

# Michael J Sadowsky

## List of Publications by Year in descending order

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462  
papers

27,138  
citations

4955

84  
h-index

10441

139  
g-index

476  
all docs

476  
docs citations

476  
times ranked

24899  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bioaugmentation with As-transforming bacteria improves arsenic availability and uptake by the hyperaccumulator plant <i>Pteris vittata</i> (L).. International Journal of Phytoremediation, 2022, 24, 420-428.	1.7	6
2	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. Science of the Total Environment, 2022, 805, 149877.	3.9	153
3	Erosion and deposition divergently affect the structure of soil bacterial communities and functionality. Catena, 2022, 209, 105805.	2.2	14
4	Climate Change Impacts on Microbiota in Beach Sand and Water: Looking Ahead. International Journal of Environmental Research and Public Health, 2022, 19, 1444.	1.2	7
5	Composition and Potential Functions of Rhizobacterial Communities in a Pioneer Plant from Andean Altiplano. Diversity, 2022, 14, 14.	0.7	5
6	Differential hydrogen sulfide production by a human cohort in response to animal- and plant-based diet interventions. Clinical Nutrition, 2022, 41, 1153-1162.	2.3	4
7	Halophytes increase rhizosphere microbial diversity, network complexity and function in inland saline ecosystem. Science of the Total Environment, 2022, 831, 154944.	3.9	28
8	Afforestation can lower microbial diversity and functionality in deep soil layers in a semiarid region. Global Change Biology, 2022, 28, 6086-6101.	4.2	40
9	Comparative decay of culturable faecal indicator bacteria, microbial source tracking marker genes, and enteric pathogens in laboratory microcosms that mimic a sub-tropical environment. Science of the Total Environment, 2021, 751, 141475.	3.9	21
10	Influence of Environmental Stressors on the Microbiota of Zebra Mussels ( <i>Dreissena polymorpha</i> ). Microbial Ecology, 2021, 81, 1042-1053.	1.4	6
11	Influence of seasonality on the aerosol microbiome of the Amazon rainforest. Science of the Total Environment, 2021, 760, 144092.	3.9	13
12	Bioturbation by the marine polychaete <i>Capitella teleta</i> alters the sediment microbial community by ingestion and defecation of sediment particles. Science of the Total Environment, 2021, 752, 142239.	3.9	4
13	Composition and predicted functions of the bacterial community in spouting pool sediments from the El Tatio Geysir field in Chile. Archives of Microbiology, 2021, 203, 389-397.	1.0	3
14	Faecal microbiota transplantation for <i>Clostridioides difficile</i> : mechanisms and pharmacology. Nature Reviews Gastroenterology and Hepatology, 2021, 18, 67-80.	8.2	91
15	Structural modifications that increase gut restriction of bile acid derivatives. RSC Medicinal Chemistry, 2021, 12, 394-405.	1.7	3
16	Lower endoscopic delivery of freeze-dried intestinal microbiota results in more rapid and efficient engraftment than oral administration. Scientific Reports, 2021, 11, 4519.	1.6	5
17	Microbial source tracking using metagenomics and other new technologies. Journal of Microbiology, 2021, 59, 259-269.	1.3	13
18	Erosion reduces soil microbial diversity, network complexity and multifunctionality. ISME Journal, 2021, 15, 2474-2489.	4.4	273

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19	Comparative genomic analysis of diverse rhizobia and effective nitrogen-fixing clover-nodulating Rhizobium strains adapted to Egyptian dry ecosystems. <i>Symbiosis</i> , 2021, 84, 39-47.	1.2	3
20	CRISPR loci-PCR as Tool for Tracking Azospirillum sp. Strain B510. <i>Microorganisms</i> , 2021, 9, 1351.	1.6	2
21	Impacts of cover crops and nitrogen fertilization on agricultural soil fungal and bacterial communities. <i>Plant and Soil</i> , 2021, 466, 139-150.	1.8	13
22	Rhizobacteria from "flowering desert" events contribute to the mitigation of water scarcity stress during tomato seedling germination and growth. <i>Scientific Reports</i> , 2021, 11, 13745.	1.6	18
23	A Combined Digital PCR and Next Generation DNA-Sequencing Based Approach for Tracking Nearshore Pollutant Dynamics Along the Southwest United States/Mexico Border. <i>Frontiers in Microbiology</i> , 2021, 12, 674214.	1.5	16
24	Biodegradation of azo dyes by bacterial or fungal consortium and identification of the biodegradation products. <i>Egyptian Journal of Aquatic Research</i> , 2021, 47, 269-276.	1.0	29
25	Gut Microbiota Associated With Different Sea Lamprey ( <i>Petromyzon marinus</i> ) Life Stages. <i>Frontiers in Microbiology</i> , 2021, 12, 706683.	1.5	3
26	Engineering Multigenerational Host-Modulated Microbiota against Soilborne Pathogens in Response to Global Climate Change. <i>Biology</i> , 2021, 10, 865.	1.3	9
27	Temperature alters dicyandiamide (DCD) efficacy for multiple reactive nitrogen species in urea-amended soils: Experiments and modeling. <i>Soil Biology and Biochemistry</i> , 2021, 160, 108341.	4.2	9
28	A hybrid DNA sequencing approach is needed to properly link genotype to phenotype in multi-drug resistant bacteria. <i>Environmental Pollution</i> , 2021, 289, 117856.	3.7	1
29	Inoculation of <i>Mimosa pudica</i> with <i>Paraburkholderia phymatum</i> ; Results in Changes to the Rhizoplane Microbial Community Structure. <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	5
30	Probable role of <i>Cutibacterium acnes</i> in the gut of the polychaete <i>Capitella teleta</i> . <i>Science of the Total Environment</i> , 2021, 809, 151127.	3.9	2
31	Inactivation of <i>Clostridioides Difficile</i> Spores in Carpeting and Upholstery to Reduce Disease Recurrence in Households and Nursing Care Facilities. <i>Journal of Public Health Issues and Practices</i> , 2021, 5, .	0.2	0
32	Source-Associated Gastroenteritis Risk from Swimming Exposure to Aging Fecal Pathogens. <i>Environmental Science &amp; Technology</i> , 2020, 54, 921-929.	4.6	13
33	Water and sediment act as reservoirs for microbial taxa associated with invasive dreissenid mussels. <i>Science of the Total Environment</i> , 2020, 703, 134915.	3.9	8
34	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>Infection and Immunity</i> , 2020, 88, .	1.0	0
35	Convenient Protocol for Production and Purification of <i>Clostridioides difficile</i> Spores for Germination Studies. <i>STAR Protocols</i> , 2020, 1, 100071.	0.5	3
36	Sequence-enabled community-based microbial source tracking in surface waters using machine learning classification: A review. <i>Journal of Microbiological Methods</i> , 2020, 177, 106050.	0.7	29

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37	Bacterial community composition in agricultural soils under long-term organic and conventional management. , 2020, 3, e20063.		3
38	Peri-operative antibiotics acutely and significantly impact intestinal microbiota following bariatric surgery. Scientific Reports, 2020, 10, 20340.	1.6	9
39	Methanogen Abundance Thresholds Capable of Differentiating In Vitro Methane Production in Human Stool Samples. Digestive Diseases and Sciences, 2020, 66, 3822-3830.	1.1	3
40	Randomised clinical study: oral aspirin 325mg daily vs placebo alters gut microbial composition and bacterial taxa associated with colorectal cancer risk. Alimentary Pharmacology and Therapeutics, 2020, 52, 976-987.	1.9	40
41	The ASM Journals Committee Values the Contributions of Black Microbiologists. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	0
42	The ASM Journals Committee Values the Contributions of Black Microbiologists. Journal of Virology, 2020, 94, .	1.5	0
43	The ASM Journals Committee Values the Contributions of Black Microbiologists. Journal of Bacteriology, 2020, 202, .	1.0	0
44	The ASM Journals Committee Values the Contributions of Black Microbiologists. Microbiology and Molecular Biology Reviews, 2020, 84, .	2.9	0
45	The ASM Journals Committee Values the Contributions of Black Microbiologists. MSystems, 2020, 5, .	1.7	0
46	The ASM Journals Committee Values the Contributions of Black Microbiologists. Microbiology Resource Announcements, 2020, 9, .	0.3	0
47	The ASM Journals Committee Values the Contributions of Black Microbiologists. MBio, 2020, 11, .	1.8	3
48	The ASM Journals Committee Values the Contributions of Black Microbiologists. Journal of Clinical Microbiology, 2020, 58, .	1.8	1
49	Niche Differentiation in the Composition, Predicted Function, and Co-occurrence Networks in Bacterial Communities Associated With Antarctic Vascular Plants. Frontiers in Microbiology, 2020, 11, 1036.	1.5	34
50	Indigenous soil bacteria and the hyperaccumulator Pteris vittata mediate phytoremediation of soil contaminated with arsenic species. Ecotoxicology and Environmental Safety, 2020, 195, 110458.	2.9	32
51	Environmental and Adaptive Changes Necessitate a Paradigm Shift for Indicators of Fecal Contamination. Microbiology Spectrum, 2020, 8, .	1.2	12
52	Lack of evidence for the role of gut microbiota in PAH biodegradation by the polychaete Capitella teleta. Science of the Total Environment, 2020, 725, 138356.	3.9	4
53	Composition, Predicted Functions and Co-occurrence Networks of Rhizobacterial Communities Impacting Flowering Desert Events in the Atacama Desert, Chile. Frontiers in Microbiology, 2020, 11, 571.	1.5	22
54	Impact of Atrazine Exposure on the Microbial Community Structure in a Brazilian Tropical Latosol Soil. Microbes and Environments, 2020, 35, n/a.	0.7	21

