

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	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.	8.6	496
2	Effect of Fecal Microbiota Transplantation on Recurrence in Multiply Recurrent <i>Clostridium difficile</i> Infection. Annals of Internal Medicine, 2016, 165, 609.	3.9	486
3	Interaction of gut microbiota with bile acid metabolism and its influence on disease states. Applied Microbiology and Biotechnology, 2017, 101, 47-64.	3.6	387
4	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. Cell Host and Microbe, 2018, 23, 229-240.e5.	11.0	292
5	Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. Journal of Applied Microbiology, 2013, 115, 1147-1158.	3.1	209
6	Environment shapes the fecal microbiome of invasive carp species. Microbiome, 2016, 4, 44.	11.1	166
7	Successful Resolution of Recurrent <i>Clostridium difficile</i> Infection using Freeze-Dried, Encapsulated Fecal Microbiota; Pragmatic Cohort Study. American Journal of Gastroenterology, 2017, 112, 940-947.	0.4	164
8	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. Journal of Experimental Medicine, 2013, 210, 2011-2024.	8.5	144
9	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. Microbiome, 2017, 5, 87.	11.1	138
10	Species sorting and seasonal dynamics primarily shape bacterial communities in the Upper Mississippi River. Science of the Total Environment, 2015, 505, 435-445.	8.0	133
11	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.	3.1	128
12	Microbes in beach sands: integrating environment, ecology and public health. Reviews in Environmental Science and Biotechnology, 2014, 13, 329-368.	8.1	127
13	Associations between soil bacterial community structure and nutrient cycling functions in long-term organic farm soils following cover crop and organic fertilizer amendment. Science of the Total Environment, 2016, 566-567, 949-959.	8.0	112
14	Complete Microbiota Engraftment Is Not Essential for Recovery from Recurrent <i>Clostridium difficile</i> Infection following Fecal Microbiota Transplantation. MBio, 2016, 7, .	4.1	97
15	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.	3.5	95
16	Microbiota-Driven Activation of Intrahepatic B Cells Aggravates NASH Through Innate and Adaptive Signaling. Hepatology, 2021, 74, 704-722.	7.3	95
17	Faecal microbiota transplantation for <i>Clostridioides difficile</i> : mechanisms and pharmacology. Nature Reviews Gastroenterology and Hepatology, 2021, 18, 67-80.	17.8	91
18	Beach sand and the potential for infectious disease transmission: observations and recommendations. Journal of the Marine Biological Association of the United Kingdom, 2016, 96, 101-120.	0.8	80

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19	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
20	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018, 6, 166.	11.1	73
21	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
22	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <i>Frontiers in Microbiology</i> , 2014, 5, 524.	3.5	70
23	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
24	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
25	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
26	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
27	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
28	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	11.1	62
29	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
30	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
31	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
32	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
33	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
34	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
35	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
36	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

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37	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
38	Environmental and Animal-Associated Enterococci. <i>Advances in Applied Microbiology</i> , 2014, 87, 147-186.	2.4	45
39	Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. <i>PLoS ONE</i> , 2015, 10, e0116705.	2.5	45
40	Sleeve gastrectomy drives persistent shifts in the gut microbiome. <i>Surgery for Obesity and Related Diseases</i> , 2017, 13, 916-924.	1.2	43
41	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
42	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
43	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
44	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
45	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
46	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
47	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
48	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
49	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
50	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
51	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
52	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
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	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

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55	Dysbiosis patterns during re-induction/salvage versus induction chemotherapy for acute leukemia. <i>Scientific Reports</i> , 2019, 9, 6083.	3.3	32
56	Gut microbiota response to antibiotics is personalized and depends on baseline microbiota. <i>Microbiome</i> , 2021, 9, 211.	11.1	32
57	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
58	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
59	Specific gut microbiota changes heralding bloodstream infection and neutropenic fever during intensive chemotherapy. <i>Leukemia</i> , 2020, 34, 312-316.	7.2	30
60	Gut dysbiosis during antileukemia chemotherapy versus allogeneic hematopoietic cell transplantation. <i>Cancer</i> , 2020, 126, 1434-1447.	4.1	30
61	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
62	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
63	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
64	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
65	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
66	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
67	Analysis of gut microbiota – An ever changing landscape. <i>Gut Microbes</i> , 2017, 8, 268-275.	9.8	25
68	Mucosal Microbiota and Metabolome along the Intestinal Tract Reveal a Location-Specific Relationship. <i>MSystems</i> , 2020, 5, .	3.8	25
69	Signal Disruption Leads to Changes in Bacterial Community Population. <i>Frontiers in Microbiology</i> , 2019, 10, 611.	3.5	24
70	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
71	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
72	Clinician Guide to Microbiome Testing. <i>Digestive Diseases and Sciences</i> , 2018, 63, 3167-3177.	2.3	22

