

Christopher Staley

List of Publications by Year in descending order

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Version: 2024-02-01

145
papers

6,347
citations

76326

40
h-index

79698

73
g-index

149
all docs

149
docs citations

149
times ranked

8513
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>In vitro</i> efficacy of a non-instrumentation technique to remove intracanal multispecies biofilm. International Endodontic Journal, 2022, 55, 495-504.	5.0	9
2	Lasting shift in the gut microbiota in patients with acute myeloid leukemia. Blood Advances, 2022, 6, 3451-3457.	5.2	10
3	Encapsulated Fecal Microbiota Transplantation: Development, Efficacy, and Clinical Application. Frontiers in Cellular and Infection Microbiology, 2022, 12, 826114.	3.9	21
4	Network-based approaches for the investigation of microbial community structure and function using metagenomics-based data. Future Microbiology, 2022, 17, 621-631.	2.0	2
5	<i>In vitro</i> physicochemical characterization of five root canal sealers and their influence on an <i>ex vivo</i> oral multi-species biofilm community. International Endodontic Journal, 2022, 55, 772-783.	5.0	8
6	Protective Effect of Intestinal <i>Blautia</i> Against Neutropenic Fever in Allogeneic Transplant Recipients. Clinical Infectious Diseases, 2022, 75, 1912-1920.	5.8	5
7	Loss of microbiota-derived protective metabolites after neutropenic fever. Scientific Reports, 2022, 12, 6244.	3.3	4
8	Reduced Enterohepatic Recirculation of Mycophenolate and Lower Blood Concentrations Are Associated with the Stool Bacterial Microbiome after Hematopoietic Cell Transplantation. Transplantation and Cellular Therapy, 2022, 28, 372.e1-372.e9.	1.2	12
9	A pilot study demonstrating the impact of surgical bowel preparation on intestinal microbiota composition following colon and rectal surgery. Scientific Reports, 2022, 12, .	3.3	14
10	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
11	Faecal microbiota transplantation for <i>Clostridioides difficile</i> : mechanisms and pharmacology. Nature Reviews Gastroenterology and Hepatology, 2021, 18, 67-80.	17.8	91
12	Effect of COVID-19 precautions on the gut microbiota and nosocomial infections. Gut Microbes, 2021, 13, 1-10.	9.8	10
13	Antibiotic Conditioning and Single Gavage Allows Stable Engraftment of Human Microbiota in Mice. Methods in Molecular Biology, 2021, 2327, 281-291.	0.9	1
14	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
15	Donor Microbiota Composition and Housing Affect Recapitulation of Obese Phenotypes in a Human Microbiota-Associated Murine Model. Frontiers in Cellular and Infection Microbiology, 2021, 11, 614218.	3.9	5
16	75200 Fecal Microbiota Transplantation to Prevent Infections in Patients with Acute Myeloid Leukemia: A Double-Blind Randomized Placebo-Controlled Phase 2 Clinical Trial. Journal of Clinical and Translational Science, 2021, 5, 36-36.	0.6	0
17	Microbiota-Driven Activation of Intrahepatic B Cells Aggravates NASH Through Innate and Adaptive Signaling. Hepatology, 2021, 74, 704-722.	7.3	95
18	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

