

# James M Tiedje

## List of Publications by Year in descending order

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Version: 2024-02-01

230  
papers

57,855  
citations

4942

84  
h-index

1152

229  
g-index

241  
all docs

241  
docs citations

241  
times ranked

52688  
citing authors

#	ARTICLE	IF	CITATIONS
1	Application of magnetic biochar/quaternary phosphonium salt to combat the antibiotic resistome in livestock wastewater. <i>Science of the Total Environment</i> , 2022, 811, 151386.	3.9	5
2	Permafrost thaw with warming reduces microbial metabolic capacities in subsurface soils. <i>Molecular Ecology</i> , 2022, 31, 1403-1415.	2.0	12
3	Microbes and Climate Change: a Research Prospectus for the Future. <i>MBio</i> , 2022, 13, e0080022.	1.8	53
4	Reduction of microbial diversity in grassland soil is driven by long-term climate warming. <i>Nature Microbiology</i> , 2022, 7, 1054-1062.	5.9	86
5	Antibiotic Resistomes and Microbiomes in the Surface Water along the Code River in Indonesia Reflect Drainage Basin Anthropogenic Activities. <i>Environmental Science &amp; Technology</i> , 2022, 56, 14994-15006.	4.6	11
6	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
7	Winter warming rapidly increases carbon degradation capacities of fungal communities in tundra soil: Potential consequences on carbon stability. <i>Molecular Ecology</i> , 2021, 30, 926-937.	2.0	16
8	Does anaerobic condition play a more positive role in dissipation of antibiotic resistance genes in soil?. <i>Science of the Total Environment</i> , 2021, 757, 143737.	3.9	16
9	Climate warming enhances microbial network complexity and stability. <i>Nature Climate Change</i> , 2021, 11, 343-348.	8.1	672
10	A new primer set for Clade I nosZ that recovers genes from a broader range of taxa. <i>Biology and Fertility of Soils</i> , 2021, 57, 523-531.	2.3	25
11	Peat-based gnotobiotic plant growth systems for Arabidopsis microbiome research. <i>Nature Protocols</i> , 2021, 16, 2450-2470.	5.5	26
12	Metagenomic analysis reveals the shared and distinct features of the soil resistome across tundra, temperate prairie, and tropical ecosystems. <i>Microbiome</i> , 2021, 9, 108.	4.9	60
13	Removal of extracellular antibiotic resistance genes using magnetic biochar/quaternary phosphonium salt in aquatic environments: A mechanistic study. <i>Journal of Hazardous Materials</i> , 2021, 411, 125048.	6.5	36
14	Long-read sequencing revealed cooccurrence, host range, and potential mobility of antibiotic resistome in cow feces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	27
15	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021, 12, 4765.	5.8	248
16	Long-term excess nitrogen fertilizer increases sensitivity of soil microbial community to seasonal change revealed by ecological network and metagenome analyses. <i>Soil Biology and Biochemistry</i> , 2021, 160, 108349.	4.2	77
17	MicroRNA-based host response to toxicant exposure is influenced by the presence of gut microbial populations. <i>Science of the Total Environment</i> , 2021, 797, 149130.	3.9	2
18	Bioaccumulation of Manure-borne antibiotic resistance genes in carrot and its exposure assessment. <i>Environment International</i> , 2021, 157, 106830.	4.8	36

