

Eoin L Brodie

List of Publications by Year in descending order

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Version: 2024-02-01

174
papers

34,048
citations

13332

70
h-index

5622

168
g-index

193
all docs

193
docs citations

193
times ranked

45461
citing authors

#	ARTICLE	IF	CITATIONS
1	Conversion of marginal land into switchgrass conditionally accrues soil carbon but reduces methane consumption. <i>ISME Journal</i> , 2022, 16, 10-25.	4.4	4
2	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.	3.9	15
3	Life and death in the soil microbiome: how ecological processes influence biogeochemistry. <i>Nature Reviews Microbiology</i> , 2022, 20, 415-430.	13.6	282
4	Spectroscopic analysis reveals that soil phosphorus availability and plant allocation strategies impact feedstock quality of nutrient-limited switchgrass. <i>Communications Biology</i> , 2022, 5, 227.	2.0	1
5	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.	2.3	8
6	Routes and rates of bacterial dispersal impact surface soil microbiome composition and functioning. <i>ISME Journal</i> , 2022, 16, 2295-2304.	4.4	26
7	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.	1.6	11
8	Modeling the Impact of Riparian Hollows on River Corridor Nitrogen Exports. <i>Frontiers in Water</i> , 2021, 3, .	1.0	15
9	Sample Identifiers and Metadata to Support Data Management and Reuse in Multidisciplinary Ecosystem Sciences. <i>Data Science Journal</i> , 2021, 20, 11.	0.6	11
10	Protist diversity and community complexity in the rhizosphere of switchgrass are dynamic as plants develop. <i>Microbiome</i> , 2021, 9, 96.	4.9	54
11	Multiple lineages of <i>Streptomyces</i> produce antimicrobials within passalid beetle galleries across eastern North America. <i>ELife</i> , 2021, 10, .	2.8	11
12	Measurement of Volatile Compounds for Real-Time Analysis of Soil Microbial Metabolic Response to Simulated Snowmelt. <i>Frontiers in Microbiology</i> , 2021, 12, 679671.	1.5	5
13	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.	1.5	8
14	The Colorado East River Community Observatory Data Collection. <i>Hydrological Processes</i> , 2021, 35, e14243.	1.1	10
15	Effect of elevation, season and accelerated snowmelt on biogeochemical processes during isolated conifer needle litter decomposition. <i>PeerJ</i> , 2021, 9, e11926.	0.9	1
16	Conceptualizing Biogeochemical Reactions With an Ohm's Law Analogy. <i>Journal of Advances in Modeling Earth Systems</i> , 2021, 13, e2021MS002469.	1.3	2
17	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, , .	4.2	8
18	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.	1.5	6

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19	Community RNA-Seq; multi-kingdom responses to living versus decaying roots in soil. ISME Communications, 2021, 1, .	1.7	8
20	Defining trait-based microbial strategies with consequences for soil carbon cycling under climate change. ISME Journal, 2020, 14, 1-9.	4.4	470
21	Integrating airborne remote sensing and field campaigns for ecology and Earth system science. Methods in Ecology and Evolution, 2020, 11, 1492-1508.	2.2	33
22	Hormonal contraception alters vaginal microbiota and cytokines in South African adolescents in a randomized trial. Nature Communications, 2020, 11, 5578.	5.8	30
23	The Snowmelt Niche Differentiates Three Microbial Life Strategies That Influence Soil Nitrogen Availability During and After Winter. Frontiers in Microbiology, 2020, 11, 871.	1.5	32
24	Taxon-specific microbial growth and mortality patterns reveal distinct temporal population responses to rewetting in a California grassland soil. ISME Journal, 2020, 14, 1520-1532.	4.4	67
25	Niche differentiation is spatially and temporally regulated in the rhizosphere. ISME Journal, 2020, 14, 999-1014.	4.4	135
26	Effect of Cover Crop on Carbon Distribution in Size and Density Separated Soil Aggregates. Soil Systems, 2020, 4, 6.	1.0	8
27	Phylogenetic conservation of soil bacterial responses to simulated global changes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190242.	1.8	46
28	Drought and plant litter chemistry alter microbial gene expression and metabolite production. ISME Journal, 2020, 14, 2236-2247.	4.4	79
29	A comparison of lodgepole and spruce needle chemistry impacts on terrestrial biogeochemical processes during isolated decomposition. PeerJ, 2020, 8, e9538.	0.9	6
30	Paired RNA Radiocarbon and Sequencing Analyses Indicate the Importance of Autotrophy in a Shallow Alluvial Aquifer. Scientific Reports, 2019, 9, 10370.	1.6	1
31	Model exploration of interactions between algal functional diversity and productivity in chemostats to represent open ponds systems across climate gradients. Ecological Modelling, 2019, 406, 121-132.	1.2	4
32	Methane Production Pathway Regulated Proximally by Substrate Availability and Distally by Temperature in a High-Latitude Mire Complex. Journal of Geophysical Research G: Biogeosciences, 2019, 124, 3057-3074.	1.3	24
33	Evidence for Microbial Mediated NO ₃ ⁻ Cycling Within Floodplain Sediments During Groundwater Fluctuations. Frontiers in Earth Science, 2019, 7, .	0.8	6
34	Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. Nature Microbiology, 2019, 4, 864-875.	5.9	68
35	P367â€¦Hormonal contraception and risk of STIs and bacterial vaginosis in south african adolescents: a randomized trial. , 2019, , .		0
36	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. MBio, 2019, 10, .	1.8	19

