

Eoin L Brodie

List of Publications by Year in descending order

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Version: 2024-02-01

174
papers

34,048
citations

11651

70
h-index

4885

168
g-index

193
all docs

193
docs citations

193
times ranked

41249
citing authors

#	ARTICLE	IF	CITATIONS
1	Greengenes, a Chimera-Checked 16S rRNA Gene Database and Workbench Compatible with ARB. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5069-5072.	3.1	9,859
2	Induction of Intestinal Th17 Cells by Segmented Filamentous Bacteria. <i>Cell</i> , 2009, 139, 485-498.	28.9	3,818
3	Dynamic root exudate chemistry and microbial substrate preferences drive patterns in rhizosphere microbial community assembly. <i>Nature Microbiology</i> , 2018, 3, 470-480.	13.3	1,268
4	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	12.8	994
5	NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , 2006, 34, W394-W399.	14.5	918
6	Airway microbiota and bronchial hyperresponsiveness in patients with suboptimally controlled asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2011, 127, 372-381.e3.	2.9	598
7	Urban aerosols harbor diverse and dynamic bacterial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 299-304.	7.1	593
8	Differential Growth Responses of Soil Bacterial Taxa to Carbon Substrates of Varying Chemical Recalcitrance. <i>Frontiers in Microbiology</i> , 2011, 2, 94.	3.5	504
9	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. <i>Science</i> , 2008, 322, 275-278.	12.6	474
10	Defining trait-based microbial strategies with consequences for soil carbon cycling under climate change. <i>ISME Journal</i> , 2020, 14, 1-9.	9.8	470
11	High-Density Universal 16S rRNA Microarray Analysis Reveals Broader Diversity than Typical Clone Library When Sampling the Environment. <i>Microbial Ecology</i> , 2007, 53, 371-383.	2.8	416
12	Application of a High-Density Oligonucleotide Microarray Approach To Study Bacterial Population Dynamics during Uranium Reduction and Reoxidation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6288-6298.	3.1	404
13	Airway Microbiota and Pathogen Abundance in Age-Stratified Cystic Fibrosis Patients. <i>PLoS ONE</i> , 2010, 5, e11044.	2.5	395
14	Rainfall-induced carbon dioxide pulses result from sequential resuscitation of phylogenetically clustered microbial groups. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10931-10936.	7.1	386
15	Design of 16S rRNA gene primers for 454 pyrosequencing of the human foregut microbiome. <i>World Journal of Gastroenterology</i> , 2010, 16, 4135.	3.3	370
16	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . <i>ISME Journal</i> , 2009, 3, 512-521.	9.8	364
17	Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. <i>Nature Communications</i> , 2015, 6, 7618.	12.8	361
18	Long-Term Sustainability of a High-Energy, Low-Diversity Crustal Biome. <i>Science</i> , 2006, 314, 479-482.	12.6	350

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19	Selective progressive response of soil microbial community to wild oat roots. ISME Journal, 2009, 3, 168-178.	9.8	306
20	A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. ISME Journal, 2008, 2, 1146-1156.	9.8	299
21	Use of 16S rRNA Gene for Identification of a Broad Range of Clinically Relevant Bacterial Pathogens. PLoS ONE, 2015, 10, e0117617.	2.5	293
22	Life and death in the soil microbiome: how ecological processes influence biogeochemistry. Nature Reviews Microbiology, 2022, 20, 415-430.	28.6	282
23	Comparative Analyses of the Bacterial Microbiota of the Human Nostril and Oropharynx. MBio, 2010, 1, .	4.1	266
24	Structure of the human gastric bacterial community in relation to <i>Helicobacter pylori</i> status. ISME Journal, 2011, 5, 574-579.	9.8	256
25	Whole-Genome Transcriptional Analysis of Heavy Metal Stresses in <i>Caulobacter crescentus</i> . Journal of Bacteriology, 2005, 187, 8437-8449.	2.2	247
26	Pre-exposure to drought increases the resistance of tropical forest soil bacterial communities to extended drought. ISME Journal, 2013, 7, 384-394.	9.8	236
27	Successional Trajectories of Rhizosphere Bacterial Communities over Consecutive Seasons. MBio, 2015, 6, e00746.	4.1	232
28	Diversity of 16S rRNA Genes within Individual Prokaryotic Genomes. Applied and Environmental Microbiology, 2010, 76, 3886-3897.	3.1	231
29	Despite strong seasonal responses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland. ISME Journal, 2009, 3, 738-744.	9.8	228
30	Soil Microbial Community Successional Patterns during Forest Ecosystem Restoration. Applied and Environmental Microbiology, 2011, 77, 6158-6164.	3.1	226
31	Dynamic cyanobacterial response to hydration and dehydration in a desert biological soil crust. ISME Journal, 2013, 7, 2178-2191.	9.8	217
32	Environmental Whole-Genome Amplification To Access Microbial Populations in Contaminated Sediments. Applied and Environmental Microbiology, 2006, 72, 3291-3301.	3.1	213
33	A Persistent and Diverse Airway Microbiota Present during Chronic Obstructive Pulmonary Disease Exacerbations. OMICS A Journal of Integrative Biology, 2010, 14, 9-59.	2.0	213
34	Integrating microbial ecology into ecosystem models: challenges and priorities. Biogeochemistry, 2012, 109, 7-18.	3.5	206
35	Man's best friend? The effect of pet ownership on house dust microbial communities. Journal of Allergy and Clinical Immunology, 2010, 126, 410-412.e3.	2.9	205
36	Relationship between cystic fibrosis respiratory tract bacterial communities and age, genotype, antibiotics and <i>Pseudomonas aeruginosa</i> . Environmental Microbiology, 2010, 12, 1293-1303.	3.8	203

