 8, 2044-2064.	2.5	123
18	Global diversity and distribution of three necrotrophic effectors in <i>Phaeosphaeria nodorum</i> and related species. New Phytologist, 2013, 199, 241-251.	7.3	101

#	ARTICLE	IF	CITATIONS
19	CfT-I: an LTR-retrotransposon in Cladosporium fulvum, a fungal pathogen of tomato. Molecular Genetics and Genomics, 1992, 233, 337-347.	2.4	98
20	Mixtures as a Fungicide Resistance Management Tactic. Phytopathology, 2014, 104, 1264-1273.	2.2	83
21	Proteinaceous necrotrophic effectors in fungal virulence. Functional Plant Biology, 2010, 37, 907.	2.1	80
22	Proposal for a unified nomenclature for targetâ€site mutations associated with resistance to fungicides. Pest Management Science, 2016, 72, 1449-1459.	3.4	76
23	Differential effector gene expression underpins epistasis in a plant fungal disease. Plant Journal, 2016, 87, 343-354.	5.7	75
24	Regulation of proteinaceous effector expression in phytopathogenic fungi. PLoS Pathogens, 2017, 13, e1006241.	4.7	75
25	Demethylase Inhibitor Fungicide Resistance in Pyrenophora teres f. sp. teres Associated with Target Site Modification and Inducible Overexpression of Cyp51. Frontiers in Microbiology, 2016, 7, 1279.	3.5	74
26	A reassessment of the risk of rust fungi developing resistance to fungicides. Pest Management Science, 2014, 70, 1641-1645.	3.4	71
27	Quantitative Variation in Effector Activity of ToxA Isoforms from <i>Stagonospora nodorum</i> and <i>Pyrenophora tritici-repentis</i>. Molecular Plant-Microbe Interactions, 2012, 25, 515-522.	2.6	70
28	A functionally conserved Zn₂Cys₆ binuclear cluster transcription factor class regulates necrotrophic effector gene expression and hostâ€specific virulence of two major Pleosporales fungal pathogens of wheat. Molecular Plant Pathology, 2017, 18, 420-434.	4.2	69
29	Resequencing and Comparative Genomics of <i>Stagonospora nodorum</i>: Sectional Gene Absence and Effector Discovery. G3: Genes, Genomes, Genetics, 2013, 3, 959-969.	1.8	66
30	Comparative genomics of the wheat fungal pathogen Pyrenophora tritici-repentis reveals chromosomal variations and genome plasticity. BMC Genomics, 2018, 19, 279.	2.8	56
31	An <i>In Planta</i> -Expressed Polyketide Synthase Produces (<i>R</i>)-Mellein in the Wheat Pathogen Parastagonospora nodorum. Applied and Environmental Microbiology, 2015, 81, 177-186.	3.1	54
32	Mannitol 1-Phosphate Metabolism Is Required for Sporulation in Planta of the Wheat Pathogen Stagonospora nodorum. Molecular Plant-Microbe Interactions, 2005, 18, 110-115.	2.6	53
33	Novel sources of resistance to Septoria nodorum blotch in the Vavilov wheat collection identified by genome-wide association studies. Theoretical and Applied Genetics, 2018, 131, 1223-1238.	3.6	53
34	A quantitative PCR approach to determine gene copy number. Fungal Genetics Reports, 2008, 55, 5-8.	0.6	53
35	Transcription factor control of virulence in phytopathogenic fungi. Molecular Plant Pathology, 2021, 22, 858-881.	4.2	50
36	Metabolite profiling identifies the mycotoxin alternariol in the pathogen Stagonospora nodorum. Metabolomics, 2009, 5, 330-335.	3.0	48

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37	Assessing European Wheat Sensitivities to Parastagonospora nodorum Necrotrophic Effectors and Fine-Mapping the Snn3-B1 Locus Conferring Sensitivity to the Effector SnTox3. Frontiers in Plant Science, 2018, 9, 881.	3.6	48
38	Comprehensive Annotation of the Parastagonospora nodorum Reference Genome Using Next-Generation Genomics, Transcriptomics and Proteogenomics. PLoS ONE, 2016, 11, e0147221.	2.5	47
