

# Christopher Staley

## List of Publications by Year in descending order

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Version: 2024-02-01

144  
papers

6,347  
citations

76196

40  
h-index

79541

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 nonâ€instrumentation technique to remove intracanal multispecies biofilm. International Endodontic Journal, 2022, 55, 495-504.	2.3	9
2	Lasting shift in the gut microbiota in patients with acute myeloid leukemia. Blood Advances, 2022, 6, 3451-3457.	2.5	10
3	Encapsulated Fecal Microbiota Transplantation: Development, Efficacy, and Clinical Application. Frontiers in Cellular and Infection Microbiology, 2022, 12, 826114.	1.8	21
4	Network-based approaches for the investigation of microbial community structure and function using metagenomics-based data. Future Microbiology, 2022, 17, 621-631.	1.0	2
5	<i>In vitro</i> physicochemical characterization of five root canal sealers and their influence on an <i>ex vivo</i> oral multiâ€species biofilm community. International Endodontic Journal, 2022, 55, 772-783.	2.3	8
6	Protective Effect of Intestinal <i>Blautia</i> Against Neutropenic Fever in Allogeneic Transplant Recipients. Clinical Infectious Diseases, 2022, 75, 1912-1920.	2.9	5
7	Loss of microbiota-derived protective metabolites after neutropenic fever. Scientific Reports, 2022, 12, 6244.	1.6	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.	0.6	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, .	1.6	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.	3.9	21
11	Faecal microbiota transplantation for Clostridioides difficile: mechanisms and pharmacology. Nature Reviews Gastroenterology and Hepatology, 2021, 18, 67-80.	8.2	91
12	Effect of COVID-19 precautions on the gut microbiota and nosocomial infections. Gut Microbes, 2021, 13, 1-10.	4.3	10
13	Antibiotic Conditioning and Single Gavage Allows Stable Engraftment of Human Microbiota in Mice. Methods in Molecular Biology, 2021, 2327, 281-291.	0.4	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.	1.6	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.	1.8	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.	0.3	0
17	Microbiotaâ€Driven Activation of Intrahepatic B Cells Aggravates NASH Through Innate and Adaptive Signaling. Hepatology, 2021, 74, 704-722.	3.6	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.	1.5	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.	2.5	12
20	Role of biliary stent and neoadjuvant chemotherapy in the pancreatic tumor microbiome. <i>BMC Microbiology</i> , 2021, 21, 280.	1.3	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, .	3.3	26
22	Gut microbiota response to antibiotics is personalized and depends on baseline microbiota. <i>Microbiome</i> , 2021, 9, 211.	4.9	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.	0.6	0
24	A nonhuman primate model of vertical sleeve gastrectomy facilitates mechanistic and translational research in human obesity. <i>IScience</i> , 2021, 24, 103421.	1.9	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.	2.9	10
26	Specific gut microbiota changes heralding bloodstream infection and neutropenic fever during intensive chemotherapy. <i>Leukemia</i> , 2020, 34, 312-316.	3.3	30
27	Gut dysbiosis during antileukemia chemotherapy versus allogeneic hematopoietic cell transplantation. <i>Cancer</i> , 2020, 126, 1434-1447.	2.0	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.	0.7	29
31	Peri-operative antibiotics acutely and significantly impact intestinal microbiota following bariatric surgery. <i>Scientific Reports</i> , 2020, 10, 20340.	1.6	9
32	Randomised clinical study: oral aspirin 325mg 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.	1.9	40
33	Circulating bacterial DNA and neutropenic fever during anti-leukaemia chemotherapy. <i>British Journal of Haematology</i> , 2020, 191, e55-e58.	1.2	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.	0.2	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.	0.2	1
36	Effect of Colorectal Operations on the Colonic Microbiome. <i>Journal of the American College of Surgeons</i> , 2020, 231, S53.	0.2	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.	1.0	6
38	Mucosal Microbiota and Metabolome along the Intestinal Tract Reveal a Location-Specific Relationship. <i>MSystems</i> , 2020, 5, .	1.7	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.	1.2	4
40	Microbiome swings with repeated insults. <i>British Journal of Haematology</i> , 2020, 189, e94-e96.	1.2	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.	0.7	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.	0.7	15
44	Structuring biofilm communities living in pesticide contaminated water. <i>Heliyon</i> , 2020, 6, e03996.	1.4	12
45	Abstract 6097: Alterations of the pancreatic tumor microbiome: the role of biliary stents. , 2020, , .		0
46	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.	2.9	74
47	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
48	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
49	Vancomycin-resistance gene cluster, vanC, in the gut microbiome of acute leukemia patients undergoing intensive chemotherapy. <i>PLoS ONE</i> , 2019, 14, e0223890.	1.1	8
50	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
51	Dysbiosis patterns during re-induction/salvage versus induction chemotherapy for acute leukemia. <i>Scientific Reports</i> , 2019, 9, 6083.	1.6	32
52	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
53	Signal Disruption Leads to Changes in Bacterial Community Population. <i>Frontiers in Microbiology</i> , 2019, 10, 611.	1.5	24
54	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