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73	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
74	Comparative decay of culturable faecal indicator bacteria, microbial source tracking marker genes, and enteric pathogens in laboratory microcosms that mimic a sub-tropical environment. <i>Science of the Total Environment</i> , 2021, 751, 141475.	8.0	21
75	Encapsulated Fecal Microbiota Transplantation: Development, Efficacy, and Clinical Application. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 826114.	3.9	21
76	Detection and differentiation of <i>Vibrio vulnificus</i> and <i>V. parahaemolyticus</i> in water and oysters of a Gulf of Mexico estuary. <i>Environmental Microbiology</i> , 2013, 15, 623-633.	3.8	20
77	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
78	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
79	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
80	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
81	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
82	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
83	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
84	Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1973-1987.	3.6	16
85	A Combined Digital PCR and Next Generation DNA-Sequencing Based Approach for Tracking Nearshore Pollutant Dynamics Along the Southwest United States/Mexico Border. <i>Frontiers in Microbiology</i> , 2021, 12, 674214.	3.5	16
86	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
87	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
88	A pilot study demonstrating the impact of surgical bowel preparation on intestinal microbiota composition following colon and rectal surgery. <i>Scientific Reports</i> , 2022, 12, .	3.3	14
89	Pre-transplant recovery of microbiome diversity without recovery of the original microbiome. <i>Bone Marrow Transplantation</i> , 2019, 54, 1115-1117.	2.4	13
90	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

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91	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
92	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
93	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
94	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
95	Structuring biofilm communities living in pesticide contaminated water. <i>Heliyon</i> , 2020, 6, e03996.	3.2	12
96	Reduced Enterohepatic Recirculation of Mycophenolate and Lower Blood Concentrations Are Associated with the Stool Bacterial Microbiome after Hematopoietic Cell Transplantation. <i>Transplantation and Cellular Therapy</i> , 2022, 28, 372.e1-372.e9.	1.2	12
97	Levaquin Gets a Pass. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, 778-781.	2.0	11
98	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
99	Effect of COVID-19 precautions on the gut microbiota and nosocomial infections. <i>Gut Microbes</i> , 2021, 13, 1-10.	9.8	10
100	Role of biliary stent and neoadjuvant chemotherapy in the pancreatic tumor microbiome. <i>BMC Microbiology</i> , 2021, 21, 280.	3.3	10
101	Lasting shift in the gut microbiota in patients with acute myeloid leukemia. <i>Blood Advances</i> , 2022, 6, 3451-3457.	5.2	10
102	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
103	Peri-operative antibiotics acutely and significantly impact intestinal microbiota following bariatric surgery. <i>Scientific Reports</i> , 2020, 10, 20340.	3.3	9
104	<i>In vitro</i> efficacy of a non-instrumentation technique to remove intracanal multispecies biofilm. <i>International Endodontic Journal</i> , 2022, 55, 495-504.	5.0	9
105	Influence of heavy metals on rhizosphere microbial communities of Siam weed (<i>Chromolaena odorata</i>) <i>Tj ETQq1 1 0.784314 rgBT /Over</i> 137-141.	0.1	8
106	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
107	Vancomycin-resistance gene cluster, <i>vanC</i> , in the gut microbiome of acute leukemia patients undergoing intensive chemotherapy. <i>PLoS ONE</i> , 2019, 14, e0223890.	2.5	8
108	<i>In vitro</i> physicochemical characterization of five root canal sealers and their influence on an <i>ex vivo</i> oral multispecies biofilm community. <i>International Endodontic Journal</i> , 2022, 55, 772-783.	5.0	8

