

Michael J Sadowsky

List of Publications by Year in descending order

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462
papers

27,138
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4960

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139
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476
all docs

476
docs citations

476
times ranked

24899
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017, 5, 10.	11.1	901
2	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.	2.2	595
3	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.	0.4	583
4	Effect of Fecal Microbiota Transplantation on Recurrence in Multiply Recurrent <i>Clostridium difficile</i> Infection. <i>Annals of Internal Medicine</i> , 2016, 165, 609.	3.9	486
5	Environmental <i>Escherichia coli</i> : ecology and public health implications-a review. <i>Journal of Applied Microbiology</i> , 2017, 123, 570-581.	3.1	477
6	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.	3.1	440
7	Use of Repetitive DNA Sequences and the PCR To Differentiate <i>Escherichia coli</i> Isolates from Human and Animal Sources. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2572-2577.	3.1	425
8	<i>Escherichia coli</i> in the Environment: Implications for Water Quality and Human Health. <i>Microbes and Environments</i> , 2008, 23, 101-108.	1.6	393
9	Interaction of gut microbiota with bile acid metabolism and its influence on disease states. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 47-64.	3.6	387
10	Understanding the mechanisms of faecal microbiota transplantation. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2016, 13, 508-516.	17.8	377
11	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.	3.4	341
12	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.	2.2	324
13	Biodegradation of atrazine and related s-triazine compounds: from enzymes to field studies. <i>Applied Microbiology and Biotechnology</i> , 2002, 58, 39-45.	3.6	305
14	Hydrothermal carbonization of microalgae. <i>Biomass and Bioenergy</i> , 2010, 34, 875-882.	5.7	301
15	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.	11.0	292
16	Erosion reduces soil microbial diversity, network complexity and multifunctionality. <i>ISME Journal</i> , 2021, 15, 2474-2489.	9.8	273
17	Genetics of Competition for Nodulation of Legumes. <i>Annual Review of Microbiology</i> , 1992, 46, 399-422.	7.3	270
18	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.	9.8	262

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19	Proposed Minimal Standards for the Description of New Genera and Species of Root- and Stem-Nodulating Bacteria. <i>International Journal of Systematic Bacteriology</i> , 1991, 41, 582-587.	2.8	240
20	The Atrazine Catabolism Genes <i>atzABC</i> Are Widespread and Highly Conserved. <i>Journal of Bacteriology</i> , 1998, 180, 1951-1954.	2.2	225
21	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.	2.2	220
22	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.	7.1	220
23	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.	11.1	218
24	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.	3.1	215
25	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.	3.1	214
26	Secrets of Soil Survival Revealed by the Genome Sequence of <i>Arthrobacter aurescens</i> TC1. <i>PLoS Genetics</i> , 2006, 2, e214.	3.5	213
27	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.	3.1	209
28	<i>Arthrobacter aurescens</i> TC1 Metabolizes Diverse s-Triazine Ring Compounds. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5973-5980.	3.1	203
29	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.	2.7	192
30	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.	4.4	190
31	Molecular Basis of a Bacterial Consortium: Interspecies Catabolism of Atrazine. <i>Applied and Environmental Microbiology</i> , 1998, 64, 178-184.	3.1	187
32	Beach Sand and Sediments are Temporal Sinks and Sources of <i>Escherichia coli</i> in Lake Superior. <i>Environmental Science & Technology</i> , 2007, 41, 2203-2209.	10.0	185
33	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.	3.8	181
34	Environment shapes the fecal microbiome of invasive carp species. <i>Microbiome</i> , 2016, 4, 44.	11.1	166
35	Comparative genomics of the core and accessory genomes of 48 <i>Sinorhizobium</i> strains comprising five genospecies. <i>Genome Biology</i> , 2013, 14, R17.	9.6	164
36	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.	0.4	164

