

Noah Fierer

List of Publications by Year in descending order

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257
papers

128,759
citations

735

120
h-index

736

251
g-index

290
all docs

290
docs citations

290
times ranked

85939
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	19.0	31,818
2	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME Journal, 2012, 6, 1621-1624.	9.8	7,430
3	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4516-4522.	7.1	7,425
4	The diversity and biogeography of soil bacterial communities. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 626-631.	7.1	4,672
5	Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11971-11975.	7.1	3,738
6	TOWARD AN ECOLOGICAL CLASSIFICATION OF SOIL BACTERIA. Ecology, 2007, 88, 1354-1364.	3.2	3,728
7	Pyrosequencing-Based Assessment of Soil pH as a Predictor of Soil Bacterial Community Structure at the Continental Scale. Applied and Environmental Microbiology, 2009, 75, 5111-5120.	3.1	3,268
8	Soil bacterial and fungal communities across a pH gradient in an arable soil. ISME Journal, 2010, 4, 1340-1351.	9.8	3,154
9	Bacterial Community Variation in Human Body Habitats Across Space and Time. Science, 2009, 326, 1694-1697.	12.6	2,713
10	Embracing the unknown: disentangling the complexities of the soil microbiome. Nature Reviews Microbiology, 2017, 15, 579-590.	28.6	2,087
11	Using network analysis to explore co-occurrence patterns in soil microbial communities. ISME Journal, 2012, 6, 343-351.	9.8	2,051
12	A communal catalogue reveals Earth's multiscale microbial diversity. Nature, 2017, 551, 457-463.	27.8	1,942
13	The influence of soil properties on the structure of bacterial and fungal communities across land-use types. Soil Biology and Biochemistry, 2008, 40, 2407-2415.	8.8	1,688
14	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	17.5	1,512
15	Variations in microbial community composition through two soil depth profiles. Soil Biology and Biochemistry, 2003, 35, 167-176.	8.8	1,409
16	Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. ISME Journal, 2012, 6, 1007-1017.	9.8	1,405
17	A global atlas of the dominant bacteria found in soil. Science, 2018, 359, 320-325.	12.6	1,386
18	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21390-21395.	7.1	1,260

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19	Assessment of Soil Microbial Community Structure by Use of Taxon-Specific Quantitative PCR Assays. Applied and Environmental Microbiology, 2005, 71, 4117-4120.	3.1	1,227
20	Examining the global distribution of dominant archaeal populations in soil. ISME Journal, 2011, 5, 908-917.	9.8	1,112
21	Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10967-10972.	7.1	1,023
22	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. ISME Journal, 2009, 3, 442-453.	9.8	984
23	The influence of sex, handedness, and washing on the diversity of hand surface bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17994-17999.	7.1	980
24	Bacterial phylogeny structures soil resistomes across habitats. Nature, 2014, 509, 612-616.	27.8	973
25	Global patterns in belowground communities. Ecology Letters, 2009, 12, 1238-1249.	6.4	957
26	Consistent effects of nitrogen amendments on soil microbial communities and processes across biomes. Global Change Biology, 2012, 18, 1918-1927.	9.5	936
27	Moving pictures of the human microbiome. Genome Biology, 2011, 12, R50.	9.6	934
28	Effects of drying–rewetting frequency on soil carbon and nitrogen transformations. Soil Biology and Biochemistry, 2002, 34, 777-787.	8.8	874
29	Cohabiting family members share microbiota with one another and with their dogs. ELife, 2013, 2, e00458.	6.0	801
30	MICROBIAL NITROGEN LIMITATION INCREASES DECOMPOSITION. Ecology, 2007, 88, 2105-2113.	3.2	765
31	Relic DNA is abundant in soil and obscures estimates of soil microbial diversity. Nature Microbiology, 2017, 2, 16242.	13.3	660
32	Testing the functional significance of microbial community composition. Ecology, 2009, 90, 441-451.	3.2	635
33	Digging deeper to find unique microbial communities: The strong effect of depth on the structure of bacterial and archaeal communities in soil. Soil Biology and Biochemistry, 2012, 50, 58-65.	8.8	614
34	The under-recognized dominance of Verrucomicrobia in soil bacterial communities. Soil Biology and Biochemistry, 2011, 43, 1450-1455.	8.8	613
35	Plant diversity predicts beta but not alpha diversity of soil microbes across grasslands worldwide. Ecology Letters, 2015, 18, 85-95.	6.4	612
36	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608

