Gaétan Le Floch

List of Publications by Year in descending order

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62 papers

2,153 citations

218381 26 h-index 253896 43 g-index

65 all docs 65 docs citations

times ranked

65

2802 citing authors

#	Article	IF	CITATIONS
1	Gene family expansions and contractions are associated with host range in plant pathogens of the genus Colletotrichum. BMC Genomics, 2016, 17, 555.	1.2	151
2	Antimicrobial, antioxidant and phytochemical investigations of sea buckthorn (Hippophaë rhamnoides) Tj ETQc	10	/Qyerlock 10
3	Radical scavenging, antioxidant and antimicrobial activities of halophytic species. Journal of Ethnopharmacology, 2008, 116, 258-262.	2.0	119
4	Biological control of plant pathogens: advantages and limitations seen through the case study of Pythium oligandrum. Environmental Science and Pollution Research, 2014, 21, 4847-4860.	2.7	107
5	Effect of tillage and static abiotic soil properties on microbial diversity. Applied Soil Ecology, 2018, 132, 135-145.	2.1	101
6	Pythium oligandrum: an example of opportunistic success. Microbiology (United Kingdom), 2012, 158, 2679-2694.	0.7	89
7	Challenges facing the biological control strategies for the management of Fusarium Head Blight of cereals caused by F. graminearum. Biological Control, 2017, 113, 26-38.	1.4	88
8	Molecular techniques for pathogen identification and fungus detection in the environment. IMA Fungus, $2011, 2, 177-189$.	1.7	81
9	New antibacterial and cytotoxic activities of falcarindiol isolated in Crithmum maritimum L. leaf extract. Food and Chemical Toxicology, 2010, 48, 553-557.	1.8	66
10	The Colletotrichum acutatum Species Complex as a Model System to Study Evolution and Host Specialization in Plant Pathogens. Frontiers in Microbiology, 2017, 8, 2001.	1.5	61
11	Influence of <i>Pythium oligandrum</i> Biocontrol on Fungal and Oomycete Population Dynamics in the Rhizosphere. Applied and Environmental Microbiology, 2009, 75, 4790-4800.	1.4	55
12	Pathogenic and beneficial microorganisms in soilless cultures. Agronomy for Sustainable Development, 2011, 31, 191-203.	2.2	55
13	Impact of auxin-compounds produced by the antagonistic fungus Pythium oligandrum or the minor pathogen Pythium group F on plant growth. Plant and Soil, 2003, 257, 459-470.	1.8	53
14	Combined Metabarcoding and Co-occurrence Network Analysis to Profile the Bacterial, Fungal and Fusarium Communities and Their Interactions in Maize Stalks. Frontiers in Microbiology, 2019, 10, 261.	1.5	51
15	Insights into Penicillium roqueforti Morphological and Genetic Diversity. PLoS ONE, 2015, 10, e0129849.	1.1	46
16	Enhancement of development and induction of resistance in tomato plants by the antagonist, Pythium oligandrum. Agronomy for Sustainable Development, 2003, 23, 455-460.	0.8	45
17	Aquatic Bacterial Communities Associated With Land Use and Environmental Factors in Agricultural Landscapes Using a Metabarcoding Approach. Frontiers in Microbiology, 2018, 9, 2301.	1.5	44
18	Combining the oomycete Pythium oligandrum with two other antagonistic fungi: Root relationships and tomato grey mold biocontrol. Biological Control, 2009, 50, 288-298.	1.4	43