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37	A unified initiative to harness Earth's microbiomes. <i>Science</i> , 2015, 350, 507-508.	12.6	195
38	Direct Cellular Lysis/Protein Extraction Protocol for Soil Metaproteomics. <i>Journal of Proteome Research</i> , 2010, 9, 6615-6622.	3.7	193
39	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. <i>ISME Journal</i> , 2012, 6, 531-541.	9.8	186
40	Exometabolite niche partitioning among sympatric soil bacteria. <i>Nature Communications</i> , 2015, 6, 8289.	12.8	178
41	Loss of Bacterial Diversity during Antibiotic Treatment of Intubated Patients Colonized with <i>Pseudomonas aeruginosa</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 1954-1962.	3.9	166
42	Reoxidation of Bioreduced Uranium under Reducing Conditions. <i>Environmental Science & Technology</i> , 2005, 39, 6162-6169.	10.0	157
43	Environmental microarray analyses of Antarctic soil microbial communities. <i>ISME Journal</i> , 2009, 3, 340-351.	9.8	156
44	Bacteria increase arid-land soil surface temperature through the production of sunscreens. <i>Nature Communications</i> , 2016, 7, 10373.	12.8	156
45	Impact of lime, nitrogen and plant species on bacterial community structure in grassland microcosms. <i>Environmental Microbiology</i> , 2004, 6, 1070-1080.	3.8	147
46	Probabilistic Invasion Underlies Natural Gut Microbiome Stability. <i>Current Biology</i> , 2017, 27, 1999-2006.e8.	3.9	144
47	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	9.8	135
48	Changes in the microbial community structure of bacteria, archaea and fungi in response to elevated CO_2 and warming in an Australian native grassland soil. <i>Environmental Microbiology</i> , 2012, 14, 3081-3096.	3.8	134
49	Toward a Predictive Understanding of Earth's Microbiomes to Address 21st Century Challenges. <i>MBio</i> , 2016, 7, .	4.1	124
50	Metatranscriptomic evidence of pervasive and diverse chemolithoautotrophy relevant to C, S, N and Fe cycling in a shallow alluvial aquifer. <i>ISME Journal</i> , 2016, 10, 2106-2117.	9.8	119
51	Soil fungal community structure in a temperate upland grassland soil. <i>FEMS Microbiology Ecology</i> , 2003, 45, 105-114.	2.7	115
52	The East River, Colorado, Watershed: A Mountainous Community Testbed for Improving Predictive Understanding of Multiscale Hydrological Biogeochemical Dynamics. <i>Vadose Zone Journal</i> , 2018, 17, 1-25.	2.2	115
53	Molecular bacterial community analysis of clean rooms where spacecraft are assembled. <i>FEMS Microbiology Ecology</i> , 2007, 61, 509-521.	2.7	113
54	Microbial legacies alter decomposition in response to simulated global change. <i>ISME Journal</i> , 2017, 11, 490-499.	9.8	112

