

Jack A Gilbert

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

243
papers

26,749
citations

72
h-index

161
g-index

314
ext. papers

35,468
ext. citations

11
avg, IF

7.14
L-index

#	Paper	IF	Citations
243	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , 2012 , 6, 1621-4	11.9	5059
242	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
241	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008 , 26, 541-7	44.5	964
240	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, 21390-5	11.5	956
239	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018 , 24, 392-400	50.5	823
238	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,	7.6	703
237	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012 , 6, 298-308	11.9	656
236	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014 , 345, 1048-52	33.3	543
235	Innate Immunity and Asthma Risk in Amish and Hutterite Farm Children. <i>New England Journal of Medicine</i> , 2016 , 375, 411-421	59.2	537
234	Metagenomics - a guide from sampling to data analysis. <i>Microbial Informatics and Experimentation</i> , 2012 , 2, 3		507
233	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , 2014 , 12, 69	7.3	501
232	The soil microbiome influences grapevine-associated microbiota. <i>MBio</i> , 2015 , 6,	7.8	465
231	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016 , 535, 94-103	50.4	443
230	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, 681-9	23.4	440
229	Geographic patterns of co-occurrence network topological features for soil microbiota at continental scale in eastern China. <i>ISME Journal</i> , 2016 , 10, 1891-901	11.9	403
228	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014 , 2, e545	3.1	395
227	Conditionally rare taxa disproportionately contribute to temporal changes in microbial diversity. <i>MBio</i> , 2014 , 5, e01371-14	7.8	359

226	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
225	Reconstructing the microbial diversity and function of pre-agricultural tallgrass prairie soils in the United States. <i>Science</i> , 2013 , 342, 621-4	33.3	324
224	Diversity, structure and convergent evolution of the global sponge microbiome. <i>Nature Communications</i> , 2016 , 7, 11870	17.4	318
223	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019 , 4, 396-403	26.6	296
222	The seasonal structure of microbial communities in the Western English Channel. <i>Environmental Microbiology</i> , 2009 , 11, 3132-9	5.2	291
221	Detection of large numbers of novel sequences in the metatranscriptomes of complex marine microbial communities. <i>PLoS ONE</i> , 2008 , 3, e3042	3.7	289
220	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014 , 8, 1464-75	11.9	262
219	Microbial metagenomics: beyond the genome. <i>Annual Review of Marine Science</i> , 2011 , 3, 347-71	15.4	258
218	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016 , 351, 158-62	33.3	256
217	Lactobacillus rhamnosus GG-supplemented formula expands butyrate-producing bacterial strains in food allergic infants. <i>ISME Journal</i> , 2016 , 10, 742-50	11.9	251
216	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012 , 30, 513-20	44.5	212
215	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	7.8	203
214	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, 251-61	7	198
213	Collagen degradation and MMP9 activation by Enterococcus faecalis contribute to intestinal anastomotic leak. <i>Science Translational Medicine</i> , 2015 , 7, 286ra68	17.5	191
212	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , 2010 , 3, 243-8		187
211	The taxonomic and functional diversity of microbes at a temperate coastal site: a 'multi-omic' study of seasonal and diel temporal variation. <i>PLoS ONE</i> , 2010 , 5, e15545	3.7	173
210	Recovering complete and draft population genomes from metagenome datasets. <i>Microbiome</i> , 2016 , 4, 8	16.6	158
209	Evidence for a persistent microbial seed bank throughout the global ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 4651-5	11.5	158