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19	Bacterial Blight Induced Shifts in Endophytic Microbiome of Rice Leaves and the Enrichment of Specific Bacterial Strains With Pathogen Antagonism. Frontiers in Plant Science, 2020, 11, 963.	1.7	40
20	Fungal Planet description sheets: 1182–1283. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2021, , .	1.6	40
21	Characterisation of the early events in atypical tomato root colonisation by a biocontrol agent, Pythium oligandrum. Plant Physiology and Biochemistry, 2005, 43, 1-11.	2.8	38
22	Rhizosphere persistence of three Pythium oligandrum strains in tomato soilless culture assessed by DNA macroarray and real-time PCR. FEMS Microbiology Ecology, 2007, 61, 317-326.	1.3	36
23	Pneumocystis jirovecii in the air surrounding patients with Pneumocystis pulmonary colonization. Diagnostic Microbiology and Infectious Disease, 2015, 82, 137-142.	0.8	34
24	Microbiota in the Rhizosphere and Seed of Rice From China, With Reference to Their Transmission and Biogeography. Frontiers in Microbiology, 2020, 11, 995.	1.5	32
25	Assessing Performance of Spore Samplers in Monitoring Aeromycobiota and Fungal Plant Pathogen Diversity in Canada. Applied and Environmental Microbiology, 2018, 84, .	1.4	31
26	Combined Metabarcoding and Multi-locus approach for Genetic characterization of Colletotrichum species associated with common walnut (Juglans regia) anthracnose in France. Scientific Reports, 2018, 8, 10765.	1.6	29
27	Polyphenol content and biological activities of Mesembryanthemum edule organs after fractionation. Industrial Crops and Products, 2013, 42, 145-152.	2.5	28
28	Draft Genome Sequence of Pantoea ananatis Strain LMG 2665 T , a Bacterial Pathogen of Pineapple Fruitlets. Genome Announcements, 2014, 2, .	0.8	28
29	Rhizosphere microbiota assemblage associated with wild and cultivated soybeans grown in three types of soil suspensions. Archives of Agronomy and Soil Science, 2019, 65, 74-87.	1.3	28
30	Interactions between the mycoparasite Pythium oligandrum and two types of sclerotia of plant-pathogenic fungi. Mycological Research, 2005, 109, 779-788.	2.5	27
31	Modelling the effect of temperature, water activity and pH on the growth of Serpula lacrymans. Journal of Applied Microbiology, 2011, 111, 1436-1446.	1.4	27
32	Development of Crop.LCA, an adaptable screening life cycle assessment tool for agricultural systems: A Canadian scenario assessment. Journal of Cleaner Production, 2018, 172, 3770-3780.	4.6	26
33	A novel metabarcoding approach to investigate Fusarium species composition in soil and plant samples. FEMS Microbiology Ecology, 2019, 95, .	1.3	25
34	The Ecobiomics project: Advancing metagenomics assessment of soil health and freshwater quality in Canada. Science of the Total Environment, 2020, 710, 135906.	3.9	25
35	Whole-Genome Sequence of the Orchid Anthracnose Pathogen <i>Colletotrichum orchidophilum</i> . Molecular Plant-Microbe Interactions, 2018, 31, 979-981.	1.4	21
36	Molecular Detection of the Seed-Borne Pathogen Colletotrichum lupini Targeting the Hyper-Variable IGS Region of the Ribosomal Cluster. Plants, 2019, 8, 222.	1.6	18

