

Richard C Hamelin

List of Publications by Year in descending order

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178
papers

10,486
citations

70961

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h-index

38300

95
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all docs

188
docs citations

188
times ranked

11575
citing authors

#	ARTICLE	IF	CITATIONS
1	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for <i>Fungi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	3.3	4,012
2	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9166-9171.	3.3	640
3	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. PLoS Pathogens, 2012, 8, e1003037.	2.1	595
4	Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau061-bau061.	1.4	272
5	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. PLoS Genetics, 2012, 8, e1003088.	1.5	226
6	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2504-2509.	3.3	218
7	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in <i>Melampsora larici-populina</i> (Poplar Leaf Rust). Molecular Plant-Microbe Interactions, 2012, 25, 279-293.	1.4	150
8	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. Genome Biology, 2009, 10, R94.	13.9	130
9	Association genetics, geography and ecophysiology link stomatal patterning in <i>Populus trichocarpa</i> with carbon gain and disease resistance trade-offs. Molecular Ecology, 2014, 23, 5771-5790.	2.0	103
10	Standardizing the Nomenclature for Clonal Lineages of the Sudden Oak Death Pathogen, <i>Phytophthora ramorum</i> . Phytopathology, 2009, 99, 792-795.	1.1	93
11	Evaluation of mitochondrial genes as DNA barcode for Basidiomycota. Molecular Ecology Resources, 2009, 9, 99-113.	2.2	91
12	Molecular Detection of <i>Phytophthora ramorum</i> by Real-Time Polymerase Chain Reaction Using TaqMan, SYBR Green, and Molecular Beacons. Phytopathology, 2007, 97, 632-642.	1.1	89
13	Development of a multiplex immunocapture RT-PCR assay for detection and differentiation of tomato and tobacco mosaic tobamoviruses. Journal of Virological Methods, 1998, 74, 167-178.	1.0	86
14	Genetic Resistance to Fusiform Rust in Southern Pines and White Pine Blister Rust in White Pines—A Contrasting Tale of Two Rust Pathosystems—Current Status and Future Prospects. Forests, 2014, 5, 2050-2083.	0.9	81
15	Molecular Profiling of Rhizosphere Microbial Communities Associated with Healthy and Diseased Black Spruce (<i>Picea mariana</i>) Seedlings Grown in a Nursery. Applied and Environmental Microbiology, 2004, 70, 3541-3551.	1.4	77
16	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen <i>Pseudocercospora fijiensis</i> (Synonym <i>Mycosphaerella fijiensis</i>) Genomes Reveal Clues for Disease Control. PLoS Genetics, 2016, 12, e1005876.	1.5	77
17	Identification of <i>Gremmeniella abietina</i> Races with Random Amplified Polymorphic DNA Markers. Applied and Environmental Microbiology, 1993, 59, 1752-1755.	1.4	75
18	The landscape of transposable elements in the finished genome of the fungal wheat pathogen <i>Mycosphaerella graminicola</i> . BMC Genomics, 2014, 15, 1132.	1.2	65