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37	An associated particle imaging system for soil-carbon measurements. , 2019, , .		1
38	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, .	1.8	28
39	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.	2.9	31
40	Dynamic root exudate chemistry and microbial substrate preferences drive patterns in rhizosphere microbial community assembly. <i>Nature Microbiology</i> , 2018, 3, 470-480.	5.9	1,268
41	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.	1.3	115
42	Water Table Dynamics and Biogeochemical Cycling in a Shallow, Variably-Saturated Floodplain. <i>Environmental Science & Technology</i> , 2017, 51, 3307-3317.	4.6	100
43	Probabilistic Invasion Underlies Natural Gut Microbiome Stability. <i>Current Biology</i> , 2017, 27, 1999-2006.e8.	1.8	144
44	Reoxidation of Chromium(III) Products Formed under Different Biogeochemical Regimes. <i>Environmental Science & Technology</i> , 2017, 51, 4918-4927.	4.6	60
45	Quantitative characterization of soil micro-aggregates: New opportunities from sub-micron resolution synchrotron X-ray microtomography. <i>Geoderma</i> , 2017, 305, 382-393.	2.3	60
46	Microdiversity of an Abundant Terrestrial Bacterium Encompasses Extensive Variation in Ecologically Relevant Traits. <i>MBio</i> , 2017, 8, .	1.8	49
47	Microbial legacies alter decomposition in response to simulated global change. <i>ISME Journal</i> , 2017, 11, 490-499.	4.4	112
48	Metatranscriptomic Analysis Reveals Unexpectedly Diverse Microbial Metabolism in a Biogeochemical Hot Spot in an Alluvial Aquifer. <i>Frontiers in Microbiology</i> , 2017, 8, 40.	1.5	14
49	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
50	Preface to the Special Issue of <i>Vadose Zone Journal</i> on Soil as Complex Systems. <i>Vadose Zone Journal</i> , 2016, 15, 1-3.	1.3	2
51	Belowground Response to Drought in a Tropical Forest Soil. II. Change in Microbial Function Impacts Carbon Composition. <i>Frontiers in Microbiology</i> , 2016, 7, 323.	1.5	46
52	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.	1.5	100
53	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.	1.5	27
54	Toward a Predictive Understanding of Earth’s Microbiomes to Address 21st Century Challenges. <i>MBio</i> , 2016, 7, .	1.8	124

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55	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	5.8	994
56	Climate and edaphic controllers influence rhizosphere community assembly for a wild annual grass. <i>Ecology</i> , 2016, 97, 1307-1318.	1.5	111
57	Bacteria increase arid-land soil surface temperature through the production of sunscreens. <i>Nature Communications</i> , 2016, 7, 10373.	5.8	156
58	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.	2.1	70
59	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.	4.4	119
60	Exometabolite niche partitioning among sympatric soil bacteria. <i>Nature Communications</i> , 2015, 6, 8289.	5.8	178
61	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.	1.6	60
62	Use of 16S rRNA Gene for Identification of a Broad Range of Clinically Relevant Bacterial Pathogens. <i>PLoS ONE</i> , 2015, 10, e0117617.	1.1	293
63	Impacts of Agricultural Nitrogen on the Environment and Strategies to Reduce these Impacts. <i>Procedia Environmental Sciences</i> , 2015, 29, 303.	1.3	29
64	Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. <i>Nature Communications</i> , 2015, 6, 7618.	5.8	361
65	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. <i>Frontiers in Microbiology</i> , 2015, 6, 277.	1.5	50
66	Solid and Suspension Microarrays for Microbial Diagnostics. <i>Methods in Microbiology</i> , 2015, , 395-431.	0.4	4
67	A unified initiative to harness Earth's microbiomes. <i>Science</i> , 2015, 350, 507-508.	6.0	195
68	Successional Trajectories of Rhizosphere Bacterial Communities over Consecutive Seasons. <i>MBio</i> , 2015, 6, e00746.	1.8	232
69	Foregut Microbiome, Development of Esophageal Adenocarcinoma, Project. , 2015, , 186-189.		1
70	Interactions between <i>Bacillus anthracis</i> and Plants May Promote Anthrax Transmission. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2903.	1.3	40
71	Cellulolytic potential under environmental changes in microbial communities from grassland litter. <i>Frontiers in Microbiology</i> , 2014, 5, 639.	1.5	61
72	Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4723-4736.	1.7	51