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55	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
56	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
57	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
58	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
59	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
60	Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1973-1987.	1.7	16
61	Pre-transplant recovery of microbiome diversity without recovery of the original microbiome. <i>Bone Marrow Transplantation</i> , 2019, 54, 1115-1117.	1.3	13
62	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
63	Abstract 5060: Effect of aspirin on gut microbiome in a pilot randomized double-blind trial. , 2019, , .		1
64	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.	0.6	0
65	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
66	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
67	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
68	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
69	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
70	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
71	Clinician Guide to Microbiome Testing. <i>Digestive Diseases and Sciences</i> , 2018, 63, 3167-3177.	1.1	22
72	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

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73	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018, 6, 166.	4.9	73
74	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
75	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
76	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
77	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
78	Sleeve gastrectomy drives persistent shifts in the gut microbiome. <i>Surgery for Obesity and Related Diseases</i> , 2017, 13, 916-924.	1.0	43
79	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
80	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
81	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
82	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.	2.3	18
83	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
84	Successful Resolution of Recurrent <i>Clostridium Difficile</i> Infection using Freeze-Dried, Encapsulated Fecal Microbiota. <i>Gastroenterology</i> , 2017, 152, S343-S344.	0.6	2
85	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
86	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
87	Analysis of gut microbiota – An ever changing landscape. <i>Gut Microbes</i> , 2017, 8, 268-275.	4.3	25
88	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.	0.2	0
89	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
90	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

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91	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
92	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
93	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
94	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, .	0.7	8
95	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	4.9	62
96	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
97	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.	1.7	34
98	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
99	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
100	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
101	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
102	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	4.9	138
103	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
104	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
105	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
106	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.	0.6	0
107	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
108	Mo1966 The Gut Microbiome Shifts Acutely and Independently From Hypocaloric Restriction Following the Vertical Sleeve Gastrectomy. <i>Gastroenterology</i> , 2016, 150, S1246.	0.6	0



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109	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
110	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
111	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
112	Environment shapes the fecal microbiome of invasive carp species. <i>Microbiome</i> , 2016, 4, 44.	4.9	166
113	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.	0.2	0
114	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.	0.6	0
115	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
116	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
117	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
118	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
119	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
120	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
121	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
122	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
123	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
124	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
125	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
126	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



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127	Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. PLoS ONE, 2015, 10, e0116705.	1.1	45
128	Core functional traits of bacterial communities in the Upper Mississippi River show limited variation in response to land cover. Frontiers in Microbiology, 2014, 5, 414.	1.5	95
129	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. Frontiers in Microbiology, 2014, 5, 524.	1.5	70
130	Microbial source tracking markers for detection of fecal contamination in environmental waters: relationships between pathogens and human health outcomes. FEMS Microbiology Reviews, 2014, 38, 1-40.	3.9	496
131	Differential Expression of a Sodium-Phosphate Cotransporter Among Vibrio vulnificus Strains. Microbial Ecology, 2014, 67, 24-33.	1.4	5
132	Environmental and Animal-Associated Enterococci. Advances in Applied Microbiology, 2014, 87, 147-186.	1.3	45
133	Microbes in beach sands: integrating environment, ecology and public health. Reviews in Environmental Science and Biotechnology, 2014, 13, 329-368.	3.9	127
134	Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. Journal of Applied Microbiology, 2013, 115, 1147-1158.	1.4	209
135	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. Journal of Experimental Medicine, 2013, 210, 2011-2024.	4.2	144
136	Detection and differentiation of <i>Vibrio vulnificus</i> and <i>V. vulnificus</i> in water and oysters of a Gulf of Mexico estuary. Environmental Microbiology, 2013, 15, 623-633.	1.8	20
137	Performance of Two Quantitative PCR Methods for Microbial Source Tracking of Human Sewage and Implications for Microbial Risk Assessment in Recreational Waters. Applied and Environmental Microbiology, 2012, 78, 7317-7326.	1.4	128
138	Assessment of sources of human pathogens and fecal contamination in a Florida freshwater lake. Water Research, 2012, 46, 5799-5812.	5.3	66
139	Microbial source tracking to identify human and ruminant sources of faecal pollution in an ephemeral Florida river. Journal of Applied Microbiology, 2012, 113, 1396-1406.	1.4	40
140	Interlaboratory Comparison of Real-Time PCR Protocols for Quantification of General Fecal Indicator Bacteria. Environmental Science & Technology, 2012, 46, 945-953.	4.6	72
141	Genetic and quantitative assessment of <i>Vibrio vulnificus</i> populations in oyster ( <i>Crassostrea</i> ) Tj ETQq1 1 0.784314 rgBT /Ov	1.0	1
142	The Use of Genetic Typing Methods to Discriminate Among Strains of <i>Vibrio cholerae</i> , <i>V. parahaemolyticus</i> , and <i>V. vulnificus</i> . Journal of AOAC INTERNATIONAL, 2010, 93, 1553-1569.	0.7	9
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> . Journal of AOAC INTERNATIONAL, 2010, 93, 1553-69.	0.7	4
144	Real-Time PCR Assays for Quantification and Differentiation of <i>Vibrio vulnificus</i> Strains in Oysters and Water. Applied and Environmental Microbiology, 2008, 74, 1704-1709.	1.4	53