

# James M Tiedje

## List of Publications by Year in descending order

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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	Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5261-5267.	1.4	17,125
2	DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 81-91.	0.8	3,968
3	Ribosomal Database Project: data and tools for high throughput rRNA analysis. <i>Nucleic Acids Research</i> , 2014, 42, D633-D642.	6.5	3,768
4	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
5	Genomic insights that advance the species definition for prokaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2567-2572.	3.3	1,869
6	Using the class 1 integron-integrase gene as a proxy for anthropogenic pollution. <i>ISME Journal</i> , 2015, 9, 1269-1279.	4.4	974
7	Towards a Genome-Based Taxonomy for Prokaryotes. <i>Journal of Bacteriology</i> , 2005, 187, 6258-6264.	1.0	966
8	In-feed antibiotic effects on the swine intestinal microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1691-1696.	3.3	942
9	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
10	Towards environmental systems biology of <i>Shewanella</i> . <i>Nature Reviews Microbiology</i> , 2008, 6, 592-603.	13.6	829
11	Revealing the Bacterial Butyrate Synthesis Pathways by Analyzing (Meta)genomic Data. <i>MBio</i> , 2014, 5, e00889.	1.8	829
12	Climate warming enhances microbial network complexity and stability. <i>Nature Climate Change</i> , 2021, 11, 343-348.	8.1	672
13	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
14	Spatial and Resource Factors Influencing High Microbial Diversity in Soil. <i>Applied and Environmental Microbiology</i> , 2002, 68, 326-334.	1.4	599
15	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
16	The bacterial species definition in the genomic era. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1929-1940.	1.8	550
17	FunGene: the functional gene pipeline and repository. <i>Frontiers in Microbiology</i> , 2013, 4, 291.	1.5	518
18	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	5.9	491

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19	A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16892-16898.	3.3	482
20	Conversion of the Amazon rainforest to agriculture results in biotic homogenization of soil bacterial communities. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 988-993.	3.3	481
21	The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of Archaea and Bacteria at the whole genome level. Nucleic Acids Research, 2018, 46, W282-W288.	6.5	458
22	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
23	Biogeography and Degree of Endemicity of Fluorescent Pseudomonas Strains in Soil. Applied and Environmental Microbiology, 2000, 66, 5448-5456.	1.4	429
24	Prokaryotic taxonomy and phylogeny in the genomic era: advancements and challenges ahead. Current Opinion in Microbiology, 2007, 10, 504-509.	2.3	403
25	Multiscale responses of microbial life to spatial distance and environmental heterogeneity in a patchy ecosystem. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2761-2766.	3.3	376
26	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. Bioinformatics, 2018, 34, 2263-2270.	1.8	375
27	Development and Evaluation of Functional Gene Arrays for Detection of Selected Genes in the Environment. Applied and Environmental Microbiology, 2001, 67, 5780-5790.	1.4	373
28	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. Science Advances, 2019, 5, eaau9124.	4.7	346
29	Burkholderia xenovorans LB400 harbors a multi-replicon, 9.73-Mbp genome shaped for versatility. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15280-15287.	3.3	339
30	Cellulosic biofuel contributions to a sustainable energy future: Choices and outcomes. Science, 2017, 356, .	6.0	314
31	Technologies and perspectives for achieving carbon neutrality. Innovation(China), 2021, 2, 100180.	5.2	306
32	Tackling soil diversity with the assembly of large, complex metagenomes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4904-4909.	3.3	305
33	Flexible Community Structure Correlates with Stable Community Function in Methanogenic Bioreactor Communities Perturbed by Glucose. Applied and Environmental Microbiology, 2000, 66, 4058-4067.	1.4	302
34	Dechlorination of Four Commercial Polychlorinated Biphenyl Mixtures (Aroclors) by Anaerobic Microorganisms from Sediments. Applied and Environmental Microbiology, 1990, 56, 2360-2369.	1.4	291
35	Metagenomic Assembly Reveals Hosts of Antibiotic Resistance Genes and the Shared Resistome in Pig, Chicken, and Human Feces. Environmental Science & Technology, 2016, 50, 420-427.	4.6	287
36	Genome sequencing of environmental <i>Escherichia coli</i> expands understanding of the ecology and speciation of the model bacterial species. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7200-7205.	3.3	279