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55	Do shared traits create the same fates? Examining the link between morphological type and the biogeography of fungal and bacterial communities. <i>Fungal Ecology</i> , 2020, 46, 100948.	0.7	15
56	Structuring biofilm communities living in pesticide contaminated water. <i>Heliyon</i> , 2020, 6, e03996.	1.4	12
57	Herbicide bioremediation: from strains to bacterial communities. <i>Heliyon</i> , 2020, 6, e05767.	1.4	43
58	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	1
59	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>MSphere</i> , 2020, 5, .	1.3	1
60	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>Molecular and Cellular Biology</i> , 2020, 40, .	1.1	0
61	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>Clinical Microbiology Reviews</i> , 2020, 33, .	5.7	1
62	Role of Rhizobacteria in Phytoremediation of Metal-Impacted Sites. , 2019, , 299-328.		8
63	Synergy between quantitative microbial source tracking (qMST) and quantitative microbial risk assessment (QMRA): A review and prospectus. <i>Environment International</i> , 2019, 130, 104703.	4.8	58
64	Impacts of a changing earth on microbial dynamics and human health risks in the continuum between beach water and sand. <i>Water Research</i> , 2019, 162, 456-470.	5.3	53
65	Durable Long-Term Bacterial Engraftment following Encapsulated Fecal Microbiota Transplantation To Treat <i>Clostridium difficile</i> Infection. <i>MBio</i> , 2019, 10, .	1.8	58
66	7-Methylation of Chenodeoxycholic Acid Derivatives Yields a Substantial Increase in TGR5 Receptor Potency. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 6824-6830.	2.9	18
67	Microbiota transplant therapy and autism: lessons for the clinic. <i>Expert Review of Gastroenterology and Hepatology</i> , 2019, 13, 1033-1037.	1.4	24
68	An Alkane Sulfonate Monooxygenase Is Required for Symbiotic Nitrogen Fixation by <i>Bradyrhizobium diazoefficiens</i> (syn. <i>Bradyrhizobium japonicum</i> ) USDA110 <sup>T</sup> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	8
69	Compositional and temporal stability of fecal taxon libraries for use with SourceTracker in sub-tropical catchments. <i>Water Research</i> , 2019, 165, 114967.	5.3	12
70	Letter to the Editor. <i>Clinical Infectious Diseases</i> , 2019, 69, 2232-2233.	2.9	1
71	Editorial: Alternative Therapeutic Approaches For Multidrug Resistant <i>Clostridium difficile</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1216.	1.5	0
72	Dietary Factors in Sulfur Metabolism and Pathogenesis of Ulcerative Colitis. <i>Nutrients</i> , 2019, 11, 931.	1.7	35

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73	Endophytic Bacterial Communities Associated with Roots and Leaves of Plants Growing in Chilean Extreme Environments. <i>Scientific Reports</i> , 2019, 9, 4950.	1.6	68
74	Breastmilk and NICU surfaces are potential sources of fungi for infant mycobiomes. <i>Fungal Genetics and Biology</i> , 2019, 128, 29-35.	0.9	27
75	Impacts of Sampling Design on Estimates of Microbial Community Diversity and Composition in Agricultural Soils. <i>Microbial Ecology</i> , 2019, 78, 753-763.	1.4	11
76	Response of dry bean ( <i>Phaseolus vulgaris</i> L.) to inoculation with indigenous and commercial <i>Rhizobium</i> strains under organic farming systems in Minnesota. <i>Symbiosis</i> , 2019, 78, 125-134.	1.2	7
77	Influence of short-term changes in dietary sulfur on the relative abundances of intestinal sulfate-reducing bacteria. <i>Gut Microbes</i> , 2019, 10, 447-457.	4.3	34
78	The deposit feeder <i>Capitella teleta</i> has a unique and relatively complex microbiome likely supporting its ability to degrade pollutants. <i>Science of the Total Environment</i> , 2019, 670, 547-554.	3.9	16
79	A microfluidic platform for the simultaneous quantification of methanogen populations in anaerobic digestion processes. <i>Environmental Microbiology</i> , 2019, 21, 1798-1808.	1.8	11
80	Signal Disruption Leads to Changes in Bacterial Community Population. <i>Frontiers in Microbiology</i> , 2019, 10, 611.	1.5	24
81	Denitrifying Bacteria Active in Woodchip Bioreactors at Low-Temperature Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 635.	1.5	33
82	Intermittent flooding of organic-rich soil promotes the formation of denitrification hot moments and hot spots. <i>Ecosphere</i> , 2019, 10, e02549.	1.0	29
83	A pilot study of fecal bile acid and microbiota profiles in inflammatory bowel disease and primary sclerosing cholangitis. <i>Clinical and Experimental Gastroenterology</i> , 2019, Volume 12, 9-19.	1.0	58
84	Influence of Library Composition on SourceTracker Predictions for Community-Based Microbial Source Tracking. <i>Environmental Science &amp; Technology</i> , 2019, 53, 60-68.	4.6	33
85	Impact of long-term grazing exclusion on soil microbial community composition and nutrient availability. <i>Biology and Fertility of Soils</i> , 2019, 55, 121-134.	2.3	66
86	Comparative decay of sewage-associated marker genes in beach water and sediment in a subtropical region. <i>Water Research</i> , 2019, 149, 511-521.	5.3	56
87	Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1973-1987.	1.7	16
88	Association between submerged aquatic vegetation and elevated levels of <i>Escherichia coli</i> and potential bacterial pathogens in freshwater lakes. <i>Science of the Total Environment</i> , 2019, 657, 319-324.	3.9	21
89	Antibiotic-induced Disruption of Intestinal Microbiota Contributes to Failure of Vertical Sleeve Gastrectomy. <i>Annals of Surgery</i> , 2019, 269, 1092-1100.	2.1	29
90	Application of SourceTracker for Accurate Identification of Fecal Pollution in Recreational Freshwater: A Double-Blinded Study. <i>Environmental Science &amp; Technology</i> , 2018, 52, 4207-4217.	4.6	59

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91	Current understanding of microbiota- and dietary-therapies for treating inflammatory bowel disease. <i>Journal of Microbiology</i> , 2018, 56, 189-198.	1.3	97
92	Comparisons of bacterial and archaeal communities in the rumen and a dual-flow continuous culture fermentation system using amplicon sequencing. <i>Journal of Animal Science</i> , 2018, 96, 1059-1072.	0.2	12
93	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. <i>Scientific Reports</i> , 2018, 8, 6219.	1.6	99
94	The Effects of Turbulence and Carbon Amendments on Nitrate Uptake and Microbial Gene Abundances in Stream Sediment. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2018, 123, 1289-1301.	1.3	12
95	Seasonal metabolic analysis of marine sediments collected from Moreton Bay in South East Queensland, Australia, using a multi-omics-based approach. <i>Science of the Total Environment</i> , 2018, 631-632, 1328-1341.	3.9	20
96	Select and resequence reveals relative fitness of bacteria in symbiotic and free-living environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2425-2430.	3.3	88
97	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. <i>Cell Host and Microbe</i> , 2018, 23, 229-240.e5.	5.1	292
98	Widespread occurrence of <i>Sinorhizobium meliloti</i> strains with a type IV secretion system. <i>Symbiosis</i> , 2018, 75, 81-91.	1.2	6
99	Genome-Wide Association Analyses in the Model Rhizobium <i>Sinorhizobium meliloti</i> . <i>MSphere</i> , 2018, 3, .	1.3	26
100	Complete Genome Sequence of <i>Sinorhizobium meliloti</i> Bacteriophage HMSP1-Susan. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
101	Practical considerations for sampling and data analysis in contemporary metagenomics-based environmental studies. <i>Journal of Microbiological Methods</i> , 2018, 154, 14-18.	0.7	12
102	Comprehensive Functional Analysis of the <i>Enterococcus faecalis</i> Core Genome Using an Ordered, Sequence-Defined Collection of Insertional Mutations in Strain OG1RF. <i>MSystems</i> , 2018, 3, .	1.7	57
103	Putative Nitrogen-Fixing Bacteria Associated With the Rhizosphere and Root Endosphere of Wheat Plants Grown in an Andisol From Southern Chile. <i>Frontiers in Microbiology</i> , 2018, 9, 2710.	1.5	81
104	Influence of Physicochemical Factors on Bacterial Communities Along the Lower Mekong River Assessed by Illumina Next-Generation Sequencing. <i>Water, Air, and Soil Pollution</i> , 2018, 229, 1.	1.1	7
105	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018, 6, 166.	4.9	73
106	Spatial and temporal characterization of epiphytic microbial communities associated with Eurasian watermilfoil: a highly invasive macrophyte in North America. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	6
107	Fecal pollution: new trends and challenges in microbial source tracking using next-generation sequencing. <i>Environmental Microbiology</i> , 2018, 20, 3132-3140.	1.8	56
108	Quantitative microbial risk assessment of microbial source tracking markers in recreational water contaminated with fresh untreated and secondary treated sewage. <i>Environment International</i> , 2018, 117, 243-249.	4.8	67

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109	Precipitation influences pathogenic bacteria and antibiotic resistance gene abundance in storm drain outfalls in coastal sub-tropical waters. <i>Environment International</i> , 2018, 116, 308-318.	4.8	92
110	<i>Bacillus megaterium</i> strains derived from water and soil exhibit differential responses to the herbicide mesotrione. <i>PLoS ONE</i> , 2018, 13, e0196166.	1.1	19
111	Urea Amendment Decreases Microbial Diversity and Selects for Specific Nitrifying Strains in Eight Contrasting Agricultural Soils. <i>Frontiers in Microbiology</i> , 2018, 9, 634.	1.5	37
112	CLOUD: a non-parametric detection test for microbiome outliers. <i>Microbiome</i> , 2018, 6, 137.	4.9	16
113	Decay of sewage-associated bacterial communities in fresh and marine environmental waters and sediment. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7159-7170.	1.7	14
114	The complete replicons of 16 <i>Ensifer meliloti</i> strains offer insights into intra- and inter-replicon gene transfer, transposon-associated loci, and repeat elements. <i>Microbial Genomics</i> , 2018, 4, .	1.0	21
115	Sleeve gastrectomy drives persistent shifts in the gut microbiome. <i>Surgery for Obesity and Related Diseases</i> , 2017, 13, 916-924.	1.0	43
116	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017, 5, 10.	4.9	901
117	Complete Genome Sequence of the Triclosan- and Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Strain B10W Isolated from Municipal Wastewater. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
118	Community dynamics drive punctuated engraftment of the fecal microbiome following transplantation using freeze-dried, encapsulated fecal microbiota. <i>Gut Microbes</i> , 2017, 8, 276-288.	4.3	39
119	Metabolic Interference of <i>sod</i> gene mutations on catalase activity in <i>Escherichia coli</i> exposed to Gramoxone® (paraquat) herbicide. <i>Ecotoxicology and Environmental Safety</i> , 2017, 139, 89-96.	2.9	13
120	Successful Resolution of Recurrent <i>Clostridium difficile</i> Infection using Freeze-Dried, Encapsulated Fecal Microbiota; Pragmatic Cohort Study. <i>American Journal of Gastroenterology</i> , 2017, 112, 940-947.	0.2	164
121	Synthesis and Biological Evaluation of Bile Acid Analogues Inhibitory to <i>Clostridium difficile</i> Spore Germination. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 3451-3471.	2.9	35
122	Nitrification gene ratio and free ammonia explain nitrite and nitrous oxide production in urea-amended soils. <i>Soil Biology and Biochemistry</i> , 2017, 111, 143-153.	4.2	76
123	The Diet and Gut Microbial Communities of Two Closely Related Combtooth Blennies, <i>Chasmodes saburrae</i> and <i>Scartella cristata</i> . <i>Copeia</i> , 2017, 105, 249-256.	1.4	5
124	Factors influencing the <i>Salmonella</i> internalization into seedpods and whole plants of <i>Arachis hypogaea</i> (L.). <i>Food Microbiology</i> , 2017, 66, 184-189.	2.1	3
125	Novel Microbial Assemblages Dominate Weathered Sulfide-Bearing Rock from Copper-Nickel Deposits in the Duluth Complex, Minnesota, USA. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	32
126	Environmental <i>Escherichia coli</i> : ecology and public health implications-a review. <i>Journal of Applied Microbiology</i> , 2017, 123, 570-581.	1.4	477



