

# Laura J Grenville-Briggs

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

3,846  
citations

279487

23  
h-index

205818

48  
g-index

51  
all docs

51  
docs citations

51  
times ranked

3549  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid emergence of boscalid resistance in Swedish populations of <i>Alternaria solani</i> revealed by a combination of field and laboratory experiments. <i>European Journal of Plant Pathology</i> , 2022, 162, 289-303.	0.8	7
2	The hunt for sustainable biocontrol of oomycete plant pathogens, a case study of <i>Phytophthora infestans</i> . <i>Fungal Biology Reviews</i> , 2022, 40, 53-69.	1.9	21
3	Reduced efficacy of biocontrol agents and plant resistance inducers against potato early blight from greenhouse to field. <i>Journal of Plant Diseases and Protection</i> , 2022, 129, 923-938.	1.6	5
4	Altitudinal Heterogeneity of UV Adaptation in <i>Phytophthora infestans</i> Is Associated with the Spatial Distribution of a DNA Repair Gene. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 245.	1.5	5
5	Pathogen-Mediated Stomatal Opening: A Previously Overlooked Pathogenicity Strategy in the Oomycete Pathogen <i>Phytophthora infestans</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 668797.	1.7	11
6	Visualising the ionome in resistant and susceptible plant-pathogen interactions. <i>Plant Journal</i> , 2021, 108, 870-885.	2.8	5
7	Transcriptome Analysis of Potato Infected with the Necrotrophic Pathogen <i>Alternaria solani</i> . <i>Plants</i> , 2021, 10, 2212.	1.6	7
8	Effect of RNA silencing suppression activity of chrysanthemum virus B p12 protein on small RNA species. <i>Archives of Virology</i> , 2020, 165, 2953-2959.	0.9	3
9	What are the Top 10 Unanswered Questions in Molecular Plant-Microbe Interactions?. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1354-1365.	1.4	47
10	Horizontal Gene Transfer and Tandem Duplication Shape the Unique CAZyme Complement of the Mycoparasitic Oomycetes <i>Pythium oligandrum</i> and <i>Pythium periplocum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 581698.	1.5	10
11	Intact salicylic acid signalling is required for potato defence against the necrotrophic fungus <i>Alternaria solani</i> . <i>Plant Molecular Biology</i> , 2020, 104, 1-19.	2.0	32
12	Monitoring and discrimination of Pandemis moths in apple orchards using semiochemicals, wing pattern morphology and DNA barcoding. <i>Crop Protection</i> , 2020, 132, 105110.	1.0	5
13	The presence of <i>Phytophthora infestans</i> in the rhizosphere of a wild <i>Solanum</i> species may contribute to off-season survival and pathogenicity. <i>Applied Soil Ecology</i> , 2020, 148, 103475.	2.1	7
14	Efficient RNA silencing suppression activity of Potato Mop-Top Virus 8K protein is driven by variability and positive selection. <i>Virology</i> , 2019, 535, 111-121.	1.1	8
15	Within-season changes in <i>Alternaria solani</i> populations in potato in response to fungicide application strategies. <i>European Journal of Plant Pathology</i> , 2019, 155, 953-965.	0.8	27
16	Infection mechanisms and putative effector repertoire of the mosquito pathogenic oomycete <i>Pythium guiyangense</i> uncovered by genomic analysis. <i>PLoS Genetics</i> , 2019, 15, e1008116.	1.5	38
17	Tolerance and overcompensation to infection by <i>Phytophthora infestans</i> in the wild perennial climber <i>Solanum dulcamara</i> . <i>Ecology and Evolution</i> , 2019, 9, 4557-4567.	0.8	6
18	Genome Sequence Resource for the Oomycete Taro Pathogen <i>Phytophthora colocasiae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 903-905.	1.4	8