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37	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
38	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
39	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
40	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021, 12, 4765.	5.8	248
41	Mapping the <i>Burkholderia cenocepacia</i> niche response via high-throughput sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3976-3981.	3.3	233
42	Biogeography: An Emerging Cornerstone for Understanding Prokaryotic Diversity, Ecology, and Evolution. <i>Microbial Ecology</i> , 2007, 53, 197-207.	1.4	228
43	Phylogenetic diversity of a bacterial community determined from Siberian tundra soil DNA. <i>Microbiology (United Kingdom)</i> , 1997, 143, 3913-3919.	0.7	213
44	Climate warming leads to divergent succession of grassland microbial communities. <i>Nature Climate Change</i> , 2018, 8, 813-818.	8.1	208
45	Clusters of Antibiotic Resistance Genes Enriched Together Stay Together in Swine Agriculture. <i>MBio</i> , 2016, 7, e02214-15.	1.8	201
46	Artificial intelligence: A powerful paradigm for scientific research. <i>Innovation(China)</i> , 2021, 2, 100179.	5.2	200
47	TerraGenome: a consortium for the sequencing of a soil metagenome. <i>Nature Reviews Microbiology</i> , 2009, 7, 252-252.	13.6	199
48	Bacterial Species Determination from DNA-DNA Hybridization by Using Genome Fragments and DNA Microarrays. <i>Applied and Environmental Microbiology</i> , 2001, 67, 3677-3682.	1.4	197
49	Toward a More Robust Assessment of Intraspecies Diversity, Using Fewer Genetic Markers. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7286-7293.	1.4	196
50	Soil Bacterial Community Shift Correlated with Change from Forest to Pasture Vegetation in a Tropical Soil. <i>Applied and Environmental Microbiology</i> , 1999, 65, 3622-3626.	1.4	194
51	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
52	Effects of pH and Oxygen and Ammonium Concentrations on the Community Structure of Nitrifying Bacteria from Wastewater. <i>Applied and Environmental Microbiology</i> , 1998, 64, 3584-3590.	1.4	180
53	Nitrous Oxide Production by Organisms Other than Nitrifiers or Denitrifiers. <i>Applied and Environmental Microbiology</i> , 1982, 44, 1342-1348.	1.4	172
54	Quantitative Detection of Microbial Genes by Using DNA Microarrays. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1425-1430.	1.4	171

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55	Classification of the biphenyl- and polychlorinated biphenyl-degrading strain LB400T and relatives as <i>Burkholderia xenovorans</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1677-1681.	0.8	171
56	High-throughput quantification of antibiotic resistance genes from an urban wastewater treatment plant. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw014.	1.3	167
57	Nonpareil 3: Fast Estimation of Metagenomic Coverage and Sequence Diversity. <i>MSystems</i> , 2018, 3, .	1.7	152
58	Intestinal microbial communities associated with acute enteric infections and disease recovery. <i>Microbiome</i> , 2015, 3, 45.	4.9	151
59	Reductive Dechlorination of DDE to DDMU in Marine Sediment Microcosms. <i>Science</i> , 1998, 280, 722-724.	6.0	145
60	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
61	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
62	Fungal Community Structure in Disease Suppressive Soils Assessed by 28S LSU Gene Sequencing. <i>PLoS ONE</i> , 2014, 9, e93893.	1.1	140
63	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	4.4	136
64	Denitrification in Soil Aggregates Analyzed with Microsensors for Nitrous Oxide and Oxygen. <i>Soil Science Society of America Journal</i> , 1994, 58, 1691-1698.	1.2	135
65	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
66	Environmental Risk Assessment of Trifluoroacetic Acid. <i>Human and Ecological Risk Assessment (HERA)</i> , 1999, 5, 59-124.	1.7	128
67	The soil microbial carbon pump: From conceptual insights to empirical assessments. <i>Global Change Biology</i> , 2020, 26, 6032-6039.	4.2	122
68	Gene-targeted-metagenomics reveals extensive diversity of aromatic dioxygenase genes in the environment. <i>ISME Journal</i> , 2010, 4, 279-285.	4.4	121
69	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
70	Bacterial community fingerprinting of amplified 16S and 16S+23S ribosomal DNA gene sequences and restriction endonuclease analysis(ARDRA)., 1995, , 289-296.		116
71	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
72	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