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37	The ecology of the phyllosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. <i>Environmental Microbiology</i> , 2010, 12, 2885-2893.	3.8	574
38	LITTER QUALITY AND THE TEMPERATURE SENSITIVITY OF DECOMPOSITION. <i>Ecology</i> , 2005, 86, 320-326.	3.2	566
39	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. <i>Environmental Microbiology</i> , 2010, 12, 2998-3006.	3.8	551
40	Conditionally Rare Taxa Disproportionately Contribute to Temporal Changes in Microbial Diversity. <i>MBio</i> , 2014, 5, e01371-14.	4.1	549
41	Forensic identification using skin bacterial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6477-6481.	7.1	507
42	Managing uncertainty in soil carbon feedbacks to climate change. <i>Nature Climate Change</i> , 2016, 6, 751-758.	18.8	491
43	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7059-7066.	3.1	480
44	Reconstructing the Microbial Diversity and Function of Pre-Agricultural Tallgrass Prairie Soils in the United States. <i>Science</i> , 2013, 342, 621-624.	12.6	480
45	Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. <i>Ecology</i> , 2010, 91, 3463-3470.	3.2	475
46	A Proposed Mechanism for the Pulse in Carbon Dioxide Production Commonly Observed Following the Rapid Rewetting of a Dry Soil. <i>Soil Science Society of America Journal</i> , 2003, 67, 798.	2.2	466
47	Shifts in bacterial community structure associated with inputs of low molecular weight carbon compounds to soil. <i>Soil Biology and Biochemistry</i> , 2010, 42, 896-903.	8.8	436
48	Global biogeography of highly diverse protistan communities in soil. <i>ISME Journal</i> , 2013, 7, 652-659.	9.8	412
49	Temporal variability in soil microbial communities across land-use types. <i>ISME Journal</i> , 2013, 7, 1641-1650.	9.8	408
50	Spatial variability in airborne bacterial communities across land-use types and their relationship to the bacterial communities of potential source environments. <i>ISME Journal</i> , 2011, 5, 601-612.	9.8	385
51	Controls on microbial CO ₂ production: a comparison of surface and subsurface soil horizons. <i>Global Change Biology</i> , 2003, 9, 1322-1332.	9.5	377
52	Continental-scale distributions of dust-associated bacteria and fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5756-5761.	7.1	372
53	Revised calibration of the MBTâ€“CBT paleotemperature proxy based on branched tetraether membrane lipids in surface soils. <i>Geochimica Et Cosmochimica Acta</i> , 2012, 96, 215-229.	3.9	369
54	Bacterial Communities Associated with the Surfaces of Fresh Fruits and Vegetables. <i>PLoS ONE</i> , 2013, 8, e59310.	2.5	366

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55	Global patterns in the biogeography of bacterial taxa. <i>Environmental Microbiology</i> , 2011, 13, 135-144.	3.8	362
56	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014, 15, 531.	8.8	355
57	Caterpillars lack a resident gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9641-9646.	7.1	355
58	Microbes do not follow the elevational diversity patterns of plants and animals. <i>Ecology</i> , 2011, 92, 797-804.	3.2	351
59	PrimerProspector: <i>de novo</i> design and taxonomic analysis of barcoded polymerase chain reaction primers. <i>Bioinformatics</i> , 2011, 27, 1159-1161.	4.1	351
60	Seasonal Variability in Bacterial and Fungal Diversity of the Near-Surface Atmosphere. <i>Environmental Science & Technology</i> , 2013, 47, 12097-12106.	10.0	349
61	Effect of storage conditions on the assessment of bacterial community structure in soil and human-associated samples. <i>FEMS Microbiology Letters</i> , 2010, 307, 80-86.	1.8	341
62	Changes through time: integrating microorganisms into the study of succession. <i>Research in Microbiology</i> , 2010, 161, 635-642.	2.1	334
63	Widespread coupling between the rate and temperature sensitivity of organic matter decay. <i>Nature Geoscience</i> , 2010, 3, 854-857.	12.9	328
64	A meta-analysis of changes in bacterial and archaeal communities with time. <i>ISME Journal</i> , 2013, 7, 1493-1506.	9.8	322
65	Bacterial Communities Associated with the Lichen Symbiosis. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1309-1314.	3.1	302
66	DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	3.9	300
67	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141988.	2.6	295
68	Linking bacterial community composition to soil salinity along environmental gradients. <i>ISME Journal</i> , 2019, 13, 836-846.	9.8	283
69	Co-habiting amphibian species harbor unique skin bacterial communities in wild populations. <i>ISME Journal</i> , 2012, 6, 588-596.	9.8	282
70	Home Life: Factors Structuring the Bacterial Diversity Found within and between Homes. <i>PLoS ONE</i> , 2013, 8, e64133.	2.5	277
71	Global drivers and patterns of microbial abundance in soil. <i>Global Ecology and Biogeography</i> , 2013, 22, 1162-1172.	5.8	274
72	Characterization of Airborne Microbial Communities at a High-Elevation Site and Their Potential To Act as Atmospheric Ice Nuclei. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5121-5130.	3.1	273

