

Etienne Yergeau

List of Publications by Year in descending order

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Version: 2024-02-01

100
papers

6,903
citations

46918

47
h-index

62479

80
g-index

105
all docs

105
docs citations

105
times ranked

7692
citing authors

#	ARTICLE	IF	CITATIONS
1	The nitrification inhibitor nitrapyrin has non-target effects on the soil microbial community structure, composition, and functions. <i>Applied Soil Ecology</i> , 2022, 171, 104350.	2.1	9
2	Plastic mulch film residues in agriculture: impact on soil suppressiveness, plant growth, and microbial communities. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	18
3	Predictive microbial-based modelling of wheat yields and grain baking quality across a 500 km ² transect in Québec. <i>FEMS Microbiology Ecology</i> , 2022, 97, .	1.3	6
4	A Drying-Rewetting Cycle Imposes More Important Shifts on Soil Microbial Communities than Does Reduced Precipitation. <i>MSystems</i> , 2022, 7, .	1.7	12
5	Rhizospheric Plant-Microbe Interactions: miRNAs as a Key Mediator. <i>Trends in Plant Science</i> , 2021, 26, 132-141.	4.3	45
6	Sows affect their piglets' faecal microbiota until fattening but not their <i>Salmonella enterica</i> shedding status. <i>Letters in Applied Microbiology</i> , 2021, 72, 113-120.	1.0	1
7	Soil Characteristics Constrain the Response of Microbial Communities and Associated Hydrocarbon Degradation Genes during Phytoremediation. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	17
8	Rhizosphere shotgun metagenomic analyses fail to show differences between ancestral and modern wheat genotypes grown under low fertilizer inputs. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	3
9	Soybean Microbiome Recovery After Disruption is Modulated by the Seed and Not the Soil Microbiome. <i>Phytobiomes Journal</i> , 2021, 5, 418-431.	1.4	23
10	Engineering the plant microbiota in the context of the theory of ecological communities. <i>Current Opinion in Biotechnology</i> , 2021, 70, 220-225.	3.3	21
11	Hydrocarbon substrate richness impacts microbial abundance, microbiome composition, and hydrocarbon loss. <i>Applied Soil Ecology</i> , 2021, 165, 104015.	2.1	3
12	Effects of arbuscular mycorrhizal fungi inoculation and crop sequence on root-associated microbiome, crop productivity and nutrient uptake in wheat-based and flax-based cropping systems. <i>Applied Soil Ecology</i> , 2021, 168, 104136.	2.1	10
13	Plant Compartments and Developmental Stages Modulate the Balance between Niche-Based and Neutral Processes in Soybean Microbiome. <i>Microbial Ecology</i> , 2021, 82, 416-428.	1.4	27
14	Temporal and spatial interactions modulate the soybean microbiome. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	17
15	The resistance of the wheat microbial community to water stress is more influenced by plant compartment than reduced water availability. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	8
16	Relative and Quantitative Rhizosphere Microbiome Profiling Results in Distinct Abundance Patterns. <i>Frontiers in Microbiology</i> , 2021, 12, 798023.	1.5	8
17	Microbial indicators are better predictors of wheat yield and quality than N fertilization. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	31
18	Phenanthrene contamination and ploidy level affect the rhizosphere bacterial communities of <i>Spartina</i> spp.. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	8