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127	Differential Impacts of Land-Based Sources of Pollution on the Microbiota of Southeast Florida Coral Reefs. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	43
128	Gut-sparing treatment of urinary tract infection in patients at high risk of <i>Clostridium difficile</i> infection. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 522-528.	1.3	18
129	Type IV Effector Proteins Involved in the <i>Medicago</i> - <i>Sinorhizobium</i> Symbiosis. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 28-34.	1.4	22
130	Analysis of gut microbiota – An ever changing landscape. <i>Gut Microbes</i> , 2017, 8, 268-275.	4.3	25
131	Phylogenetic Backgrounds and Virulence-Associated Traits of <i>Escherichia coli</i> Isolates from Surface Waters and Diverse Animals in Minnesota and Wisconsin. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	13
132	Optimization of conditions for decolorization of azo-based textile dyes by multiple fungal species. <i>Journal of Biotechnology</i> , 2017, 260, 11-17.	1.9	52
133	Influence of heavy metals on rhizosphere microbial communities of Siam weed ( <i>Chromolaena odorata</i> ) Tj ETQq1 1 0.784314 rgBT /Over 137-141.	0.4	8
134	Environmental drivers of denitrification rates and denitrifying gene abundances in channels and riparian areas. <i>Water Resources Research</i> , 2017, 53, 6523-6538.	1.7	31
135	A multi-omics based ecological analysis of coastal marine sediments from Gladstone, in Australia's Central Queensland, and Heron Island, a nearby fringing platform reef. <i>Science of the Total Environment</i> , 2017, 609, 842-853.	3.9	29
136	Transcriptomic basis of genome by genome variation in a legume-rhizobia mutualism. <i>Molecular Ecology</i> , 2017, 26, 6122-6135.	2.0	40
137	Competition between introduced <i>Bradyrhizobium japonicum</i> strains and indigenous bradyrhizobia in Minnesota organic farming systems. <i>Symbiosis</i> , 2017, 73, 155-163.	1.2	14
138	Contemporary Applications of Fecal Microbiota Transplantation to Treat Intestinal Diseases in Humans. <i>Archives of Medical Research</i> , 2017, 48, 766-773.	1.5	37
139	Effect of Different Treatment Technologies on the Fate of Antibiotic Resistance Genes and Class 1 Integrons when Residual Municipal Wastewater Solids are Applied to Soil. <i>Environmental Science &amp; Technology</i> , 2017, 51, 14225-14232.	4.6	53
140	A High-Throughput DNA-Sequencing Approach for Determining Sources of Fecal Bacteria in a Lake Superior Estuary. <i>Environmental Science &amp; Technology</i> , 2017, 51, 8263-8271.	4.6	54
141	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	4.9	62
142	Virulence and biodegradation potential of dynamic microbial communities associated with decaying <i>Cladophora</i> in Great Lakes. <i>Science of the Total Environment</i> , 2017, 574, 872-880.	3.9	22
143	Amplicon-based taxonomic characterization of bacteria in urban and peri-urban roof-harvested rainwater stored in tanks. <i>Science of the Total Environment</i> , 2017, 576, 326-334.	3.9	46
144	Recent changes to the classification of symbiotic, nitrogen-fixing, legume-associating bacteria: a review. <i>Symbiosis</i> , 2017, 71, 91-109.	1.2	69

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145	Interaction of gut microbiota with bile acid metabolism and its influence on disease states. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 47-64.	1.7	387
146	Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2017, 18, 578.	1.2	54
147	Genes and Gut Bacteria Involved in Luminal Butyrate Reduction Caused by Diet and Loperamide. <i>Genes</i> , 2017, 8, 350.	1.0	41
148	A Community Multi-Omics Approach towards the Assessment of Surface Water Quality in an Urban River System. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 303.	1.2	53
149	Increased Denitrification Rates Associated with Shifts in Prokaryotic Community Composition Caused by Varying Hydrologic Connectivity. <i>Frontiers in Microbiology</i> , 2017, 8, 2304.	1.5	22
150	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	4.9	138
151	Changes in Colonic Bile Acid Composition following Fecal Microbiota Transplantation Are Sufficient to Control <i>Clostridium difficile</i> Germination and Growth. <i>PLoS ONE</i> , 2016, 11, e0147210.	1.1	130
152	Bacterial biogeography influenced by shelf-basin exchange in the Arctic surface sediment at the Cukchi orderland. <i>Environmental Microbiology</i> , 2016, 18, 668-678.	1.8	2
153	Complete Microbiota Engraftment Is Not Essential for Recovery from Recurrent <i>Clostridium difficile</i> Infection following Fecal Microbiota Transplantation. <i>MBio</i> , 2016, 7, .	1.8	97
154	Application of metagenomics to assess microbial communities in water and other environmental matrices. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016, 96, 121-129.	0.4	30
155	Draft Genome Sequences of Four Novel Thermal- and Alkaline-Tolerant Egyptian <i>Rhizobium</i> Strains Nodulating Berseem Clover. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
156	Beach sand and the potential for infectious disease transmission: observations and recommendations. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016, 96, 101-120.	0.4	80
157	Environmental Contamination in Households of Patients with Recurrent <i>Clostridium difficile</i> Infection. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2686-2692.	1.4	33
158	Correlations between pathogen concentration and fecal indicator marker genes in beach environments. <i>Science of the Total Environment</i> , 2016, 573, 826-830.	3.9	41
159	Structure of bacterial communities in soil following cover crop and organic fertilizer incorporation. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9331-9341.	1.7	65
160	Effect of Fecal Microbiota Transplantation on Recurrence in Multiply Recurrent <i>Clostridium difficile</i> Infection. <i>Annals of Internal Medicine</i> , 2016, 165, 609.	2.0	486
161	Environment shapes the fecal microbiome of invasive carp species. <i>Microbiome</i> , 2016, 4, 44.	4.9	166
162	Faecal microbiota transplantation is promising but not a panacea. <i>Nature Microbiology</i> , 2016, 1, 16015.	5.9	24

#	ARTICLE	IF	CITATIONS
163	GST activity and membrane lipid saturation prevents mesotrione-induced cellular damage in <i>Pantoea ananatis</i> . <i>AMB Express</i> , 2016, 6, 70.	1.4	18
164	Ursodeoxycholic Acid Inhibits <i>Clostridium difficile</i> Spore Germination and Vegetative Growth, and Prevents the Recurrence of Ileal Pouchitis Associated With the Infection. <i>Journal of Clinical Gastroenterology</i> , 2016, 50, 624-630.	1.1	93
165	Understanding the mechanisms of faecal microbiota transplantation. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2016, 13, 508-516.	8.2	377
166	The symbiovar <i>trifolii</i> of <i>Rhizobium bangladeshense</i> and <i>Rhizobium aegyptiacum</i> sp. nov. nodulate <i>Trifolium alexandrinum</i> in Egypt. <i>Systematic and Applied Microbiology</i> , 2016, 39, 275-279.	1.2	44
167	Associations between soil bacterial community structure and nutrient cycling functions in long-term organic farm soils following cover crop and organic fertilizer amendment. <i>Science of the Total Environment</i> , 2016, 566-567, 949-959.	3.9	112
168	Modeling the fate of antibiotic resistance genes and class 1 integrons during thermophilic anaerobic digestion of municipal wastewater solids. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 1437-1444.	1.7	38
169	Sediments and Soils Act as Reservoirs for Taxonomic and Functional Bacterial Diversity in the Upper Mississippi River. <i>Microbial Ecology</i> , 2016, 71, 814-824.	1.4	29
170	Inflammatory Bowel Disease Affects the Outcome of Fecal Microbiota Transplantation for Recurrent <i>Clostridium difficile</i> Infection. <i>Clinical Gastroenterology and Hepatology</i> , 2016, 14, 1433-1438.	2.4	190
171	Regional Similarities and Consistent Patterns of Local Variation in Beach Sand Bacterial Communities throughout the Northern Hemisphere. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2751-2762.	1.4	42
172	Ammonium sorption and ammonia inhibition of nitrite-oxidizing bacteria explain contrasting soil N <sub>2</sub> O production. <i>Scientific Reports</i> , 2015, 5, 12153.	1.6	125
173	An Alternative Approach to "Identification of Unknowns": Designing a Protocol to Verify the Identities of Nitrogen Fixing Bacteria. <i>Journal of Microbiology and Biology Education</i> , 2015, 16, 247-253.	0.5	12
174	High-throughput functional screening reveals low frequency of antibiotic resistance genes in DNA recovered from the Upper Mississippi River. <i>Journal of Water and Health</i> , 2015, 13, 693-703.	1.1	20
175	Characterization of a Functional Role of the <i>Bradyrhizobium japonicum</i> Isocitrate Lyase in Desiccation Tolerance. <i>International Journal of Molecular Sciences</i> , 2015, 16, 16695-16709.	1.8	23
176	Secretion systems and signal exchange between nitrogen-fixing rhizobia and legumes. <i>Frontiers in Plant Science</i> , 2015, 6, 491.	1.7	150
177	Transformation of tetracycline by TetX and its subsequent degradation in a heterologous host. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv059.	1.3	21
178	A Novel Microbial Source Tracking Microarray for Pathogen Detection and Fecal Source Identification in Environmental Systems. <i>Environmental Science &amp; Technology</i> , 2015, 49, 7319-7329.	4.6	36
179	Dynamic changes in the population structure of <i>Escherichia coli</i> in the Yeongsan River basin of South Korea. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv127.	1.3	6
180	Frequencies of heavy metal resistance are associated with land cover type in the Upper Mississippi River. <i>Science of the Total Environment</i> , 2015, 511, 461-468.	3.9	19

