Rosie Bradshaw

List of Publications by Year
in descending order

74 papers	2,550 citations	304743 22 h-index	214800 47 g-index
81 all docs	81 docs citations	81 times ranked	2264 citing authors

#	Article	IF	Citations
1	CRISPR-Cas9 gene editing and rapid detection of gene-edited mutants using high-resolution melting in the apple scab fungus, Venturia inaequalis. Fungal Biology, 2022, 126, 35-46.	2.5	8
2	Targeted Gene Mutations in the Forest Pathogen Dothistroma septosporum Using CRISPR/Cas9. Plants, 2022, 11, 1016.	3.5	5
3	Signatures of Post-Glacial Genetic Isolation and Human-Driven Migration in the Dothistroma Needle Blight Pathogen in Western Canada. Phytopathology, 2021, 111, 116-127.	2.2	15
4	Apoplastic effector candidates of a foliar forest pathogen trigger cell death in host and non-host plants. Scientific Reports, 2021, 11, 19958.	3.3	11
5	Phytophthora agathidicida: research progress, cultural perspectives and knowledge gaps in the control and management of kauri dieback in New Zealand. Plant Pathology, 2020, 69, 3-16.	2.4	48
6	DsEcp2-1 is a polymorphic effector that restricts growth of Dothistroma septosporum in pine. Fungal Genetics and Biology, 2020, 135, 103300.	2.1	14
7	Functional analysis of RXLR effectors from the New Zealand kauri dieback pathogen Phytophthora agathidicida. Molecular Plant Pathology, 2020, 21, 1131-1148.	4.2	13
8	Conservation and expansion of a necrosisâ€inducing small secreted protein family from hostâ€variable phytopathogens of the Sclerotiniaceae. Molecular Plant Pathology, 2020, 21, 512-526.	4.2	23
9	Camellia Plant Resistance and Susceptibility to Petal Blight Disease Are Defined by the Timing of Defense Responses. Molecular Plant-Microbe Interactions, 2020, 33, 982-995.	2.6	2
10	Reduced Virulence of an Introduced Forest Pathogen over 50 Years. Microorganisms, 2019, 7, 420.	3.6	6
11	Global population genomics of the forest pathogen Dothistroma septosporum reveal chromosome duplications in high dothistrominâ€producing strains. Molecular Plant Pathology, 2019, 20, 784-799.	4.2	19
12	Evolutionary relics dominate the small number of secondary metabolism genes in the hemibiotrophic fungus Dothistroma septosporum. Fungal Biology, 2019, 123, 397-407.	2.5	6
13	Specific Hypersensitive Responseâ€“Associated Recognition of New Apoplastic Effectors from Cladosporium fulvum in Wild Tomato. Molecular Plant-Microbe Interactions, 2018, 31, 145-162.	2.6	50
14	Genetic diversity of Phytophthora pluvialis, a pathogen of conifers, in New Zealand and the west coast of the United States of America. Plant Pathology, 2018, 67, 1131-1139.	2.4	23
15	Chromatinâ€level regulation of the fragmented dothistromin gene cluster in the forest pathogen Dothistroma septosporum. Molecular Microbiology, 2018, 107, 508-522.	2.5	13
16	Fungal genetics. , 2018, , 35-42.		1
17	Evolution of polyketide synthesis in a Dothideomycete forest pathogen. Fungal Genetics and Biology, 2017, 106, 42-50.	2.1	8
18	Genome-scale investigation of phenotypically distinct but nearly clonalTrichodermastrains. PeerJ, 2016, 4, e2023.	2.0	3

