

# 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	Soil characteristics more strongly influence soil bacterial communities than land-use type. FEMS Microbiology Ecology, 2012, 79, 12-24.	1.3	347
2	The functional potential of high Arctic permafrost revealed by metagenomic sequencing, qPCR and microarray analyses. ISME Journal, 2010, 4, 1206-1214.	4.4	273
3	Patterns of bacterial diversity across a range of Antarctic terrestrial habitats. Environmental Microbiology, 2007, 9, 2670-2682.	1.8	267
4	Shifts in soil microorganisms in response to warming are consistent across a range of Antarctic environments. ISME Journal, 2012, 6, 692-702.	4.4	258
5	Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. ISME Journal, 2007, 1, 163-179.	4.4	232
6	Microbial expression profiles in the rhizosphere of willows depend on soil contamination. ISME Journal, 2014, 8, 344-358.	4.4	229
7	Metagenomic Analysis of the Bioremediation of Diesel-Contaminated Canadian High Arctic Soils. PLoS ONE, 2012, 7, e30058.	1.1	210
8	Size and structure of bacterial, fungal and nematode communities along an Antarctic environmental gradient. FEMS Microbiology Ecology, 2006, 59, 436-451.	1.3	202
9	Next-Generation Sequencing of Microbial Communities in the Athabasca River and Its Tributaries in Relation to Oil Sands Mining Activities. Applied and Environmental Microbiology, 2012, 78, 7626-7637.	1.4	193
10	Predictable bacterial composition and hydrocarbon degradation in Arctic soils following diesel and nutrient disturbance. ISME Journal, 2013, 7, 1200-1210.	4.4	190
11	Linkage between bacterial and fungal rhizosphere communities in hydrocarbon-contaminated soils is related to plant phylogeny. ISME Journal, 2014, 8, 331-343.	4.4	190
12	Responses of Antarctic soil microbial communities and associated functions to temperature and freeze-thaw cycle frequency. Environmental Microbiology, 2008, 10, 2223-2235.	1.8	177
13	Harnessing phytomicrobiome signaling for rhizosphere microbiome engineering. Frontiers in Plant Science, 2015, 6, 507.	1.7	176
14	Environmental microarray analyses of Antarctic soil microbial communities. ISME Journal, 2009, 3, 340-351.	4.4	156
15	Increasing phytoremediation efficiency and reliability using novel omics approaches. Trends in Biotechnology, 2014, 32, 271-280.	4.9	148
16	Omics Insights into PAH Degradation toward Improved Green Remediation Biotechnologies. Environmental Science & Technology, 2015, 49, 11281-11291.	4.6	138
17	Chicken Caecal Microbiome Modifications Induced by Campylobacter jejuni Colonization and by a Non-Antibiotic Feed Additive. PLoS ONE, 2015, 10, e0131978.	1.1	123
18	Bacterial community structure and soil properties of a subarctic tundra soil in Council, Alaska. FEMS Microbiology Ecology, 2014, 89, 465-475.	1.3	121

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19	Identification of Nitrogen-Incorporating Bacteria in Petroleum-Contaminated Arctic Soils by Using [ <sup>15</sup> N]DNA-Based Stable Isotope Probing and Pyrosequencing. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4163-4171.	1.4	120
20	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
21	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
22	Chemical dispersants enhance the activity of oil- and gas condensate-degrading marine bacteria. <i>ISME Journal</i> , 2017, 11, 2793-2808.	4.4	114
23	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
24	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
25	Rhizoremediation of petroleum hydrocarbons: a model system for plant microbiome manipulation. <i>Microbial Biotechnology</i> , 2018, 11, 819-832.	2.0	88
26	Trees, fungi and bacteria: tripartite metatranscriptomics of a root microbiome responding to soil contamination. <i>Microbiome</i> , 2018, 6, 53.	4.9	88
27	Canola Root-Associated Microbiomes in the Canadian Prairies. <i>Frontiers in Microbiology</i> , 2018, 9, 1188.	1.5	85
28	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
29	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
30	<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
31	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
32	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
33	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
34	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010, 4, 711-715.	4.4	73
35	Next-generation Sequencing of 16S Ribosomal RNA Gene Amplicons. <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	69
36	Editorial: Signaling in the Phytomicrobiome. <i>Frontiers in Plant Science</i> , 2017, 8, 611.	1.7	69

