

Michael J Sadowsky

List of Publications by Year in descending order

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462
papers

27,138
citations

4960
84
h-index

10445
139
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476
all docs

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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.	3.1	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.	8.0	153
3	Erosion and deposition divergently affect the structure of soil bacterial communities and functionality. Catena, 2022, 209, 105805.	5.0	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.	2.6	7
5	Composition and Potential Functions of Rhizobacterial Communities in a Pioneer Plant from Andean Altiplano. Diversity, 2022, 14, 14.	1.7	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.	5.0	4
7	Halophytes increase rhizosphere microbial diversity, network complexity and function in inland saline ecosystem. Science of the Total Environment, 2022, 831, 154944.	8.0	28
8	Afforestation can lower microbial diversity and functionality in deep soil layers in a semiarid region. Global Change Biology, 2022, 28, 6086-6101.	9.5	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.	8.0	21
10	Influence of Environmental Stressors on the Microbiota of Zebra Mussels (<i>Dreissena polymorpha</i>). Microbial Ecology, 2021, 81, 1042-1053.	2.8	6
11	Influence of seasonality on the aerosol microbiome of the Amazon rainforest. Science of the Total Environment, 2021, 760, 144092.	8.0	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.	8.0	4
13	Composition and predicted functions of the bacterial community in spouting pool sediments from the El Tatio Geyser field in Chile. Archives of Microbiology, 2021, 203, 389-397.	2.2	3
14	Faecal microbiota transplantation for <i>Clostridioides difficile</i> : mechanisms and pharmacology. Nature Reviews Gastroenterology and Hepatology, 2021, 18, 67-80.	17.8	91
15	Structural modifications that increase gut restriction of bile acid derivatives. RSC Medicinal Chemistry, 2021, 12, 394-405.	3.9	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.	3.3	5
17	Microbial source tracking using metagenomics and other new technologies. Journal of Microbiology, 2021, 59, 259-269.	2.8	13
18	Erosion reduces soil microbial diversity, network complexity and multifunctionality. ISME Journal, 2021, 15, 2474-2489.	9.8	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. Symbiosis, 2021, 84, 39-47.	2.3	3
20	CRISPR loci-PCR as Tool for Tracking Azospirillum sp. Strain B510. Microorganisms, 2021, 9, 1351.	3.6	2
21	Impacts of cover crops and nitrogen fertilization on agricultural soil fungal and bacterial communities. Plant and Soil, 2021, 466, 139-150.	3.7	13
22	Rhizobacteria from “flowering desert” events contribute to the mitigation of water scarcity stress during tomato seedling germination and growth. Scientific Reports, 2021, 11, 13745.	3.3	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. Frontiers in Microbiology, 2021, 12, 674214.	3.5	16
24	Biodegradation of azo dyes by bacterial or fungal consortium and identification of the biodegradation products. Egyptian Journal of Aquatic Research, 2021, 47, 269-276.	2.2	29
25	Gut Microbiota Associated With Different Sea Lamprey (Petromyzon marinus) Life Stages. Frontiers in Microbiology, 2021, 12, 706683.	3.5	3
26	Engineering Multigenerational Host-Modulated Microbiota against Soilborne Pathogens in Response to Global Climate Change. Biology, 2021, 10, 865.	2.8	9
27	Temperature alters dicyandiamide (DCD) efficacy for multiple reactive nitrogen species in urea-amended soils: Experiments and modeling. Soil Biology and Biochemistry, 2021, 160, 108341.	8.8	9
28	A hybrid DNA sequencing approach is needed to properly link genotype to phenotype in multi-drug resistant bacteria. Environmental Pollution, 2021, 289, 117856.	7.5	1
29	Inoculation of <i>Mimosa Pudica</i> with <i>Paraburkholderia phymatum</i> Results in Changes to the Rhizoplane Microbial Community Structure. Microbes and Environments, 2021, 36, n/a.	1.6	5
30	Probable role of Cutibacterium acnes in the gut of the polychaete Capitella teleta. Science of the Total Environment, 2021, 809, 151127.	8.0	2
31	Inactivation of Clostridioides Difficile Spores in Carpeting and Upholstery to Reduce Disease Recurrence in Households and Nursing Care Facilities. Journal of Public Health Issues and Practices, 2021, 5, .	0.2	0
32	Source-Associated Gastroenteritis Risk from Swimming Exposure to Aging Fecal Pathogens. Environmental Science & Technology, 2020, 54, 921-929.	10.0	13
33	Water and sediment act as reservoirs for microbial taxa associated with invasive dreissenid mussels. Science of the Total Environment, 2020, 703, 134915.	8.0	8
34	The ASM Journals Committee Values the Contributions of Black Microbiologists. Infection and Immunity, 2020, 88, .	2.2	0
35	Convenient Protocol for Production and Purification of Clostridioides difficile Spores for Germination Studies. STAR Protocols, 2020, 1, 100071.	1.2	3
36	Sequence-enabled community-based microbial source tracking in surface waters using machine learning classification: A review. Journal of Microbiological Methods, 2020, 177, 106050.	1.6	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.	3.3	9
39	Methanogen Abundance Thresholds Capable of Differentiating In Vitro Methane Production in Human Stool Samples. Digestive Diseases and Sciences, 2020, 66, 3822-3830.	2.3	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.	3.7	40
41	The ASM Journals Committee Values the Contributions of Black Microbiologists. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	0
42	The ASM Journals Committee Values the Contributions of Black Microbiologists. Journal of Virology, 2020, 94, .	3.4	0
43	The ASM Journals Committee Values the Contributions of Black Microbiologists. Journal of Bacteriology, 2020, 202, .	2.2	0
44	The ASM Journals Committee Values the Contributions of Black Microbiologists. Microbiology and Molecular Biology Reviews, 2020, 84, .	6.6	0
45	The ASM Journals Committee Values the Contributions of Black Microbiologists. MSystems, 2020, 5, .	3.8	0
46	The ASM Journals Committee Values the Contributions of Black Microbiologists. Microbiology Resource Announcements, 2020, 9, .	0.6	0
47	The ASM Journals Committee Values the Contributions of Black Microbiologists. MBio, 2020, 11, .	4.1	3
48	The ASM Journals Committee Values the Contributions of Black Microbiologists. Journal of Clinical Microbiology, 2020, 58, .	3.9	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.	3.5	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.	6.0	32