#	ARTICLE	IF	CITATIONS
181	Biodegradation of atrazine by three transgenic grasses and alfalfa expressing a modified bacterial atrazine chlorohydrolase gene. <i>Transgenic Research</i> , 2015, 24, 475-488.	1.3	15
182	Predominant populations of indigenous soybean-nodulating <i>Bradyrhizobium japonicum</i> strains obtained from organic farming systems in Minnesota. <i>Journal of Applied Microbiology</i> , 2015, 118, 1152-1164.	1.4	16
183	Prevalence of toxin-producing <i>Clostridium botulinum</i> associated with the macroalga <i>Cladophora</i> in three Great Lakes: Growth and management. <i>Science of the Total Environment</i> , 2015, 511, 523-529.	3.9	11
184	Survival and Competitiveness of <i>Bradyrhizobium japonicum</i> Strains 20 Years after Introduction into Field Locations in Poland. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5552-5559.	1.4	48
185	Toolbox Approaches Using Molecular Markers and 16S rRNA Gene Amplicon Data Sets for Identification of Fecal Pollution in Surface Water. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7067-7077.	1.4	68
186	Influence of seawater intrusion on microbial communities in groundwater. <i>Science of the Total Environment</i> , 2015, 532, 337-343.	3.9	38
187	Changes in human gut microbiota influenced by probiotic fermented milk ingestion. <i>Journal of Dairy Science</i> , 2015, 98, 3568-3576.	1.4	60
188	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection. <i>Microbiome</i> , 2015, 3, 10.	4.9	218
189	Evaluation of water sampling methodologies for amplicon-based characterization of bacterial community structure. <i>Journal of Microbiological Methods</i> , 2015, 114, 43-50.	0.7	42
190	Influence of Hyphal Inoculum potential on the Competitive Success of Fungi Colonizing Wood. <i>Microbial Ecology</i> , 2015, 69, 758-767.	1.4	28
191	Isolation and Characterization of a Novel Imidacloprid-Degrading <i>Mycobacterium</i> sp. Strain MK6 from an Egyptian Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 4721-4727.	2.4	53
192	Rapid Method Using Two Microbial Enzymes for Detection of <i>Abrin</i> in Food as a Marker for the Toxic Protein <i>Abrin</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1610-1615.	1.4	4
193	Geographic isolation of <i>Escherichia coli</i> genotypes in sediments and water of the Seven Mile Creek "A" constructed riverine watershed. <i>Science of the Total Environment</i> , 2015, 538, 78-85.	3.9	16
194	Site-specific distribution and competitive ability of indigenous bean-nodulating rhizobia isolated from organic fields in Minnesota. <i>Journal of Biotechnology</i> , 2015, 214, 158-168.	1.9	3
195	Development of Fecal Microbiota Transplantation Suitable for Mainstream Medicine. <i>Clinical Gastroenterology and Hepatology</i> , 2015, 13, 246-250.	2.4	46
196	Species sorting and seasonal dynamics primarily shape bacterial communities in the Upper Mississippi River. <i>Science of the Total Environment</i> , 2015, 505, 435-445.	3.9	133
197	Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. <i>PLoS ONE</i> , 2015, 10, e0116705.	1.1	45
198	Mechanisms of Tolerance and High Degradation Capacity of the Herbicide Mesotrione by <i>Escherichia coli</i> Strain DH5- $\lambda$ . <i>PLoS ONE</i> , 2014, 9, e99960.	1.1	34

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199	Measurement and Modeling of Denitrification in Sand-Bed Streams under Various Land Uses. <i>Journal of Environmental Quality</i> , 2014, 43, 1013-1023.	1.0	9
200	Selection on Horizontally Transferred and Duplicated Genes in <i>Sinorhizobium</i> (Ensifer), the Root-Nodule Symbionts of Medicago. <i>Genome Biology and Evolution</i> , 2014, 6, 1199-1209.	1.1	17
201	Core functional traits of bacterial communities in the Upper Mississippi River show limited variation in response to land cover. <i>Frontiers in Microbiology</i> , 2014, 5, 414.	1.5	95
202	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <i>Frontiers in Microbiology</i> , 2014, 5, 524.	1.5	70
203	Draft Genome Sequence of <i>Sphingobacterium</i> sp. Strain PM2-P1-29, a Tetracycline-Degrading TetX-Expressing Aerobic Bacterium Isolated from Agricultural Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
204	Genome-Scale Metabolic Network Validation of <i>Shewanella oneidensis</i> Using Transposon Insertion Frequency Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003848.	1.5	25
205	Near-full length sequencing of 16S rDNA and RFLP indicates that <i>Rhizobium etli</i> is the dominant species nodulating Egyptian winter Berseem clover ( <i>Trifolium alexandrinum</i> L.). <i>Systematic and Applied Microbiology</i> , 2014, 37, 121-128.	1.2	14
206	Notable decomposition products of senescing Lake Michigan <i>Cladophora glomerata</i> . <i>Journal of Great Lakes Research</i> , 2014, 40, 800-806.	0.8	9
207	Microscale measurements reveal contrasting effects of photosynthesis and epiphytes on frictional drag on the surfaces of filamentous algae. <i>Freshwater Biology</i> , 2014, 59, 312-324.	1.2	9
208	Shift of bacterial community structure in two Thai soil series affected by silver nanoparticles using ARISA. <i>World Journal of Microbiology and Biotechnology</i> , 2014, 30, 2119-2124.	1.7	17
209	Environmental and Animal-Associated Enterococci. <i>Advances in Applied Microbiology</i> , 2014, 87, 147-186.	1.3	45
210	Enhanced Nodulation and Nodule Development by <i>nolR</i> Mutants of <i>Sinorhizobium medicae</i> on Specific <i>Medicago</i> Host Genotypes. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 328-335.	1.4	14
211	Quantitative PCR for measuring biomass of decomposer fungi in planta. <i>Fungal Ecology</i> , 2014, 7, 39-46.	0.7	24
212	Microbiota transplantation restores normal fecal bile acid composition in recurrent <i>Clostridium difficile</i> infection. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 306, G310-G319.	1.6	341
213	Biodegradation in Waters from Hydraulic Fracturing: Chemistry, Microbiology, and Engineering. <i>Journal of Environmental Engineering, ASCE</i> , 2014, 140, .	0.7	70
214	Fate of Antibiotic Resistance Genes and Class 1 Integrons in Soil Microcosms Following the Application of Treated Residual Municipal Wastewater Solids. <i>Environmental Science &amp; Technology</i> , 2014, 48, 5620-5627.	4.6	99
215	Species and genus level resolution analysis of gut microbiota in <i>Clostridium difficile</i> patients following fecal microbiota transplantation. <i>Microbiome</i> , 2014, 2, 13.	4.9	98
216	Microbes in beach sands: integrating environment, ecology and public health. <i>Reviews in Environmental Science and Biotechnology</i> , 2014, 13, 329-368.	3.9	127

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217	Decay of genetic markers for fecal bacterial indicators and pathogens in sand from Lake Superior. <i>Water Research</i> , 2014, 48, 99-111.	5.3	37
218	Enteric Pathogen-Plant Interactions: Molecular Connections Leading to Colonization and Growth and Implications for Food Safety. <i>Microbes and Environments</i> , 2014, 29, 123-135.	0.7	64
219	Immune Mediated Shaping of Microflora Community Composition Depends on Barrier Site. <i>PLoS ONE</i> , 2014, 9, e84019.	1.1	34
220	Seasonal and Genotypic Changes in <i>Escherichia coli</i> Phylogenetic Groups in the Yeongsan River Basin of South Korea. <i>PLoS ONE</i> , 2014, 9, e100585.	1.1	19
221	Measurement and Modeling of Denitrification in Sand-Bed Streams under Various Land Uses. , 2014, 43, 1013.		1
222	Comparative genomics of the core and accessory genomes of 48 <i>Sinorhizobium</i> strains comprising five genospecies. <i>Genome Biology</i> , 2013, 14, R17.	13.9	164
223	Evaluation of molecular community analysis methods for discerning fecal sources and human waste. <i>Water Research</i> , 2013, 47, 6862-6872.	5.3	50
224	Amino acid substitutions in naphthalene dioxygenase from <i>Pseudomonas</i> sp. strain NCIB 9816-4 result in regio- and stereo-specific hydroxylation of flavanone and isoflavanone. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 693-704.	1.7	12
225	Air-Drying Beds Reduce the Quantities of Antibiotic Resistance Genes and Class 1 Integrons in Residual Municipal Wastewater Solids. <i>Environmental Science &amp; Technology</i> , 2013, 47, 9965-9971.	4.6	42
226	Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. <i>Journal of Applied Microbiology</i> , 2013, 115, 1147-1158.	1.4	209
227	Methanogenesis Facilitated by Geobiochemical Iron Cycle in a Novel Syntrophic Methanogenic Microbial Community. <i>Environmental Science &amp; Technology</i> , 2013, 47, 10078-10084.	4.6	78
228	Characterization of an Isoeugenol Monooxygenase ( <i>Iem</i> ) from <i>Pseudomonas nitroreducens</i> Jin1 That Transforms Isoeugenol to Vanillin. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 289-294.	0.6	23
229	Photosynthetic <i>Bradyrhizobium</i> sp. Strain ORS285 Is Capable of Forming Nitrogen-Fixing Root Nodules on Soybeans ( <i>Glycine max</i> ). <i>Applied and Environmental Microbiology</i> , 2013, 79, 2459-2462.	1.4	13
230	Evaluation of the repeatability and reproducibility of a suite of qPCR-based microbial source tracking methods. <i>Water Research</i> , 2013, 47, 6839-6848.	5.3	56
231	Multi-laboratory evaluations of the performance of <i>Catellibacillus marimammalium</i> PCR assays developed to target gull fecal sources. <i>Water Research</i> , 2013, 47, 6883-6896.	5.3	58
232	The establishment of the nuisance cyanobacteria <i>Lyngbya wollei</i> in Lake St. Clair and its potential to harbor fecal indicator bacteria. <i>Journal of Great Lakes Research</i> , 2013, 39, 560-568.	0.8	26
233	Root and Stem Nodule Bacteria of Legumes. , 2013, , 401-425.		7
234	Incidence of naturally internalized bacteria in lettuce leaves. <i>International Journal of Food Microbiology</i> , 2013, 162, 260-265.	2.1	33

