Elodie Gaulin

List of Publications by Year in descending order

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FLODIE CALLIN

#	Article	IF	CITATIONS
1	Pathogenicity of animal and plant parasitic Aphanomyces spp and their economic impact on aquaculture and agriculture. Fungal Biology Reviews, 2022, 40, 1-18.	4.7	11
2	A Comprehensive Assessment of the Secretome Responsible for Host Adaptation of the Legume Root Pathogen Aphanomyces euteiches. Journal of Fungi (Basel, Switzerland), 2022, 8, 88.	3.5	4
3	An oomycete effector targets a plant RNA helicase involved in root development and defense. New Phytologist, 2022, 233, 2232-2248.	7.3	12
4	Long-Read Genome Sequence of the Sugar Beet Rhizosphere Mycoparasite <i>Pythium oligandrum</i> . G3: Genes, Genomes, Genetics, 2020, 10, 431-436.	1.8	18
5	DNA-Damaging Effectors: New Players in the Effector Arena. Trends in Plant Science, 2019, 24, 1094-1101.	8.8	13
6	Preparation of Plant Material for Analysis of Protein–Nucleic Acid Interactions by FRET-FLIM. Methods in Molecular Biology, 2019, 1991, 69-77.	0.9	4
7	Genomics analysis of Aphanomyces spp. identifies a new class of oomycete effector associated with host adaptation. BMC Biology, 2018, 16, 43.	3.8	62
8	Detection of nucleic acid–protein interactions in plant leaves using fluorescence lifetime imaging microscopy. Nature Protocols, 2017, 12, 1933-1950.	12.0	42
9	<scp>CRN</scp> 13 candidate effectors from plant and animal eukaryotic pathogens are <scp>DNA</scp> â€binding proteins which trigger host <scp>DNA</scp> damage response. New Phytologist, 2016, 210, 602-617.	7.3	54
10	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen Saprolegnia parasitica. PLoS Genetics, 2013, 9, e1003272.	3.5	221
11	The unique architecture and function of cellulose-interacting proteins in oomycetes revealed by genomic and structural analyses. BMC Genomics, 2012, 13, 605.	2.8	40
12	Ancient class of translocated oomycete effectors targets the host nucleus. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17421-17426.	7.1	326
13	Signatures of Adaptation to Obligate Biotrophy in the <i>Hyaloperonospora arabidopsidis</i> Genome. Science, 2010, 330, 1549-1551.	12.6	492
14	Genome sequence of the necrotrophic plant pathogen Pythium ultimum reveals original pathogenicity mechanisms and effector repertoire. Genome Biology, 2010, 11, R73.	9.6	391
15	Transcriptome of Aphanomyces euteiches: New Oomycete Putative Pathogenicity Factors and Metabolic Pathways. PLoS ONE, 2008, 3, e1723.	2.5	109
16	Root rot disease of legumes caused by <i>Aphanomyces euteiches</i> . Molecular Plant Pathology, 2007, 8, 539-548.	4.2	140
17	AphanoDB: a genomic resource for Aphanomyces pathogens. BMC Genomics, 2007, 8, 471.	2.8	43
18	Cellulose Binding Domains of a Phytophthora Cell Wall Protein Are Novel Pathogen-Associated Molecular Patterns. Plant Cell, 2006, 18, 1766-1777.	6.6	149

#	Article	IF	CITATIONS
19	The CBEL glycoprotein ofPhytophthora parasiticavar-nicotianaeis involved in cell wall deposition and adhesion to cellulosic substrates. Journal of Cell Science, 2002, 115, 4565-4575.	2.0	164