51	Environmental and Adaptive Changes Necessitate a Paradigm Shift for Indicators of Fecal Contamination. Microbiology Spectrum, 2020, 8, .	3.0	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.	8.0	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.	3.5	22
54	Impact of Atrazine Exposure on the Microbial Community Structure in a Brazilian Tropical Latosol Soil. Microbes and Environments, 2020, 35, n/a.	1.6	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.	1.6	15
56	Structuring biofilm communities living in pesticide contaminated water. <i>Heliyon</i> , 2020, 6, e03996.	3.2	12
57	Herbicide bioremediation: from strains to bacterial communities. <i>Heliyon</i> , 2020, 6, e05767.	3.2	43
58	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	1
59	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>MSphere</i> , 2020, 5, .	2.9	1
60	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>Molecular and Cellular Biology</i> , 2020, 40, .	2.3	0
61	The ASM Journals Committee Values the Contributions of Black Microbiologists. <i>Clinical Microbiology Reviews</i> , 2020, 33, .	13.6	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.	10.0	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.	11.3	53
65	Durable Long-Term Bacterial Engraftment following Encapsulated Fecal Microbiota Transplantation To Treat <i>Clostridium difficile</i> Infection. <i>MBio</i> , 2019, 10, .	4.1	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.	6.4	18
67	Microbiota transplant therapy and autism: lessons for the clinic. <i>Expert Review of Gastroenterology and Hepatology</i> , 2019, 13, 1033-1037.	3.0	24
68	An Alkane Sulfonate Monooxygenase Is Required for Symbiotic Nitrogen Fixation by <i>Bradyrhizobium diazoefficiens</i> (syn. <i>Bradyrhizobium japonicum</i>) USDA110 ^T . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	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.	11.3	12
70	Letter to the Editor. <i>Clinical Infectious Diseases</i> , 2019, 69, 2232-2233.	5.8	1
71	Editorial: Alternative Therapeutic Approaches For Multidrug Resistant <i>Clostridium difficile</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1216.	3.5	0
72	Dietary Factors in Sulfur Metabolism and Pathogenesis of Ulcerative Colitis. <i>Nutrients</i> , 2019, 11, 931.	4.1	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.	3.3	68
74	Breastmilk and NICU surfaces are potential sources of fungi for infant mycobiomes. <i>Fungal Genetics and Biology</i> , 2019, 128, 29-35.	2.1	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.	2.8	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.	2.3	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.	9.8	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.	8.0	16
79	A microfluidic platform for the simultaneous quantification of methanogen populations in anaerobic digestion processes. <i>Environmental Microbiology</i> , 2019, 21, 1798-1808.	3.8	11
80	Signal Disruption Leads to Changes in Bacterial Community Population. <i>Frontiers in Microbiology</i> , 2019, 10, 611.	3.5	24
81	Denitrifying Bacteria Active in Woodchip Bioreactors at Low-Temperature Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 635.	3.5	33
82	Intermittent flooding of organic-rich soil promotes the formation of denitrification hot moments and hot spots. <i>Ecosphere</i> , 2019, 10, e02549.	2.2	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.	2.3	58
84	Influence of Library Composition on SourceTracker Predictions for Community-Based Microbial Source Tracking. <i>Environmental Science & Technology</i> , 2019, 53, 60-68.	10.0	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.	4.3	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.	11.3	56
87	Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1973-1987.	3.6	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.	8.0	21
89	Antibiotic-induced Disruption of Intestinal Microbiota Contributes to Failure of Vertical Sleeve Gastrectomy. <i>Annals of Surgery</i> , 2019, 269, 1092-1100.	4.2	29
90	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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91	Current understanding of microbiota- and dietary-therapies for treating inflammatory bowel disease. <i>Journal of Microbiology</i> , 2018, 56, 189-198.	2.8	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.	0.5	12
93	Fecal microbiota transplantation reverses antibiotic and chemotherapy-induced gut dysbiosis in mice. <i>Scientific Reports</i> , 2018, 8, 6219.	3.3	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.	3.0	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.	8.0	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.	7.1	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.	11.0	292
98	Widespread occurrence of <i>Sinorhizobium meliloti</i> strains with a type IV secretion system. <i>Symbiosis</i> , 2018, 75, 81-91.	2.3	6
99	Genome-Wide Association Analyses in the Model <i>Rhizobium</i> <i>Ensifer meliloti</i> . <i>MSphere</i> , 2018, 3, .	2.9	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.	1.6	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, .	3.8	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.	3.5	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.	2.4	7
105	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018, 6, 166.	11.1	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, .	2.7	6
107	Fecal pollution: new trends and challenges in microbial source tracking using next-generation sequencing. <i>Environmental Microbiology</i> , 2018, 20, 3132-3140.	3.8	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.	10.0	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.	10.0	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.	2.5	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.	3.5	37
112	CLOUD: a non-parametric detection test for microbiome outliers. <i>Microbiome</i> , 2018, 6, 137.	11.1	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.	3.6	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, .	2.0	21
115	Sleeve gastrectomy drives persistent shifts in the gut microbiome. <i>Surgery for Obesity and Related Diseases</i> , 2017, 13, 916-924.	1.2	43
116	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
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.	9.8	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.	6.0	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.	0.4	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.	6.4	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.	8.8	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.	1.3	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.	4.2	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, .	3.1	32
126	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

