

# Blaire Steven

## List of Publications by Year in descending order

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Version: 2024-02-01

54  
papers

2,262  
citations

236912

25  
h-index

276858

41  
g-index

60  
all docs

60  
docs citations

60  
times ranked

2952  
citing authors

#	ARTICLE	IF	CITATIONS
1	Vegetation Zonation Predicts Soil Carbon Mineralization and Microbial Communities in Southern New England Salt Marshes. <i>Estuaries and Coasts</i> , 2022, 45, 168-180.	2.2	11
2	<scp>18S rRNA</scp> gene amplicon sequencing combined with cultureâ€based surveys of maize rhizosphere protists reveal dominant, plantâ€enriched and culturable community members. <i>Environmental Microbiology Reports</i> , 2022, 14, 110-118.	2.4	8
3	Temporal and spatial dynamics in the apple flower microbiome in the presence of the phytopathogen <i>Erwinia amylovora</i>. <i>ISME Journal</i> , 2021, 15, 318-329.	9.8	49
4	Inoculation of Stigma-Colonizing Microbes to Apple Stigmas Alters Microbiome Structure and Reduces the Occurrence of Fire Blight Disease. <i>Phytobiomes Journal</i> , 2021, 5, 156-165.	2.7	18
5	Resistance, Resilience, and Recovery of Dryland Soil Bacterial Communities Across Multiple Disturbances. <i>Frontiers in Microbiology</i> , 2021, 12, 648455.	3.5	13
6	Complete Genome Sequences of Curtobacterium , Pantoea , Erwinia , and Two Pseudomonas sp. Strains, Isolated from Apple Flower Stigmas from Connecticut, USA. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
7	The Axenic and Gnotobiotic Mosquito: Emerging Models for Microbiome Host Interactions. <i>Frontiers in Microbiology</i> , 2021, 12, 714222.	3.5	23
8	Whatâ€™s under the Christmas Tree? A Soil Sulfur Amendment Lowers Soil pH and Alters Fir Tree Rhizosphere Bacterial and Eukaryotic Communities, Their Interactions, and Functional Traits. <i>Microbiology Spectrum</i> , 2021, 9, e0016621.	3.0	6
9	Limited influence of the microbiome on the transcriptional profile of female <i>Aedes aegypti</i> mosquitoes. <i>Scientific Reports</i> , 2020, 10, 10880.	3.3	21
10	Nitrogen enrichment stimulates wetland plant responses whereas salt amendments alter sediment microbial communities and biogeochemical responses. <i>PLoS ONE</i> , 2020, 15, e0235225.	2.5	3
11	Validation of a PNA Clamping Method for Reducing Host DNA Amplification and Increasing Eukaryotic Diversity in Rhizosphere Microbiome Studies. <i>Phytobiomes Journal</i> , 2020, 4, 291-302.	2.7	14
12	Title is missing!. , 2020, 15, e0235225.		0
13	Title is missing!. , 2020, 15, e0235225.		0
14	Title is missing!. , 2020, 15, e0235225.		0
15	Title is missing!. , 2020, 15, e0235225.		0
16	Title is missing!. , 2020, 15, e0235225.		0
17	Title is missing!. , 2020, 15, e0235225.		0
18	Antibiotic resistant bacteria and commensal fungi are common and conserved in the mosquito microbiome. <i>PLoS ONE</i> , 2019, 14, e0218907.	2.5	27

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2019, 14, e0218907.		0
20	Title is missing!. , 2019, 14, e0218907.		0
21	Title is missing!. , 2019, 14, e0218907.		0
22	Title is missing!. , 2019, 14, e0218907.		0
23	The Influence of Flower Anatomy and Apple Cultivar on the Apple Flower Phytobiome. <i>Phytobiomes Journal</i> , 2018, 2, 171-179.	2.7	62
24	Chronic Physical Disturbance Substantially Alters the Response of Biological Soil Crusts to a Wetting Pulse, as Characterized by Metatranscriptomic Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2382.	3.5	40
25	Generation of axenic <i>Aedes aegypti</i> demonstrate live bacteria are not required for mosquito development. <i>Nature Communications</i> , 2018, 9, 4464.	12.8	84
26	Short-Term Transcriptional Response of Microbial Communities to Nitrogen Fertilization in a Pine Forest Soil. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	16
27	Simulated rRNA/DNA Ratios Show Potential To Misclassify Active Populations as Dormant. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	55
28	Response of Sediment Bacterial Communities to Sudden Vegetation Dieback in a Coastal Wetland. <i>Phytobiomes Journal</i> , 2017, 1, 5-13.	2.7	10
29	8 The Response of Arid Soil Communities to Climate Change. , 2017, , 139-158.		1
30	1. An Introduction to Arid Soils and Their Biology. , 2017, , 1-14.		6
31	The Biology of Arid Soils. , 2017, , .		5
32	Greenhouse trace gases in deadwood. <i>Biogeochemistry</i> , 2016, 130, 215-226.	3.5	31
33	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. <i>Cell Reports</i> , 2016, 14, 945-955.	6.4	49
34	Climate Change and Physical Disturbance Manipulations Result in Distinct Biological Soil Crust Communities. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7448-7459.	3.1	66
35	Nitrogen Fertilization Has a Stronger Effect on Soil Nitrogen-Fixing Bacterial Communities than Elevated Atmospheric CO <sub>2</sub> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 3103-3112.	3.1	122
36	Common and distinguishing features of the bacterial and fungal communities in biological soil crusts and shrub root zone soils. <i>Soil Biology and Biochemistry</i> , 2014, 69, 302-312.	8.8	110