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19	Ecology and Evolution of the Sudden Oak Death Pathogen <i>Phytophthora ramorum</i>. Annual Review of Phytopathology, 2019, 57, 301-321.	3.5	64
20	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3451-3456.	3.3	63
21	Genomic biosurveillance of forest invasive alien enemies: A story written in code. Evolutionary Applications, 2020, 13, 95-115.	1.5	61
22	Comparative analysis of secreted protein evolution using expressed sequence tags from four poplar leaf rusts (<i>Melampsora</i> spp.). BMC Genomics, 2010, 11, 422.	1.2	59
23	Genetic differentiation within the European race of <i>Gremmeniella abietina</i> . Mycological Research, 1996, 100, 49-56.	2.5	57
24	Spatial Genetic Structure of a Symbiotic Beetle-Fungal System: Toward Multi-Taxa Integrated Landscape Genetics. PLoS ONE, 2011, 6, e25359.	1.1	57
25	Gene genealogies reveal cryptic species and host preferences for the pine fungal pathogen <i>Grosmannia clavigera</i>. Molecular Ecology, 2011, 20, 2581-2602.	2.0	57
26	Phylogenetics of Helotiales and Rhytismatales based on partial small subunit nuclear ribosomal DNA sequences. Mycologia, 2001, 93, 915-933.	0.8	55
27	Sexual homomorphism in dioecious trees: extensive tests fail to detect sexual dimorphism in <i>Populus</i> . Scientific Reports, 2017, 7, 1831.	1.6	54
28	Genetic and genomic evidence of niche partitioning and adaptive radiation in mountain pine beetle fungal symbionts. Molecular Ecology, 2017, 26, 2077-2091.	2.0	52
29	Molecular Detection of 10 of the Most Unwanted Alien Forest Pathogens in Canada Using Real-Time PCR. PLoS ONE, 2015, 10, e0134265.	1.1	51
30	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen <i>Phytophthora ramorum</i>. MBio, 2019, 10, .	1.8	50
31	PCR detection of <i>Gremmeniella abietina</i> , the causal agent of Scleroderris canker of pine. Mycological Research, 2000, 104, 527-532.	2.5	49
32	Unequal Recombination and Evolution of the Mating-Type (MAT) Loci in the Pathogenic Fungus <i>Grosmannia clavigera</i> and Relatives. G3: Genes, Genomes, Genetics, 2013, 3, 465-480.	0.8	49
33	Fungal pathogen (mis-) identifications: A case study with DNA barcodes on <i>Melampsora</i> rusts of aspen and white poplar. Mycological Research, 2009, 113, 713-724.	2.5	48
34	Phylogenetic species recognition reveals host-specific lineages among poplar rust fungi. Molecular Phylogenetics and Evolution, 2013, 66, 628-644.	1.2	48
35	Asexual Propagation of a Virulent Clone Complex in a Human and Feline Outbreak of Sporotrichosis. Eukaryotic Cell, 2015, 14, 158-169.	3.4	47
36	Population structure and migration pattern of a conifer pathogen, <i>Grosmannia clavigera</i>, as influenced by its symbiont, the mountain pine beetle. Molecular Ecology, 2012, 21, 71-86.	2.0	46

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37	Genetic diversity among <i>Fusarium graminearum</i> strains from Ontario and Quebec. <i>Canadian Journal of Plant Pathology</i> , 1999, 21, 308-314.	0.8	44
38	DNA barcoding in the rust genus <i>Chrysomyxa</i> and its implications for the phylogeny of the genus. <i>Mycologia</i> , 2011, 103, 1250-1266.	0.8	44
39	Duplications and losses in gene families of rust pathogens highlight putative effectors. <i>Frontiers in Plant Science</i> , 2014, 5, 299.	1.7	44
40	Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. <i>Nature Ecology and Evolution</i> , 2020, 4, 626-638.	3.4	44
41	Phylogenetics of Helotiales and Rhytismatales Based on Partial Small Subunit Nuclear Ribosomal DNA Sequences. <i>Mycologia</i> , 2001, 93, 915.	0.8	43
42	In Vivo Monitoring of Obligate Biotrophic Pathogen Growth by Kinetic PCR. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1546-1552.	1.4	43
43	Recent advances related to poplar leaf spot and canker caused by <i>Septoria musiva</i> . <i>Canadian Journal of Plant Pathology</i> , 2010, 32, 122-134.	0.8	43
44	Barrier to Gene Flow Between Eastern and Western Populations of <i>Cronartium ribicola</i> in North America. <i>Phytopathology</i> , 2000, 90, 1073-1078.	1.1	42
45	Genetic diversity in populations of <i>Cronartium ribicola</i> in plantations and natural stands of <i>Pinus strobus</i> . <i>Theoretical and Applied Genetics</i> , 1995, 91, 1214-1221.	1.8	41
46	Impact of an 8-Year-Old Transgenic Poplar Plantation on the Ectomycorrhizal Fungal Community. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7527-7536.	1.4	41
47	Molecular and Physiological Analysis of the Powdery Mildew Antagonist <i>Pseudozyma flocculosa</i> and Related Fungi. <i>Phytopathology</i> , 2001, 91, 249-254.	1.1	40
48	Genetic diversity in <i>Cronartium quercuum</i> f.sp. <i>fusiforme</i> on loblolly pines in southern U.S.. <i>Current Genetics</i> , 1994, 26, 359-363.	0.8	38
49	A spruce defensin showing strong antifungal activity and increased transcript accumulation after wounding and jasmonate treatments. <i>Physiological and Molecular Plant Pathology</i> , 2004, 64, 331-341.	1.3	37
50	Poplar rust systematics and refinement of <i>Melampsora</i> species delineation. <i>Fungal Diversity</i> , 2011, 50, 227-248.	4.7	37
51	Evaluation of Molecular Markers for <i>Phytophthora ramorum</i> Detection and Identification: Testing for Specificity Using a Standardized Library of Isolates. <i>Phytopathology</i> , 2009, 99, 390-403.	1.1	36
52	Comparative analysis of mitochondrial genomes of geographic variants of the gypsy moth, <i>Lymantria dispar</i> , reveals a previously undescribed genotypic entity. <i>Scientific Reports</i> , 2017, 7, 14245.	1.6	36
53	No Evidence of an Impact on the Rhizosphere Diazotroph Community by the Expression of <i>Bacillus thuringiensis</i> Cry1Ab Toxin by Bt White Spruce. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6577-6583.	1.4	35
54	Advancing Knowledge on Biology of Rust Fungi Through Genomics. <i>Advances in Botanical Research</i> , 2014, , 173-209.	0.5	35

