

Jack A Gilbert

List of Publications by Year in descending order

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Version: 2024-02-01

269
papers

40,787
citations

5268

83
h-index

2953

189
g-index

314
all docs

314
docs citations

314
times ranked

45432
citing authors

#	ARTICLE	IF	CITATIONS
1	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , 2012, 6, 1621-1624.	9.8	7,430
2	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
3	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	30.7	1,593
4	Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. <i>MSystems</i> , 2016, 1, .	3.8	1,364
5	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21390-21395.	7.1	1,260
6	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	17.5	1,069
7	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	9.8	928
8	Geographic patterns of co-occurrence network topological features for soil microbiota at continental scale in eastern China. <i>ISME Journal</i> , 2016, 10, 1891-1901.	9.8	758
9	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	12.6	751
10	The Soil Microbiome Influences Grapevine-Associated Microbiota. <i>MBio</i> , 2015, 6, .	4.1	747
11	Innate Immunity and Asthma Risk in Amish and Hutterite Farm Children. <i>New England Journal of Medicine</i> , 2016, 375, 411-421.	27.0	745
12	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , 2014, 12, 69.	3.8	723
13	Metagenomics - a guide from sampling to data analysis. <i>Microbial Informatics and Experimentation</i> , 2012, 2, 3.	7.6	680
14	Effects of Diurnal Variation of Gut Microbes and High-Fat Feeding on Host Circadian Clock Function and Metabolism. <i>Cell Host and Microbe</i> , 2015, 17, 681-689.	11.0	634
15	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
16	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016, 535, 94-103.	27.8	595
17	Diversity, structure and convergent evolution of the global sponge microbiome. <i>Nature Communications</i> , 2016, 7, 11870.	12.8	594
18	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	13.3	590

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19	Conditionally Rare Taxa Disproportionately Contribute to Temporal Changes in Microbial Diversity. <i>MBio</i> , 2014, 5, e01371-14.	4.1	549
20	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	2.0	535
21	Reconstructing the Microbial Diversity and Function of Pre-Agricultural Tallgrass Prairie Soils in the United States. <i>Science</i> , 2013, 342, 621-624.	12.6	480
22	<i>Lactobacillus rhamnosus</i> GG-supplemented formula expands butyrate-producing bacterial strains in food allergic infants. <i>ISME Journal</i> , 2016, 10, 742-750.	9.8	407
23	The seasonal structure of microbial communities in the Western English Channel. <i>Environmental Microbiology</i> , 2009, 11, 3132-3139.	3.8	384
24	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016, 351, 158-162.	12.6	381
25	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	9.8	325
26	Microbial Metagenomics: Beyond the Genome. <i>Annual Review of Marine Science</i> , 2011, 3, 347-371.	11.6	323
27	Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. <i>PLoS ONE</i> , 2008, 3, e3042.	2.5	321
28	Collagen degradation and MMP9 activation by <i>Enterococcus faecalis</i> contribute to intestinal anastomotic leak. <i>Science Translational Medicine</i> , 2015, 7, 286ra68.	12.4	287
29	Membership and Behavior of Ultra-Low-Diversity Pathogen Communities Present in the Gut of Humans during Prolonged Critical Illness. <i>MBio</i> , 2014, 5, e01361-14.	4.1	278
30	Recovering complete and draft population genomes from metagenome datasets. <i>Microbiome</i> , 2016, 4, 8.	11.1	254
31	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012, 30, 513-520.	17.5	250
32	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	248
33	Whole-grain wheat consumption reduces inflammation in a randomized controlled trial on overweight and obese subjects with unhealthy dietary and lifestyle behaviors: role of polyphenols bound to cereal dietary fiber. <i>American Journal of Clinical Nutrition</i> , 2015, 101, 251-261.	4.7	246
34	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020, 8, 82.	11.1	239
35	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. <i>Nature Genetics</i> , 2016, 48, 167-175.	21.4	235
36	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. <i>Standards in Genomic Sciences</i> , 2010, 3, 243-248.	1.5	228