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19	Field H2 infusion alters bacterial and archaeal communities but not fungal communities nor nitrogen cycle gene abundance. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108018.	4.2	11
20	A Gaseous Milieu: Extending the Boundaries of the Rhizosphere. <i>Trends in Microbiology</i> , 2020, 28, 536-542.	3.5	43
21	Four decades of soil water stress history together with host genotype constrain the response of the wheat microbiome to soil moisture. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	43
22	A water stress-adapted inoculum affects rhizosphere fungi, but not bacteria nor wheat. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	12
23	Manipulating Wild and Tamed Phytobiomes: Challenges and Opportunities. <i>Phytobiomes Journal</i> , 2019, 3, 3-21.	1.4	38
24	7. Techniques and approaches to quantify microbial diversity in extreme environments. , 2019, , 151-166.		0
25	Systematic processing of ribosomal RNA gene amplicon sequencing data. <i>GigaScience</i> , 2019, 8, .	3.3	49
26	<i>Salmonella</i> shedding status of the sow affects the microbiota of their piglets at weaning. <i>Journal of Applied Microbiology</i> , 2019, 126, 411-423.	1.4	16
27	The impact of reconstructed soils following oil sands exploitation on aspen and its associated belowground microbiome. <i>Scientific Reports</i> , 2018, 8, 2761.	1.6	11
28	Soil contamination alters the willow root and rhizosphere metatranscriptome and the root-rhizosphere interactome. <i>ISME Journal</i> , 2018, 12, 869-884.	4.4	91
29	Bacterial Subspecies Variation and Nematode Grazing Change P Dynamics in the Wheat Rhizosphere. <i>Frontiers in Microbiology</i> , 2018, 9, 1990.	1.5	10
30	Water stress history and wheat genotype modulate rhizosphere microbial response to drought. <i>Soil Biology and Biochemistry</i> , 2018, 126, 228-236.	4.2	45
31	Rhizoremediation of petroleum hydrocarbons: a model system for plant microbiome manipulation. <i>Microbial Biotechnology</i> , 2018, 11, 819-832.	2.0	88
32	Canola Root-Associated Microbiomes in the Canadian Prairies. <i>Frontiers in Microbiology</i> , 2018, 9, 1188.	1.5	85
33	Trees, fungi and bacteria: tripartite metatranscriptomics of a root microbiome responding to soil contamination. <i>Microbiome</i> , 2018, 6, 53.	4.9	88
34	<i>Serratia marcescens</i> Outbreak in a Neonatal Intensive Care Unit: New Insights from Next-Generation Sequencing Applications. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	34
35	Metagenomic survey of the taxonomic and functional microbial communities of seawater and sea ice from the Canadian Arctic. <i>Scientific Reports</i> , 2017, 7, 42242.	1.6	59
36	Chemical dispersants enhance the activity of oil- and gas condensate-degrading marine bacteria. <i>ISME Journal</i> , 2017, 11, 2793-2808.	4.4	114

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37	Feed presentation options in Swine early fattening mitigates <i>Salmonella</i> shedding and specifically modulates the faecal microbiota. <i>Journal of Applied Microbiology</i> , 2017, 122, 30-39.	1.4	7
38	Editorial: Signaling in the Phytomicrobiome. <i>Frontiers in Plant Science</i> , 2017, 8, 611.	1.7	69
39	Lack of Evidence That Selenium-Yeast Improves Chicken Health and Modulates the Caecal Microbiota in the Context of Colonization by <i>Campylobacter jejuni</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 451.	1.5	24
40	Reduction of <i>Salmonella</i> Shedding by Sows during Gestation in Relation to Its Fecal Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 2219.	1.5	17
41	The Willow Microbiome Is Influenced by Soil Petroleum-Hydrocarbon Concentration with Plant Compartment-Specific Effects. <i>Frontiers in Microbiology</i> , 2016, 7, 1363.	1.5	75
42	Comparison of Methods to Identify Pathogens and Associated Virulence Functional Genes in Biosolids from Two Different Wastewater Treatment Facilities in Canada. <i>PLoS ONE</i> , 2016, 11, e0153554.	1.1	16
43	A Diverse Soil Microbiome Degrades More Crude Oil than Specialized Bacterial Assemblages Obtained in Culture. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5530-5541.	1.4	63
44	Early rhizosphere microbiome composition is related to the growth and Zn uptake of willows introduced to a former landfill. <i>Environmental Microbiology</i> , 2015, 17, 3025-3038.	1.8	61
45	Metaproteomics of aquatic microbial communities in a deep and stratified estuary. <i>Proteomics</i> , 2015, 15, 3566-3579.	1.3	26
46	Transplanting Soil Microbiomes Leads to Lasting Effects on Willow Growth, but not on the Rhizosphere Microbiome. <i>Frontiers in Microbiology</i> , 2015, 6, 1436.	1.5	98
47	Chicken Caecal Microbiome Modifications Induced by <i>Campylobacter jejuni</i> Colonization and by a Non-Antibiotic Feed Additive. <i>PLoS ONE</i> , 2015, 10, e0131978.	1.1	123
48	<i>Salix purpurea</i> Stimulates the Expression of Specific Bacterial Xenobiotic Degradation Genes in a Soil Contaminated with Hydrocarbons. <i>PLoS ONE</i> , 2015, 10, e0132062.	1.1	75
49	Harnessing phytomicrobiome signaling for rhizosphere microbiome engineering. <i>Frontiers in Plant Science</i> , 2015, 6, 507.	1.7	176
50	Microbial Community Composition, Functions, and Activities in the Gulf of Mexico 1 Year after the Deepwater Horizon Accident. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5855-5866.	1.4	64
51	Diversity and complexity of microbial communities from a chlor-alkali tailings dump. <i>Soil Biology and Biochemistry</i> , 2015, 90, 101-110.	4.2	54
52	Omics Insights into PAH Degradation toward Improved Green Remediation Biotechnologies. <i>Environmental Science & Technology</i> , 2015, 49, 11281-11291.	4.6	138
53	Importance of <i>Rhodococcus</i> strains in a bacterial consortium degrading a mixture of hydrocarbons, gasoline, and diesel oil additives revealed by metatranscriptomic analysis. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 2419-2430.	1.7	47
54	Next-generation Sequencing of 16S Ribosomal RNA Gene Amplicons. <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	69

