

Paul R J Birch

List of Publications by Year in descending order

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136
papers

14,318
citations

18465

62
h-index

21521

114
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140
all docs

140
docs citations

140
times ranked

9328
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.	13.7	1,405
2	A translocation signal for delivery of oomycete effector proteins into host plant cells. <i>Nature</i> , 2007, 450, 115-118.	13.7	760
3	The Top 10 oomycete pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2015, 16, 413-434.	2.0	695
4	Differential Recognition of Highly Divergent Downy Mildew Avirulence Gene Alleles by RPP1 Resistance Genes from Two Arabidopsis Lines. <i>Plant Cell</i> , 2005, 17, 1839-1850.	3.1	416
5	An ancestral oomycete locus contains late blight avirulence gene <i>Avr3a</i> , encoding a protein that is recognized in the host cytoplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7766-7771.	3.3	414
6	<i>Phytophthora infestans</i> effector AVR3a is essential for virulence and manipulates plant immunity by stabilizing host E3 ligase CMPG1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9909-9914.	3.3	412
7	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.	2.8	402
8	Genome sequence of the enterobacterial phytopathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> and characterization of virulence factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11105-11110.	3.3	366
9	Soft rot erwiniae: from genes to genomes. <i>Molecular Plant Pathology</i> , 2003, 4, 17-30.	2.0	354
10	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2012, 8, e1002940.	2.1	321
11	Crops that feed the world 8: Potato: are the trends of increased global production sustainable?. <i>Food Security</i> , 2012, 4, 477-508.	2.4	295
12	Trafficking arms: oomycete effectors enter host plant cells. <i>Trends in Microbiology</i> , 2006, 14, 8-11.	3.5	278
13	Five Reasons to Consider <i>Phytophthora infestans</i> a Reemerging Pathogen. <i>Phytopathology</i> , 2015, 105, 966-981.	1.1	254
14	Quorum Sensing Coordinates Brute Force and Stealth Modes of Infection in the Plant Pathogen <i>Pectobacterium atrosepticum</i> . <i>PLoS Pathogens</i> , 2008, 4, e1000093.	2.1	216
15	An RxLR Effector from <i>Phytophthora infestans</i> Prevents Re-localisation of Two Plant NAC Transcription Factors from the Endoplasmic Reticulum to the Nucleus. <i>PLoS Pathogens</i> , 2013, 9, e1003670.	2.1	210
16	<i>Phytophthora infestans</i> RXLR Effector PexRD2 Interacts with Host MAPKKK1μ to Suppress Plant Immune Signaling. <i>Plant Cell</i> , 2014, 26, 1345-1359.	3.1	188
17	Exploiting Knowledge of <i>R/Avr</i> Genes to Rapidly Clone a New LZ-NBS-LRR Family of Late Blight Resistance Genes from Potato Linkage Group IV. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 630-641.	1.4	181
18	Potato Virus X-Induced Gene Silencing in Leaves and Tubers of Potato. <i>Plant Physiology</i> , 2004, 134, 1308-1316.	2.3	160

