

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2862336/publications.pdf>

Version: 2024-02-01

763
papers

314,925
citations

¹²

208
h-index

²

528
g-index

890
all docs

890
docs citations

890
times ranked

143432
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	19.0	31,818
2	UCHIME improves sensitivity and speed of chimera detection. <i>Bioinformatics</i> , 2011, 27, 2194-2200.	4.1	13,241
3	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
4	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	17.5	8,049
5	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
6	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4516-4522.	7.1	7,425
7	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8228-8235.	3.1	7,007
8	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009, 457, 480-484.	27.8	6,819
9	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	27.8	6,247
10	Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. <i>Science</i> , 2011, 334, 105-108.	12.6	5,253
11	The Human Microbiome Project. <i>Nature</i> , 2007, 449, 804-810.	27.8	4,750
12	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , 2012, 6, 610-618.	9.8	4,581
13	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012, 489, 220-230.	27.8	4,114
14	Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11971-11975.	7.1	3,738
15	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 57-59.	19.0	3,402
16	PyNASt: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , 2010, 26, 266-267.	4.1	3,400
17	Pyrosequencing-Based Assessment of Soil pH as a Predictor of Soil Bacterial Community Structure at the Continental Scale. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5111-5120.	3.1	3,268
18	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	12.6	3,171

#	ARTICLE	IF	CITATIONS
19	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	11.1	3,159
20	Soil bacterial and fungal communities across a pH gradient in an arable soil. <i>ISME Journal</i> , 2010, 4, 1340-1351.	9.8	3,154
21	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. <i>Genome Research</i> , 2011, 21, 494-504.	5.5	3,015
22	Gut Microbiota from Twins Discordant for Obesity Modulate Metabolism in Mice. <i>Science</i> , 2013, 341, 1241-1244.	12.6	3,006
23	The Impact of the Gut Microbiota on Human Health: An Integrative View. <i>Cell</i> , 2012, 148, 1258-1270.	28.9	2,920
24	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837.	17.5	2,802
25	Bacterial Community Variation in Human Body Habitats Across Space and Time. <i>Science</i> , 2009, 326, 1694-1697.	12.6	2,713
26	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	11.0	2,582
27	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	28.9	2,523
28	The Effect of Diet on the Human Gut Microbiome: A Metagenomic Analysis in Humanized Gnotobiotic Mice. <i>Science Translational Medicine</i> , 2009, 1, 6ra14.	12.4	2,492
29	Quantitative and Qualitative β Diversity Measures Lead to Different Insights into Factors That Structure Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1576-1585.	3.1	2,418
30	Gut Microbiota Regulate Motor Deficits and Neuroinflammation in a Model of Parkinson's Disease. <i>Cell</i> , 2016, 167, 1469-1480.e12.	28.9	2,399
31	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172.	9.8	2,280
32	Succession of microbial consortia in the developing infant gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4578-4585.	7.1	2,108
33	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
34	Metabolic Syndrome and Altered Gut Microbiota in Mice Lacking Toll-Like Receptor 5. <i>Science</i> , 2010, 328, 228-231.	12.6	1,804
35	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	12.6	1,712
36	The Long-Term Stability of the Human Gut Microbiota. <i>Science</i> , 2013, 341, 1237-1239.	12.6	1,696

#	ARTICLE	IF	CITATIONS
37	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	27.8	1,638
38	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. <i>Cell</i> , 2012, 150, 470-480.	28.9	1,603
39	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	30.7	1,593
40	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
41	Global patterns in bacterial diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11436-11440.	7.1	1,461
42	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	11.1	1,434
43	Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. <i>ISME Journal</i> , 2012, 6, 1007-1017.	9.8	1,405
44	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
45	High-Fat Diet Determines the Composition of the Murine Gut Microbiome Independently of Obesity. <i>Gastroenterology</i> , 2009, 137, 1716-1724.e2.	1.3	1,344
46	Worlds within worlds: evolution of the vertebrate gut microbiota. <i>Nature Reviews Microbiology</i> , 2008, 6, 776-788.	28.6	1,342
47	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	3.8	1,339
48	UniFrac--an online tool for comparing microbial community diversity in a phylogenetic context. <i>BMC Bioinformatics</i> , 2006, 7, 371.	2.6	1,321
49	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011, 8, 761-763.	19.0	1,284
50	Analysis of composition of microbiomes: a novel method for studying microbial composition. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 27663.	3.5	1,283
51	Error-correcting barcoded primers for pyrosequencing hundreds of samples in multiplex. <i>Nature Methods</i> , 2008, 5, 235-237.	19.0	1,190
52	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	28.6	1,138
53	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.0	1,125
54	Examining the global distribution of dominant archaeal populations in soil. <i>ISME Journal</i> , 2011, 5, 908-917.	9.8	1,112

