Blaire Steven

List of Publications by Year in descending order

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RIAIDE STEVEN

#	Article	IF	CITATIONS
1	Vegetation Zonation Predicts Soil Carbon Mineralization and Microbial Communities in Southern New England Salt Marshes. Estuaries and Coasts, 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. Environmental Microbiology Reports, 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> . ISME Journal, 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. Phytobiomes Journal, 2021, 5, 156-165.	2.7	18
5	Resistance, Resilience, and Recovery of Dryland Soil Bacterial Communities Across Multiple Disturbances. Frontiers in Microbiology, 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. Microbiology Resource Announcements, 2021, 10, .	0.6	2
7	The Axenic and Gnotobiotic Mosquito: Emerging Models for Microbiome Host Interactions. Frontiers in Microbiology, 2021, 12, 714222.	3.5	23
8	What'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. Microbiology Spectrum, 2021, 9, e0016621.	3.0	6
9	Limited influence of the microbiome on the transcriptional profile of female Aedes aegypti mosquitoes. Scientific Reports, 2020, 10, 10880.	3.3	21
10	Nitrogen enrichment stimulates wetland plant responses whereas salt amendments alter sediment microbial communities and biogeochemical responses. PLoS ONE, 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. Phytobiomes Journal, 2020, 4, 291-302.	2.7	14
12	Title is missing!. , 2020, 15, e0235225.		0
13	Title is missing!. , 2020, 15, e0235225.		о
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. PLoS ONE, 2019, 14, e0218907.	2.5	27

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19	Title is missing!. , 2019, 14, e0218907.		Ο
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. Phytobiomes Journal, 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. Frontiers in Microbiology, 2018, 9, 2382.	3.5	40
25	Generation of axenic Aedes aegypti demonstrate live bacteria are not required for mosquito development. Nature Communications, 2018, 9, 4464.	12.8	84
26	Short-Term Transcriptional Response of Microbial Communities to Nitrogen Fertilization in a Pine Forest Soil. Applied and Environmental Microbiology, 2018, 84, .	3.1	16
27	Simulated rRNA/DNA Ratios Show Potential To Misclassify Active Populations as Dormant. Applied and Environmental Microbiology, 2017, 83, .	3.1	55
28	Response of Sediment Bacterial Communities to Sudden Vegetation Dieback in a Coastal Wetland. Phytobiomes Journal, 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. Biogeochemistry, 2016, 130, 215-226.	3.5	31
33	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. Cell Reports, 2016, 14, 945-955.	6.4	49
34	Climate Change and Physical Disturbance Manipulations Result in Distinct Biological Soil Crust Communities. Applied and Environmental Microbiology, 2015, 81, 7448-7459.	3.1	66
35	Nitrogen Fertilization Has a Stronger Effect on Soil Nitrogen-Fixing Bacterial Communities than Elevated Atmospheric CO ₂ . Applied and Environmental Microbiology, 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. Soil Biology and Biochemistry, 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 CO2 and O3. Soil Biology and Biochemistry, 2014, 76, 227-234.	8.8	29
38	Dryland soil microbial communities display spatial biogeographic patterns associated with soil depth and soil parent material. FEMS Microbiology Ecology, 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. PLoS ONE, 2013, 8, e71489.	2.5	52
40	Dryland biological soil crust cyanobacteria show unexpected decreases in abundance under longâ€ŧerm elevated <scp>CO₂</scp> . Environmental Microbiology, 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. Environmental Microbiology Reports, 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. FEMS Microbiology Ecology, 2012, 82, 607-615.	2.7	42
43	Random transposon mutagenesis of Verrucomicrobium spinosum DSM 4136T. Archives of Microbiology, 2011, 193, 307-312.	2.2	12
44	Phylum-targeted pyrosequencing reveals diverse planctomycete populations in a eutrophic lake. Aquatic Microbial Ecology, 2011, 64, 41-49.	1.8	8
45	Virgibacillus arcticus sp. nov., a moderately halophilic, endospore-forming bacterium from permafrost in the Canadian high Arctic. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 2219-2225.	1.7	40
46	Characterization of the intestinal microbiota of two Antarctic notothenioid fish species. Extremophiles, 2009, 13, 679-685.	2.3	130
47	Bacterial and Archaeal Diversity in Permafrost. Soil Biology, 2009, , 59-72.	0.8	29
48	Microbial diversity and activity through a permafrost/ground ice core profile from the Canadian high Arctic. Environmental Microbiology, 2008, 10, 3388-3403.	3.8	154
49	Tumebacillus permanentifrigoris gen. nov., sp. nov., an aerobic, spore-forming bacterium isolated from Canadian high Arctic permafrost. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1497-1501.	1.7	62
50	Development of a sensitive radiorespiration method for detecting microbial activity at subzero temperatures. Journal of Microbiological Methods, 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. FEMS Microbiology Ecology, 2007, 59, 513-523.	2.7	235
52	Microbial ecology and biodiversity in permafrost. Extremophiles, 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. Applied and Environmental Microbiology, 2005, 71, 1035-1041.	3.1	66
54	Insertion of Transposon Tn5tac1 in the Sinorhizobium meliloti Malate Dehydrogenase (mdh) Gene Results in Conditional Polar Effects on Downstream TCA Cycle Genes. Molecular Plant-Microbe Interactions, 2004, 17, 1318-1327.	2.6	23