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37	Microbial <i>terroir</i> for wine grapes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5-6.	7.1	221
38	The Taxonomic and Functional Diversity of Microbes at a Temperate Coastal Site: A "Multi-Omic"™ Study of Seasonal and Diel Temporal Variation. PLoS ONE, 2010, 5, e15545.	2.5	219
39	Development of the preterm infant gut microbiome: a research priority. Microbiome, 2014, 2, 38.	11.1	213
40	Rhizosphere-associated bacterial network structure and spatial distribution differ significantly from bulk soil in wheat crop fields. Soil Biology and Biochemistry, 2017, 113, 275-284.	8.8	210
41	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. MBio, 2020, 11, .	4.1	204
42	Evidence for a persistent microbial seed bank throughout the global ocean. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4651-4655.	7.1	200
43	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
44	The ocean sampling day consortium. GigaScience, 2015, 4, 27.	6.4	185
45	Microbiology of the built environment. Nature Reviews Microbiology, 2018, 16, 661-670.	28.6	184
46	The Influence of Age and Gender on Skin-Associated Microbial Communities in Urban and Rural Human Populations. PLoS ONE, 2015, 10, e0141842.	2.5	181
47	The Earth Microbiome Project: Meeting report of the "1st EMP meeting on sample selection and acquisition" at Argonne National Laboratory October 6th 2010.. Standards in Genomic Sciences, 2010, 3, 249-253.	1.5	176
48	The Western English Channel contains a persistent microbial seed bank. ISME Journal, 2012, 6, 1089-1093.	9.8	170
49	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
50	Genome reduction in an abundant and ubiquitous soil bacterium "Candidatus Udaeobacter copiosus"™. Nature Microbiology, 2017, 2, 16198.	13.3	168
51	Sex-specific effects of microbiome perturbations on cerebral A β amyloidosis and microglia phenotypes. Journal of Experimental Medicine, 2019, 216, 1542-1560.	8.5	165
52	Predicting bacterial community assemblages using an artificial neural network approach. Nature Methods, 2012, 9, 621-625.	19.0	159
53	Influence of Acidic pH on Hydrogen and Acetate Production by an Electrosynthetic Microbiome. PLoS ONE, 2014, 9, e109935.	2.5	145
54	Ten questions concerning the microbiomes of buildings. Building and Environment, 2016, 109, 224-234.	6.9	143

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55	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <i>MSystems</i> , 2017, 2, .	3.8	141
56	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015, 3, 21.	11.1	140
57	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , 2014, 8, 841-853.	9.8	137
58	Tools for the Microbiome: Nano and Beyond. <i>ACS Nano</i> , 2016, 10, 6-37.	14.6	137
59	Preserving microbial diversity. <i>Science</i> , 2018, 362, 33-34.	12.6	133
60	Quantifying and Understanding Well-to-Well Contamination in Microbiome Research. <i>MSystems</i> , 2019, 4, .	3.8	132
61	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. <i>Frontiers in Microbiology</i> , 2014, 5, 298.	3.5	130
62	Studying the microbiology of the indoor environment. <i>Genome Biology</i> , 2013, 14, 202.	9.6	129
63	Corticosteroid therapy and airflow obstruction influence the bronchial microbiome, which is distinct from that of bronchoalveolar lavage in asthmatic airways. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1398-1405.e3.	2.9	128
64	Intestinal anastomotic injury alters spatially defined microbiome composition and function. <i>Microbiome</i> , 2014, 2, 35.	11.1	126
65	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021, 373, 181-186.	12.6	126
66	Temporal patterns of rarity provide a more complete view of microbial diversity. <i>Trends in Microbiology</i> , 2015, 23, 335-340.	7.7	124
67	Salinity is a key factor driving the nitrogen cycling in the mangrove sediment. <i>Science of the Total Environment</i> , 2018, 631-632, 1342-1349.	8.0	120
68	Potential Contribution of Anammox to Nitrogen Loss from Paddy Soils in Southern China. <i>Applied and Environmental Microbiology</i> , 2015, 81, 938-947.	3.1	118
69	Distinct Biogeographic Patterns for Archaea, Bacteria, and Fungi along the Vegetation Gradient at the Continental Scale in Eastern China. <i>MSystems</i> , 2017, 2, .	3.8	116
70	Human and Environmental Impacts on River Sediment Microbial Communities. <i>PLoS ONE</i> , 2014, 9, e97435.	2.5	115
71	The Gut of Geographically Disparate <i>Ciona intestinalis</i> Harbors a Core Microbiota. <i>PLoS ONE</i> , 2014, 9, e93386.	2.5	111
72	Investigating the Impact of Storage Conditions on Microbial Community Composition in Soil Samples. <i>PLoS ONE</i> , 2013, 8, e70460.	2.5	108