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19	Large-Scale Gene Discovery in the Oomycete <i>Phytophthora infestans</i> Reveals Likely Components of Phytopathogenicity Shared with True Fungi. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 229-243.	1.4	160
20	Oomycete RXLR effectors: delivery, functional redundancy and durable disease resistance. <i>Current Opinion in Plant Biology</i> , 2008, 11, 373-379.	3.5	157
21	Involvement of cathepsin B in the plant disease resistance hypersensitive response. <i>Plant Journal</i> , 2007, 52, 1-13.	2.8	147
22	The <i>Phytophthora infestans</i> Avirulence Gene <i>Avr4</i> Encodes an RXLR-dEER Effector. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1460-1470.	1.4	144
23	A Potato Gene Encoding a WRKY-like Transcription Factor Is Induced in Interactions with <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> and <i>Phytophthora infestans</i> and Is Coregulated with Class I Endochitinase Expression. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 1092-1101.	1.4	142
24	CMPG1-dependent cell death follows perception of diverse pathogen elicitors at the host plasma membrane and is suppressed by <i>Phytophthora infestans</i> RXLR effector AVR3a. <i>New Phytologist</i> , 2011, 190, 653-666.	3.5	142
25	Presence/absence, differential expression and sequence polymorphisms between <i>PiAVR2</i> and <i>PiAVR2</i> -like in <i>Phytophthora infestans</i> determine virulence on <i>R2</i> plants. <i>New Phytologist</i> , 2011, 191, 763-776.	3.5	142
26	Patterns of Diversifying Selection in the Phytotoxin-like <i>scr74</i> Gene Family of <i>Phytophthora infestans</i> . <i>Molecular Biology and Evolution</i> , 2005, 22, 659-672.	3.5	140
27	Comparative Genomics Reveals What Makes An Enterobacterial Plant Pathogen. <i>Annual Review of Phytopathology</i> , 2006, 44, 305-336.	3.5	138
28	Molecular effects of resistance elicitors from biological origin and their potential for crop protection. <i>Frontiers in Plant Science</i> , 2014, 5, 655.	1.7	138
29	The zigzag in oomycete-plant interactions. <i>Molecular Plant Pathology</i> , 2009, 10, 547-562.	2.0	136
30	Cellulose Synthesis in <i>Phytophthora infestans</i> Is Required for Normal Appressorium Formation and Successful Infection of Potato. <i>Plant Cell</i> , 2008, 20, 720-738.	3.1	133
31	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.	3.1	130
32	Analysis of the <i>Pantoea ananatis</i> pan-genome reveals factors underlying its ability to colonize and interact with plant, insect and vertebrate hosts. <i>BMC Genomics</i> , 2014, 15, 404.	1.2	127
33	A <i>Phytophthora infestans</i> RXLR effector targets plant PP1c isoforms that promote late blight disease. <i>Nature Communications</i> , 2016, 7, 10311.	5.8	123
34	Delivery of cytoplasmic and apoplastic effectors from <i>Phytophthora infestans</i> haustoria by distinct secretion pathways. <i>New Phytologist</i> , 2017, 216, 205-215.	3.5	121
35	Rotting softly and stealthily. <i>Current Opinion in Plant Biology</i> , 2005, 8, 424-429.	3.5	119
36	Functionally Redundant RXLR Effectors from <i>Phytophthora infestans</i> Act at Different Steps to Suppress Early flg22-Triggered Immunity. <i>PLoS Pathogens</i> , 2014, 10, e1004057.	2.1	115

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37	Genome Sequence of the Plant-Pathogenic Bacterium <i>Dickeya dadantii</i> 3937. <i>Journal of Bacteriology</i> , 2011, 193, 2076-2077.	1.0	113
38	Elevated amino acid biosynthesis in <i>Phytophthora infestans</i> during appressorium formation and potato infection. <i>Fungal Genetics and Biology</i> , 2005, 42, 244-256.	0.9	110
39	The cell biology of late blight disease. <i>Current Opinion in Microbiology</i> , 2016, 34, 127-135.	2.3	106
40	Gene Expression Profiling During Asexual Development of the Late Blight Pathogen <i>Phytophthora infestans</i> Reveals a Highly Dynamic Transcriptome. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 433-447.	1.4	105
41	Tolerance in banana to <i>Fusarium</i> wilt is associated with early up-regulation of cell wall-strengthening genes in the roots. <i>Molecular Plant Pathology</i> , 2007, 8, 333-341.	2.0	99
42	Functional redundancy in the <i>Arabidopsis</i> Cathepsin B gene family contributes to basal defence, the hypersensitive response and senescence. <i>New Phytologist</i> , 2009, 183, 408-418.	3.5	99
43	<i>Phytophthora infestans</i> RXLR effector AVR1 interacts with exocyst component Sec5 to manipulate plant immunity. <i>Plant Physiology</i> , 2015, 169, pp.01169.2015.	2.3	95
44	<i>Plasmodium falciparum</i> and <i>Hyaloperonospora parasitica</i> effector translocation motifs are functional in <i>Phytophthora infestans</i> . <i>Microbiology (United Kingdom)</i> , 2008, 154, 3743-3751.	0.7	94
45	Profiling and quantifying differential gene transcription in <i>Phytophthora infestans</i> prior to and during the early stages of potato infection. <i>Fungal Genetics and Biology</i> , 2003, 40, 4-14.	0.9	92
46	Towards understanding the virulence functions of RXLR effectors of the oomycete plant pathogen <i>Phytophthora infestans</i> . <i>Journal of Experimental Botany</i> , 2009, 60, 1133-1140.	2.4	92
47	All Roads Lead to Susceptibility: The Many Modes of Action of Fungal and Oomycete Intracellular Effectors. <i>Plant Communications</i> , 2020, 1, 100050.	3.6	90
48	Isolation of Potato Genes That Are Induced During an Early Stage of the Hypersensitive Response to <i>Phytophthora infestans</i> . <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 356-361.	1.4	88
49	A novel <i>Phytophthora infestans</i> haustorium-specific membrane protein is required for infection of potato. <i>Cellular Microbiology</i> , 2008, 10, 2271-2284.	1.1	87
50	GenomeDiagram: a python package for the visualization of large-scale genomic data. <i>Bioinformatics</i> , 2006, 22, 616-617.	1.8	83
51	RXLR Effector AVR2 Up-Regulates a Brassinosteroid-Responsive bHLH Transcription Factor to Suppress Immunity. <i>Plant Physiology</i> , 2017, 174, 356-369.	2.3	82
52	Novel Quorum-Sensing-Controlled Genes in <i>Erwinia carotovora</i> subsp. <i>carotovora</i> : Identification of a Fungal Elicitor Homologue in a Soft-Rotting Bacterium. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 343-353.	1.4	81
53	A Cysteine Protease Gene Is Expressed Early in Resistant Potato Interactions with <i>Phytophthora infestans</i> . <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 1114-1119.	1.4	79
54	Host-targeting protein 1 (SpHtp1) from the oomycete <i>Saprolegnia parasitica</i> translocates specifically into fish cells in a tyrosine-O-sulphate-dependent manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2096-2101.	3.3	79