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19	A worldwide perspective on the management and control of Dothistroma needle blight. Forest Pathology, 2016, 46, 472-488.	1.1	58
20	Genomeâ€wide gene expression dynamics of the fungal pathogen <scp>D</scp>othistroma septosporum throughout its infection cycle of the gymnosperm host <scp>P</scp>inus radiata. Molecular Plant Pathology, 2016, 17, 210-224.	4.2	48
21	Global geographic distribution and host range of Dothistroma species: a comprehensive review. Forest Pathology, 2016, 46, 408-442.	1.1	84
22	Growth and fruition of a pathology research community: the Dothistroma story. Forest Pathology, 2016, 46, 383-387.	1.1	3
23	LaeA negatively regulates dothistromin production in the pine needle pathogen Dothistroma septosporum. Fungal Genetics and Biology, 2016, 97, 24-32.	2.1	27
24	A review of Pinaceae resistance mechanisms against needle and shoot pathogens with a focus on the Dothistromaâ€“Pinus interaction. Forest Pathology, 2016, 46, 453-471.	1.1	26
25	A conserved proline residue in Dothideomycete Avr4 effector proteins is required to trigger a Cfâ€4â€dependent hypersensitive response. Molecular Plant Pathology, 2016, 17, 84-95.	4.2	24
26	The hemibiotrophic lifestyle of the fungal pine pathogen Dothistroma septosporum. Forest Pathology, 2015, 45, 190-202.	1.1	22
27	Regulation of the aflatoxin-like toxin dothistromin by AflJ. Fungal Biology, 2015, 119, 503-508.	2.5	4
28	Dothistromin toxin is a virulence factor in dothistroma needle blight of pines. Plant Pathology, 2015, 64, 225-234.	2.4	35
29	Development of microsatellite and mating type markers for the pine needle pathogen Lecanosticta acicola. Australasian Plant Pathology, 2014, 43, 161-165.	1.0	21
30	Detection and quantification of three distinct Neotyphodium lolii endophytes in Lolium perenne by real time PCR of secondary metabolite genes. Fungal Biology, 2014, 118, 316-324.	2.5	11
31	An improved artificial pathogenicity assay for Dothistroma needle blight on Pinus radiata. Australasian Plant Pathology, 2013, 42, 503-510.	1.0	17
32	Dothistromin genes at multiple separate loci are regulated by AflR. Fungal Genetics and Biology, 2013, 51, 12-20.	2.1	30
33	Fragmentation of an aflatoxinâ€like gene cluster in a forest pathogen. New Phytologist, 2013, 198, 525-535.	7.3	55
34	Ciborinia camelliae (Sclerotiniaceae) Induces Variable Plant Resistance Responses in Selected Species of Camellia. Phytopathology, 2013, 103, 725-732.	2.2	14
35	Dothistroma needle blight.. , 2013, , 436-457.		30
36	The Genomes of the Fungal Plant Pathogens Cladosporium fulvum and Dothistroma septosporum Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. PLoS Genetics, 2012, 8, e1003088.	3.5	226

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37	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. PLoS Pathogens, 2012, 8, e1003037.	4.7	595
38	The veA gene of the pine needle pathogen Dothistroma septosporum regulates sporulation and secondary metabolism. Fungal Genetics and Biology, 2012, 49, 141-151.	2.1	46
39	Transformation of Cyclaneusma minus with Green Fluorescent Protein (GFP) to Enable Screening of Fungi for Biocontrol Activity. Forests, 2012, 3, 83-94.	2.1	10
40	A novel GFP-based approach for screening biocontrol microorganisms in vitro against Dothistroma septosporum. Journal of Microbiological Methods, 2011, 87, 32-37.	1.6	18
41	Dothistromin biosynthesis genes allow interâ€•and intraspecific differentiation between Dothistroma pine needle blight fungi. Forest Pathology, 2011, 41, 407-416.	1.1	8
42	Genetics of Dothistromin Biosynthesis in the Peanut Pathogen Passalora arachidicola. Toxins, 2010, 2, 2738-2753.	3.4	3
43	Genetics of Dothistromin Biosynthesis of Dothistroma septosporum: An Update. Toxins, 2010, 2, 2680-2698.	3.4	20
44	Functional Analysis of a Putative Dothistromin Toxin MFS Transporter Gene. Toxins, 2009, 1, 173-187.	3.4	9
45	Dothistromin toxin is not required for dothistroma needle blight in Pinus radiata. Plant Pathology, 2009, 58, 293-304.	2.4	22
46	A novel secondary metabolite from theEucalyptuspathogenMycosphaerella cryptica. Forest Pathology, 2009, 39, 289-292.	1.1	7
47	Early expression of aflatoxin-like dothistromin genes in the forest pathogen Dothistroma septosporum. Mycological Research, 2008, 112, 138-146.	2.5	18
48	Characterization and Distribution of Mating Type Genes in the Dothistroma Needle Blight Pathogens. Phytopathology, 2007, 97, 825-834.	2.2	79
49	A fragmented aflatoxin-like gene cluster in the forest pathogen Dothistroma septosporum. Fungal Genetics and Biology, 2007, 44, 1342-1354.	2.1	35
50	From protoplasts to gene clusters. The Mycologist, 2006, 20, 133-139.	0.4	8
51	Biosynthesis of dothistromin. Mycopathologia, 2006, 162, 201-213.	3.1	28
52	A Polyketide Synthase Gene Required for Biosynthesis of the Aflatoxin-like Toxin, Dothistromin. Mycopathologia, 2006, 161, 283-294.	3.1	41
53	Genomics of the filamentous fungi â€“ moving from the shadow of the bakers yeast. The Mycologist, 2006, 20, 10-14.	0.4	7
54	Dothistroma (red-band) needle blight of pines and the dothistromin toxin: a review. Forest Pathology, 2004, 34, 163-185.	1.1	104