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19	Altered microbiota-host metabolic cross talk preceding neutropenic fever in patients with acute leukemia. <i>Blood Advances</i> , 2021, 5, 3937-3950.	5.2	12
20	Role of biliary stent and neoadjuvant chemotherapy in the pancreatic tumor microbiome. <i>BMC Microbiology</i> , 2021, 21, 280.	3.3	10
21	No evidence for colonization of oral bacteria in the distal gut in healthy adults. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	26
22	Gut microbiota response to antibiotics is personalized and depends on baseline microbiota. <i>Microbiome</i> , 2021, 9, 211.	11.1	32
23	Circulating Metabolomics Suggest Neutropenic Fever As a Metabolic Derangement Related to Intestinal Tissue Damage and Gut Dysbiosis. <i>Blood</i> , 2021, 138, 688-688.	1.4	0
24	A nonhuman primate model of vertical sleeve gastrectomy facilitates mechanistic and translational research in human obesity. <i>IScience</i> , 2021, 24, 103421.	4.1	2
25	Depot Medroxyprogesterone Acetate and the Vaginal Microbiome as Modifiers of Tenofovir Diphosphate and Lamivudine Triphosphate Concentrations in the Female Genital Tract of Ugandan Women: Implications for Tenofovir Disoproxil Fumarate/Lamivudine in Preexposure Prophylaxis. <i>Clinical Infectious Diseases</i> , 2020, 70, 1717-1724.	5.8	10
26	Specific gut microbiota changes heralding bloodstream infection and neutropenic fever during intensive chemotherapy. <i>Leukemia</i> , 2020, 34, 312-316.	7.2	30
27	Gut dysbiosis during antileukemia chemotherapy versus allogeneic hematopoietic cell transplantation. <i>Cancer</i> , 2020, 126, 1434-1447.	4.1	30
28	Levaquin Gets a Pass. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, 778-781.	2.0	11
29	Sampling, analyzing, and integrating microbiome omics data in a translational clinical setting. , 2020, , 273-279.		0
30	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.	1.6	29
31	Peri-operative antibiotics acutely and significantly impact intestinal microbiota following bariatric surgery. <i>Scientific Reports</i> , 2020, 10, 20340.	3.3	9
32	Randomised clinical study: oral aspirin 325Âmg daily vs placebo alters gut microbial composition and bacterial taxa associated with colorectal cancer risk. <i>Alimentary Pharmacology and Therapeutics</i> , 2020, 52, 976-987.	3.7	40
33	Circulating bacterial DNA and neutropenic fever during anti-leukaemia chemotherapy. <i>British Journal of Haematology</i> , 2020, 191, e55-e58.	2.5	0
34	Characterizing the Gut Microbiome in Patients with Chronic Pancreatitis before and after Total Pancreatectomy with Islet Autotransplantation. <i>Journal of the American College of Surgeons</i> , 2020, 231, S155.	0.5	0
35	Laparoscopic Vertical Sleeve Gastrectomy in Nonhuman Primates Shifts the Microbiome and Drives Changes in Microbial Metabolites. <i>Journal of the American College of Surgeons</i> , 2020, 231, S24-S25.	0.5	1
36	Effect of Colorectal Operations on the Colonic Microbiome. <i>Journal of the American College of Surgeons</i> , 2020, 231, S53.	0.5	0

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37	Intestinal organoids: a model to study the role of microbiota in the colonic tumor microenvironment. <i>Future Microbiology</i> , 2020, 15, 1583-1594.	2.0	6
38	Mucosal Microbiota and Metabolome along the Intestinal Tract Reveal a Location-Specific Relationship. <i>MSystems</i> , 2020, 5, .	3.8	25
39	An alpha-defensin gene single nucleotide polymorphism modulates the gut microbiota and may alter the risk of acute graft-versus-host disease. <i>British Journal of Haematology</i> , 2020, 189, 926-930.	2.5	4
40	Microbiome swings with repeated insults. <i>British Journal of Haematology</i> , 2020, 189, e94-e96.	2.5	3
41	An Alpha-Defensin Gene Single Nucleotide Polymorphism Modulates the Gut Microbiota and May Alter the Risk of Acute Graft-Versus-Host Disease. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, S28-S29.	2.0	0
42	Impact of Atrazine Exposure on the Microbial Community Structure in a Brazilian Tropical Latosol Soil. <i>Microbes and Environments</i> , 2020, 35, n/a.	1.6	21
43	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
44	Structuring biofilm communities living in pesticide contaminated water. <i>Heliyon</i> , 2020, 6, e03996.	3.2	12
45	Abstract 6097: Alterations of the pancreatic tumor microbiome: the role of biliary stents. , 2020, , .		0
46	Release of plant nutrients and changes in the copies of N-cycling genes in response to soil amendment with rice straw and waste from a food seasoning industry. <i>Agriculture and Natural Resources</i> , 2020, 54, .	0.1	0
47	Microbial Exposure Enhances Immunity to Pathogens Recognized by TLR2 but Increases Susceptibility to Cytokine Storm through TLR4 Sensitization. <i>Cell Reports</i> , 2019, 28, 1729-1743.e5.	6.4	74
48	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
49	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
50	Vancomycin-resistance gene cluster, vanC, in the gut microbiome of acute leukemia patients undergoing intensive chemotherapy. <i>PLoS ONE</i> , 2019, 14, e0223890.	2.5	8
51	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
52	Dysbiosis patterns during re-induction/salvage versus induction chemotherapy for acute leukemia. <i>Scientific Reports</i> , 2019, 9, 6083.	3.3	32
53	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
54	Signal Disruption Leads to Changes in Bacterial Community Population. <i>Frontiers in Microbiology</i> , 2019, 10, 611.	3.5	24