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55	Relocalization of Late Blight Resistance Protein R3a to Endosomal Compartments Is Associated with Effector Recognition and Required for the Immune Response. <i>Plant Cell</i> , 2013, 24, 5142-5158.	3.1	77
56	Genome Sequence of <i>Pantoea ananatis</i> LMG20103, the Causative Agent of Eucalyptus Blight and Dieback. <i>Journal of Bacteriology</i> , 2010, 192, 2936-2937.	1.0	75
57	Identification of a New Quorum-Sensing-Controlled Virulence Factor in <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> Secreted via the Type II Targeting Pathway. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 334-342.	1.4	73
58	Use of a Pooled Transposon Mutation Grid to Demonstrate Roles in Disease Development for <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> Putative Type III Secreted Effector (DspE/A) and Helper (HrpN) Proteins. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 943-950.	1.4	72
59	Potato NPH3/RPT2-Like Protein StNRL1, Targeted by a <i>Phytophthora infestans</i> RXLR Effector, Is a Susceptibility Factor. <i>Plant Physiology</i> , 2016, 171, 645-657.	2.3	71
60	<i>Phytophthora infestans</i> enters the genomics era. <i>Molecular Plant Pathology</i> , 2001, 2, 257-263.	2.0	70
61	Sequence diversity in the large subunit of <i>RNA</i> polymerase <i>1</i> contributes to <i>Mefenoxam</i> insensitivity in <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2014, 15, 664-676.	2.0	69
62	Utilizing <i>Omics</i> Technologies to Identify and Prioritize Novel Sources of Resistance to the Oomycete Pathogen <i>Phytophthora infestans</i> in Potato Germplasm Collections. <i>Frontiers in Plant Science</i> , 2016, 7, 672.	1.7	69
63	<i>Phytophthora infestans</i> RXLR effectors act in concert at diverse subcellular locations to enhance host colonization. <i>Journal of Experimental Botany</i> , 2019, 70, 343-356.	2.4	66
64	Phenotypic and genotypic diversity of <i>Phytophthora infestans</i> populations in Scotland (1995-97). <i>Plant Pathology</i> , 2003, 52, 181-192.	1.2	65
65	A systems biology perspective on plant-microbe interactions: Biochemical and structural targets of pathogen effectors. <i>Plant Science</i> , 2011, 180, 584-603.	1.7	65
66	The zigzag model of plant-microbe interactions: is it time to move on?. <i>Molecular Plant Pathology</i> , 2014, 15, 865-870.	2.0	64
67	Progress in Mapping and Cloning Qualitative and Quantitative Resistance Against <i>Phytophthora infestans</i> in Potato and Its Wild Relatives. <i>Potato Research</i> , 2009, 52, 215-227.	1.2	62
68	ADS1 encodes a MATE-transporter that negatively regulates plant disease resistance. <i>New Phytologist</i> , 2011, 192, 471-482.	3.5	62
69	A Host KH RNA-Binding Protein Is a Susceptibility Factor Targeted by an RXLR Effector to Promote Late Blight Disease. <i>Molecular Plant</i> , 2015, 8, 1385-1395.	3.9	62
70	The Potato MAP3K StVIK Is Required for the <i>Phytophthora infestans</i> RXLR Effector Pi17316 to Promote Disease. <i>Plant Physiology</i> , 2018, 177, 398-410.	2.3	61
71	Activation tagging in plants: a tool for gene discovery. <i>Functional and Integrative Genomics</i> , 2004, 4, 258-66.	1.4	59
72	Lignocellulose degradation by <i>Phanerochaete chrysosporium</i> : gene families and gene expression for a complex process. <i>Molecular Microbiology</i> , 1996, 19, 923-932.	1.2	55