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73	Characterizing changes in soil bacterial community structure in response to short-term warming. <i>FEMS Microbiology Ecology</i> , 2014, 89, 281-292.	2.7	107
74	Microbial diversity – exploration of natural ecosystems and microbiomes. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 66-72.	3.3	105
75	The antibiotic resistome of swine manure is significantly altered by association with the <i>Musca domestica</i> larvae gut microbiome. <i>ISME Journal</i> , 2017, 11, 100-111.	9.8	101
76	The urgent need for microbiology literacy in society. <i>Environmental Microbiology</i> , 2019, 21, 1513-1528.	3.8	99
77	Saliva from Obese Individuals Suppresses the Release of Aroma Compounds from Wine. <i>PLoS ONE</i> , 2014, 9, e85611.	2.5	98
78	The microbe-mediated mechanisms affecting topsoil carbon stock in Tibetan grasslands. <i>ISME Journal</i> , 2015, 9, 2012-2020.	9.8	98
79	Toward Effective Probiotics for Autism and Other Neurodevelopmental Disorders. <i>Cell</i> , 2013, 155, 1446-1448.	28.9	97
80	Associations between fungal and bacterial microbiota of airways and asthma endotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1214-1227.e7.	2.9	96
81	Community ecology as a framework for human microbiome research. <i>Nature Medicine</i> , 2019, 25, 884-889.	30.7	96
82	Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 4.	7.6	93
83	Hospital-associated microbiota and implications for nosocomial infections. <i>Trends in Molecular Medicine</i> , 2015, 21, 427-432.	6.7	92
84	Specific Signatures of the Gut Microbiota and Increased Levels of Butyrate in Children Treated with Fermented Cow's Milk Containing Heat-Killed <i>Lactobacillus paracasei</i> CBA L74. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	92
85	Microbial Exchange via Fomites and Implications for Human Health. <i>Current Pollution Reports</i> , 2019, 5, 198-213.	6.6	92
86	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. <i>MSystems</i> , 2017, 2, .	3.8	91
87	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. <i>MicrobiologyOpen</i> , 2014, 3, 910-921.	3.0	89
88	Ecological Succession and Viability of Human-Associated Microbiota on Restroom Surfaces. <i>Applied and Environmental Microbiology</i> , 2015, 81, 765-773.	3.1	89
89	Introducing the Microbiome into Precision Medicine. <i>Trends in Pharmacological Sciences</i> , 2017, 38, 81-91.	8.7	84
90	Life in a World without Microbes. <i>PLoS Biology</i> , 2014, 12, e1002020.	5.6	82