208	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. <i>Nature Genetics</i> , 2016 , 48, 167-75	36.3	156
207	Microbial terroir for wine grapes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5-6	11.5	155
206	Development of the preterm infant gut microbiome: a research priority. <i>Microbiome</i> , 2014 , 2, 38	16.6	153
205	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	146
204	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
203	The Earth Microbiome Project: Meeting report of the "1 EMP meeting on sample selection and acquisition" at Argonne National Laboratory October 6 2010. <i>Standards in Genomic Sciences</i> , 2010 , 3, 249-53		146
202	The Western English Channel contains a persistent microbial seed bank. <i>ISME Journal</i> , 2012 , 6, 1089-93	11.9	140
201	Predicting bacterial community assemblages using an artificial neural network approach. <i>Nature Methods</i> , 2012 , 9, 621-5	21.6	130
200	The ocean sampling day consortium. <i>GigaScience</i> , 2015 , 4, 27	7.6	126
199	The Influence of Age and Gender on Skin-Associated Microbial Communities in Urban and Rural Human Populations. <i>PLoS ONE</i> , 2015 , 10, e0141842	3.7	119
198	Rhizosphere-associated bacterial network structure and spatial distribution differ significantly from bulk soil in wheat crop fields. <i>Soil Biology and Biochemistry</i> , 2017 , 113, 275-284	7.5	115
197	Influence of acidic pH on hydrogen and acetate production by an electrosynthetic microbiome. <i>PLoS ONE</i> , 2014 , 9, e109935	3.7	112
196	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , 2014 , 8, 841-53	11.9	111
195	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015 , 3, 21	16.6	108
194	Ten questions concerning the microbiomes of buildings. <i>Building and Environment</i> , 2016 , 109, 224-234	6.5	104
193	Tools for the Microbiome: Nano and Beyond. <i>ACS Nano</i> , 2016 , 10, 6-37	16.7	99
192	Genome reduction in an abundant and ubiquitous soil bacterium 'Candidatus <i>Udaeobacter copiosus</i> '. <i>Nature Microbiology</i> , 2016 , 2, 16198	26.6	99
191	Intestinal anastomotic injury alters spatially defined microbiome composition and function. <i>Microbiome</i> , 2014 , 2, 35	16.6	99

190	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. <i>Frontiers in Microbiology</i> , 2014 , 5, 298	5.7	98
189	Potential contribution of anammox to nitrogen loss from paddy soils in Southern China. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 938-47	4.8	97
188	Microbiology of the built environment. <i>Nature Reviews Microbiology</i> , 2018 , 16, 661-670	22.2	97
187	Studying the microbiology of the indoor environment. <i>Genome Biology</i> , 2013 , 14, 202	18.3	97
186	Sex-specific effects of microbiome perturbations on cerebral Amyloidosis and microglia phenotypes. <i>Journal of Experimental Medicine</i> , 2019 , 216, 1542-1560	16.6	93
185	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	11.5	89
184	Investigating the impact of storage conditions on microbial community composition in soil samples. <i>PLoS ONE</i> , 2013 , 8, e70460	3.7	86
183	Preserving microbial diversity. <i>Science</i> , 2018 , 362, 33-34	33.3	84
182	Human and environmental impacts on river sediment microbial communities. <i>PLoS ONE</i> , 2014 , 9, e97435	3.7	83
181	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <i>MSystems</i> , 2017 , 2,	7.6	80
180	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020 , 8, 82	16.6	80
179	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020 , 11,	7.8	79
178	Temporal patterns of rarity provide a more complete view of microbial diversity. <i>Trends in Microbiology</i> , 2015 , 23, 335-40	12.4	78
177	The gut of geographically disparate <i>Ciona intestinalis</i> harbors a core microbiota. <i>PLoS ONE</i> , 2014 , 9, e93386	3.6	78
176	Characterizing changes in soil bacterial community structure in response to short-term warming. <i>FEMS Microbiology Ecology</i> , 2014 , 89, 281-92	4.3	75
175	Quantifying and Understanding Well-to-Well Contamination in Microbiome Research. <i>MSystems</i> , 2019 , 4,	7.6	73
174	Toward effective probiotics for autism and other neurodevelopmental disorders. <i>Cell</i> , 2013 , 155, 1446-8	5.2	73
173	Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. <i>Microbial Informatics and Experimentation</i> , 2011 , 1, 4		73