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73	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. <i>ELife</i> , 2013, 2, e01104.	6.0	270
74	Litter quality is in the eye of the beholder: initial decomposition rates as a function of inoculum characteristics. <i>Functional Ecology</i> , 2009, 23, 627-636.	3.6	264
75	High proportions of bacteria and archaea across most biomes remain uncultured. <i>ISME Journal</i> , 2019, 13, 3126-3130.	9.8	264
76	The global-scale distributions of soil protists and their contributions to belowground systems. <i>Science Advances</i> , 2020, 6, eaax8787.	10.3	263
77	Changes in Bacterial and Fungal Communities across Compost Recipes, Preparation Methods, and Composting Times. <i>PLoS ONE</i> , 2013, 8, e79512.	2.5	258
78	Influence of balsam poplar tannin fractions on carbon and nitrogen dynamics in Alaskan taiga floodplain soils. <i>Soil Biology and Biochemistry</i> , 2001, 33, 1827-1839.	8.8	254
79	The Evolution of Stomach Acidity and Its Relevance to the Human Microbiome. <i>PLoS ONE</i> , 2015, 10, e0134116.	2.5	253
80	The effects of chronic nitrogen fertilization on alpine tundra soil microbial communities: implications for carbon and nitrogen cycling. <i>Environmental Microbiology</i> , 2008, 10, 3093-3105.	3.8	252
81	Short-Term Temporal Variability in Airborne Bacterial and Fungal Populations. <i>Applied and Environmental Microbiology</i> , 2008, 74, 200-207.	3.1	250
82	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012, 30, 513-520.	17.5	250
83	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. <i>Nature Methods</i> , 2010, 7, 813-819.	19.0	249
84	Nitrogen fertilization inhibits soil microbial respiration regardless of the form of nitrogen applied. <i>Soil Biology and Biochemistry</i> , 2010, 42, 2336-2338.	8.8	246
85	Why are some microbes more ubiquitous than others? Predicting the habitat breadth of soil bacteria. <i>Ecology Letters</i> , 2014, 17, 794-802.	6.4	243
86	Sources of Bacteria in Outdoor Air across Cities in the Midwestern United States. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6350-6356.	3.1	237
87	Seasonal variability in airborne bacterial communities at a high-elevation site. <i>Atmospheric Environment</i> , 2012, 50, 41-49.	4.1	226
88	Bacterial Succession on the Leaf Surface: A Novel System for Studying Successional Dynamics. <i>Microbial Ecology</i> , 2009, 58, 189-198.	2.8	223
89	Predicting the temperature dependence of microbial respiration in soil: A continental-scale analysis. <i>Global Biogeochemical Cycles</i> , 2006, 20, n/a-n/a.	4.9	222
90	Microbial Biogeography of Public Restroom Surfaces. <i>PLoS ONE</i> , 2011, 6, e28132.	2.5	222