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19	Strategy for Mitigating Antibiotic Resistance by Biochar and Hyperaccumulators in Cadmium and Oxytetracycline Co-contaminated Soil. <i>Environmental Science &amp; Technology</i> , 2021, 55, 16369-16378.	4.6	46
20	Artificial intelligence: A powerful paradigm for scientific research. <i>Innovation(China)</i> , 2021, 2, 100179.	5.2	200
21	Technologies and perspectives for achieving carbon neutrality. <i>Innovation(China)</i> , 2021, 2, 100180.	5.2	306
22	Bioavailability of clay-adsorbed dioxin to <i>Sphingomonas wittichii</i> RW1 and its associated genome-wide shifts in gene expression. <i>Science of the Total Environment</i> , 2020, 712, 135525.	3.9	6
23	Organic amendments change soil organic C structure and microbial community but not total organic matter on sub-decadal scales. <i>Soil Biology and Biochemistry</i> , 2020, 150, 107986.	4.2	7
24	Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming. <i>Nature Communications</i> , 2020, 11, 4897.	5.8	67
25	Editorial: The Environmental Dimension of Antibiotic Resistance. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	23
26	The soil microbial carbon pump: From conceptual insights to empirical assessments. <i>Global Change Biology</i> , 2020, 26, 6032-6039.	4.2	122
27	Antibiotic Resistance in Soil. <i>Handbook of Environmental Chemistry</i> , 2020, , 267-293.	0.2	5
28	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. <i>Microbiome</i> , 2020, 8, 84.	4.9	47
29	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
30	Targeted assemblies of <i>cas1</i> suggest CRISPR-Cas™s response to soil warming. <i>ISME Journal</i> , 2020, 14, 1651-1662.	4.4	6
31	Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. <i>Microbiome</i> , 2020, 8, 3.	4.9	75
32	A general framework for quantitatively assessing ecological stochasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16892-16898.	3.3	482
33	Composting increased persistence of manure-borne antibiotic resistance genes in soils with different fertilization history. <i>Science of the Total Environment</i> , 2019, 689, 1172-1180.	3.9	40
34	Tundra microbial community taxa and traits predict decomposition parameters of stable, old soil organic carbon. <i>ISME Journal</i> , 2019, 13, 2901-2915.	4.4	24
35	Responses of tundra soil microbial communities to half a decade of experimental warming at two critical depths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15096-15105.	3.3	83
36	Pharmaceutical exposure changed antibiotic resistance genes and bacterial communities in soil-surface- and overhead-irrigated greenhouse lettuce. <i>Environment International</i> , 2019, 131, 105031.	4.8	48

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37	Diazotroph Diversity and Nitrogen Fixation in Summer Active Perennial Grasses in a Mediterranean Region Agricultural Soil. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 115.	1.6	34
38	Antibiotic Resistance Genes in the Human-Impacted Environment: A One Health Perspective. <i>Pedosphere</i> , 2019, 29, 273-282.	2.1	100
39	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	5.9	491
40	Bacillus-Dominant Airborne Bacterial Communities Identified During Asian Dust Events. <i>Microbial Ecology</i> , 2019, 78, 677-687.	1.4	13
41	Long-Term Warming in Alaska Enlarges the Diazotrophic Community in Deep Soils. <i>MBio</i> , 2019, 10, .	1.8	22
42	Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. <i>Nature Ecology and Evolution</i> , 2019, 3, 612-619.	3.4	82
43	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. <i>Science Advances</i> , 2019, 5, eaau9124.	4.7	346
44	Community shift of microbial ammonia oxidizers in air-dried rice soils after 22 years of nitrogen fertilization. <i>Biology and Fertility of Soils</i> , 2019, 55, 419-424.	2.3	16
45	Editorial: Environmental aspects of antibiotic resistance. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	2
46	Genomic Variations Underlying Speciation and Niche Specialization of <i>Shewanella baltica</i> . <i>MSystems</i> , 2019, 4, .	1.7	10
47	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. <i>Frontiers in Genetics</i> , 2019, 10, 957.	1.1	8
48	Deforestation impacts network co-occurrence patterns of microbial communities in Amazon soils. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	34
49	Isotopic evidence for episodic nitrogen fixation in switchgrass ( <i>Panicum virgatum</i> L.). <i>Soil Biology and Biochemistry</i> , 2019, 129, 90-98.	4.2	59
50	Effect of LSU and ITS genetic markers and reference databases on analyses of fungal communities. <i>Biology and Fertility of Soils</i> , 2019, 55, 79-88.	2.3	33
51	Glucose addition increases the magnitude and decreases the age of soil respired carbon in a long-term permafrost incubation study. <i>Soil Biology and Biochemistry</i> , 2019, 129, 201-211.	4.2	26
52	<i>Bacillus cabrialesii</i> sp. nov., an endophytic plant growth promoting bacterium isolated from wheat ( <i>Triticum turgidum</i> subsp. durum) in the Yaqui Valley, Mexico. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3939-3945.	0.8	40
53	Comment on "The whole-soil carbon flux in response to warming". <i>Science</i> , 2018, 359, .	6.0	12
54	Bacterial Community Shift and Coexisting/Coexcluding Patterns Revealed by Network Analysis in a Uranium-Contaminated Site after Bioreduction Followed by Reoxidation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	37