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73	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.	1.5	108
74	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.	3.9	6
75	Seasonal patterns in microbial communities inhabiting the hot springs of <i>Tengchong</i> , <i>Yunnan</i> Province, <i>China</i> . <i>Environmental Microbiology</i> , 2014, 16, 1579-1591.	1.8	57
76	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.	4.4	80
77	Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenius disjunctus</i> . <i>ISME Journal</i> , 2014, 8, 6-18.	4.4	80
78	Divergent Aquifer Biogeochemical Systems Converge on Similar and Unexpected Cr(VI) Reduction Products. <i>Environmental Science & Technology</i> , 2014, 48, 10699-10706.	4.6	24
79	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.	1.6	17
80	Dynamic cyanobacterial response to hydration and dehydration in a desert biological soil crust. <i>ISME Journal</i> , 2013, 7, 2178-2191.	4.4	217
81	Pre-exposure to drought increases the resistance of tropical forest soil bacterial communities to extended drought. <i>ISME Journal</i> , 2013, 7, 384-394.	4.4	236
82	Microbial distributions detected by an oligonucleotide microarray across geochemical zones associated with methane in marine sediments from the Ulleung Basin. <i>Marine and Petroleum Geology</i> , 2013, 47, 147-154.	1.5	11
83	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.	4.2	28
84	Biogeography of bacterioplankton in the tropical seawaters of Singapore. <i>FEMS Microbiology Ecology</i> , 2013, 84, 259-269.	1.3	19
85	Export of submicron particulate organic matter to mesopelagic depth in an oligotrophic gyre. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12565-12570.	3.3	47
86	Cystic fibrosis transmembrane conductance regulator knockout mice exhibit aberrant gastrointestinal microbiota. <i>Gut Microbes</i> , 2013, 4, 41-47.	4.3	85
87	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.	1.4	65
88	Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. <i>Frontiers in Microbiology</i> , 2013, 4, 282.	1.5	44
89	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.	3.3	386
90	Trait-Based Representation of Biological Nitrification: Model Development, Testing, and Predicted Community Composition. <i>Frontiers in Microbiology</i> , 2012, 3, 364.	1.5	94

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91	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. ISME Journal, 2012, 6, 531-541.	4.4	186
92	Influence of geogenic factors on microbial communities in metallogenic Australian soils. ISME Journal, 2012, 6, 2107-2118.	4.4	79
93	Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. Environmental Science & Technology, 2012, 46, 1044-1054.	4.6	36
94	Differences in crop bacterial community structure between hoatzins from different geographical locations. Research in Microbiology, 2012, 163, 211-220.	1.0	23
95	High-throughput isotopic analysis of RNA microarrays to quantify microbial resource use. ISME Journal, 2012, 6, 1210-1221.	4.4	70
96	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. Environmental Microbiology, 2012, 14, 3081-3096.	1.8	134
97	Metagenomic analysis of a stable trichloroethene-degrading microbial community. ISME Journal, 2012, 6, 1702-1714.	4.4	58
98	A technique to dissect the alimentary canal of the coffee berry borer (<i>Hypothenemus hampei</i>), with isolation of internal microorganisms. Journal of Entomological and Acarological Research, 2012, 44, 21.	0.3	3
99	Diversity and structure of soil bacterial communities associated with vultures in an African savanna. Ecosphere, 2012, 3, 1-18.	1.0	19
100	Integrating microbial ecology into ecosystem models: challenges and priorities. Biogeochemistry, 2012, 109, 7-18.	1.7	206
101	Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. FEMS Microbiology Ecology, 2012, 79, 298-311.	1.3	69
102	Soil bacterial communities of a calcium-supplemented and a reference watershed at the Hubbard Brook Experimental Forest (HBEF), New Hampshire, USA. FEMS Microbiology Ecology, 2012, 79, 728-740.	1.3	34
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.	4.2	41
104	Foregut Microbiome, Development of Esophageal Adenocarcinoma, Project. , 2012, , 1-5.		1
105	PCR Amplification-Independent Methods for Detection of Microbial Communities by the High-Density Microarray PhyloChip. Applied and Environmental Microbiology, 2011, 77, 6313-6322.	1.4	74
106	Airway microbiota and bronchial hyperresponsiveness in patients with suboptimally controlled asthma. Journal of Allergy and Clinical Immunology, 2011, 127, 372-381.e3.	1.5	598
107	16S rRNA Gene Microarray Analysis of Microbial Communities in Ethanol-Stimulated Subsurface Sediment. Microbes and Environments, 2011, 26, 261-265.	0.7	2
108	Differential Growth Responses of Soil Bacterial Taxa to Carbon Substrates of Varying Chemical Recalcitrance. Frontiers in Microbiology, 2011, 2, 94.	1.5	504