#	ARTICLE	IF	CITATIONS
55	EMPeror: a tool for visualizing high-throughput microbial community data. <i>GigaScience</i> , 2013, 2, 16.	6.4	1,096
56	Fast UniFrac: facilitating high-throughput phylogenetic analyses of microbial communities including analysis of pyrosequencing and PhyloChip data. <i>ISME Journal</i> , 2010, 4, 17-27.	9.8	1,025
57	Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. <i>Science</i> , 2013, 339, 548-554.	12.6	1,012
58	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , 2009, 3, 442-453.	9.8	984
59	The influence of sex, handedness, and washing on the diversity of hand surface bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17994-17999.	7.1	980
60	Bacterial phylogeny structures soil resistomes across habitats. <i>Nature</i> , 2014, 509, 612-616.	27.8	973
61	Human oral, gut, and plaque microbiota in patients with atherosclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4592-4598.	7.1	943
62	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	9.6	934
63	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	27.8	929
64	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	9.8	928
65	The gut-liver axis and the intersection with the microbiome. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018, 15, 397-411.	17.8	905
66	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	11.0	831
67	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	13.3	830
68	Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. <i>Molecular Ecology</i> , 2012, 21, 3363-3378.	3.9	814
69	Microbial community profiling for human microbiome projects: Tools, techniques, and challenges. <i>Genome Research</i> , 2009, 19, 1141-1152.	5.5	805
70	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013, 2, e00458.	6.0	801
71	Defining the human microbiome. <i>Nutrition Reviews</i> , 2012, 70, S38-S44.	5.8	789
72	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	12.6	751

#	ARTICLE	IF	CITATIONS
73	Contribution of human hippocampal region to novelty detection. <i>Nature</i> , 1996, 383, 256-259.	27.8	743
74	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016, 22, 250-253.	30.7	736
75	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , 2014, 12, 69.	3.8	723
76	The microbiome of uncontacted Amerindians. <i>Science Advances</i> , 2015, 1, .	10.3	721
77	Gut Microbes and the Brain: Paradigm Shift in Neuroscience. <i>Journal of Neuroscience</i> , 2014, 34, 15490-15496.	3.6	719
78	Microbiota Regulate Intestinal Absorption and Metabolism of Fatty Acids in the Zebrafish. <i>Cell Host and Microbe</i> , 2012, 12, 277-288.	11.0	717
79	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
80	Gut bacteria from multiple sclerosis patients modulate human T cells and exacerbate symptoms in mouse models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10713-10718.	7.1	709
81	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	28.9	701
82	Meta-analyses of human gut microbes associated with obesity and IBD. <i>FEBS Letters</i> , 2014, 588, 4223-4233.	2.8	697
83	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. <i>Science</i> , 2017, 357, 802-806.	12.6	694
84	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , 2020, 579, 567-574.	27.8	691
85	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
86	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012, 1, 7.	6.4	671
87	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. <i>Trends in Microbiology</i> , 2019, 27, 105-117.	7.7	652
88	Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. <i>Movement Disorders</i> , 2017, 32, 739-749.	3.9	649
89	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. <i>Nature Methods</i> , 2010, 7, 668-669.	19.0	647
90	Short pyrosequencing reads suffice for accurate microbial community analysis. <i>Nucleic Acids Research</i> , 2007, 35, e120-e120.	14.5	638