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55	ARGs-OAP v2.0 with an expanded SARG database and Hidden Markov Models for enhancement characterization and quantification of antibiotic resistance genes in environmental metagenomes. <i>Bioinformatics</i> , 2018, 34, 2263-2270.	1.8	375
56	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
57	Biomass and biofuel crop effects on biodiversity and ecosystem services in the North Central US. <i>Biomass and Bioenergy</i> , 2018, 114, 18-29.	2.9	61
58	The Microbiome of Eucalyptus Roots under Different Management Conditions and Its Potential for Biological Nitrogen Fixation. <i>Microbial Ecology</i> , 2018, 75, 183-191.	1.4	45
59	Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. <i>Global Change Biology</i> , 2018, 24, 297-307.	4.2	22
60	Divergence in Gene Regulation Contributes to Sympatric Speciation of <i>Shewanella baltica</i> Strains. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	5
61	Antibiotic Resistance Gene Detection in the Microbiome Context. <i>Microbial Drug Resistance</i> , 2018, 24, 542-546.	0.9	14
62	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
63	Nonpareil 3: Fast Estimation of Metagenomic Coverage and Sequence Diversity. <i>MSystems</i> , 2018, 3, .	1.7	152
64	Long-Term Effect of Different Fertilization and Cropping Systems on the Soil Antibiotic Resistome. <i>Environmental Science &amp; Technology</i> , 2018, 52, 13037-13046.	4.6	88
65	Associative nitrogen fixation (ANF) in switchgrass ( <i>Panicum virgatum</i> ) across a nitrogen input gradient. <i>PLoS ONE</i> , 2018, 13, e0197320.	1.1	71
66	Root-Associated Microbiome of Maize Genotypes with Contrasting Phosphorus Use Efficiency. <i>Phytobiomes Journal</i> , 2018, 2, 129-137.	1.4	59
67	Microbial Community Structure and Functional Potential in Cultivated and Native Tallgrass Prairie Soils of the Midwestern United States. <i>Frontiers in Microbiology</i> , 2018, 9, 1775.	1.5	36
68	Biotic responses buffer warming-induced soil organic carbon loss in Arctic tundra. <i>Global Change Biology</i> , 2018, 24, 4946-4959.	4.2	21
69	Antibiotic Resistome Associated with Small-Scale Poultry Production in Rural Ecuador. <i>Environmental Science &amp; Technology</i> , 2018, 52, 8165-8172.	4.6	40
70	Primer set 2.0 for highly parallel qPCR array targeting antibiotic resistance genes and mobile genetic elements. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	95
71	Conserved phylogenetic distribution and limited antibiotic resistance of class 1 integrons revealed by assessing the bacterial genome and plasmid collection. <i>Microbiome</i> , 2018, 6, 130.	4.9	83
72	Taxonomic and Functional Responses of Soil Microbial Communities to Annual Removal of Aboveground Plant Biomass. <i>Frontiers in Microbiology</i> , 2018, 9, 954.	1.5	11