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91	Network-based metabolic analysis and microbial community modeling. <i>Current Opinion in Microbiology</i> , 2016, 31, 124-131.	5.1	79
92	From genomics to metagenomics. <i>Current Opinion in Biotechnology</i> , 2012, 23, 72-76.	6.6	77
93	The microbial nitrogen cycling potential is impacted by polyaromatic hydrocarbon pollution of marine sediments. <i>Frontiers in Microbiology</i> , 2014, 5, 108.	3.5	76
94	Phylogenetic imprint of woody plants on the soil mycobiome in natural mountain forests of eastern China. <i>ISME Journal</i> , 2019, 13, 686-697.	9.8	76
95	Re-examining causes of surgical site infections following elective surgery in the era of asepsis. <i>Lancet Infectious Diseases</i> , The, 2020, 20, e38-e43.	9.1	76
96	Fecal microbiota transplant rescues mice from human pathogen mediated sepsis by restoring systemic immunity. <i>Nature Communications</i> , 2020, 11, 2354.	12.8	75
97	Understanding Cultivar-Specificity and Soil Determinants of the Cannabis Microbiome. <i>PLoS ONE</i> , 2014, 9, e99641.	2.5	73
98	Beyond the genome: community-level analysis of the microbial world. <i>Biology and Philosophy</i> , 2013, 28, 261-282.	1.4	72
99	The complete genome sequence for putative <i>H₂S</i> -oxidizer <i>Candidatus Sulfuricurvum sp.</i> , assembled <i>de novo</i> from an aquifer-derived metagenome. <i>Environmental Microbiology</i> , 2014, 16, 3443-3462.	3.8	69
100	Metabolic potential of fatty acid oxidation and anaerobic respiration by abundant members of Thaumarchaeota and Thermoplasmata in deep anoxic peat. <i>ISME Journal</i> , 2015, 9, 2740-2744.	9.8	69
101	Migraines Are Correlated with Higher Levels of Nitrate-, Nitrite-, and Nitric Oxide-Reducing Oral Microbes in the American Gut Project Cohort. <i>MSystems</i> , 2016, 1, .	3.8	63
102	Genetic correlation network prediction of forest soil microbial functional organization. <i>ISME Journal</i> , 2018, 12, 2492-2505.	9.8	63
103	The Oral and Skin Microbiomes of Captive Komodo Dragons Are Significantly Shared with Their Habitat. <i>MSystems</i> , 2016, 1, .	3.8	61
104	The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , 2011, 5, 1565-1567.	9.8	59
105	Responses of Microbial Communities to Hydrocarbon Exposures. <i>Oceanography</i> , 2016, 29, 136-149.	1.0	59
106	Longitudinal survey of microbiome associated with particulate matter in a megacity. <i>Genome Biology</i> , 2020, 21, 55.	8.8	59
107	The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 309, E840-E851.	3.5	57
108	Potential for phosphonoacetate utilization by marine bacteria in temperate coastal waters. <i>Environmental Microbiology</i> , 2009, 11, 111-125.	3.8	55

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109	The human microbiome: an emerging tool in forensics. <i>Microbial Biotechnology</i> , 2017, 10, 228-230.	4.2	55
110	Spatial and Temporal Variations in Indoor Environmental Conditions, Human Occupancy, and Operational Characteristics in a New Hospital Building. <i>PLoS ONE</i> , 2015, 10, e0118207.	2.5	54
111	Ecology and Host Identity Outweigh Evolutionary History in Shaping the Bat Microbiome. <i>MSystems</i> , 2019, 4, .	3.8	54
112	Reconstructing an ancestral genotype of two hexachlorocyclohexane-degrading <i>Sphingobium</i> species using metagenomic sequence data. <i>ISME Journal</i> , 2014, 8, 398-408.	9.8	53
113	Key metabolic pathways involved in xenobiotic biotransformation and stress responses revealed by transcriptomics of the mangrove oyster <i>Crassostrea brasiliana</i> . <i>Aquatic Toxicology</i> , 2015, 166, 10-20.	4.0	53
114	Methods to assess human occupancy and occupant activity in hospital patient rooms. <i>Building and Environment</i> , 2015, 90, 136-145.	6.9	53
115	Western Diet Promotes Intestinal Colonization by Collagenolytic Microbes and Promotes Tumor Formation After Colorectal Surgery. <i>Gastroenterology</i> , 2020, 158, 958-970.e2.	1.3	53
116	Diverse protist grazers select for virulence-related traits in <i>Legionella</i> . <i>ISME Journal</i> , 2015, 9, 1607-1618.	9.8	52
117	The Microbiome-Mitochondrion Connection: Common Ancestries, Common Mechanisms, Common Goals. <i>MSystems</i> , 2017, 2, .	3.8	51
118	Soil Bacterial Diversity Is Associated with Human Population Density in Urban Greenspaces. <i>Environmental Science & Technology</i> , 2018, 52, 5115-5124.	10.0	50
119	Pharmacomicrobiomics: The Holy Grail to Variability in Drug Response?. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 317-328.	4.7	49
120	Suppression of local type I interferon by gut microbiota-derived butyrate impairs antitumor effects of ionizing radiation. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	49
121	Modeling microbial communities: Current, developing, and future technologies for predicting microbial community interaction. <i>Journal of Biotechnology</i> , 2012, 160, 17-24.	3.8	48
122	Soil pH determines bacterial distribution and assembly processes in natural mountain forests of eastern China. <i>Global Ecology and Biogeography</i> , 2021, 30, 2164-2177.	5.8	48
123	Arsenic rich Himalayan hot spring metagenomics reveal genetically novel predator-prey genotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 812-823.	2.4	47
124	Age and Mothers: Potent Influences of Children's Skin Microbiota. <i>Journal of Investigative Dermatology</i> , 2019, 139, 2497-2505.e6.	0.7	46
125	Microbial and metabolic succession on common building materials under high humidity conditions. <i>Nature Communications</i> , 2019, 10, 1767.	12.8	46
126	Role of Carbon Monoxide in Host-Gut Microbiome Communication. <i>Chemical Reviews</i> , 2020, 120, 13273-13311.	47.7	45