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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, .	3.1	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.	3.0	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.	2.6	22
130	Analysis of gut microbiota – An ever changing landscape. <i>Gut Microbes</i> , 2017, 8, 268-275.	9.8	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, .	3.1	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.	3.8	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.	0.1	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.	4.2	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.	8.0	29
136	Transcriptomic basis of genome by genome variation in a legume-rhizobia mutualism. <i>Molecular Ecology</i> , 2017, 26, 6122-6135.	3.9	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.	2.3	14
138	Contemporary Applications of Fecal Microbiota Transplantation to Treat Intestinal Diseases in Humans. <i>Archives of Medical Research</i> , 2017, 48, 766-773.	3.3	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 & Technology</i> , 2017, 51, 14225-14232.	10.0	53
140	A High-Throughput DNA-Sequencing Approach for Determining Sources of Fecal Bacteria in a Lake Superior Estuary. <i>Environmental Science & Technology</i> , 2017, 51, 8263-8271.	10.0	54
141	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	11.1	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.	8.0	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.	8.0	46
144	Recent changes to the classification of symbiotic, nitrogen-fixing, legume-associating bacteria: a review. <i>Symbiosis</i> , 2017, 71, 91-109.	2.3	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.	3.6	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.	2.8	54
147	Genes and Gut Bacteria Involved in Luminal Butyrate Reduction Caused by Diet and Loperamide. <i>Genes</i> , 2017, 8, 350.	2.4	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.	2.6	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.	3.5	22
150	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	11.1	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.	2.5	130
152	Bacterial biogeography influenced by shelf-basin exchange in the Arctic surface sediment at the C&B&orderland. <i>Environmental Microbiology</i> , 2016, 18, 668-678.	3.8	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, .	4.1	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.	0.8	30
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