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55	Climate and edaphic controllers influence rhizosphere community assembly for a wild annual grass. <i>Ecology</i> , 2016, 97, 1307-1318.	3.2	111
56	Human Papillomavirus Community in Healthy Persons, Defined by Metagenomics Analysis of Human Microbiome Project Shotgun Sequencing Data Sets. <i>Journal of Virology</i> , 2014, 88, 4786-4797.	3.4	108
57	<i>Lactobacillus casei</i> Abundance Is Associated with Profound Shifts in the Infant Gut Microbiome. <i>PLoS ONE</i> , 2010, 5, e8745.	2.5	107
58	Belowground Response to Drought in a Tropical Forest Soil. I. Changes in Microbial Functional Potential and Metabolism. <i>Frontiers in Microbiology</i> , 2016, 7, 525.	3.5	100
59	Water Table Dynamics and Biogeochemical Cycling in a Shallow, Variably-Saturated Floodplain. <i>Environmental Science & Technology</i> , 2017, 51, 3307-3317.	10.0	100
60	Trait-Based Representation of Biological Nitrification: Model Development, Testing, and Predicted Community Composition. <i>Frontiers in Microbiology</i> , 2012, 3, 364.	3.5	94
61	Bacterial Community Dynamics across a Floristic Gradient in a Temperate Upland Grassland Ecosystem. <i>Microbial Ecology</i> , 2002, 44, 260-270.	2.8	92
62	Role of the <i>rapA</i> Gene in Controlling Antibiotic Resistance of <i>Escherichia coli</i> Biofilms. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 3650-3658.	3.2	90
63	In Situ Long-Term Reductive Bioimmobilization of Cr(VI) in Groundwater Using Hydrogen Release Compound. <i>Environmental Science & Technology</i> , 2008, 42, 8478-8485.	10.0	86
64	Cystic fibrosis transmembrane conductance regulator knockout mice exhibit aberrant gastrointestinal microbiota. <i>Gut Microbes</i> , 2013, 4, 41-47.	9.8	85
65	Avian Incubation Inhibits Growth and Diversification of Bacterial Assemblages on Eggs. <i>PLoS ONE</i> , 2009, 4, e4522.	2.5	82
66	Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in <i>Orbicella faveolata</i> . <i>ISME Journal</i> , 2014, 8, 2411-2422.	9.8	80
67	Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenius disjunctus</i> . <i>ISME Journal</i> , 2014, 8, 6-18.	9.8	80
68	Influence of geogenic factors on microbial communities in metallogenic Australian soils. <i>ISME Journal</i> , 2012, 6, 2107-2118.	9.8	79
69	Drought and plant litter chemistry alter microbial gene expression and metabolite production. <i>ISME Journal</i> , 2020, 14, 2236-2247.	9.8	79
70	Role and Regulation of <i>lfs</i> in General Resistance Conferred by Low-Shear Simulated Microgravity in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2004, 186, 8207-8212.	2.2	74
71	PCR Amplification-Independent Methods for Detection of Microbial Communities by the High-Density Microarray PhyloChip. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6313-6322.	3.1	74
72	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010, 4, 711-715.	9.8	73

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73	Physiological and Transcriptional Studies of Cr(VI) Reduction under Aerobic and Denitrifying Conditions by an Aquifer-Derived Pseudomonad. <i>Environmental Science & Technology</i> , 2010, 44, 7491-7497.	10.0	73
74	Temporal Transcriptomic Microarray Analysis of <i>Dehalococcoides ethenogenes</i> Strain 195 during the Transition into Stationary Phase. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2864-2872.	3.1	72
75	High-throughput isotopic analysis of RNA microarrays to quantify microbial resource use. <i>ISME Journal</i> , 2012, 6, 1210-1221.	9.8	70
76	Sewage sludge addition modifies soil microbial communities and plant performance depending on the sludge stabilization process. <i>Applied Soil Ecology</i> , 2016, 101, 37-46.	4.3	70
77	Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. <i>FEMS Microbiology Ecology</i> , 2012, 79, 298-311.	2.7	69
78	Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. <i>Nature Microbiology</i> , 2019, 4, 864-875.	13.3	68
79	Taxon-specific microbial growth and mortality patterns reveal distinct temporal population responses to rewetting in a California grassland soil. <i>ISME Journal</i> , 2020, 14, 1520-1532.	9.8	67
80	Characterization of Coastal Urban Watershed Bacterial Communities Leads to Alternative Community-Based Indicators. <i>PLoS ONE</i> , 2010, 5, e11285.	2.5	66
81	Genomic and Physiological Characterization of the Chromate-Reducing, Aquifer-Derived Firmicute <i>Pelosinus</i> sp. Strain HCF1. <i>Applied and Environmental Microbiology</i> , 2013, 79, 63-73.	3.1	65
82	Metabolite Identification in <i>Synechococcus</i> sp. PCC 7002 Using Untargeted Stable Isotope Assisted Metabolite Profiling. <i>Analytical Chemistry</i> , 2010, 82, 9034-9042.	6.5	64
83	Cellulolytic potential under environmental changes in microbial communities from grassland litter. <i>Frontiers in Microbiology</i> , 2014, 5, 639.	3.5	61
84	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, <i>Hypothenemus hampei</i> . <i>Scientific Reports</i> , 2015, 5, 12525.	3.3	60
85	Reoxidation of Chromium(III) Products Formed under Different Biogeochemical Regimes. <i>Environmental Science & Technology</i> , 2017, 51, 4918-4927.	10.0	60
86	Quantitative characterization of soil micro-aggregates: New opportunities from sub-micron resolution synchrotron X-ray microtomography. <i>Geoderma</i> , 2017, 305, 382-393.	5.1	60
87	Metagenomic analysis of a stable trichloroethene-degrading microbial community. <i>ISME Journal</i> , 2012, 6, 1702-1714.	9.8	58
88	Seasonal patterns in microbial communities inhabiting the hot springs of Tengchong, Yunnan Province, China. <i>Environmental Microbiology</i> , 2014, 16, 1579-1591.	3.8	57
89	Developmental microbial ecology of the crop of the folivorous hoatzin. <i>ISME Journal</i> , 2010, 4, 611-620.	9.8	55
90	Field Evidence for Co-Metabolism of Trichloroethene Stimulated by Addition of Electron Donor to Groundwater. <i>Environmental Science & Technology</i> , 2010, 44, 4697-4704.	10.0	55