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37	Transcriptional and Physiological Responses of <i>Bradyrhizobium japonicum</i> to Desiccation-Induced Stress. <i>Journal of Bacteriology</i> , 2007, 189, 6751-6762.	2.2	162
38	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.	3.1	156
39	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.	2.5	156
40	AtzC Is a New Member of the Amidohydrolase Protein Superfamily and Is Homologous to Other Atrazine-Metabolizing Enzymes. <i>Journal of Bacteriology</i> , 1998, 180, 152-158.	2.2	154
41	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. <i>Science of the Total Environment</i> , 2022, 805, 149877.	8.0	153
42	<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.	3.1	150
43	Secretion systems and signal exchange between nitrogen-fixing rhizobia and legumes. <i>Frontiers in Plant Science</i> , 2015, 6, 491.	3.6	150
44	The <i>atzB</i> gene of <i>Pseudomonas</i> sp. strain ADP encodes the second enzyme of a novel atrazine degradation pathway. <i>Applied and Environmental Microbiology</i> , 1997, 63, 916-923.	3.1	149
45	Environmental Fate of Two Sulfonamide Antimicrobial Agents in Soil. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 2677-2682.	5.2	144
46	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. <i>Journal of Experimental Medicine</i> , 2013, 210, 2011-2024.	8.5	144
47	Genomes of the Symbiotic Nitrogen-Fixing Bacteria of Legumes. <i>Plant Physiology</i> , 2007, 144, 615-622.	4.8	141
48	Hydrothermal carbonization of microalgae II. Fatty acid, char, and algal nutrient products. <i>Applied Energy</i> , 2011, 88, 3286-3290.	10.1	139
49	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	11.1	138
50	The <i>Bradyrhizobium japonicum</i> <i>nolA</i> gene and its involvement in the genotype-specific nodulation of soybeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 637-641.	7.1	137
51	Field-scale remediation of atrazine-contaminated soil using recombinant <i>Escherichia coli</i> expressing atrazine chlorohydrolase. <i>Environmental Microbiology</i> , 2000, 2, 91-98.	3.8	137
52	The <i>atzABC</i> Genes Encoding Atrazine Catabolism Are Located on a Self-Transmissible Plasmid in <i>Pseudomonas</i> sp. Strain ADP. <i>Applied and Environmental Microbiology</i> , 1998, 64, 2323-2326.	3.1	136
53	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.	8.0	133
54	Soybean Metabolites Regulated in Root Hairs in Response to the Symbiotic Bacterium <i>Bradyrhizobium japonicum</i> . <i>Plant Physiology</i> , 2010, 153, 1808-1822.	4.8	132

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55	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.	2.5	130
56	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.	3.1	130
57	Hydrothermal carbonization of distiller's grains. <i>Biomass and Bioenergy</i> , 2011, 35, 2526-2533.	5.7	129
58	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.	7.1	127
59	Microbes in beach sands: integrating environment, ecology and public health. <i>Reviews in Environmental Science and Biotechnology</i> , 2014, 13, 329-368.	8.1	127
60	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.	3.1	127
61	Ammonium sorption and ammonia inhibition of nitrite-oxidizing bacteria explain contrasting soil N ₂ O production. <i>Scientific Reports</i> , 2015, 5, 12153.	3.3	125
62	Melamine Deaminase and Atrazine Chlorohydrolase: 98 Percent Identical but Functionally Different. <i>Journal of Bacteriology</i> , 2001, 183, 2405-2410.	2.2	119
63	Microbial community changes in the rhizospheres of white clover and perennial ryegrass exposed to Free Air Carbon dioxide Enrichment (FACE). <i>Soil Biology and Biochemistry</i> , 1996, 28, 1717-1724.	8.8	118
64	Peptide-mediated shape- and size-tunable synthesis of gold nanostructures. <i>Acta Biomaterialia</i> , 2010, 6, 2681-2689.	8.3	118
65	Applications of the rep-PCR DNA fingerprinting technique to study microbial diversity, ecology and evolution. <i>Environmental Microbiology</i> , 2009, 11, 733-740.	3.8	116
66	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.	8.0	112
67	Use of Barcoded Pyrosequencing and Shared OTUs To Determine Sources of Fecal Bacteria in Watersheds. <i>Environmental Science & Technology</i> , 2010, 44, 7777-7782.	10.0	108
68	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.	3.1	104
69	Metabolism of polyhalogenated compounds by a genetically engineered bacterium. <i>Nature</i> , 1994, 368, 627-629.	27.8	103
70	<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.	3.1	103
71	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.	3.1	102
72	Presence and Sources of Fecal Coliform Bacteria in Epilithic Periphyton Communities of Lake Superior. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3771-3778.	3.1	99