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109	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.	1.0	16
110	Structure of the human gastric bacterial community in relation to <i>Helicobacter pylori</i> status. <i>ISME Journal</i> , 2011, 5, 574-579.	4.4	256
111	Comparative genomics of two newly isolated <i>Dehalococcoides</i> strains and an enrichment using a genus microarray. <i>ISME Journal</i> , 2011, 5, 1014-1024.	4.4	54
112	Microbial community response to addition of polylactate compounds to stimulate hexavalent chromium reduction in groundwater. <i>Chemosphere</i> , 2011, 85, 660-665.	4.2	50
113	Proteomic and targeted qPCR analyses of subsurface microbial communities for presence of methane monoxygenase. <i>Biodegradation</i> , 2011, 22, 1045-1059.	1.5	30
114	Bacterial Diversity of Terrestrial Crystalline Volcanic Rocks, Iceland. <i>Microbial Ecology</i> , 2011, 62, 69-79.	1.4	51
115	Simrank: Rapid and sensitive general-purpose k-mer search tool. <i>BMC Ecology</i> , 2011, 11, 11.	3.0	24
116	Macroscopic Biofilms in Fracture-Dominated Sediment That Anaerobically Oxidize Methane. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6780-6787.	1.4	37
117	Soil Microbial Community Successional Patterns during Forest Ecosystem Restoration. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6158-6164.	1.4	226
118	Design of 16S rRNA gene primers for 454 pyrosequencing of the human foregut microbiome. <i>World Journal of Gastroenterology</i> , 2010, 16, 4135.	1.4	370
119	Direct Cellular Lysis/Protein Extraction Protocol for Soil Metaproteomics. <i>Journal of Proteome Research</i> , 2010, 9, 6615-6622.	1.8	193
120	Deep space and hidden depths: understanding the evolution and ecology of fungal entomopathogens. <i>BioControl</i> , 2010, 55, 1-6.	0.9	29
121	Developmental microbial ecology of the crop of the folivorous hoatzin. <i>ISME Journal</i> , 2010, 4, 611-620.	4.4	55
122	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010, 4, 711-715.	4.4	73
123	Relationship between cystic fibrosis respiratory tract bacterial communities and age, genotype, antibiotics and <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2010, 12, 1293-1303.	1.8	203
124	Foregut microbiome in development of esophageal adenocarcinoma. <i>Nature Precedings</i> , 2010, , .	0.1	1
125	The Impact Of Pet Ownership On Microbial Communities In Settled House Dust. , 2010, , .		0
126	Diversity of 16S rRNA Genes within Individual Prokaryotic Genomes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3886-3897.	1.4	231