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91	Comparative genomics of two newly isolated <i>Dehalococcoides</i> strains and an enrichment using a genus microarray. ISME Journal, 2011, 5, 1014-1024.	9.8	54
92	Protist diversity and community complexity in the rhizosphere of switchgrass are dynamic as plants develop. Microbiome, 2021, 9, 96.	11.1	54
93	Comparative Genomics of <i>Dehalococcoides ethenogenes</i> 195 and an Enrichment Culture Containing Unsequenced <i>Dehalococcoides</i> Strains. Applied and Environmental Microbiology, 2008, 74, 3533-3540.	3.1	53
94	Bacterial Diversity of Terrestrial Crystalline Volcanic Rocks, Iceland. Microbial Ecology, 2011, 62, 69-79.	2.8	51
95	Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. Applied Microbiology and Biotechnology, 2014, 98, 4723-4736.	3.6	51
96	Microbial community response to addition of polylactate compounds to stimulate hexavalent chromium reduction in groundwater. Chemosphere, 2011, 85, 660-665.	8.2	50
97	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. Frontiers in Microbiology, 2015, 6, 277.	3.5	50
98	Microdiversity of an Abundant Terrestrial Bacterium Encompasses Extensive Variation in Ecologically Relevant Traits. MBio, 2017, 8, .	4.1	49
99	Export of submicron particulate organic matter to mesopelagic depth in an oligotrophic gyre. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12565-12570.	7.1	47
100	Belowground Response to Drought in a Tropical Forest Soil. II. Change in Microbial Function Impacts Carbon Composition. Frontiers in Microbiology, 2016, 7, 323.	3.5	46
101	Phylogenetic conservation of soil bacterial responses to simulated global changes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190242.	4.0	46
102	Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. Frontiers in Microbiology, 2013, 4, 282.	3.5	44
103	Bacterial community structure of contrasting soils underlying Bornean rain forests: Inferences from microarray and next-generation sequencing methods. Soil Biology and Biochemistry, 2012, 55, 48-59.	8.8	41
104	Interactions between <i>Bacillus anthracis</i> and Plants May Promote Anthrax Transmission. PLoS Neglected Tropical Diseases, 2014, 8, e2903.	3.0	40
105	Macroscopic Biofilms in Fracture-Dominated Sediment That Anaerobically Oxidize Methane. Applied and Environmental Microbiology, 2011, 77, 6780-6787.	3.1	37
106	Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. Environmental Science & Technology, 2012, 46, 1044-1054.	10.0	36
107	Mineralogical, Chemical and Biological Characterization of an Anaerobic Biofilm Collected from a Borehole in a Deep Gold Mine in South Africa. Geomicrobiology Journal, 2007, 24, 491-504.	2.0	35
108	Seasonal influences on fungal community structure in unimproved and improved upland grassland soils. Canadian Journal of Microbiology, 2006, 52, 689-694.	1.7	34