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127	Gut microbiota-driven brain A β amyloidosis in mice requires microglia. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	44
128	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. <i>ISME Journal</i> , 2010, 4, 1236-1242.	9.8	43
129	The Future of microbial metagenomics (or is ignorance bliss?). <i>ISME Journal</i> , 2011, 5, 777-779.	9.8	42
130	Our interface with the built environment: immunity and the indoor microbiota. <i>Trends in Immunology</i> , 2015, 36, 121-123.	6.8	42
131	Agricultural intensification and the functional capacity of soil microbes on smallholder African farms. <i>Journal of Applied Ecology</i> , 2015, 52, 744-752.	4.0	42
132	Decreased microbial co-occurrence network stability and SCFA receptor level correlates with obesity in African-origin women. <i>Scientific Reports</i> , 2018, 8, 17135.	3.3	42
133	Analysis of gut microbiome, nutrition and immune status in autism spectrum disorder: a case-control study in Ecuador. <i>Gut Microbes</i> , 2020, 11, 453-464.	9.8	41
134	The obese gut microbiome across the epidemiologic transition. <i>Emerging Themes in Epidemiology</i> , 2016, 13, 2.	2.7	40
135	16Stimator: statistical estimation of ribosomal gene copy numbers from draft genome assemblies. <i>ISME Journal</i> , 2016, 10, 1020-1024.	9.8	40
136	Introducing the Mangrove Microbiome Initiative: Identifying Microbial Research Priorities and Approaches To Better Understand, Protect, and Rehabilitate Mangrove Ecosystems. <i>MSystems</i> , 2020, 5, .	3.8	40
137	Modeling microbial community structure and functional diversity across time and space. <i>FEMS Microbiology Letters</i> , 2012, 332, 91-98.	1.8	38
138	Implication of gut microbiota in the association between infant antibiotic exposure and childhood obesity and adiposity accumulation. <i>International Journal of Obesity</i> , 2020, 44, 1508-1520.	3.4	38
139	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	11.1	37
140	Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. <i>Briefings in Bioinformatics</i> , 2012, 13, 420-429.	6.5	36
141	Athletic equipment microbiota are shaped by interactions with human skin. <i>Microbiome</i> , 2015, 3, 25.	11.1	36
142	Housefly Larva Vermicomposting Efficiently Attenuates Antibiotic Resistance Genes in Swine Manure, with Concomitant Bacterial Population Changes. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7668-7679.	3.1	36
143	Bias in assessments of marine microbial biodiversity in fosmid libraries as evaluated by pyrosequencing. <i>ISME Journal</i> , 2009, 3, 792-796.	9.8	35
144	Carbon constrains fungal endophyte assemblages along the timberline. <i>Environmental Microbiology</i> , 2016, 18, 2455-2469.	3.8	35