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55	Biosurveillance of forest insects: part I—integration and application of genomic tools to the surveillance of non-native forest insects. <i>Journal of Pest Science</i> , 2019, 92, 51-70.	1.9	35
56	Oh the places they™ go: improving species distribution modelling for invasive forest pests in an uncertain world. <i>Biological Invasions</i> , 2021, 23, 297-349.	1.2	34
57	Genetic Structure of <i>Cronartium ribicola</i> Populations in Eastern Canada. <i>Phytopathology</i> , 1999, 89, 915-919.	1.1	33
58	Fungal Diversity, Dominance, and Community Structure in the Rhizosphere of Clonal <i>Picea mariana</i> Plants Throughout Nursery Production Chronosequences. <i>Microbial Ecology</i> , 2007, 54, 672-684.	1.4	33
59	Approaches to molecular characterization of fungal biocontrol agents: some case studies. <i>Canadian Journal of Plant Pathology</i> , 2001, 23, 8-12.	0.8	32
60	Assessing the potential of genotyping-by-sequencing-derived single nucleotide polymorphisms to identify the geographic origins of intercepted gypsy moth (<i>Lymantria dispar</i>) specimens: A proof-of-concept study. <i>Evolutionary Applications</i> , 2018, 11, 325-339.	1.5	32
61	Molecular Evidence of Distinct Introductions of the European Race of <i>Gremmeniella abietina</i> into North America. <i>Phytopathology</i> , 1998, 88, 582-588.	1.1	31
62	The effects of high-tannin leaf litter from transgenic poplars on microbial communities in microcosm soils. <i>Frontiers in Microbiology</i> , 2013, 4, 290.	1.5	31
63	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015, 10, e0142864.	1.1	31
64	A Multi-Species TaqMan PCR Assay for the Identification of Asian Gypsy Moths (<i>Lymantria</i> spp.) and Other Invasive Lymantriines of Biosecurity Concern to North America. <i>PLoS ONE</i> , 2016, 11, e0160878.	1.1	31
65	CRISPR/Cas9 Gene Editing: An Unexplored Frontier for Forest Pathology. <i>Frontiers in Plant Science</i> , 2020, 11, 1126.	1.7	31
66	Genetic Diversity Between and Within Cankers of the White Pine Blister Rust. <i>Phytopathology</i> , 1996, 86, 875.	1.1	31
67	Association Analysis Identifies <i>Melampsora</i> — <i>columbiana</i> Poplar Leaf Rust Resistance SNPs. <i>PLoS ONE</i> , 2013, 8, e78423.	1.1	31
68	Alteration of Soil Rhizosphere Communities following Genetic Transformation of White Spruce. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4128-4134.	1.4	30
69	Population Structure of Mountain Pine Beetle Symbiont <i>Leptographium longiclavatum</i> and the Implication on the Multipartite Beetle-Fungi Relationships. <i>PLoS ONE</i> , 2014, 9, e105455.	1.1	30
70	Genetic Structure of <i>Mycosphaerella populorum</i> (Anamorph <i>Septoria musiva</i>) Populations in North-Central and Northeastern North America. <i>Phytopathology</i> , 2005, 95, 608-616.	1.1	29
71	Putative origin of clonal lineages of <i>Amylostereum areolatum</i> , the fungal symbiont associated with <i>Sirex noctilio</i> , retrieved from <i>Pinus sylvestris</i> , in eastern Canada. <i>Fungal Biology</i> , 2011, 115, 750-758.	1.1	29
72	Genome sequences of six <i>Phytophthora</i> species threatening forest ecosystems. <i>Genomics Data</i> , 2016, 10, 85-88.	1.3	29