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109	Effects of Organic Carbon Supply Rates on Uranium Mobility in a Previously Bioreduced Contaminated Sediment. <i>Environmental Science & Technology</i> , 2008, 42, 7573-7579.	10.0	34
110	Soil bacterial communities of a calcium-supplemented and a reference watershed at the Hubbard Brook Experimental Forest (HBEF), New Hampshire, USA. <i>FEMS Microbiology Ecology</i> , 2012, 79, 728-740.	2.7	34
111	Integrating airborne remote sensing and field campaigns for ecology and Earth system science. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1492-1508.	5.2	33
112	The Snowmelt Niche Differentiates Three Microbial Life Strategies That Influence Soil Nitrogen Availability During and After Winter. <i>Frontiers in Microbiology</i> , 2020, 11, 871.	3.5	32
113	Feeding-Related Gut Microbial Composition Associates With Peripheral T-Cell Activation and Mucosal Gene Expression in African Infants. <i>Clinical Infectious Diseases</i> , 2018, 67, 1237-1246.	5.8	31
114	Proteomic and targeted qPCR analyses of subsurface microbial communities for presence of methane monooxygenase. <i>Biodegradation</i> , 2011, 22, 1045-1059.	3.0	30
115	Hormonal contraception alters vaginal microbiota and cytokines in South African adolescents in a randomized trial. <i>Nature Communications</i> , 2020, 11, 5578.	12.8	30
116	Deep space and hidden depths: understanding the evolution and ecology of fungal entomopathogens. <i>BioControl</i> , 2010, 55, 1-6.	2.0	29
117	Impacts of Agricultural Nitrogen on the Environment and Strategies to Reduce these Impacts. <i>Procedia Environmental Sciences</i> , 2015, 29, 303.	1.4	29
118	Shifts in the phylogenetic structure and functional capacity of soil microbial communities follow alteration of native tussock grassland ecosystems. <i>Soil Biology and Biochemistry</i> , 2013, 57, 675-682.	8.8	28
119	Large Blooms of <i>Bacillales</i> (<i>Firmicutes</i>) Underlie the Response to Wetting of Cyanobacterial Biocrusts at Various Stages of Maturity. <i>MBio</i> , 2018, 9, .	4.1	28
120	Effect of Different Lignocellulosic Diets on Bacterial Microbiota and Hydrolytic Enzyme Activities in the Gut of the Cotton Boll Weevil (<i>Anthonomus grandis</i>). <i>Frontiers in Microbiology</i> , 2016, 07, 2093.	3.5	27
121	Routes and rates of bacterial dispersal impact surface soil microbiome composition and functioning. <i>ISME Journal</i> , 2022, 16, 2295-2304.	9.8	26
122	Influences of Organic Carbon Supply Rate on Uranium Bioreduction in Initially Oxidizing, Contaminated Sediment. <i>Environmental Science & Technology</i> , 2008, 42, 8901-8907.	10.0	25
123	Simrank: Rapid and sensitive general-purpose k-mer search tool. <i>BMC Ecology</i> , 2011, 11, 11.	3.0	24
124	Divergent Aquifer Biogeochemical Systems Converge on Similar and Unexpected Cr(VI) Reduction Products. <i>Environmental Science & Technology</i> , 2014, 48, 10699-10706.	10.0	24
125	Methane Production Pathway Regulated Proximally by Substrate Availability and Distally by Temperature in a High-latitude Mire Complex. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 3057-3074.	3.0	24
126	¹³ C-Isotopomer-based metabolomics of microbial groups isolated from two forest soils. <i>Metabolomics</i> , 2009, 5, 108-122.	3.0	23