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91	A Proposed Mechanism for the Pulse in Carbon Dioxide Production Commonly Observed Following the Rapid Rewetting of a Dry Soil. Soil Science Society of America Journal, 2003, 67, 798-805.	2.2	219
92	ENVIRONMENTAL CONTROLS ON THE LANDSCAPE-SCALE BIOGEOGRAPHY OF STREAM BACTERIAL COMMUNITIES. Ecology, 2007, 88, 2162-2173.	3.2	216
93	Predicting the structure of soil communities from plant community taxonomy, phylogeny, and traits. ISME Journal, 2018, 12, 1794-1805.	9.8	210
94	The generation and maintenance of diversity in microbial communities. American Journal of Botany, 2011, 98, 439-448.	1.7	209
95	The ecology of microscopic life in household dust. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20151139.	2.6	205
96	Volatile organic compound (VOC) emissions from soil and litter samples. Soil Biology and Biochemistry, 2008, 40, 1629-1636.	8.8	199
97	Lake microbial communities are resilient after a whole-ecosystem disturbance. ISME Journal, 2012, 6, 2153-2167.	9.8	198
98	Microbes follow Humboldt: temperature drives plant and soil microbial diversity patterns from the Amazon to the Andes. Ecology, 2018, 99, 2455-2466.	3.2	197
99	How microbes can, and cannot, be used to assess soil health. Soil Biology and Biochemistry, 2021, 153, 108111.	8.8	196
100	Not all animals need a microbiome. FEMS Microbiology Letters, 2019, 366, .	1.8	189
101	Plant domestication and the assembly of bacterial and fungal communities associated with strains of the common sunflower, <i>Helianthus annuus</i> . New Phytologist, 2017, 214, 412-423.	7.3	185
102	Relating belowground microbial composition to the taxonomic, phylogenetic, and functional trait distributions of trees in a tropical forest. Ecology Letters, 2015, 18, 1397-1405.	6.4	183
103	The Earth Microbiome Project: Meeting report of the 1st EMP meeting on sample selection and acquisition at Argonne National Laboratory October 6th 2010.. Standards in Genomic Sciences, 2010, 3, 249-253.	1.5	176
104	Resuscitation of the rare biosphere contributes to pulses of ecosystem activity. Frontiers in Microbiology, 2015, 6, 24.	3.5	174
105	Digging the New York City Skyline: Soil Fungal Communities in Green Roofs and City Parks. PLoS ONE, 2013, 8, e58020.	2.5	174
106	Diversity, distribution and sources of bacteria in residential kitchens. Environmental Microbiology, 2013, 15, 588-596.	3.8	170
107	A method for simultaneous measurement of soil bacterial abundances and community composition via 16S rRNA gene sequencing. Soil Biology and Biochemistry, 2016, 96, 145-151.	8.8	170
108	Genome reduction in an abundant and ubiquitous soil bacterium <i>Candidatus Udaeobacter copiosus</i> . Nature Microbiology, 2017, 2, 16198.	13.3	168

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109	The influence of microbial communities, management, and soil texture on soil organic matter chemistry. <i>Geoderma</i> , 2009, 150, 278-286.	5.1	163
110	Fungal diversity regulates plant-soil feedbacks in temperate grassland. <i>Science Advances</i> , 2018, 4, eaau4578.	10.3	161
111	A Cross-Taxon Analysis of Insect-Associated Bacterial Diversity. <i>PLoS ONE</i> , 2013, 8, e61218.	2.5	157
112	Changes in belowground biodiversity during ecosystem development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6891-6896.	7.1	151
113	Global ecological predictors of the soil priming effect. <i>Nature Communications</i> , 2019, 10, 3481.	12.8	148
114	Metamorphosis of a Butterfly-Associated Bacterial Community. <i>PLoS ONE</i> , 2014, 9, e86995.	2.5	144
115	Ten questions concerning the microbiomes of buildings. <i>Building and Environment</i> , 2016, 109, 224-234.	6.9	143
116	Identifying the microbial taxa that consistently respond to soil warming across time and space. <i>Global Change Biology</i> , 2017, 23, 2117-2129.	9.5	143
117	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , 2010, 11, 210.	9.6	134
118	Microbial Processes in the Vadose Zone. <i>Vadose Zone Journal</i> , 2005, 4, 1-21.	2.2	132
119	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. <i>Frontiers in Microbiology</i> , 2014, 5, 298.	3.5	130
120	The Biogeography of Ammonia-Oxidizing Bacterial Communities in Soil. <i>Microbial Ecology</i> , 2009, 58, 435-445.	2.8	128
121	Geological and Geochemical Controls on Subsurface Microbial Life in the Samail Ophiolite, Oman. <i>Frontiers in Microbiology</i> , 2017, 8, 56.	3.5	126
122	Searching for unifying principles in soil ecology. <i>Soil Biology and Biochemistry</i> , 2009, 41, 2249-2256.	8.8	124
123	Fungal Community Composition in Neotropical Rain Forests: the Influence of Tree Diversity and Precipitation. <i>Microbial Ecology</i> , 2012, 63, 804-812.	2.8	121
124	Sensitivity of soil respiration and microbial communities to altered snowfall. <i>Soil Biology and Biochemistry</i> , 2013, 57, 217-227.	8.8	121
125	Molecular mechanisms underlying the close association between soil <i>Burkholderia</i> and fungi. <i>ISME Journal</i> , 2016, 10, 253-264.	9.8	118
126	Nitrogen and phosphorus fertilization consistently favor pathogenic over mutualistic fungi in grassland soils. <i>Nature Communications</i> , 2021, 12, 3484.	12.8	116