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145	Environmental Sources of Bacteria Differentially Influence Host-Associated Microbial Dynamics. <i>MSystems</i> , 2018, 3, .	3.8	35
146	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	3.8	35
147	Mice Fed an Obesogenic Western Diet, Administered Antibiotics, and Subjected to a Sterile Surgical Procedure Develop Lethal Septicemia with Multidrug-Resistant Pathobionts. <i>MBio</i> , 2019, 10, .	4.1	34
148	Is triclosan harming your microbiome?. <i>Science</i> , 2016, 353, 348-349.	12.6	33
149	Comparative genomic analysis of novel <i>Acinetobacter</i> symbionts: A combined systems biology and genomics approach. <i>Scientific Reports</i> , 2016, 6, 29043.	3.3	33
150	Longitudinal homogenization of the microbiome between both occupants and the built environment in a cohort of United States Air Force Cadets. <i>Microbiome</i> , 2019, 7, 70.	11.1	33
151	The Future of Microbiome-Based Therapeutics in Clinical Applications. <i>Clinical Pharmacology and Therapeutics</i> , 2020, 107, 123-128.	4.7	33
152	Taxonomic and functional patterns across soil microbial communities of global biomes. <i>Science of the Total Environment</i> , 2017, 609, 1064-1074.	8.0	32
153	Microbial exposure and human health. <i>Current Opinion in Microbiology</i> , 2018, 44, 79-87.	5.1	32
154	Gut microbiota, short chain fatty acids, and obesity across the epidemiologic transition: the METS-Microbiome study protocol. <i>BMC Public Health</i> , 2018, 18, 978.	2.9	32
155	Dietary Selection Pressures and Their Impact on the Gut Microbiome. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 13, 7-18.	4.5	32
156	Microbial Similarity between Students in a Common Dormitory Environment Reveals the Forensic Potential of Individual Microbial Signatures. <i>MBio</i> , 2019, 10, .	4.1	31
157	Concurrent measurement of microbiome and allergens in the air of bedrooms of allergy disease patients in the Chicago area. <i>Microbiome</i> , 2019, 7, 82.	11.1	31
158	Agricultural Risk Factors Influence Microbial Ecology in Honghu Lake. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 76-90.	6.9	31
159	A New N -Acyl Homoserine Lactone Synthase in an Uncultured Symbiont of the Red Sea Sponge <i>Theonella swinhoei</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 1274-1285.	3.1	30
160	The human microbiota is associated with cardiometabolic risk across the epidemiologic transition. <i>PLoS ONE</i> , 2019, 14, e0215262.	2.5	29
161	Systems biology of the human microbiome. <i>Current Opinion in Biotechnology</i> , 2018, 51, 146-153.	6.6	28
162	Impacts of indoor surface finishes on bacterial viability. <i>Indoor Air</i> , 2019, 29, 551-562.	4.3	28

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163	ZIKV “CDB: A Collaborative Database to Guide Research Linking SncRNAs and ZIKA Virus Disease Symptoms. PLoS Neglected Tropical Diseases, 2016, 10, e0004817.	3.0	28
164	Stool consistency as a major confounding factor affecting microbiota composition: an ignored variable?. Gut, 2016, 65, 1-2.	12.1	27
165	Bacterial and Archaeal Viruses of Himalayan Hot Springs at Manikaran Modulate Host Genomes. Frontiers in Microbiology, 2018, 9, 3095.	3.5	27
166	Permissive microbiome characterizes human subjects with a neurovascular disease cavernous angioma. Nature Communications, 2020, 11, 2659.	12.8	27
167	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	26
168	Effects of Extended Postmortem Interval on Microbial Communities in Organs of the Human Cadaver. Frontiers in Microbiology, 2020, 11, 569630.	3.5	26
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