

Paul R J Birch

List of Publications by Year in descending order

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136
papers

14,318
citations

18465

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21521

114
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all docs

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docs citations

140
times ranked

9328
citing authors

#	ARTICLE	IF	CITATIONS
1	Blueâ€light receptor phototropin 1 suppresses immunity to promote <i>Phytophthora infestans</i> infection. <i>New Phytologist</i> , 2022, 233, 2282-2293.	3.5	5
2	Yeast Two-Hybrid Screening for Identification of in. <i>Methods in Molecular Biology</i> , 2021, 2354, 95-110.	0.4	2
3	Haustorium formation and a distinct biotrophic transcriptome characterize infection of <i>Nicotiana benthamiana</i> by the tree pathogen <i>Phytophthora kernoviae</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 954-968.	2.0	5
4	Evolutionarily distinct resistance proteins detect a pathogen effector through its association with different host targets. <i>New Phytologist</i> , 2021, 232, 1368-1381.	3.5	6
5	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
6	Devastating intimacy: the cell biology of plantâ€ <i>Phytophthora</i> interactions. <i>New Phytologist</i> , 2020, 228, 445-458.	3.5	48
7	Divergent Evolution of PcF/SCR74 Effectors in Oomycetes Is Associated with Distinct Recognition Patterns in Solanaceous Plants. <i>MBio</i> , 2020, 11, .	1.8	11
8	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
9	<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
10	Highlights of the miniâ€symposium on extracellular vesicles in interâ€organismal communication, held in Munich, Germany, August 2018. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1590116.	5.5	16
11	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
12	<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
13	<i>Phytophthora infestans</i> effector SFI3 targets potato UBK to suppress early immune transcriptional responses. <i>New Phytologist</i> , 2019, 222, 438-454.	3.5	33
14	The oomycete microbe-associated molecular pattern Pep-13 triggers SERK3/BAK1-independent plant immunity. <i>Plant Cell Reports</i> , 2019, 38, 173-182.	2.8	8
15	Pathogen enrichment sequencing (PenSeq) enables population genomic studies in oomycetes. <i>New Phytologist</i> , 2019, 221, 1634-1648.	3.5	43
16	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
17	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
18	<i>Phytophthora infestans</i> RXLR effector SFI5 requires association with calmodulin for PTI/MTI suppressing activity. <i>New Phytologist</i> , 2018, 219, 1433-1446.	3.5	42