172	Ecological succession and viability of human-associated microbiota on restroom surfaces. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 765-73	4.8	72
171	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	11.9	72
170	Hospital-associated microbiota and implications for nosocomial infections. <i>Trends in Molecular Medicine</i> , 2015 , 21, 427-32	11.5	71
169	Saliva from obese individuals suppresses the release of aroma compounds from wine. <i>PLoS ONE</i> , 2014 , 9, e85611	3.7	70
168	Microbial diversity--exploration of natural ecosystems and microbiomes. <i>Current Opinion in Genetics and Development</i> , 2015 , 35, 66-72	4.9	68
167	From genomics to metagenomics. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 72-6	11.4	65
166	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. <i>MicrobiologyOpen</i> , 2014 , 3, 910-21	3.4	64
165	Distinct Biogeographic Patterns for Archaea, Bacteria, and Fungi along the Vegetation Gradient at the Continental Scale in Eastern China. <i>MSystems</i> , 2017 , 2,	7.6	63
164	Beyond the genome: community-level analysis of the microbial world. <i>Biology and Philosophy</i> , 2013 , 28, 261-282	1.7	62
163	The microbe-mediated mechanisms affecting topsoil carbon stock in Tibetan grasslands. <i>ISME Journal</i> , 2015 , 9, 2012-20	11.9	60
162	Introducing the Microbiome into Precision Medicine. <i>Trends in Pharmacological Sciences</i> , 2017 , 38, 81-91	13.2	58
161	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	10.2	57
160	Life in a World without Microbes. <i>PLoS Biology</i> , 2014 , 12, e1002020	9.7	57
159	Microbial Exchange via Fomites and Implications for Human Health. <i>Current Pollution Reports</i> , 2019 , 5, 198-213	7.6	56
158	Network-based metabolic analysis and microbial community modeling. <i>Current Opinion in Microbiology</i> , 2016 , 31, 124-131	7.9	56
157	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,	4.8	55
156	Community ecology as a framework for human microbiome research. <i>Nature Medicine</i> , 2019 , 25, 884-889	50.5	54
155	Invasive Plants Rapidly Reshape Soil Properties in a Grassland Ecosystem. <i>MSystems</i> , 2017 , 2,	7.6	53

154	The microbial nitrogen cycling potential is impacted by polyaromatic hydrocarbon pollution of marine sediments. <i>Frontiers in Microbiology</i> , 2014 , 5, 108	5.7	53
153	The complete genome sequence for putative H ₂ S-oxidizer <i>Candidatus Sulfuricurvum</i> sp., assembled de novo from an aquifer-derived metagenome. <i>Environmental Microbiology</i> , 2014 , 16, 3443-62	5.2	51
152	Potential for phosphonoacetate utilization by marine bacteria in temperate coastal waters. <i>Environmental Microbiology</i> , 2009 , 11, 111-25	5.2	49
151	The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , 2011 , 5, 1565-7	11.9	48
150	Responses of Microbial Communities to Hydrocarbon Exposures. <i>Oceanography</i> , 2016 , 29, 136-149	2.3	47
149	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, 2740-4	11.9	46
148	Associations between fungal and bacterial microbiota of airways and asthma endotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 144, 1214-1227.e7	11.5	45
147	Understanding cultivar-specificity and soil determinants of the cannabis microbiome. <i>PLoS ONE</i> , 2014 , 9, e99641	3.7	45
146	Reconstructing an ancestral genotype of two hexachlorocyclohexane-degrading <i>Sphingobium</i> species using metagenomic sequence data. <i>ISME Journal</i> , 2014 , 8, 398-408	11.9	45
145	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	3.7	43
144	Methods to assess human occupancy and occupant activity in hospital patient rooms. <i>Building and Environment</i> , 2015 , 90, 136-145	6.5	42
143	The short-chain fatty acid receptor, FFA2, contributes to gestational glucose homeostasis. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015 , 309, E840-51	6	42
142	The Oral and Skin Microbiomes of Captive Komodo Dragons Are Significantly Shared with Their Habitat. <i>MSystems</i> , 2016 , 1,	7.6	41
141	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	5.1	40
140	Fecal microbiota transplant rescues mice from human pathogen mediated sepsis by restoring systemic immunity. <i>Nature Communications</i> , 2020 , 11, 2354	17.4	40
139	Genetic correlation network prediction of forest soil microbial functional organization. <i>ISME Journal</i> , 2018 , 12, 2492-2505	11.9	40
138	Modeling microbial communities: current, developing, and future technologies for predicting microbial community interaction. <i>Journal of Biotechnology</i> , 2012 , 160, 17-24	3.7	40
137	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. <i>ISME Journal</i> , 2010 , 4, 1236-42	11.9	39