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73	<i>Shewanella loihica</i> sp. nov., isolated from iron-rich microbial mats in the Pacific Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1911-1916.	0.8	109
74	Characterization of the Dominant and Rare Members of a Young Hawaiian Soil Bacterial Community with Small-Subunit Ribosomal DNA Amplified from DNA Fractionated on the Basis of Its Guanine and Cytosine Composition. <i>Applied and Environmental Microbiology</i> , 1998, 64, 1283-1289.	1.4	108
75	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
76	Characterization of potential stress responses in ancient Siberian permafrost psychroactive bacteria. <i>FEMS Microbiology Ecology</i> , 2005, 53, 103-115.	1.3	106
77	Strategies to improve reference databases for soil microbiomes. <i>ISME Journal</i> , 2017, 11, 829-834.	4.4	106
78	<i>Shewanella</i> —the environmentally versatile genome. <i>Nature Biotechnology</i> , 2002, 20, 1093-1094.	9.4	102
79	Respiratory Nitrate Ammonification by <i>Shewanella oneidensis</i> MR-1. <i>Journal of Bacteriology</i> , 2007, 189, 656-662.	1.0	102
80	Significant Association between Sulfate-Reducing Bacteria and Uranium-Reducing Microbial Communities as Revealed by a Combined Massively Parallel Sequencing-Indicator Species Approach. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6778-6786.	1.4	102
81	Antibiotic Resistance Genes in the Human-Impacted Environment: A One Health Perspective. <i>Pedosphere</i> , 2019, 29, 273-282.	2.1	100
82	Deforestation alters denitrification in a lowland tropical rain forest. <i>Nature</i> , 1988, 336, 756-759.	13.7	98
83	Comparative systems biology across an evolutionary gradient within the <i>Shewanella</i> genus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15909-15914.	3.3	96
84	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
85	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
86	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
87	Impacts of <i>Shewanella oneidensis</i> c-type cytochromes on aerobic and anaerobic respiration. <i>Microbial Biotechnology</i> , 2010, 3, 455-466.	2.0	91
88	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
89	Validation of a more sensitive method for using spotted oligonucleotide DNA microarrays for functional genomics studies on bacterial communities. <i>Environmental Microbiology</i> , 2003, 5, 933-943.	1.8	87
90	Bacterial community comparisons by taxonomy-supervised analysis independent of sequence alignment and clustering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14637-14642.	3.3	87

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91	Construction and Characterization of Two Recombinant Bacteria That Grow on <i>ortho</i> - and <i>para</i> -Substituted Chlorobiphenyls. <i>Applied and Environmental Microbiology</i> , 1999, 65, 2163-2169.	1.4	86
92	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
93	Xander: employing a novel method for efficient gene-targeted metagenomic assembly. <i>Microbiome</i> , 2015, 3, 32.	4.9	83
94	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
95	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
96	Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. <i>Nature Ecology and Evolution</i> , 2019, 3, 612-619.	3.4	82
97	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
98	Degradation of Aroclor 1242 Dechlorination Products in Sediments by <i>Burkholderia xenovorans</i> LB400( ohb ) and <i>Rhodococcus</i> sp. Strain RHA1( fcb ). <i>Applied and Environmental Microbiology</i> , 2006, 72, 2476-2482.	1.4	78
99	Soil microbial communities under model biofuel cropping systems in southern Wisconsin, USA: Impact of crop species and soil properties. <i>Applied Soil Ecology</i> , 2012, 54, 24-31.	2.1	78
100	Development and Experimental Validation of a Predictive Threshold Cycle Equation for Quantification of Virulence and Marker Genes by High-Throughput Nanoliter-Volume PCR on the OpenArray Platform. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3831-3838.	1.4	77
101	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
102	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
103	Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. <i>Microbiome</i> , 2020, 8, 3.	4.9	75
104	Microbial Community Analysis with Ribosomal Gene Fragments from Shotgun Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 157-166.	1.4	73
105	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
106	Degradation of anaerobic reductive dechlorination products of Aroclor 1242 by four aerobic bacteria. <i>Biodegradation</i> , 1999, 10, 363-371.	1.5	70
107	Comparative Analysis of Differentially Expressed Genes in <i>Shewanella oneidensis</i> MR-1 following Exposure to UVC, UVB, and UVA Radiation. <i>Journal of Bacteriology</i> , 2005, 187, 3556-3564.	1.0	70
108	More replenishment than priming loss of soil organic carbon with additional carbon input. <i>Nature Communications</i> , 2018, 9, 3175.	5.8	69