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127	Emissions of volatile organic compounds during the decomposition of plant litter. Journal of Geophysical Research, 2010, 115, .	3.3	115
128	Consistent changes in the taxonomic structure and functional attributes of bacterial communities during primary succession. ISME Journal, 2018, 12, 1658-1667.	9.8	113
129	Microbial consumption and production of volatile organic compounds at the soil-litter interface. Biogeochemistry, 2010, 99, 97-107.	3.5	110
130	Ecological and Genomic Attributes of Novel Bacterial Taxa That Thrive in Subsurface Soil Horizons. MBio, 2019, 10, .	4.1	108
131	Seeing the forest for the genes: using metagenomics to infer the aggregated traits of microbial communities. Frontiers in Microbiology, 2014, 5, 614.	3.5	107
132	The microbial contribution to macroecology. Frontiers in Microbiology, 2014, 5, 203.	3.5	106
133	Genus-wide acid tolerance accounts for the biogeographical distribution of soil <i>Burkholderia</i> populations. Environmental Microbiology, 2014, 16, 1503-1512.	3.8	105
134	Phylogenetic factorization of compositional data yields lineage-level associations in microbiome datasets. PeerJ, 2017, 5, e2969.	2.0	105
135	Seasonal Shifts in Diet and Gut Microbiota of the American Bison (<i>Bison bison</i>). PLoS ONE, 2015, 10, e0142409.	2.5	104
136	Modern water/rock reactions in Oman hyperalkaline peridotite aquifers and implications for microbial habitability. Geochimica Et Cosmochimica Acta, 2016, 179, 217-241.	3.9	102
137	Predicting the responsiveness of soil biodiversity to deforestation: a cross-biome study. Global Change Biology, 2014, 20, 2983-2994.	9.5	101
138	Cross-biome patterns in soil microbial respiration predictable from evolutionary theory on thermal adaptation. Nature Ecology and Evolution, 2019, 3, 223-231.	7.8	100
139	Evidence-based recommendations on storing and handling specimens for analyses of insect microbiota. PeerJ, 2015, 3, e1190.	2.0	99
140	Review of human hand microbiome research. Journal of Dermatological Science, 2015, 80, 3-12.	1.9	99
141	Global gaps in soil biodiversity data. Nature Ecology and Evolution, 2018, 2, 1042-1043.	7.8	99
142	Cell Size Distributions of Soil Bacterial and Archaeal Taxa. Applied and Environmental Microbiology, 2013, 79, 7610-7617.	3.1	98
143	Spatial structuring of bacterial communities within individual <i>Ginkgo biloba</i> trees. Environmental Microbiology, 2015, 17, 2352-2361.	3.8	94
144	Lambda Interferon Restructures the Nasal Microbiome and Increases Susceptibility to <i>Staphylococcus aureus</i> Superinfection. MBio, 2016, 7, e01939-15.	4.1	94