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235	Transcriptional and functional responses of <i>Escherichia coli</i> O157:H7 growing in the lettuce rhizosphere. <i>Food Microbiology</i> , 2013, 35, 136-142.	2.1	24
236	Antimicrobial Peptides Targeting Gram-negative Pathogens, Produced and Delivered by Lactic Acid Bacteria. <i>ACS Synthetic Biology</i> , 2013, 2, 643-650.	1.9	60
237	Pathogenic <i>Escherichia coli</i> Strains Producing Extended-Spectrum $\beta$ -Lactamases in the Yeongsan River Basin of South Korea. <i>Environmental Science &amp; Technology</i> , 2013, 47, 1128-1136.	4.6	42
238	Distribution of Genetic Markers of Fecal Pollution on a Freshwater Sandy Shoreline in Proximity to Wastewater Effluent. <i>Environmental Science &amp; Technology</i> , 2013, 47, 3395-3402.	4.6	30
239	Association of Toxin-Producing <i>Clostridium botulinum</i> with the Macroalga <i>Cladophora</i> in the Great Lakes. <i>Environmental Science &amp; Technology</i> , 2013, 47, 2587-2594.	4.6	45
240	Complete Genome Sequence of the <i>Sesbania</i> Symbiont and Rice Growth-Promoting Endophyte <i>Rhizobium</i> sp. Strain IRBG74. <i>Genome Announcements</i> , 2013, 1, .	0.8	39
241	Resolution of Severe <i>Clostridium difficile</i> Infection Following Sequential Fecal Microbiota Transplantation. <i>Journal of Clinical Gastroenterology</i> , 2013, 47, 735-737.	1.1	80
242	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. <i>Journal of Experimental Medicine</i> , 2013, 210, 2011-2024.	4.2	144
243	High-throughput DNA sequence analysis reveals stable engraftment of gut microbiota following transplantation of previously frozen fecal bacteria. <i>Gut Microbes</i> , 2013, 4, 125-135.	4.3	262
244	Occurrence, Genetic Diversity, and Persistence of Enterococci in a Lake Superior Watershed. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3067-3075.	1.4	26
245	Influence of Elevated Atmospheric Carbon Dioxide on Transcriptional Responses of <i>Bradyrhizobium japonicum</i> in the Soybean Rhizosphere. <i>Microbes and Environments</i> , 2013, 28, 217-227.	0.7	15
246	Characterization of a Self-sufficient Trans-Anethole Oxygenase from <i>Pseudomonas putida</i> JYR-1. <i>PLoS ONE</i> , 2013, 8, e73350.	1.1	6
247	Candidate Genes and Genetic Architecture of Symbiotic and Agronomic Traits Revealed by Whole-Genome, Sequence-Based Association Genetics in <i>Medicago truncatula</i> . <i>PLoS ONE</i> , 2013, 8, e65688.	1.1	156
248	Aerobic digestion reduces the quantity of antibiotic resistance genes in residual municipal wastewater solids. <i>Frontiers in Microbiology</i> , 2013, 4, 17.	1.5	66
249	Plasmid Localization and Organization of Melamine Degradation Genes in <i>Rhodococcus</i> sp. Strain Mel. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1397-1403.	1.4	22
250	Transcriptional Responses of <i>Escherichia coli</i> K-12 and O157:H7 Associated with Lettuce Leaves. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1752-1764.	1.4	102
251	Transcriptional Control of the Isoeugenol Monooxygenase of <i>Pseudomonas nitroreducens</i> in <i>Escherichia coli</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1891-1896.	0.6	11
252	Transcriptional Responses of <i>Escherichia coli</i> K-12 and O157:H7 Associated with Lettuce Leaves. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3783-3783.	1.4	2

#	ARTICLE	IF	CITATIONS
253	Defining Sequence Space and Reaction Products within the Cyanuric Acid Hydrolase (AtzD)/Barbiturase Protein Family. <i>Journal of Bacteriology</i> , 2012, 194, 4579-4588.	1.0	27
254	Reactive Biomaterial for the Treatment of Herbicide Contaminated Drinking Water: Atrazine Dechlorination. , 2012, , .		0
255	Gene expression profiling of <i>Escherichia coli</i> in response to interactions with the lettuce rhizosphere. <i>Journal of Applied Microbiology</i> , 2012, 113, 1076-1086.	1.4	30
256	Integrated Online System for a Pyrosequencing-Based Microbial Source Tracking Method that Targets Bacteroidetes 16S rDNA. <i>Environmental Science &amp; Technology</i> , 2012, 46, 93-98.	4.6	34
257	A model laboratory system to study the synergistic interaction and growth of environmental <i>Escherichia coli</i> with macrophytic green algae. <i>Journal of Great Lakes Research</i> , 2012, 38, 390-395.	0.8	3
258	Silica gel-encapsulated AtzA biocatalyst for atrazine biodegradation. <i>Applied Microbiology and Biotechnology</i> , 2012, 96, 231-240.	1.7	31
259	Standardized Frozen Preparation for Transplantation of Fecal Microbiota for Recurrent <i>Clostridium difficile</i> Infection. <i>American Journal of Gastroenterology</i> , 2012, 107, 761-767.	0.2	583
260	Legume-“Microbe Symbioses. , 2012, , 73-88.		0
261	Phylogenetic and phenotypic analyses of arsenic-reducing bacteria isolated from an old tin mine area in Thailand. <i>World Journal of Microbiology and Biotechnology</i> , 2012, 28, 2287-2292.	1.7	5
262	Competition between two wood-degrading fungi with distinct influences on residues. <i>FEMS Microbiology Ecology</i> , 2012, 79, 109-117.	1.3	32
263	Isolation of mesotrione-degrading bacteria from aquatic environments in Brazil. <i>Chemosphere</i> , 2012, 86, 1127-1132.	4.2	42
264	The population structure of <i>Escherichia coli</i> isolated from subtropical and temperate soils. <i>Science of the Total Environment</i> , 2012, 417-418, 273-279.	3.9	46
265	Population Genomics of the Facultatively Mutualistic Bacteria <i>Sinorhizobium meliloti</i> and <i>S. medicae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002868.	1.5	69
266	Synthesis of chalcogenide ternary and quaternary nanotubes through directed compositional alterations of bacterial As-“S nanotubes. <i>Journal of Materials Chemistry</i> , 2011, 21, 10277.	6.7	8
267	Bacterial formation of extracellular U(vi) nanowires. <i>Chemical Communications</i> , 2011, 47, 8076.	2.2	18
268	Biodegradation and Mineralization of Metolachlor and Alachlor by <i>Candida xestobii</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 619-627.	2.4	58
269	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E864-70.	3.3	220
270	New Family of Biuret Hydrolases Involved in <i>s</i> -Triazine Ring Metabolism. <i>ACS Catalysis</i> , 2011, 1, 1075-1082.	5.5	24



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271	Simultaneous Synthesis of Temperature-Tunable Peptide and Gold Nanoparticle Hybrid Spheres. <i>Biomacromolecules</i> , 2011, 12, 2518-2523.	2.6	24
272	Multi-scale temporal and spatial variation in genotypic composition of <i>Cladophora</i> -borne <i>Escherichia coli</i> populations in Lake Michigan. <i>Water Research</i> , 2011, 45, 721-731.	5.3	24
273	<i>E. coli</i> Histidine Triad Nucleotide Binding Protein 1 (ecHtnT) Is a Catalytic Regulator of D-Alanine Dehydrogenase (DadA) Activity In Vivo. <i>PLoS ONE</i> , 2011, 6, e20897.	1.1	14
274	Expression and Functional Roles of <i>Bradyrhizobium japonicum</i> Genes Involved in the Utilization of Inorganic and Organic Sulfur Compounds in Free-Living and Symbiotic Conditions. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 451-457.	1.4	12
275	Waterfowl Abundance Does Not Predict the Dominant Avian Source of Beach <i>Escherichia coli</i> . <i>Journal of Environmental Quality</i> , 2011, 40, 1924-1931.	1.0	10
276	Genotypic and Phenotypic Trends in Antibiotic Resistant Pathogenic <i>Escherichia coli</i> Isolated from Humans and Farm Animals in South Korea. <i>Microbes and Environments</i> , 2011, 26, 198-204.	0.7	14
277	Prevalence of season-specific <i>Escherichia coli</i> strains in the Yeongsan River Basin of South Korea. <i>Environmental Microbiology</i> , 2011, 13, 3103-3113.	1.8	15
278	Soil nitrogen transformations under elevated atmospheric CO <sub>2</sub> and O <sub>3</sub> during the soybean growing season. <i>Environmental Pollution</i> , 2011, 159, 401-407.	3.7	25
279	The occurrence of virulence traits among high-level aminoglycosides resistant <i>Enterococcus</i> isolates obtained from feces of humans, animals, and birds in South Korea. <i>International Journal of Food Microbiology</i> , 2011, 144, 387-392.	2.1	45
280	Hydrothermal carbonization of microalgae II. Fatty acid, char, and algal nutrient products. <i>Applied Energy</i> , 2011, 88, 3286-3290.	5.1	139
281	Hydrothermal carbonization of distiller's grains. <i>Biomass and Bioenergy</i> , 2011, 35, 2526-2533.	2.9	129
282	Therapeutic transplantation of the distal gut microbiota. <i>Mucosal Immunology</i> , 2011, 4, 4-7.	2.7	75
283	Factors Controlling Long-Term Survival and Growth of Naturalized <i>Escherichia coli</i> Populations in Temperate Field Soils. <i>Microbes and Environments</i> , 2010, 25, 8-14.	0.7	58
284	Changes in the Composition of the Human Fecal Microbiome After Bacteriotherapy for Recurrent <i>Clostridium difficile</i> -associated Diarrhea. <i>Journal of Clinical Gastroenterology</i> , 2010, 44, 354-360.	1.1	595
285	Laser imaging for rapid Microbial Source Tracking. <i>International Journal of Computational Biology and Drug Design</i> , 2010, 3, 177.	0.3	3
286	Isoeugenol monooxygenase and its putative regulatory gene are located in the eugenol metabolic gene cluster in <i>Pseudomonas nitroreducens</i> Jin1. <i>Archives of Microbiology</i> , 2010, 192, 201-209.	1.0	18
287	High diversity and abundance of antibiotic-resistant <i>Escherichia coli</i> isolated from humans and farm animal hosts in Jeonnam Province, South Korea. <i>Science of the Total Environment</i> , 2010, 408, 3499-3506.	3.9	22
288	Peptide-mediated shape- and size-tunable synthesis of gold nanostructures. <i>Acta Biomaterialia</i> , 2010, 6, 2681-2689.	4.1	118