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37	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
38	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
39	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
40	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
41	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
42	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
43	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
44	Alteration of microbial community structure affects diesel biodegradation in an Arctic soil. <i>FEMS Microbiology Ecology</i> , 2013, 85, 51-61.	1.3	54
45	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
46	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
47	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
48	Systematic processing of ribosomal RNA gene amplicon sequencing data. <i>GigaScience</i> , 2019, 8, .	3.3	49
49	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
50	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
51	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
52	Atmospheric methane oxidizers are present and active in Canadian high Arctic soils. <i>FEMS Microbiology Ecology</i> , 2014, 89, 257-269.	1.3	45
53	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
54	Rhizospheric Plant-Microbe Interactions: miRNAs as a Key Mediator. <i>Trends in Plant Science</i> , 2021, 26, 132-141.	4.3	45

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55	A Gaseous Milieu: Extending the Boundaries of the Rhizosphere. <i>Trends in Microbiology</i> , 2020, 28, 536-542.	3.5	43
56	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
57	Manipulating Wild and Tamed Phytobiomes: Challenges and Opportunities. <i>Phytobiomes Journal</i> , 2019, 3, 3-21.	1.4	38
58	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
59	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
60	<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
61	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
62	Microbial indicators are better predictors of wheat yield and quality than N fertilization. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	31
63	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
64	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
65	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
66	Metaproteomics of aquatic microbial communities in a deep and stratified estuary. <i>Proteomics</i> , 2015, 15, 3566-3579.	1.3	26
67	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
68	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
69	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
70	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
71	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
72	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

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73	Temporal and spatial interactions modulate the soybean microbiome. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	17
74	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
75	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
76	<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
77	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
78	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
79	A water stress-adapted inoculum affects rhizosphere fungi, but not bacteria nor wheat. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	12
80	A Drying-Rewetting Cycle Imposes More Important Shifts on Soil Microbial Communities than Does Reduced Precipitation. <i>MSystems</i> , 2022, 7, .	1.7	12
81	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
82	Field H <sub>2</sub> 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
83	Bacterial Subspecies Variation and Nematode Grazing Change P Dynamics in the Wheat Rhizosphere. <i>Frontiers in Microbiology</i> , 2018, 9, 1990.	1.5	10
84	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
85	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
86	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
87	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
88	Relative and Quantitative Rhizosphere Microbiome Profiling Results in Distinct Abundance Patterns. <i>Frontiers in Microbiology</i> , 2021, 12, 798023.	1.5	8
89	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
90	Predictive microbial-based modelling of wheat yields and grain baking quality across a 500 km <sup>2</sup> transect in Qu <sup>À</sup> bec. <i>FEMS Microbiology Ecology</i> , 2022, 97, .	1.3	6

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91	Fell-Field Soil Microbiology. , 2014, , 115-129.		4
92	Rhizosphere shotgun metagenomic analyses fail to show differences between ancestral and modern wheat genotypes grown under low fertilizer inputs. FEMS Microbiology Ecology, 2021, 97, .	1.3	3
93	Hydrocarbon substrate richness impacts microbial abundance, microbiome composition, and hydrocarbon loss. Applied Soil Ecology, 2021, 165, 104015.	2.1	3
94	Metagenomics Potential for Bioremediation. , 2012, , 1-11.		1
95	Sows affect their pigletsâ€™ faecal microbiota until fattening but not their Salmonella enterica shedding status. Letters in Applied Microbiology, 2021, 72, 113-120.	1.0	1
96	7. Techniques and approaches to quantify microbial diversity in extreme environments. , 2019, , 151-166.		0
97	Digestive microbiota changes during application of an effective, feed presentation based, mitigation option against Salmonella shedding in pigs. , 0, , .		0
98	Climate Change and Microbial Populations. , 2014, , 249-261.		0
99	Metagenomic Analysis of Polar Ecosystems. , 0, , 156-165.		0
100	Evolution of Salmonella excretion by sows during gestation in link with the faecal microbiome. , 0, , .		0