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73	Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818.	8.1	208
74	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1635.	1.5	51
75	More replenishment than priming loss of soil organic carbon with additional carbon input. <i>Nature Communications</i> , 2018, 9, 3175.	5.8	69
76	The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of Archaea and Bacteria at the whole genome level. <i>Nucleic Acids Research</i> , 2018, 46, W282-W288.	6.5	458
77	Virulence factor activity relationships (VFARs): a bioinformatics perspective. <i>Environmental Sciences: Processes and Impacts</i> , 2017, 19, 247-260.	1.7	16
78	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	4.4	136
79	Influence of Manure Application on the Environmental Resistome under Finnish Agricultural Practice with Restricted Antibiotic Use. <i>Environmental Science &amp; Technology</i> , 2017, 51, 5989-5999.	4.6	142
80	Isothermal assay targeting class 1 integrase gene for environmental surveillance of antibiotic resistance markers. <i>Journal of Environmental Management</i> , 2017, 198, 213-220.	3.8	17
81	TCDD influences reservoir of antibiotic resistance genes in murine gut microbiome. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	32
82	Soil depth and crop determinants of bacterial communities under ten biofuel cropping systems. <i>Soil Biology and Biochemistry</i> , 2017, 112, 140-152.	4.2	61
83	Strategies to improve reference databases for soil microbiomes. <i>ISME Journal</i> , 2017, 11, 829-834.	4.4	106
84	Soil Organic Carbon in a Changing World. <i>Pedosphere</i> , 2017, 27, 789-791.	2.1	33
85	TCDD administered on activated carbon eliminates bioavailability and subsequent shifts to a key murine gut commensal. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7409-7415.	1.7	9
86	Cellulosic biofuel contributions to a sustainable energy future: Choices and outcomes. <i>Science</i> , 2017, 356, .	6.0	314
87	Quantification of microRNAs directly from body fluids using a base-stacking isothermal amplification method in a point-of-care device. <i>Biomedical Microdevices</i> , 2017, 19, 45.	1.4	7
88	Most probable number - loop mediated isothermal amplification (MPN-LAMP) for quantifying waterborne pathogens in <math>25\text{ min}</math>. <i>Journal of Microbiological Methods</i> , 2017, 132, 27-33.	0.7	27
89	Hypoxia and Inactivity Related Physiological Changes (Constipation, Inflammation) Are Not Reflected at the Level of Gut Metabolites and Butyrate Producing Microbial Community: The PlanHab Study. <i>Frontiers in Physiology</i> , 2017, 8, 250.	1.3	32
90	Modeling Hybridization Kinetics of Gene Probes in a DNA Biochip Using FEMLAB. <i>Microarrays (Basel)</i> , Tj ETQq0 0 0 ggBT /Overlock 10 Tt		

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91	Modulatory Influence of Segmented Filamentous Bacteria on Transcriptomic Response of Gnotobiotic Mice Exposed to TCDD. <i>Frontiers in Microbiology</i> , 2017, 8, 1708.	1.5	12
92	MicroRNAs-Based Inter-Domain Communication between the Host and Members of the Gut Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1896.	1.5	46
93	Evaluation of Nucleic Acid Isothermal Amplification Methods for Human Clinical Microbial Infection Detection. <i>Frontiers in Microbiology</i> , 2017, 8, 2211.	1.5	17
94	Hypoxia and inactivity related physiological changes precede or take place in absence of significant rearrangements in bacterial community structure: The PlanHab randomized trial pilot study. <i>PLoS ONE</i> , 2017, 12, e0188556.	1.1	20
95	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	1.5	66
96	Size Matters: Assessing Optimum Soil Sample Size for Fungal and Bacterial Community Structure Analyses Using High Throughput Sequencing of rRNA Gene Amplicons. <i>Frontiers in Microbiology</i> , 2016, 7, 824.	1.5	58
97	NifH-Harboring Bacterial Community Composition across an Alaskan Permafrost Thaw Gradient. <i>Frontiers in Microbiology</i> , 2016, 7, 1894.	1.5	35
98	<i>Sphingomonas wittichii</i> Strain RW1 Genome-Wide Gene Expression Shifts in Response to Dioxins and Clay. <i>PLoS ONE</i> , 2016, 11, e0157008.	1.1	24
99	Editorial: Special section of FEMS Microbiology Ecology on the environmental dimension of antibiotic resistance. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw172.	1.3	9
100	Clusters of Antibiotic Resistance Genes Enriched Together Stay Together in Swine Agriculture. <i>MBio</i> , 2016, 7, e02214-15.	1.8	201
101	Influence of corn, switchgrass, and prairie cropping systems on soil microbial communities in the upper Midwest of the United States. <i>GCB Bioenergy</i> , 2016, 8, 481-494.	2.5	79
102	Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. <i>MBio</i> , 2016, 7, .	1.8	43
103	Land use intensification in the humid tropics increased both alpha and beta diversity of soil bacteria. <i>Ecology</i> , 2016, 97, 2760-2771.	1.5	92
104	<i>Shewanella baltica</i> Ecotypes Have Wide Transcriptional Variation under the Same Growth Conditions. <i>MSphere</i> , 2016, 1, .	1.3	3
105	Methodologies for probing the metatranscriptome of grassland soil. <i>Journal of Microbiological Methods</i> , 2016, 131, 122-129.	0.7	19
106	Influence of Soil Characteristics and Proximity to Antarctic Research Stations on Abundance of Antibiotic Resistance Genes in Soils. <i>Environmental Science &amp; Technology</i> , 2016, 50, 12621-12629.	4.6	107
107	Aquaculture changes the profile of antibiotic resistance and mobile genetic element associated genes in Baltic Sea sediments. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw052.	1.3	142
108	Soil fungal and bacterial responses to conversion of open land to short-rotation woody biomass crops. <i>GCB Bioenergy</i> , 2016, 8, 723-736.	2.5	20