39	The isolation of Ant1, a transposable element from Aspergillus niger. Molecular Genetics and Genomics, 1995, 249, 432-438.	2.4	46
40	Structural Characterisation of the Interaction between Triticum aestivum and the Dothideomycete Pathogen Stagonospora nodorum. European Journal of Plant Pathology, 2006, 114, 275-282.	1.7	46
41	A Signaling-Regulated, Short-Chain Dehydrogenase of <i>Stagonospora nodorum</i> Regulates Asexual Development. Eukaryotic Cell, 2008, 7, 1916-1929.	3.4	45
42	Generation of a ToxA knockout strain of the wheat tan spot pathogen P yrenophora triticiâ€‐repentis. Molecular Plant Pathology, 2014, 15, 918-926.	4.2	45
43	Pan-Parastagonospora Comparative Genome Analysisâ€"Effector Prediction and Genome Evolution. Genome Biology and Evolution, 2018, 10, 2443-2457.	2.5	43
44	The Medicago truncatula reference accession A17 has an aberrant chromosomal configuration. New Phytologist, 2007, 174, 299-303.	7.3	42
45	â€œCATAStrophy,â€•a Genome-Informed Trophic Classification of Filamentous Plant Pathogens â€" How Many Different Types of Filamentous Plant Pathogens Are There?. Frontiers in Microbiology, 2019, 10, 3088.	3.5	41
46	Pulsed field gel electrophoresis reveals chromosome length differences between strains of Cladosporium fulvum (syn. Fulvia fulva). Molecular Genetics and Genomics, 1991, 229, 267-272.	2.4	40
47	Fine-Mapping the Wheat <i>Snn1</i> Locus Conferring Sensitivity to the <i>Parastagonospora nodorum</i> Necrotrophic Effector SnTox1 Using an Eight Founder Multiparent Advanced Generation Inter-Cross Population. G3: Genes, Genomes, Genetics, 2015, 5, 2257-2266.	1.8	38
48	Cloning and characterisation of telomeric DNA from Cladosporium fulvum. Gene, 1993, 132, 67-73.	2.2	37
49	Sensitivity to three Parastagonospora nodorum necrotrophic effectors in current Australian wheat cultivars and the presence of further fungal effectors. Crop and Pasture Science, 2014, 65, 150.	1.5	37
50	Codon optimization underpins generalist parasitism in fungi. ELife, 2017, 6, .	6.0	36
51	Genomic tillage and the harvest of fungal phytopathogens. New Phytologist, 2012, 196, 1015-1023.	7.3	34
52	A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle on wheat. Scientific Reports, 2019, 9, 15884.	3.3	34
53	Functional redundancy of necrotrophic effectors â€" consequences for exploitation for breeding. Frontiers in Plant Science, 2015, 6, 501.	3.6	33
54	Genetic analysis of wheat sensitivity to the ToxB fungal effector from Pyrenophora tritici-repentis, the causal agent of tan spot. Theoretical and Applied Genetics, 2020, 133, 935-950.	3.6	31

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55	High frequency of fungicide resistanceâ€associated mutations in the wheat yellow rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i>. Pest Management Science, 2021, 77, 3358-3371.	3.4	30
56	Heterologous Expression of the Pyrenophora tritici-repentis Effector Proteins ToxA and ToxB, and the Prevalence of Effector Sensitivity in Australian Cereal Crops. Frontiers in Microbiology, 2019, 10, 182.	3.5	28
57	Transformation frequencies are enhanced and vector DNA is targeted during retransformation of Leptosphaeria maculans, a fungal plant pathogen. Molecular Genetics and Genomics, 1992, 231, 243-247.	2.4	24
58	Improved Detection and Monitoring of Fungicide Resistance in Blumeria graminis f. sp. hordei With High-Throughput Genotype Quantification by Digital PCR. Frontiers in Microbiology, 2018, 9, 706.	3.5	24