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73	Poplar leaf rusts: model pathogens for a model tree This minireview is one of a selection of papers published in the Special Issue on Poplar Research in Canada.. Canadian Journal of Botany, 2007, 85, 1127-1135.	1.2	27
74	Multiplex real-time polymerase chain reaction (PCR) for detection of <i>Phytophthora ramorum</i> , the causal agent of sudden oak death. Canadian Journal of Plant Pathology, 2009, 31, 195-210.	0.8	27
75	Effects of Transgenic Hybrid Aspen Overexpressing Polyphenol Oxidase on Rhizosphere Diversity. Applied and Environmental Microbiology, 2008, 74, 5340-5348.	1.4	26
76	Discrimination between alfalfa and potato isolates of <i>Verticillium albo-atrum</i> using RAPD markers. Mycological Research, 1995, 99, 1507-1512.	2.5	25
77	Identification of mycobacteria in peat moss processing plants: application of molecular biology approaches. Canadian Journal of Microbiology, 2007, 53, 92-99.	0.8	24
78	Rapid identification and detection of pine pathogenic fungi associated with mountain pine beetles by padlock probes. Journal of Microbiological Methods, 2010, 83, 26-33.	0.7	24
79	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. PeerJ, 2018, 6, e4392.	0.9	24
80	Phylogeny of <i>Gremmeniella</i> spp. based on sequences of the 5.8S rDNA and internal transcribed spacer region. Canadian Journal of Botany, 1997, 75, 693-698.	1.2	23
81	Overexpression of AtGOLS3 and CsRFS in poplar enhances ROS tolerance and represses defense response to leaf rust disease. Tree Physiology, 2018, 38, 457-470.	1.4	23
82	Genetic diversity of <i>Phytophthora pluvialis</i> , a pathogen of conifers, in New Zealand and the west coast of the United States of America. Plant Pathology, 2018, 67, 1131-1139.	1.2	23
83	Attributes and congruence of three molecular data sets: Inferring phylogenies among Septoria-related species from woody perennial plants. Molecular Phylogenetics and Evolution, 2006, 40, 808-829.	1.2	22
84	Impact of Endochitinase-Transformed White Spruce on Soil Fungal Biomass and Ectendomycorrhizal Symbiosis. Applied and Environmental Microbiology, 2010, 76, 2607-2614.	1.4	22
85	Current state of genetically modified plant impact on target and non-target fungi. Environmental Reviews, 2010, 18, 441-475.	2.1	21
86	Evolution and Adaptation of Forest and Crop Pathogens in the Anthropocene. Phytopathology, 2021, 111, 49-67.	1.1	21
87	Fine-Level Genetic Structure of White Pine Blister Rust Populations. Phytopathology, 1998, 88, 1187-1191.	1.1	20
88	Biosurveillance of forest insects: part II – adoption of genomic tools by end user communities and barriers to integration. Journal of Pest Science, 2019, 92, 71-82.	1.9	20
89	<i>Morchella tomentosa</i> : a unique belowground structure and a new clade of morels. Mycologia, 2010, 102, 1082-1088.	0.8	19
90	Colonization History, Host Distribution, Anthropogenic Influence and Landscape Features Shape Populations of White Pine Blister Rust, an Invasive Alien Tree Pathogen. PLoS ONE, 2015, 10, e0127916.	1.1	19