136	Our interface with the built environment: immunity and the indoor microbiota. <i>Trends in Immunology</i> , 2015 , 36, 121-3	14.4	38
135	Phylogenetic imprint of woody plants on the soil mycobiome in natural mountain forests of eastern China. <i>ISME Journal</i> , 2019 , 13, 686-697	11.9	37
134	Diverse protist grazers select for virulence-related traits in <i>Legionella</i> . <i>ISME Journal</i> , 2015 , 9, 1607-18	11.9	36
133	Arsenic rich Himalayan hot spring metagenomics reveal genetically novel predator-prey genotypes. <i>Environmental Microbiology Reports</i> , 2015 , 7, 812-23	3.7	36
132	Longitudinal survey of microbiome associated with particulate matter in a megacity. <i>Genome Biology</i> , 2020 , 21, 55	18.3	35
131	The Microbiome-Mitochondrion Connection: Common Ancestries, Common Mechanisms, Common Goals. <i>MSystems</i> , 2017 , 2,	7.6	34
130	Bias in assessments of marine microbial biodiversity in fosmid libraries as evaluated by pyrosequencing. <i>ISME Journal</i> , 2009 , 3, 792-6	11.9	34
129	Pharmacomicrobiomics: The Holy Grail to Variability in Drug Response?. <i>Clinical Pharmacology and Therapeutics</i> , 2019 , 106, 317-328	6.1	33
128	The obese gut microbiome across the epidemiologic transition. <i>Emerging Themes in Epidemiology</i> , 2016 , 13, 2	3.9	33
127	Modeling microbial community structure and functional diversity across time and space. <i>FEMS Microbiology Letters</i> , 2012 , 332, 91-8	2.9	33
126	Housefly Larva Vermicomposting Efficiently Attenuates Antibiotic Resistance Genes in Swine Manure, with Concomitant Bacterial Population Changes. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7668-79	4.8	32
125	Athletic equipment microbiota are shaped by interactions with human skin. <i>Microbiome</i> , 2015 , 3, 25	16.6	31
124	Agricultural intensification and the functional capacity of soil microbes on smallholder African farms. <i>Journal of Applied Ecology</i> , 2015 , 52, 744-752	5.8	31
123	Measuring the microbiome: perspectives on advances in DNA-based techniques for exploring microbial life. <i>Briefings in Bioinformatics</i> , 2012 , 13, 420-9	13.4	31
122	The future of microbial metagenomics (or is ignorance bliss?). <i>ISME Journal</i> , 2011 , 5, 777-9	11.9	31
121	Microbial and metabolic succession on common building materials under high humidity conditions. <i>Nature Communications</i> , 2019 , 10, 1767	17.4	30
120	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,	7.6	29
119	Re-examining causes of surgical site infections following elective surgery in the era of asepsis. <i>Lancet Infectious Diseases</i> , 2020 , 20, e38-e43	25.5	27

118	MICROBIOME. Is triclosan harming your microbiome?. <i>Science</i> , 2016 , 353, 348-9	33.3	26
117	Carbon constrains fungal endophyte assemblages along the timberline. <i>Environmental Microbiology</i> , 2016 , 18, 2455-69	5.2	25
116	Western Diet Promotes Intestinal Colonization by Collagenolytic Microbes and Promotes Tumor Formation After Colorectal Surgery. <i>Gastroenterology</i> , 2020 , 158, 958-970.e2	13.3	25
115	Taxonomic and functional patterns across soil microbial communities of global biomes. <i>Science of the Total Environment</i> , 2017 , 609, 1064-1074	10.2	24
114	A rare SAR11 fosmid clone confirming genetic variability in the 'Candidatus Pelagibacter ubique' genome. <i>ISME Journal</i> , 2008 , 2, 790-3	11.9	24
113	Systems biology of the human microbiome. <i>Current Opinion in Biotechnology</i> , 2018 , 51, 146-153	11.4	22
112	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,	7.8	22
111	Ecology and Host Identity Outweigh Evolutionary History in Shaping the Bat Microbiome. <i>MSystems</i> , 2019 , 4,	7.6	22
110	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021 , 373, 181-186	13.3	22
109	Soil Bacterial Diversity Is Associated with Human Population Density in Urban Greenspaces. <i>Environmental Science & Technology</i> , 2018 , 52, 5115-5124	10.3	21
108	Genomic standards consortium projects. <i>Standards in Genomic Sciences</i> , 2014 , 9, 599-601		21
107	16Stimator: statistical estimation of ribosomal gene copy numbers from draft genome assemblies. <i>ISME Journal</i> , 2016 , 10, 1020-4	11.9	20
106	Stool consistency as a major confounding factor affecting microbiota composition: an ignored variable?. <i>Gut</i> , 2016 , 65, 1-2	19.2	19
105	Celebrating parasites. <i>Nature Genetics</i> , 2017 , 49, 483-484	36.3	19
104	Identifying the plant-associated microbiome across aquatic and terrestrial environments: the effects of amplification method on taxa discovery. <i>Molecular Ecology Resources</i> , 2017 , 17, 931-942	8.4	19
103	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	4.8	19
102	A call for an international network of genomic observatories (GOs). <i>GigaScience</i> , 2012 , 1, 5	7.6	19
101	The importance of metagenomic surveys to microbial ecology: or why Darwin would have been a metagenomic scientist. <i>Microbial Informatics and Experimentation</i> , 2011 , 1, 5		19