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73	A new proteinaceous pathogen-associated molecular pattern (<scp>PAMP</scp>) identified in Ascomycete fungi induces cell death in Solanaceae. <i>New Phytologist</i> , 2017, 214, 1657-1672.	3.5	55
74	Plant pathogen effector utilizes host susceptibility factor NRL1 to degrade the immune regulator SWAP70. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7834-E7843.	3.3	55
75	The <i>Phytophthora infestans</i> Haustorium Is a Site for Secretion of Diverse Classes of Infection-Associated Proteins. <i>MBio</i> , 2018, 9, .	1.8	54
76	Intraspecific comparative genomics to identify avirulence genes from <i>Phytophthora</i> . <i>New Phytologist</i> , 2003, 159, 63-72.	3.5	50
77	Potato oxysterol binding protein and cathepsin B are rapidly up-regulated in independent defence pathways that distinguish R gene-mediated and field resistances to <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2004, 5, 45-56.	2.0	50
78	Bacterial chemoattraction towards jasmonate plays a role in the entry of <i>Dickeya dadantii</i> through wounded tissues. <i>Molecular Microbiology</i> , 2009, 74, 662-671.	1.2	50
79	The <i>Erwinia chrysanthemi</i> 3937 PhoQ Sensor Kinase Regulates Several Virulence Determinants. <i>Journal of Bacteriology</i> , 2006, 188, 3088-3098.	1.0	48
80	Genome-wide identification of potato long intergenic noncoding RNAs responsive to <i>Pectobacterium carotovorum</i> subspecies <i>brasiliense</i> infection. <i>BMC Genomics</i> , 2016, 17, 614.	1.2	48
81	Devastating intimacy: the cell biology of plant- <i>Phytophthora</i> interactions. <i>New Phytologist</i> , 2020, 228, 445-458.	3.5	48
82	U-box E3 ubiquitin ligase PUB17 acts in the nucleus to promote specific immune pathways triggered by <i>Phytophthora infestans</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 3189-3199.	2.4	47
83	Detection of the Virulent Form of AVR3a from <i>Phytophthora infestans</i> following Artificial Evolution of Potato Resistance Gene R3a. <i>PLoS ONE</i> , 2014, 9, e110158.	1.1	45
84	Effector gene birth in plant parasitic nematodes: Neofunctionalization of a housekeeping glutathione synthetase gene. <i>PLoS Genetics</i> , 2018, 14, e1007310.	1.5	44
85	Efflux Pump Gene Expression in <i>Erwinia chrysanthemi</i> Is Induced by Exposure to Phenolic Acids. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 313-320.	1.4	43
86	Pathogen enrichment sequencing (PenSeq) enables population genomic studies in oomycetes. <i>New Phytologist</i> , 2019, 221, 1634-1648.	3.5	43
87	<i>Phytophthora infestans</i> <scp>RXLR</scp> effector <scp>SFI</scp>5 requires association with calmodulin for PTI/MTI suppressing activity. <i>New Phytologist</i> , 2018, 219, 1433-1446.	3.5	42
88	Oomycetes Seek Help from the Plant: <i>Phytophthora infestans</i> Effectors Target Host Susceptibility Factors. <i>Molecular Plant</i> , 2016, 9, 636-638.	3.9	41
89	BTB-BACK Domain Protein POB1 Suppresses Immune Cell Death by Targeting Ubiquitin E3 ligase PUB17 for Degradation. <i>PLoS Genetics</i> , 2017, 13, e1006540.	1.5	41
90	Title is missing!. <i>European Journal of Plant Pathology</i> , 1997, 103, 809-814.	0.8	39