59	Septoria Nodorum Blotch of Wheat: Disease Management and Resistance Breeding in the Face of Shifting Disease Dynamics and a Changing Environment. Phytopathology, 2021, 111, 906-920.	2.2	24
60	Genomeâ€Wide Association Mapping of Resistance to Septoria Nodorum Leaf Blotch in a Nordic Spring Wheat Collection. Plant Genome, 2019, 12, 180105.	2.8	22
61	Fungicide resistance characterized across seven modes of action in <i>Botrytis cinerea</i> isolated from Australian vineyards. Pest Management Science, 2022, 78, 1326-1340.	3.4	21
62	Inheritance and alteration of transforming DNA during an induced parasexual cycle in the imperfect fungus Cladosporium fulvum. Current Genetics, 1993, 23, 508-511.	1.7	19
63	Overview of genomic and bioinformatic resources for Zymoseptoria tritici. Fungal Genetics and Biology, 2015, 79, 13-16.	2.1	17
64	Analysis of mutations in West Australian populations of <i>Blumeria graminis</i> f. sp. <i>hordei CYP51</i> conferring resistance to DMI fungicides. Pest Management Science, 2020, 76, 1265-1272.	3.4	17
65	Genomic distribution of a novel Pyrenophora tritici-repentis ToxA insertion element. PLoS ONE, 2018, 13, e0206586.	2.5	16
66	Low Amplitude Boom-and-Bust Cycles Define the Septoria Nodorum Blotch Interaction. Frontiers in Plant Science, 2019, 10, 1785.	3.6	16
67	Rapid in situ quantification of the strobilurin resistance mutation G143A in the wheat pathogen Blumeria graminis f. sp. tritici. Scientific Reports, 2021, 11, 4526.	3.3	16
68	Reference Genome Assembly for Australian<i>Ascochyta rabiei</i>Isolate ArME14. G3: Genes, Genomes, Genetics, 2020, 10, 2131-2140.	1.8	15
69	Dissecting the role of G-protein signalling in primary metabolism in the wheat pathogen Stagonospora nodorum. Microbiology (United Kingdom), 2013, 159, 1972-1985.	1.8	14
70	Fungal Plant Pathogenesis Mediated by Effectors. Microbiology Spectrum, 2016, 4, .	3.0	12
71	The identification and deletion of the polyketide synthaseâ€nonribosomal peptide synthase gene responsible for the production of the phytotoxic triticone A/B in the wheat fungal pathogen Pyrenophora triticiâ€repentis. Environmental Microbiology, 2019, 21, 4875-4886.	3.8	12
72	Adult resistance genes to barley powdery mildew confer basal penetration resistance associated with broadâ€spectrum resistance. Plant Genome, 2021, 14, e20129.	2.8	12

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73	Î´-Aminolaevulinic acid synthesis is required for virulence of the wheat pathogen Stagonospora nodorum. Microbiology (United Kingdom), 2006, 152, 1533-1538.	1.8	11
74	Dissecting the role of histidine kinase and HOG1 mitogen-activated protein kinase signalling in stress tolerance and pathogenicity of Parastagonospora nodorum on wheat. Microbiology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 697 T	1.8	9
75	Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat. PLoS Pathogens, 2022, 18, e1010149.	4.7	9
76	Evaluation of a Multilocus Indel DNA Region for the Detection of the Wheat Tan Spot Pathogen Pyrenophora tritici-repentis. Plant Disease, 2016, 100, 2215-2225.	1.4	8
77	The rise of necrotrophic effectors. New Phytologist, 2022, 233, 11-14.	7.3	7
78	The novel avirulence effector AlAvr1 from <i>Ascochyta lentis</i> mediates host cultivar specificity of ascochyta blight in lentil. Molecular Plant Pathology, 2022, , .	4.2	5
79	Globalizing plant health. Plant Pathology, 2022, 71, 226-235.	2.4	3
80	Fungal Plant Pathogenesis Mediated by Effectors. , 0, , 767-785.		1
81	Plant Health in a One Health context Special Issue. Plant Pathology, 2022, 71, 3-4.	2.4	0