100	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
99	Microbial Similarity between Students in a Common Dormitory Environment Reveals the Forensic Potential of Individual Microbial Signatures. <i>MBio</i> , 2019 , 10,	7.8	18
98	ZIKV - CDB: A Collaborative Database to Guide Research Linking SncRNAs and ZIKA Virus Disease Symptoms. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004817	4.8	18
97	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	16.6	17
96	Age and Mothers: Potent Influences of Children's Skin Microbiota. <i>Journal of Investigative Dermatology</i> , 2019 , 139, 2497-2505.e6	4.3	17
95	Environmental Sources of Bacteria Differentially Influence Host-Associated Microbial Dynamics. <i>MSystems</i> , 2018 , 3,	7.6	17
94	Impacts of indoor surface finishes on bacterial viability. <i>Indoor Air</i> , 2019 , 29, 551-562	5.4	16
93	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	4.1	16
92	The human microbiota is associated with cardiometabolic risk across the epidemiologic transition. <i>PLoS ONE</i> , 2019 , 14, e0215262	3.7	16
91	Enteric dysbiosis and fecal calprotectin expression in premature infants. <i>Pediatric Research</i> , 2019 , 85, 361-368	3.2	16
90	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	8.8	16
89	The Future of Microbiome-Based Therapeutics in Clinical Applications. <i>Clinical Pharmacology and Therapeutics</i> , 2020 , 107, 123-128	6.1	16
88	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	5.5	15
87	Satellite remote sensing data can be used to model marine microbial metabolite turnover. <i>ISME Journal</i> , 2015 , 9, 166-79	11.9	15
86	The role of macrobiota in structuring microbial communities along rocky shores. <i>PeerJ</i> , 2014 , 2, e631	3.1	15
85	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021 , 9, 132	16.6	15
84	Decreased microbial co-occurrence network stability and SCFA receptor level correlates with obesity in African-origin women. <i>Scientific Reports</i> , 2018 , 8, 17135	4.9	15
83	Microbial exposure and human health. <i>Current Opinion in Microbiology</i> , 2018 , 44, 79-87	7.9	15

82	Comparative genomic analysis of novel Acinetobacter symbionts: A combined systems biology and genomics approach. <i>Scientific Reports</i> , 2016 , 6, 29043	4.9	14
81	Role of Carbon Monoxide in Host-Gut Microbiome Communication. <i>Chemical Reviews</i> , 2020 , 120, 13273-13311	13.1	14
80	Preparing the Bowel for Surgery: Learning from the Past and Planning for the Future. <i>Journal of the American College of Surgeons</i> , 2017 , 225, 324-332	4.4	13
79	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	16.6	13
78	A simple novel device for air sampling by electrokinetic capture. <i>Microbiome</i> , 2015 , 3, 79	16.6	13
77	Towards large-cohort comparative studies to define the factors influencing the gut microbial community structure of ASD patients. <i>Microbial Ecology in Health and Disease</i> , 2015 , 26, 26555		13
76	Bacterial and Archaeal Viruses of Himalayan Hot Springs at Manikaran Modulate Host Genomes. <i>Frontiers in Microbiology</i> , 2018 , 9, 3095	5.7	13
75	Agricultural Risk Factors Influence Microbial Ecology in Honghu Lake. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 76-90	6.5	12
74	Metagenomic analysis of basal ice from an Alaskan glacier. <i>Microbiome</i> , 2018 , 6, 123	16.6	12
73	Social behavior and the microbiome. <i>ELife</i> , 2015 , 4,	8.9	12
72	Introducing the Mangrove Microbiome Initiative: Identifying Microbial Research Priorities and Approaches To Better Understand, Protect, and Rehabilitate Mangrove Ecosystems. <i>MSystems</i> , 2020 , 5,	7.6	12
71	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,	16.6	12
70	Predicting ecosystem emergent properties at multiple scales. <i>Environmental Microbiology Reports</i> , 2015 , 7, 20-2	3.7	11
69	American Gut: an Open Platform for Citizen-Science Microbiome Research		11
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