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109	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
110	Antimicrobial resistance dashboard application for mapping environmental occurrence and resistant pathogens. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw020.	1.3	32
111	High-throughput quantification of antibiotic resistance genes from an urban wastewater treatment plant. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw014.	1.3	167
112	ARGs-OAP: online analysis pipeline for antibiotic resistance genes detection from metagenomic data using an integrated structured ARG-database. <i>Bioinformatics</i> , 2016, 32, 2346-2351.	1.8	254
113	Metagenomic Assembly Reveals Hosts of Antibiotic Resistance Genes and the Shared Resistome in Pig, Chicken, and Human Feces. <i>Environmental Science &amp; Technology</i> , 2016, 50, 420-427.	4.6	287
114	Switchgrass rhizospheres stimulate microbial biomass but deplete microbial necromass in agricultural soils of the upper Midwest, USA. <i>Soil Biology and Biochemistry</i> , 2016, 94, 173-180.	4.2	32
115	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 157-166.	1.4	73
116	The Resistome of Farmed Fish Feces Contributes to the Enrichment of Antibiotic Resistance Genes in Sediments below Baltic Sea Fish Farms. <i>Frontiers in Microbiology</i> , 2016, 7, 2137.	1.5	119
117	Functional roles of CymA and NapC in reduction of nitrate and nitrite by <i>Shewanella putrefaciens</i> W3-18-1. <i>Microbiology (United Kingdom)</i> , 2016, 162, 930-941.	0.7	14
118	Xander: employing a novel method for efficient gene-targeted metagenomic assembly. <i>Microbiome</i> , 2015, 3, 32.	4.9	83
119	Intestinal microbial communities associated with acute enteric infections and disease recovery. <i>Microbiome</i> , 2015, 3, 45.	4.9	151
120	Denitrifying and diazotrophic community responses to artificial warming in permafrost and tallgrass prairie soils. <i>Frontiers in Microbiology</i> , 2015, 6, 746.	1.5	19
121	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
122	Differential Response of Acidobacteria Subgroups to Forest-to-Pasture Conversion and Their Biogeographic Patterns in the Western Brazilian Amazon. <i>Frontiers in Microbiology</i> , 2015, 6, 1443.	1.5	111
123	Intercropped Silviculture Systems, a Key to Achieving Soil Fungal Community Management in Eucalyptus Plantations. <i>PLoS ONE</i> , 2015, 10, e0118515.	1.1	38
124	Alterations of the Murine Gut Microbiome with Age and Allergic Airway Disease. <i>Journal of Immunology Research</i> , 2015, 2015, 1-8.	0.9	47
125	Gene expression analysis of <i>E. coli</i> strains provides insights into the role of gene regulation in diversification. <i>ISME Journal</i> , 2015, 9, 1130-1140.	4.4	63
126	Methane-derived carbon flow through microbial communities in arctic lake sediments. <i>Environmental Microbiology</i> , 2015, 17, 3233-3250.	1.8	31