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55	Outpatient-to-Inpatient Transition Causes Marked Dysbiosis in Allogeneic Hematopoietic Cell Transplantation Recipients. <i>Biology of Blood and Marrow Transplantation</i> , 2019, 25, S47.	2.0	1
56	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
57	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
58	Gut Dysbiosis Increases Gut Barrier Damage during Anti-Leukemia Chemotherapy: Implications for Acute Graft-Versus-Host Disease. <i>Biology of Blood and Marrow Transplantation</i> , 2019, 25, S142-S143.	2.0	0
59	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
60	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
61	Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1973-1987.	3.6	16
62	Pre-transplant recovery of microbiome diversity without recovery of the original microbiome. <i>Bone Marrow Transplantation</i> , 2019, 54, 1115-1117.	2.4	13
63	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
64	Abstract 5060: Effect of aspirin on gut microbiome in a pilot randomized double-blind trial. , 2019, , .		1
65	Pre-Transplant Serum Claudin-3 Predicts Intestinal Graft-Versus-Host Disease and Non-Relapse Mortality Risk after Allogeneic Hematopoietic Cell Transplantation. <i>Blood</i> , 2019, 134, 39-39.	1.4	0
66	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
67	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
68	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
69	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
70	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
71	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
72	Clinician Guide to Microbiome Testing. <i>Digestive Diseases and Sciences</i> , 2018, 63, 3167-3177.	2.3	22

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73	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
74	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018, 6, 166.	11.1	73
75	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
76	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
77	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
78	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
79	Sleeve gastrectomy drives persistent shifts in the gut microbiome. <i>Surgery for Obesity and Related Diseases</i> , 2017, 13, 916-924.	1.2	43
80	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
81	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
82	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
83	Next-generation sequencing and culture-based techniques offer complementary insights into fungi and prokaryotes in beach sands. <i>Marine Pollution Bulletin</i> , 2017, 119, 351-358.	5.0	18
84	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
85	Successful Resolution of Recurrent <i>Clostridium Difficile</i> Infection using Freeze-Dried, Encapsulated Fecal Microbiota. <i>Gastroenterology</i> , 2017, 152, S343-S344.	1.3	2
86	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
87	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
88	Analysis of gut microbiota – An ever changing landscape. <i>Gut Microbes</i> , 2017, 8, 268-275.	9.8	25
89	Postoperative Disruption of Intestinal Microbiota Composition Attenuates the Metabolic Efficacy of Vertical Sleeve Gastrectomy. <i>Journal of the American College of Surgeons</i> , 2017, 225, S17.	0.5	0
90	Influence of heavy metals on rhizosphere microbial communities of Siam weed (<i>Chromolaena odorata</i>) Tj ETQq0 0 0 rgBT /Overlock 10 137-141.	0.1	8

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91	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
92	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
93	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
94	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
95	Peculiar citric acid cycle of hydrothermal vent chemolithoautotroph <i>Hydrogenovibrio crunogenus</i> , and insights into carbon metabolism by obligate autotrophs. <i>FEMS Microbiology Letters</i> , 2017, 364, .	1.8	8
96	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	11.1	62
97	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
98	Amplicon-based profiling of bacteria in raw and secondary treated wastewater from treatment plants across Australia. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1253-1266.	3.6	34
99	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
100	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
101	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
102	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
103	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	11.1	138
104	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
105	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
106	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
107	Mo1290 Treatment of Urinary Tract Infections Without Affecting the Gut Microbiota in Patients With Recurrent <i>Clostridium difficile</i> Infection. <i>Gastroenterology</i> , 2016, 150, S689.	1.3	0
108	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