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91	Use of suppression subtractive hybridization to identify downy mildew genes expressed during infection of <i>Arabidopsis thaliana</i> . <i>Molecular Plant Pathology</i> , 2003, 4, 501-507.	2.0	39
92	High-throughput screening of suppression subtractive hybridization cDNA libraries using DNA microarray analysis. <i>BioTechniques</i> , 2004, 37, 818-824.	0.8	37
93	cDNA-AFLP analysis of differential gene expression in the prokaryotic plant pathogen <i>Erwinia carotovora</i> The GenBank accession numbers for the EL1, EL2, EL3, EP5, EP22, EP26, EP11 and EP21 sequences determined in this work are AJ274641â€“AJ274648, respectively.. <i>Microbiology (United Kingdom)</i> Tj ETQq1 1 0.784314 rgBT /Overlo	0.7	37
94	Why did filamentous plant pathogens evolve the potential to secrete hundreds of effectors to enable disease?. <i>Molecular Plant Pathology</i> , 2018, 19, 781-785.	2.0	34
95	<i>Phytophthora infestans</i> RXLR Effectors Target Parallel Steps in an Immune Signal Transduction Pathway. <i>Plant Physiology</i> , 2019, 180, 2227-2239.	2.3	33
96	<i>Phytophthora infestans</i> effector SFL3 targets potato UBK to suppress early immune transcriptional responses. <i>New Phytologist</i> , 2019, 222, 438-454.	3.5	33
97	A genetic interval and physical contig spanning the <i>Peronospora parasitica</i> (At) avirulence gene locus ATR1Nd. <i>Fungal Genetics and Biology</i> , 2003, 38, 33-42.	0.9	31
98	Sample sequencing of a selected region of the genome of <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> reveals candidate phytopathogenicity genes and allows comparison with <i>Escherichia coli</i> The GenBank accession numbers for the 424 sequences determined in this work are BH614193 to BH614616.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 1367-1378.	0.7	31
99	PCR-based detection of <i>Xanthomonas campestris</i> pv. <i>phaseoli</i> var. <i>fuscans</i> in plant material and its differentiation from <i>X. c.</i> pv. <i>phaseoli</i> . <i>Journal of Applied Microbiology</i> , 1998, 85, 327-336.	1.4	30
100	A putative DEAD-box RNA-helicase is required for normal zoospore development in the late blight pathogen <i>Phytophthora infestans</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 954-962.	0.9	30
101	Opening the Effector Protein Toolbox for Plantâ€“Parasitic Cyst Nematode Interactions. <i>Molecular Plant</i> , 2016, 9, 1451-1453.	3.9	29
102	Avirulence Protein 3a (AVR3a) from the Potato Pathogen <i>Phytophthora infestans</i> Forms Homodimers through Its Predicted Translocation Region and Does Not Specifically Bind Phospholipids. <i>Journal of Biological Chemistry</i> , 2012, 287, 38101-38109.	1.6	28
103	A transcriptional reference map of defence hormone responses in potato. <i>Scientific Reports</i> , 2015, 5, 15229.	1.6	28
104	A novel non-protein-coding infection-specific gene family is clustered throughout the genome of <i>Phytophthora infestans</i> . <i>Microbiology (United Kingdom)</i> , 2007, 153, 747-759.	0.7	27
105	AVR2 Targets BSL Family Members, Which Act as Susceptibility Factors to Suppress Host Immunity. <i>Plant Physiology</i> , 2019, 180, 571-581.	2.3	27
106	Characterisation of early transcriptional changes involving multiple signalling pathways in the Mla13 barley interaction with powdery mildew (<i>Blumeria graminis</i> f. sp. <i>hordei</i>). <i>Planta</i> , 2004, 218, 803-813.	1.6	26
107	Genome-Wide Identification of HrpL-Regulated Genes in the Necrotrophic Phytopathogen <i>Dickeya dadantii</i> 3937. <i>PLoS ONE</i> , 2010, 5, e13472.	1.1	25
108	A competitive PCR-based method for the detection and quantification of <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> on potato tubers. <i>Letters in Applied Microbiology</i> , 2000, 30, 330-335.	1.0	21