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127	Comparative Analyses of the Bacterial Microbiota of the Human Nostril and Oropharynx. MBio, 2010, 1, .	1.8	266
128	Physiological and Transcriptional Studies of Cr(VI) Reduction under Aerobic and Denitrifying Conditions by an Aquifer-Derived Pseudomonad. Environmental Science & Technology, 2010, 44, 7491-7497.	4.6	73
129	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.	1.5	205
130	A Persistent and Diverse Airway Microbiota Present during Chronic Obstructive Pulmonary Disease Exacerbations. OMICS A Journal of Integrative Biology, 2010, 14, 9-59.	1.0	213
131	Field Evidence for Co-Metabolism of Trichloroethene Stimulated by Addition of Electron Donor to Groundwater. Environmental Science & Technology, 2010, 44, 4697-4704.	4.6	55
132	Metabolite Identification in <i>Synechococcus</i> sp. PCC 7002 Using Untargeted Stable Isotope Assisted Metabolite Profiling. Analytical Chemistry, 2010, 82, 9034-9042.	3.2	64
133	<i>Lactobacillus casei</i> Abundance Is Associated with Profound Shifts in the Infant Gut Microbiome. PLoS ONE, 2010, 5, e8745.	1.1	107
134	Airway Microbiota and Pathogen Abundance in Age-Stratified Cystic Fibrosis Patients. PLoS ONE, 2010, 5, e11044.	1.1	395
135	Characterization of Coastal Urban Watershed Bacterial Communities Leads to Alternative Community-Based Indicators. PLoS ONE, 2010, 5, e11285.	1.1	66
136	Avian Incubation Inhibits Growth and Diversification of Bacterial Assemblages on Eggs. PLoS ONE, 2009, 4, e4522.	1.1	82
137	¹³ C-Isotopomer-based metabolomics of microbial groups isolated from two forest soils. Metabolomics, 2009, 5, 108-122.	1.4	23
138	Influence of trace erythromycin and erythromycin-H ₂ O on carbon and nutrients removal and on resistance selection in sequencing batch reactors (SBRs). Applied Microbiology and Biotechnology, 2009, 85, 185-195.	1.7	21
139	Selective progressive response of soil microbial community to wild oat roots. ISME Journal, 2009, 3, 168-178.	4.4	306
140	Environmental microarray analyses of Antarctic soil microbial communities. ISME Journal, 2009, 3, 340-351.	4.4	156
141	Bacterial diversity and White Plague Disease-associated community changes in the Caribbean coral <i>Montastraea faveolata</i> . ISME Journal, 2009, 3, 512-521.	4.4	364
142	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.	4.4	228
143	Induction of Intestinal Th17 Cells by Segmented Filamentous Bacteria. Cell, 2009, 139, 485-498.	13.5	3,818
144	Deep space and hidden depths: understanding the evolution and ecology of fungal entomopathogens. , 2009, , 1-6.		2

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145	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. <i>Science</i> , 2008, 322, 275-278.	6.0	474
146	A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. <i>ISME Journal</i> , 2008, 2, 1146-1156.	4.4	299
147	Effects of Organic Carbon Supply Rates on Uranium Mobility in a Previously Bioreduced Contaminated Sediment. <i>Environmental Science & Technology</i> , 2008, 42, 7573-7579.	4.6	34
148	Influences of Organic Carbon Supply Rate on Uranium Bioreduction in Initially Oxidizing, Contaminated Sediment. <i>Environmental Science & Technology</i> , 2008, 42, 8901-8907.	4.6	25
149	In Situ Long-Term Reductive Bioimmobilization of Cr(VI) in Groundwater Using Hydrogen Release Compound. <i>Environmental Science & Technology</i> , 2008, 42, 8478-8485.	4.6	86
150	Comparative Genomics of <i>Dehalococcoides ethenogenes</i> 195 and an Enrichment Culture Containing Unsequenced <i>Dehalococcoides</i> Strains. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3533-3540.	1.4	53
151	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.	1.4	72
152	Culture-Independent Bacterial Population Analysis – Clinical Implications for Respiratory and Other Infections. <i>Current Respiratory Medicine Reviews</i> , 2008, 4, 35-39.	0.1	1
153	Section 3 Update - High density DNA microarray analysis for monitoring microbial community composition and dynamics. , 2008, , 1806-1822.		0
154	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.	3.3	593
155	Exploration for Facultative Endosymbionts of Glassy-Winged Sharpshooter (Hemiptera: Cicadellidae). <i>Annals of the Entomological Society of America</i> , 2007, 100, 345-349.	1.3	14
156	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.	1.4	90
157	Mineralogical, Chemical and Biological Characterization of an Anaerobic Biofilm Collected from a Borehole in a Deep Gold Mine in South Africa. <i>Geomicrobiology Journal</i> , 2007, 24, 491-504.	1.0	35
158	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.	1.8	166
159	Molecular bacterial community analysis of clean rooms where spacecraft are assembled. <i>FEMS Microbiology Ecology</i> , 2007, 61, 509-521.	1.3	113
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