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91	Genetic Diversity and the Presence of Two Distinct Groups in <i>Ophiostoma clavigerum</i> Associated with <i>Dendroctonus ponderosae</i> in British Columbia and the Northern Rocky Mountains. <i>Phytopathology</i> , 2007, 97, 1177-1185.	1.1	18
92	Molecular Epidemiology of White Pine Blister Rust: Recombination and Spatial Distribution. <i>Phytopathology</i> , 2005, 95, 793-799.	1.1	17
93	Differentiation of European and North American genotypes of <i>Phytophthora ramorum</i> by real-time polymerase chain reaction primer extension. <i>Canadian Journal of Plant Pathology</i> , 2007, 29, 408-420.	0.8	17
94	Impact of endochitinase-transformed white spruce on soil fungal communities under greenhouse conditions. <i>FEMS Microbiology Ecology</i> , 2011, 76, 199-208.	1.3	17
95	Extensive Functional Pleiotropy of REVOLUTA Substantiated through Forward Genetics. <i>Plant Physiology</i> , 2014, 164, 548-554.	2.3	17
96	Genetic patterns reveal historical and contemporary dispersal of a tree pathogen. <i>Biological Invasions</i> , 2016, 18, 1781-1799.	1.2	17
97	Anthropogenic signature in the incidence and distribution of an emerging pathogen of poplars. <i>Biological Invasions</i> , 2016, 18, 1147-1161.	1.2	17
98	In Situ Processing and Efficient Environmental Detection (iSPEED) of tree pests and pathogens using point-of-use real-time PCR. <i>PLoS ONE</i> , 2020, 15, e0226863.	1.1	17
99	Real-time PCR assay to distinguish <i>Phytophthora ramorum</i> lineages using the cellulose binding elicitor lectin (CBEL) locus. <i>Canadian Journal of Plant Pathology</i> , 2014, 36, 367-376.	0.8	16
100	Prediction of poplar leaf rust epidemics from a leaf-disk assay. <i>Canadian Journal of Forest Research</i> , 1994, 24, 2085-2088.	0.8	15
101	Sequence-tagged sites (STS) for studies of molecular epidemiology of scleroderris canker of conifers. <i>Theoretical and Applied Genetics</i> , 1998, 97, 789-796.	1.8	15
102	Variability of Nuclear SSU-rDNA Group Introns Within <i>Septoria</i> Species: Incongruence with Host Sequence Phylogenies. <i>Journal of Molecular Evolution</i> , 2007, 64, 489-499.	0.8	15
103	Signatures of Post-Glacial Genetic Isolation and Human-Driven Migration in the <i>Dothistroma</i> Needle Blight Pathogen in Western Canada. <i>Phytopathology</i> , 2021, 111, 116-127.	1.1	15
104	Detection and validation of EST-derived SNPs for poplar leaf rust <i>Melampsora medusae</i> f. sp. <i>deltoidae</i> . <i>Molecular Ecology Notes</i> , 2007, 7, 1222-1228.	1.7	14
105	Improved detection and identification of the sudden oak death pathogen <i>Phytophthora ramorum</i> and the Port Orford cedar root pathogen <i>Phytophthora lateralis</i> . <i>Plant Pathology</i> , 2019, 68, 878-888.	1.2	14
106	Genome-enhanced detection and identification of fungal pathogens responsible for pine and poplar rust diseases. <i>PLoS ONE</i> , 2019, 14, e0210952.	1.1	14
107	Population Genomic Analyses Reveal Connectivity via Human-Mediated Transport across <i>Populus</i> Plantations in North America and an Undescribed Subpopulation of <i>Sphaerulina musiva</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 189-199.	1.4	14
108	Worldwide Genetic Structure Elucidates the Eurasian Origin and Invasion Pathways of <i>Dothistroma septosporum</i> , Causal Agent of <i>Dothistroma</i> Needle Blight. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 111.	1.5	14

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109	DNA polymorphism and molecular diagnosis in <i>Inonotus</i> spp.. Canadian Journal of Plant Pathology, 2002, 24, 194-199.	0.8	13
110	A comparative study of genetic diversity of populations of <i>Nectria galligena</i> and <i>N. coccinea</i> var. <i>faginata</i> in North America. Mycological Research, 2002, 106, 183-193.	2.5	13
111	Single nucleotide polymorphism discovery in <i>Lepptographium longiclavatum</i> , a mountain pine beetle-associated symbiotic fungus, using whole genome resequencing. Molecular Ecology Resources, 2014, 14, 401-410.	2.2	13
112	Real-time PCR assays for the detection of <i>Heterobasidion irregulare</i> , <i>H. occidentale</i> , <i>H. annosum</i> sensu stricto and the <i>Heterobasidion annosum</i> complex. Forest Pathology, 2017, 47, e12321.	0.5	13
113	Say hello to my little friends: how microbiota can modulate tree health. New Phytologist, 2017, 215, 508-510.	3.5	13
114	Adaptation of poplar leaf rust to Eastern cottonwood. Euphytica, 1992, 62, 69-75.	0.6	12
115	Comparison of RAPD technique and somatic incompatibility tests for the identification of <i>Phlebiopsis gigantea</i> strains. Canadian Journal of Botany, 1997, 75, 2097-2104.	1.2	12
116	Genetic Variability of Canadian Populations of the Sapstain Fungus <i>Ophiostoma piceae</i> . Phytopathology, 2001, 91, 369-376.	1.1	12
117	Target-specific PCR primers can detect and differentiate ophiostomatoid fungi from microbial communities associated with the mountain pine beetle <i>Dendroctonus ponderosae</i> . Fungal Biology, 2010, 114, 825-833.	1.1	12
118	The MAT1-1:MAT1-2 Ratio of <i>Sporothrix globosa</i> Isolates in Japan. Mycopathologia, 2015, 179, 81-86.	1.3	12
119	Development and Validation of Polymorphic Microsatellite Loci for the NA2 Lineage of <i>Phytophthora ramorum</i> from Whole Genome Sequence Data. Plant Disease, 2017, 101, 666-673.	0.7	12
120	The contribution of genetics and genomics to understanding the ecology of the mountain pine beetle system. Canadian Journal of Forest Research, 2019, 49, 721-730.	0.8	12
121	An Applied Empirical Framework for Invasion Science: Confronting Biological Invasion Through Collaborative Research Aimed at Tool Production. Annals of the Entomological Society of America, 2020, 113, 230-245.	1.3	12
122	Transcriptional profile of oil palm pathogen, <i>Ganoderma boninense</i> , reveals activation of lignin degradation machinery and possible evasion of host immune response. BMC Genomics, 2021, 22, 326.	1.2	12
123	Quantification of Disease Progress and Defoliation in the Poplar Leaf Rust-Eastern Cottonwood Pathosystem. Phytopathology, 1993, 83, 140.	1.1	12
124	Functional categorization of unique expressed sequence tags obtained from the yeast-like growth phase of the elm pathogen <i>Ophiostoma novo-ulmi</i> . BMC Genomics, 2011, 12, 431.	1.2	11
125	Nucleotide polymorphisms in three genes support host and geographic speciation in tree pathogens belonging to <i>Gremmeniellasp.</i> . Canadian Journal of Botany, 2002, 80, 1151-1159.	1.2	10
126	Genetic Diversity in Poplar Leaf Rust (<i>Melampsora medusae</i> f. sp. <i>deltoidae</i>) in the Zones of Host Sympatry and Allopatry. Phytopathology, 2007, 97, 603-610.	1.1	10