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109	Genetic and quantitative assessment of <i>Vibrio vulnificus</i> populations in oyster (<i>Crassostrea</i>) Tj ETQq1 1 0,784314 rgBT /Overl	2.4	7
110	Influence of Physicochemical Factors on Bacterial Communities Along the Lower Mekong River Assessed by Illumina Next-Generation Sequencing. Water, Air, and Soil Pollution, 2018, 229, 1.	2.4	7
111	Intestinal organoids: a model to study the role of microbiota in the colonic tumor microenvironment. Future Microbiology, 2020, 15, 1583-1594.	2.0	6
112	Differential Expression of a Sodium-Phosphate Cotransporter Among <i>Vibrio vulnificus</i> Strains. Microbial Ecology, 2014, 67, 24-33.	2.8	5
113	The Diet and Gut Microbial Communities of Two Closely Related Combtooth Blennies, <i>Chasmodes saburrae</i> and <i>Scartella cristata</i> . Copeia, 2017, 105, 249-256.	1.3	5
114	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
115	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
116	Protective Effect of Intestinal <i>Blautia</i> Against Neutropenic Fever in Allogeneic Transplant Recipients. Clinical Infectious Diseases, 2022, 75, 1912-1920.	5.8	5
117	An alpha-defensin gene single nucleotide polymorphism modulates the gut microbiota and may alter the risk of acute graft-versus host disease. British Journal of Haematology, 2020, 189, 926-930.	2.5	4
118	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.	1.5	4
119	Loss of microbiota-derived protective metabolites after neutropenic fever. Scientific Reports, 2022, 12, 6244.	3.3	4
120	Site-specific distribution and competitive ability of indigenous bean-nodulating rhizobia isolated from organic fields in Minnesota. Journal of Biotechnology, 2015, 214, 158-168.	3.8	3
121	Microbiome swings with repeated insults. British Journal of Haematology, 2020, 189, e94-e96.	2.5	3
122	Draft Genome Sequences of Four Novel Thermal- and Alkaline-Tolerant Egyptian <i>Rhizobium</i> Strains Nodulating Berseem Clover. Genome Announcements, 2016, 4, .	0.8	2
123	Successful Resolution of Recurrent <i>Clostridium Difficile</i> Infection using Freeze-Dried, Encapsulated Fecal Microbiota. Gastroenterology, 2017, 152, S343-S344.	1.3	2
124	A nonhuman primate model of vertical sleeve gastrectomy facilitates mechanistic and translational research in human obesity. IScience, 2021, 24, 103421.	4.1	2
125	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
126	Outpatient-to-Inpatient Transition Causes Marked Dysbiosis in Allogeneic Hematopoietic Cell Transplantation Recipients. Biology of Blood and Marrow Transplantation, 2019, 25, S47.	2.0	1

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127	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
128	Antibiotic Conditioning and Single Gavage Allows Stable Engraftment of Human Microbiota in Mice. <i>Methods in Molecular Biology</i> , 2021, 2327, 281-291.	0.9	1
129	Abstract 5060: Effect of aspirin on gut microbiome in a pilot randomized double-blind trial. , 2019, , .		1
130	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
131	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
132	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
133	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
134	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
135	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
136	Sampling, analyzing, and integrating microbiome "omics data in a translational clinical setting. , 2020, , 273-279.		0
137	Circulating bacterial DNA and neutropenic fever during anti-leukaemia chemotherapy. <i>British Journal of Haematology</i> , 2020, 191, e55-e58.	2.5	0
138	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
139	Effect of Colorectal Operations on the Colonic Microbiome. <i>Journal of the American College of Surgeons</i> , 2020, 231, S53.	0.5	0
140	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
141	75200 Fecal Microbiota Transplantation to Prevent Infections in Patients with Acute Myeloid Leukemia: A Double-Blind Randomized Placebo-Controlled Phase 2 Clinical Trial. <i>Journal of Clinical and Translational Science</i> , 2021, 5, 36-36.	0.6	0
142	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
143	Abstract 6097: Alterations of the pancreatic tumor microbiome: the role of biliary stents. , 2020, , .		0
144	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

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145	Circulating Metabolomics Suggest Neutropenic Fever As a Metabolic Derangement Related to Intestinal Tissue Damage and Gut Dysbiosis. Blood, 2021, 138, 688-688.	1.4	0