#	ARTICLE	IF	CITATIONS
289	Hydrothermal carbonization of microalgae. <i>Biomass and Bioenergy</i> , 2010, 34, 875-882.	2.9	301
290	Identification of a <i>Brevibacterium</i> marker gene specific to poultry litter and development of a quantitative PCR assay. <i>Journal of Applied Microbiology</i> , 2010, 109, 334-347.	1.4	63
291	Functional Role of <i>Bradyrhizobium japonicum</i> Trehalose Biosynthesis and Metabolism Genes during Physiological Stress and Nodulation. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1071-1081.	1.4	78
292	Bacterial Ammeline Metabolism via Guanine Deaminase. <i>Journal of Bacteriology</i> , 2010, 192, 1106-1112.	1.0	33
293	X-ray Structure and Mutational Analysis of the Atrazine Chlorohydrolase TrzN. <i>Journal of Biological Chemistry</i> , 2010, 285, 30606-30614.	1.6	28
294	Soybean Metabolites Regulated in Root Hairs in Response to the Symbiotic Bacterium <i>Bradyrhizobium japonicum</i> . <i>Plant Physiology</i> , 2010, 153, 1808-1822.	2.3	132
295	Use of Barcoded Pyrosequencing and Shared OTUs To Determine Sources of Fecal Bacteria in Watersheds. <i>Environmental Science &amp; Technology</i> , 2010, 44, 7777-7782.	4.6	108
296	Large scale analysis of virulence genes in <i>Escherichia coli</i> strains isolated from Avalon Bay, CA. <i>Water Research</i> , 2010, 44, 5463-5473.	5.3	55
297	Bioavailability of Organoclay Formulations of Atrazine in Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 11857-11863.	2.4	13
298	Shewanella-mediated synthesis of selenium nanowires and nanoribbons. <i>Journal of Materials Chemistry</i> , 2010, 20, 5899.	6.7	30
299	Structure and Diversity of Arsenic Resistant Bacteria in an Old Tin Mine Area of Thailand. <i>Journal of Microbiology and Biotechnology</i> , 2010, 20, 169-178.	0.9	19
300	Structure and diversity of arsenic resistant bacteria in an old tin mine area of Thailand. <i>Journal of Microbiology and Biotechnology</i> , 2010, 20, 169-78.	0.9	4
301	<i>Arthrobacter</i> sp. strain KU001 isolated from a Thai soil degrades atrazine in the presence of inorganic nitrogen sources. <i>Journal of Microbiology and Biotechnology</i> , 2010, 20, 602-8.	0.9	14
302	<i>Escherichia coli</i> Populations in Great Lakes Waterfowl Exhibit Spatial Stability and Temporal Shifting. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1546-1551.	1.4	16
303	Absence of <i>Escherichia coli</i> Phylogenetic Group B2 Strains in Humans and Domesticated Animals from Jeonnam Province, Republic of Korea. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5659-5666.	1.4	46
304	Thermostable Cyanuric Acid Hydrolase from <i>Moorella thermoacetica</i> ATCC 39073. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6986-6991.	1.4	16
305	Rapid identification and discrimination among Egyptian genotypes of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> and <i>Sinorhizobium meliloti</i> nodulating faba bean ( <i>Vicia faba</i> L.) by analysis of <i>nodC</i> , ARDRA, and rDNA sequence analysis. <i>Soil Biology and Biochemistry</i> , 2009, 41, 45-53.	4.2	30
306	<i>Sphingobacterium</i> sp. strain PM2-P1-29 harbours a functional <i>tet(X)</i> gene encoding for the degradation of tetracycline. <i>Journal of Applied Microbiology</i> , 2009, 106, 1336-1342.	1.4	95

#	ARTICLE	IF	CITATIONS
307	Applications of the repêPCR DNA fingerprinting technique to study microbial diversity, ecology and evolution. <i>Environmental Microbiology</i> , 2009, 11, 733-740.	1.8	116
308	Rapid and Complete Degradation of the Herbicide Picloram by <i>Lipomyces kononenkoae</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 4878-4882.	2.4	14
309	Biogenic Formation of As-S Nanotubes by Diverse <i>Shewanella</i> Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6896-6899.	1.4	58
310	Seasonal stability of <i>Cladophora</i> -associated <i>Salmonella</i> in Lake Michigan watersheds. <i>Water Research</i> , 2009, 43, 806-814.	5.3	80
311	Identification of a <i>Brevibacterium</i> Marker Gene Specific to Poultry Litter and Development of a Quantitative PCR Assay. <i>Journal of Applied Microbiology</i> , 2009, 109, 334.	1.4	2
312	Insights learned from pBTAi1, a 229-kb accessory plasmid from <i>Bradyrhizobium</i> sp. strain BTAi1 and prevalence of accessory plasmids in other <i>Bradyrhizobium</i> sp. strains. <i>ISME Journal</i> , 2008, 2, 158-170.	4.4	28
313	Sources and Sinks of <i>Escherichia coli</i> in Benthic and Pelagic Fish. <i>Journal of Great Lakes Research</i> , 2008, 34, 228-234.	0.8	21
314	Mineralization of the <i>Bacillus thuringiensis</i> Cry1Ac Endotoxin in Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 1025-1028.	2.4	19
315	Microbial Degradation of s-Triazine Herbicides. , 2008, , 301-328.		16
316	Availability of Triazine Herbicides in Aged Soils Amended with Olive Oil Mill Waste. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 4112-4119.	2.4	36
317	Nodulation Gene Regulation and Quorum Sensing Control Density-Dependent Suppression and Restriction of Nodulation in the <i>Bradyrhizobium japonicum</i> -Soybean Symbiosis. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3749-3756.	1.4	41
318	Whole-Genome Transcriptional Profiling of <i>Bradyrhizobium japonicum</i> during Chemoautotrophic Growth. <i>Journal of Bacteriology</i> , 2008, 190, 6697-6705.	1.0	47
319	<i>Escherichia coli</i> in the Environment: Implications for Water Quality and Human Health. <i>Microbes and Environments</i> , 2008, 23, 101-108.	0.7	393
320	Biogenic formation of photoactive arsenic-sulfide nanotubes by <i>Shewanella</i> sp. strain HN-41. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20410-20415.	3.3	127
321	High-Throughput and Quantitative Procedure for Determining Sources of <i>Escherichia coli</i> in Waterways by Using Host-Specific DNA Marker Genes. <i>Applied and Environmental Microbiology</i> , 2007, 73, 890-896.	1.4	24
322	Presence and Sources of Fecal Coliform Bacteria in Epilithic Periphyton Communities of Lake Superior. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3771-3778.	1.4	99
323	Relationship between Phylogenetic Groups, Genotypic Clusters, and Virulence Gene Profiles of <i>Escherichia coli</i> Strains from Diverse Human and Animal Sources. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5703-5710.	1.4	104
324	Genomes of the Symbiotic Nitrogen-Fixing Bacteria of Legumes. <i>Plant Physiology</i> , 2007, 144, 615-622.	2.3	141

#	ARTICLE	IF	CITATIONS
325	Hydroxyatrazine <i>N</i> -Ethylaminohydrolase (AtzB): an Amidohydrolase Superfamily Enzyme Catalyzing Deamination and Dechlorination. <i>Journal of Bacteriology</i> , 2007, 189, 6989-6997.	1.0	29
326	Evolution of Catabolic Pathways: Genomic Insights into Microbial s-Triazine Metabolism. <i>Journal of Bacteriology</i> , 2007, 189, 674-682.	1.0	98
327	Transcriptional and Physiological Responses of <i>Bradyrhizobium japonicum</i> to Desiccation-Induced Stress. <i>Journal of Bacteriology</i> , 2007, 189, 9150-9150.	1.0	4
328	An Oligonucleotide Microarray Resource for Transcriptional Profiling of <i>Bradyrhizobium japonicum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1298-1307.	1.4	71
329	Population structure of <i>Cladophora</i> -borne <i>Escherichia coli</i> in nearshore water of Lake Michigan. <i>Water Research</i> , 2007, 41, 3649-3654.	5.3	50
330	Determining Sources of Fecal Bacteria in Waterways. <i>Environmental Monitoring and Assessment</i> , 2007, 129, 97-106.	1.3	36
331	Transcriptional and Physiological Responses of <i>Bradyrhizobium japonicum</i> to Desiccation-Induced Stress. <i>Journal of Bacteriology</i> , 2007, 189, 6751-6762.	1.0	162
332	Beach Sand and Sediments are Temporal Sinks and Sources of <i>Escherichia coli</i> in Lake Superior. <i>Environmental Science &amp; Technology</i> , 2007, 41, 2203-2209.	4.6	185
333	Environmental Fate of Two Sulfonamide Antimicrobial Agents in Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 2677-2682.	2.4	144
334	Root and Stem Nodule Bacteria of Legumes. , 2006, , 818-841.		6
335	Influence of Soil Aging on Sorption and Bioavailability of Simazine. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 1373-1379.	2.4	63
336	Influence of Cry1Ac Toxin on Mineralization and Bioavailability of Glyphosate in Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 164-169.	2.4	6
337	The <i>argRB</i> of <i>Escherichia coli</i> is rare in isolates obtained from natural sources. <i>Gene</i> , 2006, 376, 240-247.	1.0	4
338	Automated Robotic Assay of Phosphomonoesterase Activity in Soils. <i>Soil Science Society of America Journal</i> , 2006, 70, 378-381.	1.2	5
339	Population structure, persistence, and seasonality of autochthonous <i>Escherichia coli</i> in temperate, coastal forest soil from a Great Lakes watershed. <i>Environmental Microbiology</i> , 2006, 8, 504-513.	1.8	181
340	Secrets of Soil Survival Revealed by the Genome Sequence of <i>Arthrobacter aurescens</i> TC1. <i>PLoS Genetics</i> , 2006, 2, e214.	1.5	213
341	TrzN from <i>Arthrobacter aurescens</i> TC1 Is a Zinc Amidohydrolase. <i>Journal of Bacteriology</i> , 2006, 188, 5859-5864.	1.0	47
342	Purification and Characterization of TrzF: Biuret Hydrolysis by Allophanate Hydrolase Supports Growth. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2491-2495.	1.4	27