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127	Optimization of a real-time PCR assay for the detection of the quarantine pathogen <i>Melampsora medusae</i> f. sp. <i>deltoidae</i> . <i>Fungal Biology</i> , 2013, 117, 389-398.	1.1	10
128	Comparative Gene Expression Analysis Reveals Mechanism of <i>Pinus contorta</i> Response to the Fungal Pathogen <i>Dothistroma septosporum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 397-409.	1.4	10
129	Influence of leaf wetness, temperature, and rain on poplar leaf rust epidemics. <i>Canadian Journal of Forest Research</i> , 1992, 22, 1249-1254.	0.8	9
130	Molecular epidemiology of forest pathogens: from genes to landscape. <i>Canadian Journal of Plant Pathology</i> , 2006, 28, 167-181.	0.8	9
131	Characterization of microsatellite loci in the fungus, <i>Grosmannia clavigera</i> , a pine pathogen associated with the mountain pine beetle. <i>Molecular Ecology Resources</i> , 2009, 9, 1500-1503.	2.2	9
132	Simultaneous monitoring and quantification of <i>Melampsora alliâ€populina</i> and <i>Melampsora lariciâ€populina</i> on infected poplar leaves using a duplex real-time <i>scp</i> PCR assay. <i>Plant Pathology</i> , 2016, 65, 380-391.	1.2	9
133	Molecular assays to detect the presence and viability of <i>Phytophthora ramorum</i> and <i>Grosmannia clavigera</i> . <i>PLoS ONE</i> , 2020, 15, e0221742.	1.1	9
134	Potential Differences and Methods of Determining Gypsy Moth Female Flight Capabilities: Implications for the Establishment and Spread in Novel Habitats. <i>Forests</i> , 2021, 12, 103.	0.9	9
135	Urban environments harbor greater oomycete and <i>Phytophthora</i> diversity, creating a bridgehead for potential new pathogens to natural ecosystems. <i>Environmental DNA</i> , 2022, 4, 1039-1051.	3.1	9
136	A sensitive real-time PCR assay for the detection of the two <i>Melampsora medusae</i> formae speciales on infected poplar leaves. <i>European Journal of Plant Pathology</i> , 2013, 136, 433-441.	0.8	8
137	Cryptic Speciation in Western North America and Eastern Eurasia of the Pathogens Responsible for Laminated Root Rot. <i>Phytopathology</i> , 2019, 109, 456-468.	1.1	8
138	Expansion of LINEs and species-specific DNA repeats drives genome expansion in Asian Gypsy Moths. <i>Scientific Reports</i> , 2019, 9, 16413.	1.6	8
139	Long-term effects of stump removal and tree species composition on the diversity and structure of soil fungal communities. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	8
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