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55	Dothistroma pini , a Forest Pathogen, Contains Homologs of Aflatoxin Biosynthetic Pathway Genes. Applied and Environmental Microbiology, 2002, 68, 2885-2892.	3.1	45
56	First report of apothecia of Tapesia yallundae occurring on the wild grass Holcus lanatus (Yorkshire) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.4	4
57	Cytochrome c is not essential for viability of the fungus Aspergillus nidulans. Molecular Genetics and Genomics, 2001, 266, 48-55.	2.1	14
58	Rapid identification of polymorphic microsatellite loci in a forest pathogen, Dothistroma pini, using anchored PCR. Mycological Research, 2001, 105, 1075-1078.	2.5	10
59	High levels of dothistromin toxin produced by the forest pathogen Dothistroma pini. Mycological Research, 2000, 104, 325-332.	2.5	62
60	Identification of putative regulatory signals including the HAP1 binding site in the upstream sequence of the Aspergillus nidulans cytochrome c gene (cycA).. Fungal Genetics Reports, 1998, 45, 15-18.	0.6	0
61	Transformation of the fungal forest pathogen Dothistroma pini to hygromycin resistance. Mycological Research, 1997, 101, 1247-1250.	2.5	16
62	Gene targeting is locus dependent in the filamentous fungus Aspergillus nidulans. Molecular Genetics and Genomics, 1997, 255, 219-225.	2.4	59
63	A mutualistic fungal symbiont of perennial ryegrass contains two different pyr4 genes, both expressing orotidine-5â€²-monophosphate decarboxylase. Gene, 1995, 158, 31-39.	2.2	22
64	Cloning and characterisation of the cytochrome c gene of Aspergillus nidulans. Molecular Genetics and Genomics, 1994, 242, 17-22.	2.4	13
65	Isolation and nucleotide sequence of the 5-aminolevulinate synthase gene from Aspergillus nidulans. Current Genetics, 1993, 23, 501-507.	1.7	16
66	Isolation and Northern blotting of RNA from Aspergillus nidulans. Journal of Microbiological Methods, 1992, 15, 1-5.	1.6	5
67	Isolation and nucleotide sequence of the ribosomal protein S16-encoding gene from Aspergillus nidulans. Gene, 1991, 108, 157-162.	2.2	6
68	Heat shock and stationary phase induce transcription of the Saccharomyces cerevisiae iso-2 cytochrome c gene. Current Genetics, 1991, 20, 185-188.	1.7	22
69	Aspects of penicillin production in Aspergillus hybrids. Enzyme and Microbial Technology, 1984, 6, 121-126.	3.2	6
70	Protoplast fusion in Aspergillus: selection of interspecific heterokaryons using antifungal inhibitors. Journal of Microbiological Methods, 1984, 3, 27-32.	1.6	9
71	Genetic analysis in Aspergillus rugulosus using the parasexual cycle. Transactions of the British Mycological Society, 1983, 81, 15-19.	0.6	3
72	Efficient protoplast isolation from fungi using commercial enzymes. Enzyme and Microbial Technology, 1981, 3, 321-325.	3.2	155

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73	The secreted proteome of necrotrophic Ciborinia camelliae causes nonâ€hostâ€specific virulence. Plant Pathology, 0, , .	2.4	1
74	In vitro assays of Phytophthora agathidicida on kauri leaves suggest variability in pathogen virulence and host response. New Zealand Plant Protection, 0, 71, 285-288.	0.3	7