#	ARTICLE	IF	CITATIONS
343	Development of Goose- and Duck-Specific DNA Markers To Determine Sources of <i>Escherichia coli</i> in Waterways. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4012-4019.	1.4	48
344	<i>Cladophora</i> (Chlorophyta) spp. Harbor Human Bacterial Pathogens in Nearshore Water of Lake Michigan. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4545-4553.	1.4	150
345	Presence and Growth of Naturalized <i>Escherichia coli</i> in Temperate Soils from Lake Superior Watersheds. <i>Applied and Environmental Microbiology</i> , 2006, 72, 612-621.	1.4	440
346	Biological Nitrogen Fixation: A Key Process for the Response of Grassland Ecosystems to Elevated Atmospheric [CO <sub>2</sub> ]. <i>Ecological Studies</i> , 2006, , 325-336.	0.4	5
347	Biodegradation of atrazine in transgenic plants expressing a modified bacterial atrazine chlorohydrolase ( <i>atzA</i> ) gene. <i>Plant Biotechnology Journal</i> , 2005, 3, 475-486.	4.1	86
348	Detection of Homoserine Lactone-Like Quorum Sensing Molecules in <i>Bradyrhizobium</i> Strains. <i>Current Microbiology</i> , 2005, 51, 250-254.	1.0	30
349	The role of histidine 200 in MndD, the Mn(II)-dependent 3,4-dihydroxyphenylacetate 2,3-dioxygenase from <i>Arthrobacter globiformis</i> CM-2, a site-directed mutagenesis study. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 751-760.	1.1	29
350	Allophanate Hydrolase, Not Urease, Functions in Bacterial Cyanuric Acid Metabolism. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4437-4445.	1.4	64
351	Purification and Characterization of Allophanate Hydrolase ( <i>AtzF</i> ) from <i>Pseudomonas</i> sp. Strain ADP. <i>Journal of Bacteriology</i> , 2005, 187, 3731-3738.	1.0	52
352	Substrate Specificity and Colorimetric Assay for Recombinant <i>TrzN</i> Derived from <i>Arthrobacter aurescens</i> TC1. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2214-2220.	1.4	51
353	Effects of Incorporated Corn Residues on Glyphosate Mineralization and Sorption in Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 4110-4117.	2.4	49
354	Soil Stress Factors Influencing Symbiotic Nitrogen Fixation. , 2005, , 89-112.		30
355	Arsenic Availability from Chromated Copper Arsenate (CCA)â€Treated Wood. <i>Journal of Environmental Quality</i> , 2004, 33, 173.	1.0	5
356	<i>Arthrobacter aurescens</i> TC1 Atrazine Catabolism Genes <i>trzN</i> , <i>atzB</i> , and <i>atzC</i> Are Linked on a 160-Kilobase Region and Are Functional in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 4402-4407.	1.4	103
357	Frequency and Distribution of Tetracycline Resistance Genes in Genetically Diverse, Nonselected, and Nonclinical <i>Escherichia coli</i> Strains Isolated from Diverse Human and Animal Sources. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2503-2507.	1.4	215
358	Sample Size, Library Composition, and Genotypic Diversity among Natural Populations of <i>Escherichia coli</i> from Different Animals Influence Accuracy of Determining Sources of Fecal Pollution. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4478-4485.	1.4	156
359	Solvent Extraction Characterization of Bioavailability of Atrazine Residues in Soils. <i>Journal of Agricultural and Food Chemistry</i> , 2004, 52, 6552-6556.	2.4	66
360	Phylogeny and distribution of extra-slow-growing <i>Bradyrhizobium japonicum</i> harboring high copy numbers of <i>RS</i> ±, <i>RS</i> ² and IS1631. <i>FEMS Microbiology Ecology</i> , 2003, 44, 191-202.	1.3	40

#	ARTICLE	IF	CITATIONS
361	Growth and survival of <i>Escherichia coli</i> and enterococci populations in the macro-alga <i>Cladophora</i> (Chlorophyta). <i>FEMS Microbiology Ecology</i> , 2003, 46, 203-211.	1.3	192
362	On the Origins of Cyanuric Acid Hydrolase: Purification, Substrates, and Prevalence of AtzD from <i>Pseudomonas</i> sp. Strain ADP. <i>Applied and Environmental Microbiology</i> , 2003, 69, 3653-3657.	1.4	68
363	Comparison of genotypic-based microbial source tracking methods requiring a host origin database. <i>Journal of Water and Health</i> , 2003, 1, 167-180.	1.1	63
364	Purification, Substrate Range, and Metal Center of AtzC: the N-Isopropylammelide Aminohydrolase Involved in Bacterial Atrazine Metabolism. <i>Journal of Bacteriology</i> , 2002, 184, 5376-5384.	1.0	51
365	Novel psbA1 Gene from a Naturally Occurring Atrazine-Resistant Cyanobacterial Isolate. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1358-1366.	1.4	15
366	Enzymatic Degradation of Chlorodiamino- s-Triazine. <i>Applied and Environmental Microbiology</i> , 2002, 68, 4672-4675.	1.4	31
367	<i>Arthrobacter aurescens</i> TC1 Metabolizes Diverse s-Triazine Ring Compounds. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5973-5980.	1.4	203
368	Atrazine Chlorohydrolase from <i>Pseudomonas</i> Sp. Strain ADP Is a Metalloenzyme. <i>Biochemistry</i> , 2002, 41, 14430-14437.	1.2	53
369	Biodegradation of atrazine and related s-triazine compounds: from enzymes to field studies. <i>Applied Microbiology and Biotechnology</i> , 2002, 58, 39-45.	1.7	305
370	Title is missing!. <i>Plant and Soil</i> , 2002, 243, 197-207.	1.8	78
371	Complete Nucleotide Sequence and Organization of the Atrazine Catabolic Plasmid pADP-1 from <i>Pseudomonas</i> sp. Strain ADP. <i>Journal of Bacteriology</i> , 2001, 183, 5684-5697.	1.0	324
372	Agricultural Microbes Genome 2. <i>Comparative and Functional Genomics</i> , 2001, 2, 10-13.	2.0	0
373	A Marker-Dense Physical Map of the <i>Bradyrhizobium japonicum</i> Genome. <i>Genome Research</i> , 2001, 11, 1434-1440.	2.4	11
374	Melamine Deaminase and Atrazine Chlorohydrolase: 98 Percent Identical but Functionally Different. <i>Journal of Bacteriology</i> , 2001, 183, 2405-2410.	1.0	119
375	Field-scale remediation of atrazine-contaminated soil using recombinant <i>Escherichia coli</i> expressing atrazine chlorohydrolase. <i>Environmental Microbiology</i> , 2000, 2, 91-98.	1.8	137
376	Elevated atmospheric CO <sub>2</sub> alters microbial population structure in a pasture ecosystem. <i>Global Change Biology</i> , 2000, 6, 475-482.	4.2	67
377	Substrate Specificity of Atrazine Chlorohydrolase and Atrazine-Catabolizing Bacteria. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4247-4252.	1.4	65
378	Genetics of Atrazine and s-Triazine Degradation by <i>Pseudomonas</i> sp. Strain ADP and Other Bacteria. <i>ACS Symposium Series</i> , 2000, , 268-282.	0.5	3

#	ARTICLE	IF	CITATIONS
379	Use of Repetitive DNA Sequences and the PCR To Differentiate Escherichia coli Isolates from Human and Animal Sources. Applied and Environmental Microbiology, 2000, 66, 2572-2577.	1.4	425
380	The Bradyrhizobium japonicum nola Gene Encodes Three Functionally Distinct Proteins. Journal of Bacteriology, 1999, 181, 1544-1554.	1.0	29
381	Genetics of Atrazine Degradation in Pseudomonas sp. Strain ADP. ACS Symposium Series, 1998, , 88-94.	0.5	1
382	Soil Biology of the Rhizobiaceae. , 1998, , 155-172.		42
383	Use of Endogenous Repeated Sequences to Fingerprint Bacterial Genomic DNA. , 1998, , 399-413.		9
384	The Bradyrhizobium japonicum noeD Gene: A Negatively Acting, Genotype-Specific Nodulation Gene for Soybean. Molecular Plant-Microbe Interactions, 1998, 11, 476-488.	1.4	16
385	The Atrazine Catabolism Genes <i>atzABC</i> Are Widespread and Highly Conserved. Journal of Bacteriology, 1998, 180, 1951-1954.	1.0	225
386	Molecular Basis of a Bacterial Consortium: Interspecies Catabolism of Atrazine. Applied and Environmental Microbiology, 1998, 64, 178-184.	1.4	187
387	The <i>atzABC</i> Genes Encoding Atrazine Catabolism Are Located on a Self-Transmissible Plasmid in <i>Pseudomonas</i> sp. Strain ADP. Applied and Environmental Microbiology, 1998, 64, 2323-2326.	1.4	136
388	AtzC Is a New Member of the Amidohydrolase Protein Superfamily and Is Homologous to Other Atrazine-Metabolizing Enzymes. Journal of Bacteriology, 1998, 180, 152-158.	1.0	154
389	A Host-Controlled, Serogroup-Specific, Ineffective-Nodulation System in the Bradyrhizobium-Soybean (Glycine max) Symbiosis. Molecular Plant-Microbe Interactions, 1997, 10, 994-1001.	1.4	9
390	Manganese(II) Active Site Mutants of 3,4-Dihydroxyphenylacetate 2,3-Dioxygenase from Arthrobacter globiformis Strain CM-2. Biochemistry, 1997, 36, 2147-2153.	1.2	37
391	Relationship between root length density and soil microorganisms in the rhizospheres of white clover and perennial ryegrass. Communications in Soil Science and Plant Analysis, 1997, 28, 1675-1682.	0.6	9
392	Plasmid Transfer between Spatially Separated Donor and Recipient Bacteria in Earthworm-Containing Soil Microcosms. Applied and Environmental Microbiology, 1997, 63, 679-686.	1.4	44
393	The <i>atzB</i> gene of Pseudomonas sp. strain ADP encodes the second enzyme of a novel atrazine degradation pathway. Applied and Environmental Microbiology, 1997, 63, 916-923.	1.4	149
394	Host-Controlled Restriction of Nodulation by Bradyrhizobium Japonicum Strain USDA 110 and Characterization of a Gene Regulating Nodulation. , 1997, , 137-141.		0
395	Microbial community changes in the rhizospheres of white clover and perennial ryegrass exposed to Free Air Carbon dioxide Enrichment (FACE). Soil Biology and Biochemistry, 1996, 28, 1717-1724.	4.2	118
396	Inheritance of Host-Controlled Restriction of Nodulation by Bradyrhizobium japonicum Strain USDA 110. Crop Science, 1996, 36, 1271-1276.	0.8	25

