

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	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.	3.9	496
2	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
3	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
4	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
5	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.	1.4	209
6	Environment shapes the fecal microbiome of invasive carp species. <i>Microbiome</i> , 2016, 4, 44.	4.9	166
7	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
8	Intestinal lamina propria dendritic cells maintain T cell homeostasis but do not affect commensalism. <i>Journal of Experimental Medicine</i> , 2013, 210, 2011-2024.	4.2	144
9	Stable engraftment of human microbiota into mice with a single oral gavage following antibiotic conditioning. <i>Microbiome</i> , 2017, 5, 87.	4.9	138
10	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
11	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.	1.4	128
12	Microbes in beach sands: integrating environment, ecology and public health. <i>Reviews in Environmental Science and Biotechnology</i> , 2014, 13, 329-368.	3.9	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. <i>Science of the Total Environment</i> , 2016, 566-567, 949-959.	3.9	112
14	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
15	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.	1.5	95
16	Microbiota-Driven Activation of Intrahepatic B Cells Aggravates NASH Through Innate and Adaptive Signaling. <i>Hepatology</i> , 2021, 74, 704-722.	3.6	95
17	Faecal microbiota transplantation for <i>Clostridioides difficile</i> : mechanisms and pharmacology. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2021, 18, 67-80.	8.2	91
18	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

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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.	2.9	74
20	Predicting recurrence of <i>Clostridium difficile</i> infection following encapsulated fecal microbiota transplantation. <i>Microbiome</i> , 2018, 6, 166.	4.9	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.	4.6	72
22	Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. <i>Frontiers in Microbiology</i> , 2014, 5, 524.	1.5	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.	1.4	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.	4.8	67
25	Assessment of sources of human pathogens and fecal contamination in a Florida freshwater lake. <i>Water Research</i> , 2012, 46, 5799-5812.	5.3	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.	2.3	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.	1.7	65
28	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	4.9	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.	4.6	59
30	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
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.	1.0	58
32	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
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.	4.6	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.	1.4	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.	1.2	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.	5.3	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.	3.9	46
38	Environmental and Animal-Associated Enterococci. <i>Advances in Applied Microbiology</i> , 2014, 87, 147-186.	1.3	45
39	Complementary Amplicon-Based Genomic Approaches for the Study of Fungal Communities in Humans. <i>PLoS ONE</i> , 2015, 10, e0116705.	1.1	45
40	Sleeve gastrectomy drives persistent shifts in the gut microbiome. <i>Surgery for Obesity and Related Diseases</i> , 2017, 13, 916-924.	1.0	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, .	1.4	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.	0.7	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.	1.4	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.	3.9	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.	1.4	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.	1.9	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.	4.3	39
48	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
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.	1.5	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.	4.6	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.	2.9	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.	1.7	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.	4.3	34
54	Influence of Library Composition on SourceTracker Predictions for Community-Based Microbial Source Tracking. <i>Environmental Science & Technology</i> , 2019, 53, 60-68.	4.6	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.	1.6	32
56	Gut microbiota response to antibiotics is personalized and depends on baseline microbiota. <i>Microbiome</i> , 2021, 9, 211.	4.9	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.	1.7	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.	0.4	30
59	Specific gut microbiota changes heralding bloodstream infection and neutropenic fever during intensive chemotherapy. <i>Leukemia</i> , 2020, 34, 312-316.	3.3	30
60	Gut dysbiosis during antileukemia chemotherapy versus allogeneic hematopoietic cell transplantation. <i>Cancer</i> , 2020, 126, 1434-1447.	2.0	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.	1.4	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.	3.9	29
63	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
64	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
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.	0.7	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, .	3.3	26
67	Analysis of gut microbiota – An ever changing landscape. <i>Gut Microbes</i> , 2017, 8, 268-275.	4.3	25
68	Mucosal Microbiota and Metabolome along the Intestinal Tract Reveal a Location-Specific Relationship. <i>MSystems</i> , 2020, 5, .	1.7	25
69	Signal Disruption Leads to Changes in Bacterial Community Population. <i>Frontiers in Microbiology</i> , 2019, 10, 611.	1.5	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.	3.9	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.	1.5	22