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73	Fate of Antibiotic Resistance Genes and Class 1 Integrons in Soil Microcosms Following the Application of Treated Residual Municipal Wastewater Solids. <i>Environmental Science & Technology</i> , 2014, 48, 5620-5627.	10.0	99
74	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. <i>Scientific Reports</i> , 2018, 8, 6219.	3.3	99
75	Influence of soil variables on in situ plasmid transfer from <i>Escherichia coli</i> to <i>Rhizobium fredii</i> . <i>Applied and Environmental Microbiology</i> , 1989, 55, 1730-1734.	3.1	99
76	Evolution of Catabolic Pathways: Genomic Insights into Microbial s -Triazine Metabolism. <i>Journal of Bacteriology</i> , 2007, 189, 674-682.	2.2	98
77	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.	11.1	98
78	Complete Microbiota Engraftment Is Not Essential for Recovery from Recurrent <i>Clostridium difficile</i> Infection following Fecal Microbiota Transplantation. <i>MBio</i> , 2016, 7, .	4.1	97
79	Current understanding of microbiota- and dietary-therapies for treating inflammatory bowel disease. <i>Journal of Microbiology</i> , 2018, 56, 189-198.	2.8	97
80	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.	2.2	95
81	<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.	3.1	95
82	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.	3.5	95
83	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.	2.2	93
84	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.	10.0	92
85	Faecal microbiota transplantation for <i>Clostridioides difficile</i> : mechanisms and pharmacology. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2021, 18, 67-80.	17.8	91
86	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.	7.1	88
87	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.	8.3	86
88	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.	3.5	81
89	Seasonal stability of <i>Cladophora</i> -associated <i>Salmonella</i> in Lake Michigan watersheds. <i>Water Research</i> , 2009, 43, 806-814.	11.3	80
90	Resolution of Severe <i>Clostridium difficile</i> Infection Following Sequential Fecal Microbiota Transplantation. <i>Journal of Clinical Gastroenterology</i> , 2013, 47, 735-737.	2.2	80

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91	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.	0.8	80
92	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.	3.1	79
93	Title is missing!. <i>Plant and Soil</i> , 2002, 243, 197-207.	3.7	78
94	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.	3.1	78
95	Methanogenesis Facilitated by Geobiochemical Iron Cycle in a Novel Syntrophic Methanogenic Microbial Community. <i>Environmental Science & Technology</i> , 2013, 47, 10078-10084.	10.0	78
96	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.	8.8	76
97	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
98	Therapeutic transplantation of the distal gut microbiota. <i>Mucosal Immunology</i> , 2011, 4, 4-7.	6.0	75
99	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018, 6, 166.	11.1	73
100	An Oligonucleotide Microarray Resource for Transcriptional Profiling of <i>Bradyrhizobium japonicum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1298-1307.	2.6	71
101	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <i>Frontiers in Microbiology</i> , 2014, 5, 524.	3.5	70
102	Biodegradation in Waters from Hydraulic Fracturing: Chemistry, Microbiology, and Engineering. <i>Journal of Environmental Engineering, ASCE</i> , 2014, 140, .	1.4	70
103	Two host-inducible genes of <i>Rhizobium fredii</i> and characterization of the inducing compound. <i>Journal of Bacteriology</i> , 1988, 170, 171-178.	2.2	69
104	Recent changes to the classification of symbiotic, nitrogen-fixing, legume-associating bacteria: a review. <i>Symbiosis</i> , 2017, 71, 91-109.	2.3	69
105	Population Genomics of the Facultatively Mutualistic Bacteria <i>Sinorhizobium meliloti</i> and <i>S. medicae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002868.	3.5	69
106	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.	3.1	68
107	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.	3.1	68
108	Endophytic Bacterial Communities Associated with Roots and Leaves of Plants Growing in Chilean Extreme Environments. <i>Scientific Reports</i> , 2019, 9, 4950.	3.3	68