#	ARTICLE	IF	CITATIONS
397	Atrazine chlorohydrolase from <i>Pseudomonas</i> sp. strain ADP: gene sequence, enzyme purification, and protein characterization. <i>Journal of Bacteriology</i> , 1996, 178, 4894-4900.	1.0	220
398	Influence of earthworm activity on gene transfer from <i>Pseudomonas fluorescens</i> to indigenous soil bacteria. <i>Applied and Environmental Microbiology</i> , 1996, 62, 515-521.	1.4	79
399	Use of repetitive intergenic DNA sequences to classify pathogenic and disease-suppressive <i>Streptomyces</i> strains. <i>Applied and Environmental Microbiology</i> , 1996, 62, 3489-3493.	1.4	46
400	A manganese-dependent dioxygenase from <i>Arthrobacter globiformis</i> CM-2 belongs to the major extradiol dioxygenase family. <i>Journal of Bacteriology</i> , 1995, 177, 1225-1232.	1.0	95
401	Differences among strains of <i>Bradyrhizobium</i> in fatty acid methyl ester analysis. <i>Canadian Journal of Microbiology</i> , 1995, 41, 1038-1042.	0.8	26
402	Native prairie grasses and microbial community responses to reclamation of taconite iron ore tailing. <i>Canadian Journal of Botany</i> , 1995, 73, 1645-1654.	1.2	15
403	Restriction of Nodulation by <i>Bradyrhizobium japonicum</i> Is Mediated by Factors Present in the Roots of <i>Glycine max.</i> <i>Applied and Environmental Microbiology</i> , 1995, 61, 832-836.	1.4	22
404	Diversity among Field Populations of <i>Bradyrhizobium japonicum</i> in Poland. <i>Applied and Environmental Microbiology</i> , 1995, 61, 1194-1200.	1.4	51
405	Host-Controlled Restriction of Nodulation by <i>Bradyrhizobium japonicum</i> Strains in Serogroup 110. <i>Applied and Environmental Microbiology</i> , 1995, 61, 2378-2383.	1.4	29
406	Cloning, characterization, and expression of a gene region from <i>Pseudomonas</i> sp. strain ADP involved in the dechlorination of atrazine. <i>Applied and Environmental Microbiology</i> , 1995, 61, 3373-3378.	1.4	127
407	Metabolism of polyhalogenated compounds by a genetically engineered bacterium. <i>Nature</i> , 1994, 368, 627-629.	13.7	103
408	Metabolism of chlorofluorocarbons and polybrominated compounds by <i>Pseudomonas putida</i> G786(pHG-2) via an engineered metabolic pathway. <i>Applied and Environmental Microbiology</i> , 1994, 60, 4148-4154.	1.4	24
409	A Selective Medium for the Isolation and Quantification of <i>Bradyrhizobium japonicum</i> and <i>Bradyrhizobium elkanii</i> Strains from Soils and Inoculants. <i>Applied and Environmental Microbiology</i> , 1994, 60, 581-586.	1.4	64
410	Tellurium and Selenium Resistance in Rhizobia and Its Potential Use for Direct Isolation of <i>Rhizobium meliloti</i> from Soil. <i>Applied and Environmental Microbiology</i> , 1994, 60, 1674-1677.	1.4	53
411	Isolation of a <i>Bradyrhizobium japonicum</i> serogroup 123 mutant which has an extended host range for nodulation-restricting soybean genotypes. <i>FEMS Microbiology Letters</i> , 1993, 106, 205-209.	0.7	9
412	The <i>Bradyrhizobium japonicum</i> serocluster 123 hyperreiterated DNA region, HRS1, has DNA and amino acid sequence homology to IS1380, an insertion sequence from <i>Acetobacter pasteurianus</i> . <i>Applied and Environmental Microbiology</i> , 1993, 59, 1656-1661.	1.4	13
413	Use of repetitive sequences and the polymerase chain reaction technique to classify genetically related <i>Bradyrhizobium japonicum</i> serocluster 123 strains. <i>Applied and Environmental Microbiology</i> , 1993, 59, 1702-1708.	1.4	130
414	Plasmids pJP4 and r68.45 Can Be Transferred between Populations of <i>Bradyrhizobia</i> in Nonsterile Soil. <i>Applied and Environmental Microbiology</i> , 1993, 59, 1762-1766.	1.4	56



#	ARTICLE	IF	CITATIONS
415	Genetics of Competition for Nodulation of Legumes. Annual Review of Microbiology, 1992, 46, 399-422.	2.9	270
416	Lysogeny in <i>Bradyrhizobium japonicum</i> and Its Effect on Soybean Nodulation. Applied and Environmental Microbiology, 1992, 58, 3360-3366.	1.4	19
417	The Soybean <i>Rj4</i> Allele Restricts Nodulation by <i>Bradyrhizobium japonicum</i> Serogroup 123 Strains. Applied and Environmental Microbiology, 1992, 58, 720-723.	1.4	32
418	Hyperreiterated DNA regions are conserved among <i>Bradyrhizobium japonicum</i> serocluster 123 strains. Applied and Environmental Microbiology, 1992, 58, 1878-1885.	1.4	15
419	Characterization of cytochromes c550 and c555 from <i>Bradyrhizobium japonicum</i> : cloning, mutagenesis, and sequencing of the c555 gene ( <i>cycC</i> ). Journal of Bacteriology, 1991, 173, 7887-7895.	1.0	21
420	The <i>Bradyrhizobium japonicum</i> <i>nolA</i> gene and its involvement in the genotype-specific nodulation of soybeans.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 637-641.	3.3	137
421	Proposed Minimal Standards for the Description of New Genera and Species of Root- and Stem-Nodulating Bacteria. International Journal of Systematic Bacteriology, 1991, 41, 582-587.	2.8	240
422	Gene-for-gene interaction in the legume-Rhizobium symbiosis. , 1991, , 163-171.		2
423	Microbial influence on gene-for-gene interactions in legume-Rhizobium symbioses. , 1991, , 173-180.		1
424	Microbial influence on gene-for-gene interactions in legume-Rhizobium symbioses. Plant and Soil, 1990, 129, 53-60.	1.8	16
425	DNA Hybridization Probe for Use in Determining Restricted Nodulation among <i>Bradyrhizobium japonicum</i> Serocluster 123 Field Isolates. Applied and Environmental Microbiology, 1990, 56, 1768-1774.	1.4	27
426	Genome analysis of <i>Bradyrhizobium japonicum</i> serocluster 123 field isolates by using field inversion gel electrophoresis. Applied and Environmental Microbiology, 1990, 56, 1949-1953.	1.4	22
427	Cytochrome Mutants of <i>Bradyrhizobium</i> Induced by Transposon Tn5. Plant Physiology, 1989, 90, 553-559.	2.3	28
428	Host Plant Effects on Nodulation and Competitiveness of the <i>Bradyrhizobium japonicum</i> Serotype Strains Constituting Serocluster 123. Applied and Environmental Microbiology, 1989, 55, 2532-2536.	1.4	51
429	Influence of soil variables on in situ plasmid transfer from <i>Escherichia coli</i> to <i>Rhizobium fredii</i> . Applied and Environmental Microbiology, 1989, 55, 1730-1734.	1.4	99
430	Soybean Genotype Restricting Nodulation of a Previously Unrestricted Serocluster 123 <i>Bradyrhizobia</i> . Crop Science, 1989, 29, 307.	0.8	49
431	Two host-inducible genes of <i>Rhizobium fredii</i> and characterization of the inducing compound. Journal of Bacteriology, 1988, 170, 171-178.	1.0	69
432	Nodulation and Nitrogen Fixation Efficacy of <i>Rhizobium fredii</i> with <i>Phaseolus vulgaris</i> Genotypes. Applied and Environmental Microbiology, 1988, 54, 1907-1910.	1.4	32

#	ARTICLE	IF	CITATIONS
433	Genetic Diversity in <i>Bradyrhizobium japonicum</i> Serogroup 123 and Its Relation to Genotype-Specific Nodulation of Soybean. <i>Applied and Environmental Microbiology</i> , 1987, 53, 2624-2630.	1.4	214
434	Serological Relatedness of <i>Rhizobium fredii</i> to Other Rhizobia and to the Bradyrhizobia. <i>Applied and Environmental Microbiology</i> , 1987, 53, 1785-1789.	1.4	38
435	Symbiotically defective histidine auxotrophs of <i>Bradyrhizobium japonicum</i> . <i>Archives of Microbiology</i> , 1986, 144, 334-339.	1.0	24
436	Rapid Colored-Nodule Assay for Assessing Root Exudate-Enhanced Competitiveness of <i>Bradyrhizobium japonicum</i> . <i>Applied and Environmental Microbiology</i> , 1986, 52, 847-851.	1.4	9
437	Growth of Fast- and Slow-Growing Rhizobia on Ethanol. <i>Applied and Environmental Microbiology</i> , 1986, 52, 951-953.	1.4	9
438	Identification of Genes Involved in the Rhizobium-Legume Symbiosis by Mu-dI (Kan, lac)-Generated Transcription Fusions. <i>Bio/technology</i> , 1985, 3, 143-149.	1.9	29
439	Biochemical Characterization of Fast- and Slow-Growing Rhizobia That Nodulate Soybeans. <i>International Journal of Systematic Bacteriology</i> , 1983, 33, 716-722.	2.8	75
440	Competition of <i>Rhizobium japonicum</i> Strains in Early Stages of Soybean Nodulation. <i>Applied and Environmental Microbiology</i> , 1983, 46, 870-873.	1.4	63
441	Possible Involvement of a Megaplasmid in Nodulation of Soybeans by Fast-Growing Rhizobia from China. <i>Applied and Environmental Microbiology</i> , 1983, 46, 906-911.	1.4	32
442	Diversity and evolution of micro-organisms and pathways for the degradation of environmental contaminants: a case study with the s-triazine herbicides. , 0, , 205-225.		3
443	Fecal Pollution, Public Health, and Microbial Source Tracking. , 0, , 1-32.		15
444	Assumptions and Limitations Associated with Microbial Source Tracking Methods. , 0, , 33-64.		7
445	Molecular Detection and Characterization Tools. , 0, , 65-91.		3
446	Molecular Subtyping, Source Tracking, and Food Safety. , 0, , 93-136.		9
447	Statistical Issues in Microbial Source Identification. , 0, , 181-210.		1
448	The Future of Microbial Source Tracking Studies. , 0, , 235-277.		13
449	The Fecal Environment, The Gut. , 0, , 1-21.		5
450	Prevalence and Fate of Gut-Associated Human Pathogens in the Environment. , 0, , 217-240.		2

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451	Classical and Molecular Methods to Measure Fecal Bacteria. , 0, , 241-273.		2
452	Taxonomy, Phylogeny, and Physiology of Fecal Indicator Bacteria. , 0, , 23-38.		4
453	Animals and Humans as Sources of Fecal Indicator Bacteria. , 0, , 67-91.		9
454	Environmental Sources of Fecal Bacteria. , 0, , 93-110.		13
455	Physical and Biological Factors Influencing Environmental Sources of Fecal Indicator Bacteria in Surface Water. , 0, , 111-134.		5
456	Impacts of Fecal Bacteria on Human and Animal Health-Pathogens and Virulence Genes. , 0, , 135-164.		1
457	Modeling Fate and Transport of Fecal Bacteria in Surface Water. , 0, , 165-188.		11
458	Microbial Source Tracking. , 0, , 189-216.		3
459	The Gut Microbiota: Ecology and Function. , 0, , 39-65.		1
460	Conclusions and Future Use of Fecal Indicator Bacteria for Monitoring Water Quality and Protecting Human Health. , 0, , 295-302.		0
461	Fecal Bacteria and Foods. , 0, , 275-293.		0
462	Shellfish and Microbial Source Tracking. , 0, , 137-179.		0