72	Clinician Guide to Microbiome Testing. <i>Digestive Diseases and Sciences</i> , 2018, 63, 3167-3177.	1.1	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.	0.7	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.	3.9	21
75	Encapsulated Fecal Microbiota Transplantation: Development, Efficacy, and Clinical Application. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 826114.	1.8	21
76	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.	1.8	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.	1.1	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.	3.9	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.	3.9	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.	2.3	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.	1.3	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.	1.4	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.	3.9	16
84	Cultivar and phosphorus effects on switchgrass yield and rhizosphere microbial diversity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1973-1987.	1.7	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.	1.5	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.	0.7	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.	1.7	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, .	1.6	14
89	Pre-transplant recovery of microbiome diversity without recovery of the original microbiome. <i>Bone Marrow Transplantation</i> , 2019, 54, 1115-1117.	1.3	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.	0.2	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.	1.3	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.	0.7	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.	5.3	12
94	Altered microbiota-host metabolic cross talk preceding neutropenic fever in patients with acute leukemia. <i>Blood Advances</i> , 2021, 5, 3937-3950.	2.5	12
95	Structuring biofilm communities living in pesticide contaminated water. <i>Heliyon</i> , 2020, 6, e03996.	1.4	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.	0.6	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.	2.9	10
99	Effect of COVID-19 precautions on the gut microbiota and nosocomial infections. <i>Gut Microbes</i> , 2021, 13, 1-10.	4.3	10
100	Role of biliary stent and neoadjuvant chemotherapy in the pancreatic tumor microbiome. <i>BMC Microbiology</i> , 2021, 21, 280.	1.3	10
101	Lasting shift in the gut microbiota in patients with acute myeloid leukemia. <i>Blood Advances</i> , 2022, 6, 3451-3457.	2.5	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.	0.7	9
103	Peri-operative antibiotics acutely and significantly impact intestinal microbiota following bariatric surgery. <i>Scientific Reports</i> , 2020, 10, 20340.	1.6	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.	2.3	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.	0.4	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, .	0.7	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.	1.1	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.	2.3	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 /Ov	1.0	7
110	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
111	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
112	Differential Expression of a Sodium-Phosphate Cotransporter Among <i>Vibrio vulnificus</i> Strains. <i>Microbial Ecology</i> , 2014, 67, 24-33.	1.4	5
113	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
114	Lower endoscopic delivery of freeze-dried intestinal microbiota results in more rapid and efficient engraftment than oral administration. <i>Scientific Reports</i> , 2021, 11, 4519.	1.6	5
115	Donor Microbiota Composition and Housing Affect Recapitulation of Obese Phenotypes in a Human Microbiota-Associated Murine Model. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 614218.	1.8	5
116	Protective Effect of Intestinal <i>Blautia</i> Against Neutropenic Fever in Allogeneic Transplant Recipients. <i>Clinical Infectious Diseases</i> , 2022, 75, 1912-1920.	2.9	5
117	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
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> . <i>Journal of AOAC INTERNATIONAL</i> , 2010, 93, 1553-69.	0.7	4
119	Loss of microbiota-derived protective metabolites after neutropenic fever. <i>Scientific Reports</i> , 2022, 12, 6244.	1.6	4
120	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
121	Microbiome swings with repeated insults. <i>British Journal of Haematology</i> , 2020, 189, e94-e96.	1.2	3
122	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
123	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
124	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
125	Network-based approaches for the investigation of microbial community structure and function using metagenomics-based data. <i>Future Microbiology</i> , 2022, 17, 621-631.	1.0	2
126	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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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.	0.2	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.	0.4	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.	0.6	0
131	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
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.	0.2	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.	0.6	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.	0.2	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.	1.2	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.	0.2	0
139	Effect of Colorectal Operations on the Colonic Microbiome. <i>Journal of the American College of Surgeons</i> , 2020, 231, S53.	0.2	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.	0.3	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.	0.6	0
143	Abstract 6097: Alterations of the pancreatic tumor microbiome: the role of biliary stents. , 2020, , .		0
144	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