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109	Mo1966 The Gut Microbiome Shifts Acutely and Independently From Hypocaloric Restriction Following the Vertical Sleeve Gastrectomy. <i>Gastroenterology</i> , 2016, 150, S1246.	1.3	0
110	Correlations between pathogen concentration and fecal indicator marker genes in beach environments. <i>Science of the Total Environment</i> , 2016, 573, 826-830.	8.0	41
111	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
112	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
113	Environment shapes the fecal microbiome of invasive carp species. <i>Microbiome</i> , 2016, 4, 44.	11.1	166
114	Preoperative Antibiotics Drive Short-Term Changes in the Gut Microbiome after Vertical Sleeve Gastrectomy. <i>Journal of the American College of Surgeons</i> , 2016, 223, S17.	0.5	0
115	Su1743 Characterization of Fecal Microbiota in Response to Heterologous Versus Autologous (Placebo) Fecal Microbial Transplantation: Results From a Dual-Center, Randomized, Placebo-Controlled Trial. <i>Gastroenterology</i> , 2016, 150, S542.	1.3	0
116	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
117	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.	2.8	29
118	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.	3.1	42
119	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.	2.6	20
120	A Novel Microbial Source Tracking Microarray for Pathogen Detection and Fecal Source Identification in Environmental Systems. <i>Environmental Science & Technology</i> , 2015, 49, 7319-7329.	10.0	36
121	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.	8.0	19
122	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.	3.1	16
123	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
124	Evaluation of water sampling methodologies for amplicon-based characterization of bacterial community structure. <i>Journal of Microbiological Methods</i> , 2015, 114, 43-50.	1.6	42
125	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.	8.0	16
126	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.	3.8	3

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127	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
128	Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. <i>PLoS ONE</i> , 2015, 10, e0116705.	2.5	45
129	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
130	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <i>Frontiers in Microbiology</i> , 2014, 5, 524.	3.5	70
131	Microbial source tracking markers for detection of fecal contamination in environmental waters: relationships between pathogens and human health outcomes. <i>FEMS Microbiology Reviews</i> , 2014, 38, 1-40.	8.6	496
132	Differential Expression of a Sodium-Phosphate Cotransporter Among <i>Vibrio vulnificus</i> Strains. <i>Microbial Ecology</i> , 2014, 67, 24-33.	2.8	5
133	Environmental and Animal-Associated Enterococci. <i>Advances in Applied Microbiology</i> , 2014, 87, 147-186.	2.4	45
134	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
135	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
136	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
137	Detection and differentiation of <i>Vibrio vulnificus</i> and <i>V. vulnificus</i> in water and oysters of a Gulf of Mexico estuary. <i>Environmental Microbiology</i> , 2013, 15, 623-633.	3.8	20
138	Performance of Two Quantitative PCR Methods for Microbial Source Tracking of Human Sewage and Implications for Microbial Risk Assessment in Recreational Waters. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7317-7326.	3.1	128
139	Assessment of sources of human pathogens and fecal contamination in a Florida freshwater lake. <i>Water Research</i> , 2012, 46, 5799-5812.	11.3	66
140	Microbial source tracking to identify human and ruminant sources of faecal pollution in an ephemeral Florida river. <i>Journal of Applied Microbiology</i> , 2012, 113, 1396-1406.	3.1	40
141	Interlaboratory Comparison of Real-Time PCR Protocols for Quantification of General Fecal Indicator Bacteria. <i>Environmental Science & Technology</i> , 2012, 46, 945-953.	10.0	72
142	Genetic and quantitative assessment of <i>Vibrio vulnificus</i> populations in oyster (<i>Crassostrea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.4	7
143	The Use of Genetic Typing Methods to Discriminate Among Strains of <i>Vibrio cholerae</i> , <i>V. parahaemolyticus</i> , and <i>V. vulnificus</i> . <i>Journal of AOAC INTERNATIONAL</i> , 2010, 93, 1553-1569.	1.5	9
144	The use of genetic typing methods to discriminate among strains of <i>Vibrio cholerae</i> , <i>V. parahaemolyticus</i> , and <i>V. vulnificus</i> . <i>Journal of AOAC INTERNATIONAL</i> , 2010, 93, 1553-69.	1.5	4

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145	Real-Time PCR Assays for Quantification and Differentiation of <i>Vibrio vulnificus</i> Strains in Oysters and Water. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1704-1709.	3.1	53