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109	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
110	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
111	Recently Deglaciaded 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
112	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
113	Factors Controlling the Rate of DDE Dechlorination to DDMU in Palos Verdes Margin Sediments under Anaerobic Conditions. <i>Environmental Science &amp; Technology</i> , 2001, 35, 286-291.	4.6	65
114	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
115	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
116	On-chip non-equilibrium dissociation curves and dissociation rate constants as methods to assess specificity of oligonucleotide probes. <i>Nucleic Acids Research</i> , 2006, 34, e26-e26.	6.5	61
117	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
118	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
119	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
120	Cloning, Expression, and Nucleotide Sequence of the <i>Pseudomonas aeruginosa</i> 142 <i>ohb</i> Genes Coding for Oxygenolytic <i>ortho</i> Dehalogenation of Halobenzoates. <i>Applied and Environmental Microbiology</i> , 1999, 65, 2151-2162.	1.4	60
121	Root-Associated Microbiome of Maize Genotypes with Contrasting Phosphorus Use Efficiency. <i>Phytobiomes Journal</i> , 2018, 2, 129-137.	1.4	59
122	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
123	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
124	Coping with Polychlorinated Biphenyl (PCB) Toxicity: Physiological and Genome-Wide Responses of <i>Burkholderia xenovorans</i> LB400 to PCB-Mediated Stress. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6607-6614.	1.4	57
125	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
126	Tetrachloroethene and 3-chlorobenzoate dechlorination activities are co-induced in <i>Desulfomonile tiedjei</i> DCB-1. <i>Biodegradation</i> , 1995, 6, 167-172.	1.5	54



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127	Microbes and Climate Change: a Research Prospectus for the Future. MBio, 2022, 13, e0080022.	1.8	53
128	Microbial Diversity of a Mediterranean Soil and Its Changes after Biotransformed Dry Olive Residue Amendment. PLoS ONE, 2014, 9, e103035.	1.1	52
129	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. Frontiers in Microbiology, 2018, 9, 1635.	1.5	51
130	Pharmaceutical exposure changed antibiotic resistance genes and bacterial communities in soil-surface- and overhead-irrigated greenhouse lettuce. Environment International, 2019, 131, 105031.	4.8	48
131	Alterations of the Murine Gut Microbiome with Age and Allergic Airway Disease. Journal of Immunology Research, 2015, 2015, 1-8.	0.9	47
132	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. Applied and Environmental Microbiology, 2018, 84, .	1.4	47
133	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. Microbiome, 2020, 8, 84.	4.9	47
134	MicroRNAs-Based Inter-Domain Communication between the Host and Members of the Gut Microbiome. Frontiers in Microbiology, 2017, 8, 1896.	1.5	46
135	Strategy for Mitigating Antibiotic Resistance by Biochar and Hyperaccumulators in Cadmium and Oxytetracycline Co-contaminated Soil. Environmental Science & Technology, 2021, 55, 16369-16378.	4.6	46
136	Potential of DNA microarrays for developing parallel detection tools (PDTs) for microorganisms relevant to biodefense and related research needs. Biosensors and Bioelectronics, 2004, 20, 668-683.	5.3	45
137	The Microbiome of Eucalyptus Roots under Different Management Conditions and Its Potential for Biological Nitrogen Fixation. Microbial Ecology, 2018, 75, 183-191.	1.4	45
138	Identification of Potential Therapeutic Targets for Burkholderia cenocepacia by Comparative Transcriptomics. PLoS ONE, 2010, 5, e8724.	1.1	45
139	In Situ-Synthesized Virulence and Marker Gene Biochip for Detection of Bacterial Pathogens in Water. Applied and Environmental Microbiology, 2008, 74, 2200-2209.	1.4	44
140	Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. MBio, 2016, 7, .	1.8	43
141	Development of a Rhodococcus Recombinant Strain for Degradation of Products from Anaerobic Dechlorination of PCBs. Environmental Science & Technology, 2001, 35, 663-668.	4.6	42
142	Bacterial Communities in the Rhizosphere of Biofuel Crops Grown on Marginal Lands as Evaluated by 16S rRNA Gene Pyrosequences. Bioenergy Research, 2010, 3, 20-27.	2.2	40
143	Antibiotic Resistome Associated with Small-Scale Poultry Production in Rural Ecuador. Environmental Science & Technology, 2018, 52, 8165-8172.	4.6	40
144	Composting increased persistence of manure-borne antibiotic resistance genes in soils with different fertilization history. Science of the Total Environment, 2019, 689, 1172-1180.	3.9	40

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145	<i>Bacillus cabrialesii</i> sp. nov., an endophytic plant growth promoting bacterium isolated from wheat ( <i>Triticum turgidum</i> subsp. <i>durum</i> ) in the Yaqui Valley, Mexico. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3939-3945.	0.8	40
146	<i>Agromyces albus</i> sp. nov., isolated from a plant ( <i>Androsace</i> sp.). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1435-1438.	0.8	38
147	Intercropped Silviculture Systems, a Key to Achieving Soil Fungal Community Management in Eucalyptus Plantations. <i>PLoS ONE</i> , 2015, 10, e0118515.	1.1	38
148	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
149	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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