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37	Surface soil fungal and bacterial communities in aspen stands are resilient to eleven years of elevated CO <sub>2</sub> and O <sub>3</sub> . <i>Soil Biology and Biochemistry</i> , 2014, 76, 227-234.	8.8	29
38	Dryland soil microbial communities display spatial biogeographic patterns associated with soil depth and soil parent material. <i>FEMS Microbiology Ecology</i> , 2013, 86, 101-113.	2.7	164
39	High Bacterial Diversity of Biological Soil Crusts in Water Tracks over Permafrost in the High Arctic Polar Desert. <i>PLoS ONE</i> , 2013, 8, e71489.	2.5	52
40	Dryland biological soil crust cyanobacteria show unexpected decreases in abundance under long-term elevated CO <sub>2</sub> . <i>Environmental Microbiology</i> , 2012, 14, 3247-3258.	3.8	61
41	Targeted and shotgun metagenomic approaches provide different descriptions of dryland soil microbial communities in a manipulated field study. <i>Environmental Microbiology Reports</i> , 2012, 4, 248-256.	2.4	58
42	Pyrosequencing of plastid 23S rRNA genes reveals diverse and dynamic cyanobacterial and algal populations in two eutrophic lakes. <i>FEMS Microbiology Ecology</i> , 2012, 82, 607-615.	2.7	42
43	Random transposon mutagenesis of <i>Verrucomicrobium spinosum</i> DSM 4136T. <i>Archives of Microbiology</i> , 2011, 193, 307-312.	2.2	12
44	Phylum-targeted pyrosequencing reveals diverse planctomycete populations in a eutrophic lake. <i>Aquatic Microbial Ecology</i> , 2011, 64, 41-49.	1.8	8
45	<i>Virgibacillus arcticus</i> sp. nov., a moderately halophilic, endospore-forming bacterium from permafrost in the Canadian high Arctic. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2219-2225.	1.7	40
46	Characterization of the intestinal microbiota of two Antarctic notothenioid fish species. <i>Extremophiles</i> , 2009, 13, 679-685.	2.3	130
47	Bacterial and Archaeal Diversity in Permafrost. <i>Soil Biology</i> , 2009, , 59-72.	0.8	29
48	Microbial diversity and activity through a permafrost/ground ice core profile from the Canadian high Arctic. <i>Environmental Microbiology</i> , 2008, 10, 3388-3403.	3.8	154
49	<i>Tumebacillus permanentifrigoris</i> gen. nov., sp. nov., an aerobic, spore-forming bacterium isolated from Canadian high Arctic permafrost. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 1497-1501.	1.7	62
50	Development of a sensitive radiorespiration method for detecting microbial activity at subzero temperatures. <i>Journal of Microbiological Methods</i> , 2007, 71, 275-280.	1.6	33
51	Characterization of the microbial diversity in a permafrost sample from the Canadian high Arctic using culture-dependent and culture-independent methods. <i>FEMS Microbiology Ecology</i> , 2007, 59, 513-523.	2.7	235
52	Microbial ecology and biodiversity in permafrost. <i>Extremophiles</i> , 2006, 10, 259-267.	2.3	195
53	Utilization of Fluorescent Microspheres and a Green Fluorescent Protein-Marked Strain for Assessment of Microbiological Contamination of Permafrost and Ground Ice Core Samples from the Canadian High Arctic. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1035-1041.	3.1	66
54	Insertion of Transposon Tn5tac1 in the <i>Sinorhizobium meliloti</i> Malate Dehydrogenase (mdh) Gene Results in Conditional Polar Effects on Downstream TCA Cycle Genes. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1318-1327.	2.6	23