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109	Discovery and profiling of small RNAs responsive to stress conditions in the plant pathogen <i>Pectobacterium atrosepticum</i> . <i>BMC Genomics</i> , 2016, 17, 47.	1.2	19
110	Imaging Fluorescently Tagged <i>Phytophthora</i> Effector Proteins Inside Infected Plant Tissue. <i>Methods in Molecular Biology</i> , 2011, 712, 195-209.	0.4	18
111	Nucleotide sequence of a gene from <i>Phanerochaete chrysosporium</i> that shows homology to the <i>facA</i> gene of <i>Aspergillus nidulans</i> . <i>DNA Sequence</i> , 1992, 2, 319-323.	0.7	17
112	<i>Phanerochaete chrysosporium</i> and its natural substrate. <i>FEMS Microbiology Reviews</i> , 1994, 13, 189-195.	3.9	16
113	RNA-seq Profiling Reveals Defense Responses in a Tolerant Potato Cultivar to Stem Infection by <i>Pectobacterium carotovorum</i> ssp. <i>brasiliense</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1905.	1.7	16
114	Highlights of the mini-symposium on extracellular vesicles in inter-organismal communication, held in Munich, Germany, August 2018. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1590116.	5.5	16
115	The Ubiquitin E3 Ligase PUB17 Positively Regulates Immunity by Targeting a Negative Regulator, KH17, for Degradation. <i>Plant Communications</i> , 2020, 1, 100020.	3.6	15
116	Targeted differential display of abundantly expressed sequences from the basidiomycete <i>Phanerochaete chrysosporium</i> which contain regions coding for fungal cellulose-binding domains. <i>Current Genetics</i> , 1998, 33, 70-76.	0.8	14
117	A potato gene, <i>erg-1</i> , is rapidly induced by <i>Erwinia carotovora</i> ssp. <i>atroseptica</i> , <i>Phytophthora infestans</i> , ethylene and salicylic acid. <i>Journal of Plant Physiology</i> , 2000, 157, 201-205.	1.6	13
118	The potato <i>Phytophthora infestans</i> interaction transcriptome. <i>Canadian Journal of Plant Pathology</i> , 2003, 25, 226-231.	0.8	12
119	A potato STRUBBELIG-RECEPTOR FAMILY member, <i>StLRPK1</i> , associates with <i>StSERK3A/BAK1</i> and activates immunity. <i>Journal of Experimental Botany</i> , 2018, 69, 5573-5586.	2.4	12
120	The early days of late blight. <i>ELife</i> , 2013, 2, e00954.	2.8	12
121	A reporter system for analysis of regulatable promoter functions in the basidiomycete fungus <i>Phanerochaete chrysosporium</i> . <i>Journal of Applied Microbiology</i> , 1998, 85, 417-424.	1.4	11
122	Divergent Evolution of <i>PcF/SCR74</i> Effectors in Oomycetes Is Associated with Distinct Recognition Patterns in Solanaceous Plants. <i>MBio</i> , 2020, 11, .	1.8	11
123	In Vivo Protein-Protein Interaction Studies with BiFC: Conditions, Cautions, and Caveats. <i>Methods in Molecular Biology</i> , 2014, 1127, 81-90.	0.4	10
124	Microarray Comparative Genomic Hybridisation Analysis Incorporating Genomic Organisation, and Application to Enterobacterial Plant Pathogens. <i>PLoS Computational Biology</i> , 2009, 5, e1000473.	1.5	9
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130	The Hypersensitive Response in PAMP- and Effector-Triggered Immune Responses. , 2015, , 235-268.		4
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