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127	Differences in crop bacterial community structure between hoatzins from different geographical locations. <i>Research in Microbiology</i> , 2012, 163, 211-220.	2.1	23
128	Uranium Reduction in Sediments under Diffusion-Limited Transport of Organic Carbon. <i>Environmental Science & Technology</i> , 2005, 39, 7077-7083.	10.0	22
129	Influence of trace erythromycin and erythromycin-H ₂ O on carbon and nutrients removal and on resistance selection in sequencing batch reactors (SBRs). <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 185-195.	3.6	21
130	Diversity and structure of soil bacterial communities associated with vultures in an African savanna. <i>Ecosphere</i> , 2012, 3, 1-18.	2.2	19
131	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , 2013, 84, 259-269.	2.7	19
132	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019, 10, .	4.1	19
133	A large column analog experiment of stable isotope variations during reactive transport: II. Carbon mass balance, microbial community structure and predation. <i>Geochimica Et Cosmochimica Acta</i> , 2014, 124, 394-409.	3.9	17
134	Microbial community structure of a slow sand filter schmutzdecke: a phylogenetic snapshot based on rRNA sequence analysis. <i>Water Science and Technology: Water Supply</i> , 2011, 11, 426-436.	2.1	16
135	Modeling the Impact of Riparian Hollows on River Corridor Nitrogen Exports. <i>Frontiers in Water</i> , 2021, 3, .	2.3	15
136	Plant organic matter inputs exert a strong control on soil organic matter decomposition in a thawing permafrost peatland. <i>Science of the Total Environment</i> , 2022, 820, 152757.	8.0	15
137	Exploration for Facultative Endosymbionts of Glassy-Winged Sharpshooter (Hemiptera: Cicadellidae). <i>Annals of the Entomological Society of America</i> , 2007, 100, 345-349.	2.5	14
138	Metatranscriptomic Analysis Reveals Unexpectedly Diverse Microbial Metabolism in a Biogeochemical Hot Spot in an Alluvial Aquifer. <i>Frontiers in Microbiology</i> , 2017, 8, 40.	3.5	14
139	Microbial distributions detected by an oligonucleotide microarray across geochemical zones associated with methane in marine sediments from the Ullung Basin. <i>Marine and Petroleum Geology</i> , 2013, 47, 147-154.	3.3	11
140	A novel d-xylose isomerase from the gut of the wood feeding beetle <i>Odontotaenius disjunctus</i> efficiently expressed in <i>Saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2021, 11, 4766.	3.3	11
141	Sample Identifiers and Metadata to Support Data Management and Reuse in Multidisciplinary Ecosystem Sciences. <i>Data Science Journal</i> , 2021, 20, 11.	1.3	11
142	Multiple lineages of <i>Streptomyces</i> produce antimicrobials within passalid beetle galleries across eastern North America. <i>ELife</i> , 2021, 10, .	6.0	11
143	The Colorado East River Community Observatory Data Collection. <i>Hydrological Processes</i> , 2021, 35, e14243.	2.6	10
144	Effect of Cover Crop on Carbon Distribution in Size and Density Separated Soil Aggregates. <i>Soil Systems</i> , 2020, 4, 6.	2.6	8

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145	Microbial Phosphorus Mobilization Strategies Across a Natural Nutrient Limitation Gradient and Evidence for Linkage With Iron Solubilization Traits. <i>Frontiers in Microbiology</i> , 2021, 12, 572212.	3.5	8
146	Coupling plant litter quantity to a novel metric for litter quality explains C storage changes in a thawing permafrost peatland. <i>Global Change Biology</i> , 2021, , .	9.5	8
147	Community RNA-Seq: multi-kingdom responses to living versus decaying roots in soil. <i>ISME Communications</i> , 2021, 1, .	4.2	8
148	Progressive dysbiosis of human orodigestive microbiota along the sequence of gastroesophageal reflux, Barrett's esophagus and esophageal adenocarcinoma. <i>International Journal of Cancer</i> , 2022, 151, 1703-1716.	5.1	8
149	Noninvasive Mapping of Photosynthetic Heterogeneity in Biological Soil Crusts by Positron Emission Tomography: Carbon Fixation. <i>Environmental Science and Technology Letters</i> , 2014, 1, 393-398.	8.7	6
150	Evidence for Microbial Mediated NO ₃ ⁻ Cycling Within Floodplain Sediments During Groundwater Fluctuations. <i>Frontiers in Earth Science</i> , 2019, 7, .	1.8	6
151	A comparison of lodgepole and spruce needle chemistry impacts on terrestrial biogeochemical processes during isolated decomposition. <i>PeerJ</i> , 2020, 8, e9538.	2.0	6
152	Kinetic Properties of Microbial Exoenzymes Vary With Soil Depth but Have Similar Temperature Sensitivities Through the Soil Profile. <i>Frontiers in Microbiology</i> , 2021, 12, 735282.	3.5	6
153	Metagenomic analysis of intertidal hypersaline microbial mats from Elkhorn Slough, California, grown with and without molybdate. <i>Standards in Genomic Sciences</i> , 2017, 12, 67.	1.5	5
154	Measurement of Volatile Compounds for Real-Time Analysis of Soil Microbial Metabolic Response to Simulated Snowmelt. <i>Frontiers in Microbiology</i> , 2021, 12, 679671.	3.5	5
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