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109	Elevated atmospheric CO ₂ alters microbial population structure in a pasture ecosystem. <i>Global Change Biology</i> , 2000, 6, 475-482.	9.5	67
110	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.	10.0	67
111	Solvent Extraction Characterization of Bioavailability of Atrazine Residues in Soils. <i>Journal of Agricultural and Food Chemistry</i> , 2004, 52, 6552-6556.	5.2	66
112	Aerobic digestion reduces the quantity of antibiotic resistance genes in residual municipal wastewater solids. <i>Frontiers in Microbiology</i> , 2013, 4, 17.	3.5	66
113	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.	4.3	66
114	Substrate Specificity of Atrazine Chlorohydrolase and Atrazine-Catabolizing Bacteria. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4247-4252.	3.1	65
115	Structure of bacterial communities in soil following cover crop and organic fertilizer incorporation. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9331-9341.	3.6	65
116	Allophanate Hydrolase, Not Urease, Functions in Bacterial Cyanuric Acid Metabolism. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4437-4445.	3.1	64
117	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.	1.6	64
118	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.	3.1	64
119	Comparison of genotypic-based microbial source tracking methods requiring a host origin database. <i>Journal of Water and Health</i> , 2003, 1, 167-180.	2.6	63
120	Influence of Soil Aging on Sorption and Bioavailability of Simazine. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 1373-1379.	5.2	63
121	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.	3.1	63
122	Competition of <i>Rhizobium japonicum</i> Strains in Early Stages of Soybean Nodulation. <i>Applied and Environmental Microbiology</i> , 1983, 46, 870-873.	3.1	63
123	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	11.1	62
124	Antimicrobial Peptides Targeting Gram-negative Pathogens, Produced and Delivered by Lactic Acid Bacteria. <i>ACS Synthetic Biology</i> , 2013, 2, 643-650.	3.8	60
125	Changes in human gut microbiota influenced by probiotic fermented milk ingestion. <i>Journal of Dairy Science</i> , 2015, 98, 3568-3576.	3.4	60
126	Application of SourceTracker for Accurate Identification of Fecal Pollution in Recreational Freshwater: A Double-Blinded Study. <i>Environmental Science & Technology</i> , 2018, 52, 4207-4217.	10.0	59

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127	Biogenic Formation of As-S Nanotubes by Diverse <i>Shewanella</i> Strains. Applied and Environmental Microbiology, 2009, 75, 6896-6899.	3.1	58
128	Factors Controlling Long-Term Survival and Growth of Naturalized Escherichia coli Populations in Temperate Field Soils. Microbes and Environments, 2010, 25, 8-14.	1.6	58
129	Biodegradation and Mineralization of Metolachlor and Alachlor by Candida xestobii. Journal of Agricultural and Food Chemistry, 2011, 59, 619-627.	5.2	58
130	Multi-laboratory evaluations of the performance of Catellicoccus marimammalium PCR assays developed to target gull fecal sources. Water Research, 2013, 47, 6883-6896.	11.3	58
131	Synergy between quantitative microbial source tracking (qMST) and quantitative microbial risk assessment (QMRA): A review and prospectus. Environment International, 2019, 130, 104703.	10.0	58
132	Durable Long-Term Bacterial Engraftment following Encapsulated Fecal Microbiota Transplantation To Treat Clostridium difficile Infection. MBio, 2019, 10, .	4.1	58
133	A pilot study of fecal bile acid and microbiota profiles in inflammatory bowel disease and primary sclerosing cholangitis. Clinical and Experimental Gastroenterology, 2019, Volume 12, 9-19.	2.3	58
134	Comprehensive Functional Analysis of the Enterococcus faecalis Core Genome Using an Ordered, Sequence-Defined Collection of Insertional Mutations in Strain OG1RF. MSystems, 2018, 3, .	3.8	57
135	Evaluation of the repeatability and reproducibility of a suite of qPCR-based microbial source tracking methods. Water Research, 2013, 47, 6839-6848.	11.3	56
136	Fecal pollution: new trends and challenges in microbial source tracking using next-generation sequencing. Environmental Microbiology, 2018, 20, 3132-3140.	3.8	56
137	Comparative decay of sewage-associated marker genes in beach water and sediment in a subtropical region. Water Research, 2019, 149, 511-521.	11.3	56
138	Plasmids pJP4 and r68.45 Can Be Transferred between Populations of Bradyrhizobia in Nonsterile Soil. Applied and Environmental Microbiology, 1993, 59, 1762-1766.	3.1	56
139	Large scale analysis of virulence genes in Escherichia coli strains isolated from Avalon Bay, CA. Water Research, 2010, 44, 5463-5473.	11.3	55
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