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19	Screening of alternative products for integrated pest management of cucurbit powdery mildew in Sweden. <i>European Journal of Plant Pathology</i> , 2018, 150, 127-138.	0.8	22
20	Draft Genome Sequence for the Tree Pathogen <i>Phytophthora plurivora</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 2432-2442.	1.1	19
21	Draft Genome Sequence of the Mycoparasitic Oomycete <i>Pythium periplocum</i> Strain CBS 532.74. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
22	Draft genome of the oomycete pathogen <i>Phytophthora cactorum</i> strain LV007 isolated from European beech ( <i>Fagus sylvatica</i> ). <i>Genomics Data</i> , 2017, 12, 155-156.	1.3	18
23	<i>Phytophthora infestans</i> effector Pi14054 is a novel candidate suppressor of host silencing mechanisms. <i>European Journal of Plant Pathology</i> , 2017, 149, 771-777.	0.8	17
24	Draft Genome Sequence of the Mycoparasitic Oomycete <i>Pythium oligandrum</i> Strain CBS 530.74. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
25	Proteomic Analysis of <i>Phytophthora infestans</i> Reveals the Importance of Cell Wall Proteins in Pathogenicity. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1958-1971.	2.5	31
26	Earlier occurrence and increased explanatory power of climate for the first incidence of potato late blight caused by <i>Phytophthora infestans</i> in Fennoscandia. <i>PLoS ONE</i> , 2017, 12, e0177580.	1.1	26
27	The occurrence of pathogen suppressive soils in Sweden in relation to soil biota, soil properties, and farming practices. <i>Applied Soil Ecology</i> , 2016, 107, 57-65.	2.1	78
28	Infection of the brown alga <i>Enteromorpha flexilis</i> by the oomycete <i>Urychasma dicksonii</i> induces oxidative stress and halogen metabolism. <i>Plant, Cell and Environment</i> , 2016, 39, 259-271.	2.8	30
29	Comparative mitochondrial genome analysis of <i>Pythium insidiosum</i> and related oomycete species provides new insights into genetic variation and phylogenetic relationships. <i>Gene</i> , 2016, 575, 34-41.	1.0	11
30	Draft Genome Sequence of the Pathogenic Oomycete <i>Pythium insidiosum</i> Strain Pi-S, Isolated from a Patient with Pythiosis. <i>Genome Announcements</i> , 2015, 3, .	0.8	47
31	Auto-aggregation in zoospores of <i>Phytophthora infestans</i> : the cooperative roles of bioconvection and chemotaxis. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140017.	1.5	27
32	Functional characterization of a tyrosinase gene from the oomycete <i>Saprolegnia parasitica</i> by RNAi silencing. <i>Fungal Biology</i> , 2014, 118, 621-629.	1.1	12
33	A family of small tyrosine rich proteins is essential for oogonial and oospore cell wall development of the mycoparasitic oomycete <i>Pythium oligandrum</i> . <i>Fungal Biology</i> , 2013, 117, 163-172.	1.1	14
34	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen <i>Saprolegnia parasitica</i> . <i>PLoS Genetics</i> , 2013, 9, e1003272.	1.5	221
35	The oomycete <i>Pythium oligandrum</i> expresses putative effectors during mycoparasitism of <i>Phytophthora infestans</i> and is amenable to transformation. <i>Fungal Biology</i> , 2012, 116, 24-41.	1.1	74
36	Evidence for involvement of Dicer-like, Argonaute and histone deacetylase proteins in gene silencing in <i>Phytophthora infestans</i> . <i>Molecular Plant Pathology</i> , 2011, 12, 772-785.	2.0	64

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37	Self-directed student research through analysis of microarray datasets: A computer-based functional genomics practical class for masters-level students. <i>Biochemistry and Molecular Biology Education</i> , 2011, 39, 440-447.	0.5	0
38	A Molecular Insight into Algal-Oomycete Warfare: cDNA Analysis of <i>Ectocarpus siliculosus</i> Infected with the Basal Oomycete <i>Eurychasma dicksonii</i> . <i>PLoS ONE</i> , 2011, 6, e24500.	1.1	33
39	Identification of appressorial and mycelial cell wall proteins and a survey of the membrane proteome of <i>Phytophthora infestans</i> . <i>Fungal Biology</i> , 2010, 114, 702-723.	1.1	41
40	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	13.9	391
41	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
42	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
43	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
44	Internuclear gene silencing in <i>Phytophthora infestans</i> is established through chromatin remodelling. <i>Microbiology (United Kingdom)</i> , 2008, 154, 1482-1490.	0.7	71
45	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
46	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
47	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
48	The Biotrophic Stages of Oomycete-Plant Interactions. <i>Advances in Applied Microbiology</i> , 2005, 57, 217-243.	1.3	39
49	Host-Parasite Coevolutionary Conflict Between <i>Arabidopsis</i> and Downy Mildew. <i>Science</i> , 2004, 306, 1957-1960.	6.0	406