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19	Plant pathogen effector utilizes host susceptibility factor NRL1 to degrade the immune regulator SWAP70. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7834-E7843.	3.3	55
20	Effector gene birth in plant parasitic nematodes: Neofunctionalization of a housekeeping glutathione synthetase gene. PLoS Genetics, 2018, 14, e1007310.	1.5	44
21	A potato STRUBBELIG-RECEPTOR FAMILY member, StLRPK1, associates with StSERK3A/BAK1 and activates immunity. Journal of Experimental Botany, 2018, 69, 5573-5586.	2.4	12
22	The <i>Phytophthora infestans</i> Haustorium Is a Site for Secretion of Diverse Classes of Infection-Associated Proteins. MBio, 2018, 9, .	1.8	54
23	RXLR Effector AVR2 Up-Regulates a Brassinosteroid-Responsive bHLH Transcription Factor to Suppress Immunity. Plant Physiology, 2017, 174, 356-369.	2.3	82
24	A new proteinaceous pathogen-associated molecular pattern (PAMP) identified in Ascomycete fungi induces cell death in Solanaceae. New Phytologist, 2017, 214, 1657-1672.	3.5	55
25	Delivery of cytoplasmic and apoplastic effectors from <i>Phytophthora infestans</i> haustoria by distinct secretion pathways. New Phytologist, 2017, 216, 205-215.	3.5	121
26	BTB-BACK Domain Protein POB1 Suppresses Immune Cell Death by Targeting Ubiquitin E3 ligase PUB17 for Degradation. PLoS Genetics, 2017, 13, e1006540.	1.5	41
27	Utilizing Omic Technologies to Identify and Prioritize Novel Sources of Resistance to the Oomycete Pathogen <i>Phytophthora infestans</i> in Potato Germplasm Collections. Frontiers in Plant Science, 2016, 7, 672.	1.7	69
28	RNA-seq Profiling Reveals Defense Responses in a Tolerant Potato Cultivar to Stem Infection by <i>Pectobacterium carotovorum</i> ssp. <i>brasiliense</i> . Frontiers in Plant Science, 2016, 7, 1905.	1.7	16
29	Oomycetes Seek Help from the Plant: <i>Phytophthora infestans</i> Effectors Target Host Susceptibility Factors. Molecular Plant, 2016, 9, 636-638.	3.9	41
30	Potato NPH3/RPT2-Like Protein StNRL1, Targeted by a <i>Phytophthora infestans</i> RXLR Effector, Is a Susceptibility Factor. Plant Physiology, 2016, 171, 645-657.	2.3	71
31	The cell biology of late blight disease. Current Opinion in Microbiology, 2016, 34, 127-135.	2.3	106
32	Genome-wide identification of potato long intergenic noncoding RNAs responsive to <i>Pectobacterium carotovorum</i> subspecies <i>brasiliense</i> infection. BMC Genomics, 2016, 17, 614.	1.2	48
33	Opening the Effector Protein Toolbox for Plant-Parasitic Cyst Nematode Interactions. Molecular Plant, 2016, 9, 1451-1453.	3.9	29
34	Discovery and profiling of small RNAs responsive to stress conditions in the plant pathogen <i>Pectobacterium atrosepticum</i> . BMC Genomics, 2016, 17, 47.	1.2	19
35	A <i>Phytophthora infestans</i> RXLR effector targets plant PP1c isoforms that promote late blight disease. Nature Communications, 2016, 7, 10311.	5.8	123
36	A transcriptional reference map of defence hormone responses in potato. Scientific Reports, 2015, 5, 15229.	1.6	28

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37	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
38	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
39	Five Reasons to Consider <i>Phytophthora infestans</i> a Reemerging Pathogen. <i>Phytopathology</i> , 2015, 105, 966-981.	1.1	254
40	The Hypersensitive Response in PAMP- and Effector-Triggered Immune Responses. , 2015, , 235-268.		4
41	<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
42	The Top 10 oomycete pathogens in molecular plant pathology. <i>Molecular Plant Pathology</i> , 2015, 16, 413-434.	2.0	695
43	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
44	<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
45	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
46	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
47	Sequence diversity in the large subunit of RNA polymerase I contributes to Mefenoxam insensitivity in <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2014, 15, 664-676.	2.0	69
48	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
49	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
50	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
51	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
52	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
53	The early days of late blight. <i>ELife</i> , 2013, 2, e00954.	2.8	12
54	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

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55	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
56	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
57	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2012, 8, e1002940.	2.1	321
58	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
59	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
60	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
61	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
62	ADS1 encodes a MATE-transporter that negatively regulates plant disease resistance. <i>New Phytologist</i> , 2011, 192, 471-482.	3.5	62
63	Genome Sequence of the Plant-Pathogenic Bacterium <i>Dickeya dadantii</i> 3937. <i>Journal of Bacteriology</i> , 2011, 193, 2076-2077.	1.0	113
64	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
65	Reverse Engineering Gene Regulatory Networks Related to Quorum Sensing in the Plant Pathogen <i>Pectobacterium atrosepticum</i> . <i>Methods in Molecular Biology</i> , 2010, 673, 253-281.	0.4	3
66	Towards an understanding on how RxLR-effector proteins are translocated from oomycetes into host cells. <i>Fungal Biology Reviews</i> , 2010, 24, 27-36.	1.9	9
67	<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
68	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
69	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
70	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
71	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
72	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