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127	Metagenomic and network analysis reveal wide distribution and co-occurrence of environmental antibiotic resistance genes. <i>ISME Journal</i> , 2015, 9, 2490-2502.	4.4	928
128	Evaluation of the Ion Torrent Personal Genome Machine for Gene-Targeted Studies Using Amplicons of the Nitrogenase Gene <i>nifH</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 4536-4545.	1.4	26
129	Dynamic Succession of Groundwater Functional Microbial Communities in Response to Emulsified Vegetable Oil Amendment during Sustained <i>In Situ</i> U(VI) Reduction. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4164-4172.	1.4	24
130	Selection of fluorescent DNA dyes for real-time LAMP with portable and simple optics. <i>Journal of Microbiological Methods</i> , 2015, 119, 223-227.	0.7	37
131	Using the class 1 integron-integrase gene as a proxy for anthropogenic pollution. <i>ISME Journal</i> , 2015, 9, 1269-1279.	4.4	974
132	Diet is a major factor governing the fecal butyrate-producing community structure across <i>Mammalia</i> , <i>Aves</i> and <i>Reptilia</i> . <i>ISME Journal</i> , 2015, 9, 832-843.	4.4	93
133	Microbial communities biostimulated by ethanol during uranium (VI) bioremediation in contaminated sediment as shown by stable isotope probing. <i>Frontiers of Environmental Science and Engineering</i> , 2015, 9, 453-464.	3.3	22
134	History and impact of RDP. <i>RNA Biology</i> , 2014, 11, 239-243.	1.5	19
135	Tackling soil diversity with the assembly of large, complex metagenomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4904-4909.	3.3	305
136	Revealing the Bacterial Butyrate Synthesis Pathways by Analyzing (Meta)genomic Data. <i>MBio</i> , 2014, 5, e00889.	1.8	829
137	Ribosomal Database Project: data and tools for high throughput rRNA analysis. <i>Nucleic Acids Research</i> , 2014, 42, D633-D642.	6.5	3,768
138	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
139	Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E836-45.	3.3	595
140	Role of Tetracycline Speciation in the Bioavailability to <i>Escherichia coli</i> for Uptake and Expression of Antibiotic Resistance. <i>Environmental Science &amp; Technology</i> , 2014, 48, 4893-4900.	4.6	57
141	Editorial overview: Ecology and industrial microbiology. <i>Current Opinion in Microbiology</i> , 2014, 19, v-vii.	2.3	2
142	Stability, genotypic and phenotypic diversity of <i>S. hewanella baltica</i> in the redox transition zone of the <i>Baltic Sea</i> . <i>Environmental Microbiology</i> , 2014, 16, 1854-1866.	1.8	26
143	Fungal Community Structure in Disease Suppressive Soils Assessed by 28S LSU Gene Sequencing. <i>PLoS ONE</i> , 2014, 9, e93893.	1.1	140
144	Microbial Diversity of a Mediterranean Soil and Its Changes after Biotransformed Dry Olive Residue Amendment. <i>PLoS ONE</i> , 2014, 9, e103035.	1.1	52

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145	Fungal Diversity in Permafrost and Tallgrass Prairie Soils under Experimental Warming Conditions. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7063-7072.	1.4	66
146	Effect of storage conditions on the stability and fermentability of enzymatic lignocellulosic hydrolysate. <i>Bioresource Technology</i> , 2013, 147, 212-220.	4.8	19
147	Ecological Patterns of <i>nifH</i> Genes in Four Terrestrial Climatic Zones Explored with Targeted Metagenomics Using FrameBot, a New Informatics Tool. <i>MBio</i> , 2013, 4, e00592-13.	1.8	279
148	FunGene: the functional gene pipeline and repository. <i>Frontiers in Microbiology</i> , 2013, 4, 291.	1.5	518
149	Diverse and abundant antibiotic resistance genes in Chinese swine farms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3435-3440.	3.3	1,925
150	Conversion of the Amazon rainforest to agriculture results in biotic homogenization of soil bacterial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 988-993.	3.3	481
151	Recently Deglaciated High-Altitude Soils of the Himalaya: Diverse Environments, Heterogenous Bacterial Communities and Long-Range Dust Inputs from the Upper Troposphere. <i>PLoS ONE</i> , 2013, 8, e76440.	1.1	66
152	Denitrifying Bacteria from the Genus <i>Rhodanobacter</i> Dominate Bacterial Communities in the Highly Contaminated Subsurface of a Nuclear Legacy Waste Site. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1039-1047.	1.4	184
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