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55	Bacterial community structure and soil properties of a subarctic tundra soil in Council, Alaska. <i>FEMS Microbiology Ecology</i> , 2014, 89, 465-475.	1.3	121
56	Linkage between bacterial and fungal rhizosphere communities in hydrocarbon-contaminated soils is related to plant phylogeny. <i>ISME Journal</i> , 2014, 8, 331-343.	4.4	190
57	Atmospheric methane oxidizers are present and active in Canadian high Arctic soils. <i>FEMS Microbiology Ecology</i> , 2014, 89, 257-269.	1.3	45
58	Increasing phytoremediation efficiency and reliability using novel omics approaches. <i>Trends in Biotechnology</i> , 2014, 32, 271-280.	4.9	148
59	Microbial expression profiles in the rhizosphere of willows depend on soil contamination. <i>ISME Journal</i> , 2014, 8, 344-358.	4.4	229
60	Biogeochemical activity of microbial biofilms in the water column overlying uranium mine tailings. <i>Journal of Applied Microbiology</i> , 2014, 117, 1079-1094.	1.4	16
61	Fell-Field Soil Microbiology. , 2014, , 115-129.		4
62	Microbial Functional Potential and Community Composition in Permafrost-Affected Soils of the NW Canadian Arctic. <i>PLoS ONE</i> , 2014, 9, e84761.	1.1	79
63	Climate Change and Microbial Populations. , 2014, , 249-261.		0
64	Impact of water quality on the bacterial populations and off-flavours in recirculating aquaculture systems. <i>FEMS Microbiology Ecology</i> , 2013, 84, 235-247.	1.3	45
65	Microbial communities in low permeability, high pH uranium mine tailings: characterization and potential effects. <i>Journal of Applied Microbiology</i> , 2013, 114, 1671-1686.	1.4	74
66	Alteration of microbial community structure affects diesel biodegradation in an Arctic soil. <i>FEMS Microbiology Ecology</i> , 2013, 85, 51-61.	1.3	54
67	Increased microbial activity and nitrogen mineralization coupled to changes in microbial community structure in the rhizosphere of Bt corn. <i>Applied Soil Ecology</i> , 2013, 68, 46-56.	2.1	13
68	Predictable bacterial composition and hydrocarbon degradation in Arctic soils following diesel and nutrient disturbance. <i>ISME Journal</i> , 2013, 7, 1200-1210.	4.4	190
69	Aerobic Biofilms Grown from Athabasca Watershed Sediments Are Inhibited by Increasing Concentrations of Bituminous Compounds. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7398-7412.	1.4	26
70	Defining the Functional Potential and Active Community Members of a Sediment Microbial Community in a High-Arctic Hypersaline Subzero Spring. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3637-3648.	1.4	51
71	Plant and Bird Presence Strongly Influences the Microbial Communities in Soils of Admiralty Bay, Maritime Antarctica. <i>PLoS ONE</i> , 2013, 8, e66109.	1.1	35
72	Metagenomics Potential for Bioremediation. , 2012, , 1-11.		1