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145	Ecological Analyses of Mycobacteria in Showerhead Biofilms and Their Relevance to Human Health. MBio, 2018, 9, .	4.1	90
146	Microbial Biogeography: Patterns in Microbial Diversity across Space and Time. , 0, , 95-115.		90
147	Structure, inter-annual recurrence, and global-scale connectivity of airborne microbial communities. Science of the Total Environment, 2014, 487, 187-195.	8.0	89
148	Impacts of Flood Damage on Airborne Bacteria and Fungi in Homes after the 2013 Colorado Front Range Flood. Environmental Science & Technology, 2015, 49, 2675-2684.	10.0	88
149	Novel bacterial lineages associated with boreal moss species. Environmental Microbiology, 2018, 20, 2625-2638.	3.8	86
150	Production of CO ₂ in Soil Profiles of a California Annual Grassland. Ecosystems, 2005, 8, 412-429.	3.4	84
151	Microbial Processes in the Vadose Zone. Vadose Zone Journal, 2005, 4, 1-21.	2.2	84
152	Temporal variability in the diversity and composition of stream bacterioplankton communities. Environmental Microbiology, 2012, 14, 2417-2428.	3.8	83
153	Global homogenization of the structure and function in the soil microbiome of urban greenspaces. Science Advances, 2021, 7, .	10.3	83
154	Evolutionary histories of soil fungi are reflected in their large-scale biogeography. Ecology Letters, 2014, 17, 1086-1093.	6.4	80
155	The diversity and function of sourdough starter microbiomes. ELife, 2021, 10, .	6.0	77
156	From the litter layer to the saprolite: Chemical changes in water-soluble soil organic matter and their correlation to microbial community composition. Soil Biology and Biochemistry, 2014, 68, 166-176.	8.8	75
157	Climatic warming and the future of bison as grazers. Scientific Reports, 2015, 5, 16738.	3.3	72
158	Palaeoclimate explains a unique proportion of the global variation in soil bacterial communities. Nature Ecology and Evolution, 2017, 1, 1339-1347.	7.8	70
159	Effects of Spatial Variability and Relic DNA Removal on the Detection of Temporal Dynamics in Soil Microbial Communities. MBio, 2020, 11, .	4.1	70
160	Ectomycorrhizal-Dominated Boreal and Tropical Forests Have Distinct Fungal Communities, but Analogous Spatial Patterns across Soil Horizons. PLoS ONE, 2013, 8, e68278.	2.5	69
161	Hiding in Plain Sight: Mining Bacterial Species Records for Phenotypic Trait Information. MSphere, 2017, 2, .	2.9	69
162	The Role of Phosphorus Limitation in Shaping Soil Bacterial Communities and Their Metabolic Capabilities. MBio, 2020, 11, .	4.1	69

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163	A Jungle in There: Bacteria in Belly Buttons are Highly Diverse, but Predictable. PLoS ONE, 2012, 7, e47712.	2.5	69
164	From Animalcules to an Ecosystem: Application of Ecological Concepts to the Human Microbiome. Annual Review of Ecology, Evolution, and Systematics, 2012, 43, 137-155.	8.3	68
165	A preliminary survey of lichen associated eukaryotes using pyrosequencing. Lichenologist, 2012, 44, 137-146.	0.8	67
166	Treating cattle with antibiotics affects greenhouse gas emissions, and microbiota in dung and dung beetles. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160150.	2.6	67
167	Infection with a Shoot-Specific Fungal Endophyte (<i>Epichloa</i>) Alters Tall Fescue Soil Microbial Communities. Microbial Ecology, 2016, 72, 197-206.	2.8	67
168	Microbial responses to warming enhance soil carbon loss following translocation across a tropical forest elevation gradient. Ecology Letters, 2019, 22, 1889-1899.	6.4	65
169	Wild plant species growing closely connected in a subalpine meadow host distinct root-associated bacterial communities. PeerJ, 2015, 3, e804.	2.0	65
170	Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig (<i>Sus</i>) in the Philippines. PLoS ONE, 2019, 14, e0204621.	1.9	63
171	Tales from the tomb: the microbial ecology of exposed rock surfaces. Environmental Microbiology, 2018, 20, 958-970.	3.8	63
172	Variable influences of soil and seed-associated bacterial communities on the assembly of seedling microbiomes. ISME Journal, 2021, 15, 2748-2762.	9.8	63
173	Response of soil microbial community composition and function to a bottomland forest restoration intensity gradient. Applied Soil Ecology, 2017, 119, 317-326.	4.3	62
174	Fungal growth on a common wood substrate across a tropical elevation gradient: Temperature sensitivity, community composition, and potential for above-ground decomposition. Soil Biology and Biochemistry, 2010, 42, 1083-1090.	8.8	61
175	A Direct PCR Approach to Accelerate Analyses of Human-Associated Microbial Communities. PLoS ONE, 2012, 7, e44563.	2.5	60
176	Consequences of tropical forest conversion to oil palm on soil bacterial community and network structure. Soil Biology and Biochemistry, 2017, 112, 258-268.	8.8	60
177	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	5.3	59
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