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73	The zig-zag-zig in oomycete-plant interactions. <i>Molecular Plant Pathology</i> , 2009, 10, 547-562.	2.0	136
74	The zig-zag-zig in oomycete-plant interactions. <i>Molecular Plant Pathology</i> , 2009, 10, 717-717.	2.0	1
75	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
76	Bacterial chemoattraction towards jasmonate plays a role in the entry of <i>Dickeya dadantii</i> through wounded tissues. <i>Molecular Microbiology</i> , 2009, 74, 1543-1543.	1.2	1
77	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
78	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
79	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
80	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
81	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
82	Oomycete RXLR effectors: delivery, functional redundancy and durable disease resistance. <i>Current Opinion in Plant Biology</i> , 2008, 11, 373-379.	3.5	157
83	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
84	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
85	<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
86	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
87	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
88	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
89	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
90	A translocation signal for delivery of oomycete effector proteins into host plant cells. <i>Nature</i> , 2007, 450, 115-118.	13.7	760

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91	Involvement of cathepsin B in the plant disease resistance hypersensitive response. <i>Plant Journal</i> , 2007, 52, 1-13.	2.8	147
92	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
93	Comparative Genomics Reveals What Makes An Enterobacterial Plant Pathogen. <i>Annual Review of Phytopathology</i> , 2006, 44, 305-336.	3.5	138
94	GenomeDiagram: a python package for the visualization of large-scale genomic data. <i>Bioinformatics</i> , 2006, 22, 616-617.	1.8	83
95	Trafficking arms: oomycete effectors enter host plant cells. <i>Trends in Microbiology</i> , 2006, 14, 8-11.	3.5	278
96	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
97	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
98	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
99	Rotting softly and stealthily. <i>Current Opinion in Plant Biology</i> , 2005, 8, 424-429.	3.5	119
100	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
101	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
102	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
103	Differential Recognition of Highly Divergent Downy Mildew Avirulence Gene Alleles by RPP1 Resistance Genes from Two <i>Arabidopsis</i> Lines. <i>Plant Cell</i> , 2005, 17, 1839-1850.	3.1	416
104	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
105	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
106	High-throughput screening of suppression subtractive hybridization cDNA libraries using DNA microarray analysis. <i>BioTechniques</i> , 2004, 37, 818-824.	0.8	37
107	Potato Virus X-Induced Gene Silencing in Leaves and Tubers of Potato. <i>Plant Physiology</i> , 2004, 134, 1308-1316.	2.3	160
108	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

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109	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
110	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
111	Activation tagging in plants: a tool for gene discovery. <i>Functional and Integrative Genomics</i> , 2004, 4, 258-66.	1.4	59
112	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
113	Mechanisms of Infection: Oomycetes. , 2004, , 697-700.		3
114	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
115	Intraspecific comparative genomics to identify avirulence genes from <i>Phytophthora</i> . <i>New Phytologist</i> , 2003, 159, 63-72.	3.5	50
116	Soft rot erwiniae: from genes to genomes. <i>Molecular Plant Pathology</i> , 2003, 4, 17-30.	2.0	354
117	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
118	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
119	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
120	The potato "Phytophthora infestans interaction transcriptome. <i>Canadian Journal of Plant Pathology</i> , 2003, 25, 226-231.	0.8	12
121	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
122	<i>Phytophthora infestans</i> enters the genomics era. <i>Molecular Plant Pathology</i> , 2001, 2, 257-263.	2.0	70
123	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
124	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
125	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
126	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 AJ274641" AJ274648, respectively.. <i>Microbiology (United)</i> Tj ETQq0 0 0 rgBT /Overl 10 Tf 5	0.7	37

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127	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
128	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
129	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
130	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
131	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
132	Title is missing!. <i>European Journal of Plant Pathology</i> , 1997, 103, 809-814.	0.8	39
133	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
134	<i>Phanerochaete chrysosporium</i> and its natural substrate. <i>FEMS Microbiology Reviews</i> , 1994, 13, 189-195.	3.9	16
135	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
136	Gene Expression Profiling. , 0, , 477-492.		0