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37	Phylogenetic Diversity and Effect of Temperature on Pathogenicity of Colletotrichum lupini. Plant Disease, 2020, 104, 938-950.	0.7	18
38	Deciphering the Infectious Process of Colletotrichum lupini in Lupin through Transcriptomic and Proteomic Analysis. Microorganisms, 2020, 8, 1621.	1.6	18
39	Evolution of the amino acid fingerprint in the unsterilized rhizosphere of a legume in relation to plant maturity. Soil Biology and Biochemistry, 2016, 101, 226-236.	4.2	17
40	Improved molecular methods to characterise Serpula lacrymans and other Basidiomycetes involved in wood decay. Journal of Microbiological Methods, 2011, 84, 208-215.	0.7	16
41	Application of denaturing high-performance liquid chromatography (DHPLC) for yeasts identification in red smear cheese surfaces. Letters in Applied Microbiology, 2010, 51, no-no.	1.0	15
42	Co-occurrence analysis reveal that biotic and abiotic factors influence soil fungistasis against Fusarium graminearum. FEMS Microbiology Ecology, 2019, 95, .	1.3	15
43	First Report of <i>Colletotrichum fructicola</i> Causing Apple Bitter Rot in Europe. Plant Disease, 2019, 103, 1767.	0.7	13
44	Development of qPCR assays to monitor the ability of Gliocladium catenulatum J1446 to reduce the cereal pathogen Fusarium graminearum inoculum in soils. European Journal of Plant Pathology, 2018, 152, 285-295.	0.8	12
45	Phylogeny of Canadian ergot fungi and a detection assay by real-time polymerase chain reaction. Mycologia, 2019, 111, 493-505.	0.8	12
46	First Report of Apple Bitter Rot Caused by <i>Colletotrichum fioriniae</i> in Brittany, France. Plant Disease, 2016, 100, 1497-1497.	0.7	11
47	Towards Improved Detection and Identification of Rust Fungal Pathogens in Environmental Samples Using a Metabarcoding Approach. Phytopathology, 2022, 112, 535-548.	1.1	10
48	Complete Genome Sequence of the plant pathogenic fungus Colletotrichum lupini Molecular Plant-Microbe Interactions, 2021, , MPMI07210173A.	1.4	9
49	Draft Genome Sequences of Three <i>Arcobacter</i> Strains of Pig and Dairy Cattle Manure Origin. Genome Announcements, 2014, 2, .	0.8	8
50	Influence of Maize Residues in Shaping Soil Microbiota and Fusarium spp. Communities. Microbial Ecology, 2022, 83, 702-713.	1.4	8
51	Population structure of Serpula lacrymans in Europe with an outlook to the French population. Mycologia, 2014, 106, 889-895.	0.8	7
52	First Report of Pear Bitter Rot Caused by <i>Colletotrichum fioriniae</i> in France. Plant Disease, 2017, 101, 1319-1319.	0.7	7
53	Pollination, Fertilization and Floral Traits Co-Segregating with Autofertility in Faba Bean. Journal of New Seeds, 2009, 10, 14-30.	0.3	6
54	Identification and Characterization of a New Type III Polyketide Synthase from a Marine Yeast, Naganishia uzbekistanensis. Marine Drugs, 2020, 18, 637.	2.2	4

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55	Eelgrass Slabs, a Soilless Culture Substrate That Inhibits Adhesion of Fungi and Oomycetes and Enhances Antioxidant Activity in Tomato. Journal of Agricultural and Food Chemistry, 2011, 59, 10913-10918.	2.4	3
56	Draft Genome Sequence of Pectobacterium wasabiae Strain CFIA1002. Genome Announcements, 2014, 2, .	0.8	3
57	Water Microbiota in Greenhouses With Soilless Cultures of Tomato by Metabarcoding and Culture-Dependent Approaches. Frontiers in Microbiology, 2020, 11, 1354.	1.5	3
58	L'unité biologique du bulbe d'Échalote au cours du temps. Acta Botanica Gallica, 1999, 146, 169-178.	0.9	2
59	Improving Complementarity Effect of Legume Intercrop by Earthworm Facilitation for Wheat Performance. Journal of Agricultural Science, 2019, 10, 1.	0.1	1
60	<i>Colletotrichum</i> : new pathogen in walnut orchards – characterization of the fungus and research on control methods. Acta Horticulturae, 2021, , 147-150.	0.1	0
61	Capacité des sols forestiers tropicaux de Guyane et de la Réunion à dépolluer les bois imprégnés de biocides. Bois Et Forets Des Tropiques, 2013, 318, 51.	0.2	0
62	Draft Genome Sequence of <i>Helicobacter</i> sp. Strain CaF467b, Isolated from a Pig Manure Storage Tank. Microbiology Resource Announcements, 0, , .	0.3	0