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73	Next-Generation Sequencing of Microbial Communities in the Athabasca River and Its Tributaries in Relation to Oil Sands Mining Activities. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7626-7637.	1.4	193
74	Shifts in soil microorganisms in response to warming are consistent across a range of Antarctic environments. <i>ISME Journal</i> , 2012, 6, 692-702.	4.4	258
75	Metagenomic Analysis of the Bioremediation of Diesel-Contaminated Canadian High Arctic Soils. <i>PLoS ONE</i> , 2012, 7, e30058.	1.1	210
76	Soil characteristics more strongly influence soil bacterial communities than land-use type. <i>FEMS Microbiology Ecology</i> , 2012, 79, 12-24.	1.3	347
77	Subinhibitory concentrations of different pharmaceutical products affect the metatranscriptome of river biofilm communities cultivated in rotating annular reactors. <i>Environmental Microbiology Reports</i> , 2012, 4, 350-359.	1.0	46
78	Community patterns of soil bacteria and nematodes in relation to geographic distance. <i>Soil Biology and Biochemistry</i> , 2012, 45, 1-7.	4.2	56
79	Identification of Nitrogen-Incorporating Bacteria in Petroleum-Contaminated Arctic Soils by Using [¹⁵ N]DNA-Based Stable Isotope Probing and Pyrosequencing. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4163-4171.	1.4	120
80	Influences of space, soil, nematodes and plants on microbial community composition of chalk grassland soils. <i>Environmental Microbiology</i> , 2010, 12, 2096-2106.	1.8	54
81	Patterns of <i>Fusarium</i> community structure and abundance in relation to spatial, abiotic and biotic factors in soil. <i>FEMS Microbiology Ecology</i> , 2010, 71, 34-42.	1.3	32
82	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010, 4, 711-715.	4.4	73
83	The functional potential of high Arctic permafrost revealed by metagenomic sequencing, qPCR and microarray analyses. <i>ISME Journal</i> , 2010, 4, 1206-1214.	4.4	273
84	Metatranscriptomic Analysis of the Response of River Biofilms to Pharmaceutical Products, Using Anonymous DNA Microarrays. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5432-5439.	1.4	50
85	Temperature adaptation of soil bacterial communities along an Antarctic climate gradient: predicting responses to climate warming. <i>Global Change Biology</i> , 2009, 15, 2615-2625.	4.2	119
86	Environmental microarray analyses of Antarctic soil microbial communities. <i>ISME Journal</i> , 2009, 3, 340-351.	4.4	156
87	Microarray and Real-Time PCR Analyses of the Responses of High-Arctic Soil Bacteria to Hydrocarbon Pollution and Bioremediation Treatments. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6258-6267.	1.4	115
88	Responses of Antarctic soil microbial communities and associated functions to temperature and freeze-thaw cycle frequency. <i>Environmental Microbiology</i> , 2008, 10, 2223-2235.	1.8	177
89	Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. <i>ISME Journal</i> , 2007, 1, 163-179.	4.4	232
90	Patterns of bacterial diversity across a range of Antarctic terrestrial habitats. <i>Environmental Microbiology</i> , 2007, 9, 2670-2682.	1.8	267

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91	Impact of elevated carbon dioxide on the rhizosphere communities of <i>Carex arenaria</i> and <i>Festuca rubra</i> . <i>Global Change Biology</i> , 2007, 13, 2396-2410.	4.2	73
92	Assessing Bacterial and Fungal Community Structure in Soil Using Ribosomal RNA and Other Structural Gene Markers. <i>Soil Biology</i> , 2006, , 159-188.	0.6	15
93	Relationships between <i>Fusarium</i> population structure, soil nutrient status and disease incidence in field-grown asparagus. <i>FEMS Microbiology Ecology</i> , 2006, 58, 394-403.	1.3	35
94	Size and structure of bacterial, fungal and nematode communities along an Antarctic environmental gradient. <i>FEMS Microbiology Ecology</i> , 2006, 59, 436-451.	1.3	202
95	Biodiversity and Biogeography of <i>Fusarium</i> Species from Northeastern North American Asparagus Fields Based on Microbiological and Molecular Approaches. <i>Microbial Ecology</i> , 2006, 51, 242-255.	1.4	56
96	Changes in Communities of <i>Fusarium</i> and Arbuscular Mycorrhizal Fungi as Related to Different Asparagus Cultural Factors. <i>Microbial Ecology</i> , 2006, 52, 104-113.	1.4	28
97	A PCR-denaturing gradient gel electrophoresis approach to assess <i>Fusarium</i> diversity in asparagus. <i>Journal of Microbiological Methods</i> , 2005, 60, 143-154.	0.7	83
98	Digestive microbiota changes during application of an effective, feed presentation based, mitigation option against <i>Salmonella</i> shedding in pigs. , 0, , .		0
99	Metagenomic Analysis of Polar Ecosystems. , 0, , 156-165.		0
100	Evolution of <i>Salmonella</i> excretion by sows during gestation in link with the faecal microbiome. , 0, , .		0