#	ARTICLE	IF	CITATIONS
91	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , 2018, 24, 1532-1535.	30.7	629
92	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , 2015, 17, 603-616.	11.0	628
93	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	28.9	625
94	The under-recognized dominance of Verrucomicrobia in soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2011, 43, 1450-1455.	8.8	613
95	Identifying Genetic Determinants Needed to Establish a Human Gut Symbiont in Its Habitat. <i>Cell Host and Microbe</i> , 2009, 6, 279-289.	11.0	612
96	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	17.5	608
97	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
98	Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2012, 13, 47-58.	16.3	601
99	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016, 535, 94-103.	27.8	595
100	Diversity, structure and convergent evolution of the global sponge microbiome. <i>Nature Communications</i> , 2016, 7, 11870.	12.8	594
101	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	9.8	593
102	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	13.3	590
103	The ecology of the phyllosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. <i>Environmental Microbiology</i> , 2010, 12, 2885-2893.	3.8	574
104	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	1.0	553
105	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. <i>Environmental Microbiology</i> , 2010, 12, 2998-3006.	3.8	551
106	Conditionally Rare Taxa Disproportionately Contribute to Temporal Changes in Microbial Diversity. <i>MBio</i> , 2014, 5, e01371-14.	4.1	549
107	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <i>ISME Journal</i> , 2012, 6, 94-103.	9.8	537
108	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	2.0	535

#	ARTICLE	IF	CITATIONS
109	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. <i>Nucleic Acids Research</i> , 2008, 36, e120-e120.	14.5	508
110	Forensic identification using skin bacterial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6477-6481.	7.1	507
111	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. <i>Current Protocols in Bioinformatics</i> , 2011, 36, Unit 10.7..	25.8	507
112	The microbiome and human cancer. <i>Science</i> , 2021, 371, .	12.6	506
113	Role of the microbiome in human development. <i>Gut</i> , 2019, 68, 1108-1114.	12.1	496
114	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. <i>Current Protocols in Microbiology</i> , 2012, 27, Unit 1E.5..	6.5	486
115	Geographic distance and pH drive bacterial distribution in alkaline lake sediments across Tibetan Plateau. <i>Environmental Microbiology</i> , 2012, 14, 2457-2466.	3.8	484
116	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7059-7066.	3.1	480
117	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
118	Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. <i>Ecology</i> , 2010, 91, 3463-3470.	3.2	475
119	Fast-Find: a novel computational approach to analyzing combinatorial motifs. <i>BMC Bioinformatics</i> , 2006, 7, 1.	2.6	467
120	Genetic Control of Obesity and Gut Microbiota Composition in Response to High-Fat, High-Sucrose Diet in Mice. <i>Cell Metabolism</i> , 2013, 17, 141-152.	16.2	464
121	Individual diet has sex-dependent effects on vertebrate gut microbiota. <i>Nature Communications</i> , 2014, 5, 4500.	12.8	464
122	Microbiota restoration: natural and supplemented recovery of human microbial communities. <i>Nature Reviews Microbiology</i> , 2011, 9, 27-38.	28.6	461
123	Transient Inability to Manage Proteobacteria Promotes Chronic Gut Inflammation in TLR5-Deficient Mice. <i>Cell Host and Microbe</i> , 2012, 12, 139-152.	11.0	459
124	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	19.0	459
125	The Impact of a Consortium of Fermented Milk Strains on the Gut Microbiome of Gnotobiotic Mice and Monozygotic Twins. <i>Science Translational Medicine</i> , 2011, 3, 106ra106.	12.4	456
126	Specialized Metabolites from the Microbiome in Health and Disease. <i>Cell Metabolism</i> , 2014, 20, 719-730.	16.2	454

#	ARTICLE	IF	CITATIONS
127	Subsistence strategies in traditional societies distinguish gut microbiomes. <i>Nature Communications</i> , 2015, 6, 6505.	12.8	449
128	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	12.6	447
129	A Guide to Enterotypes across the Human Body: Meta-Analysis of Microbial Community Structures in Human Microbiome Datasets. <i>PLoS Computational Biology</i> , 2013, 9, e1002863.	3.2	446
130	Microbial endocrinology: the interplay between the microbiota and the endocrine system. <i>FEMS Microbiology Reviews</i> , 2015, 39, 509-521.	8.6	439
131	Shifts in bacterial community structure associated with inputs of low molecular weight carbon compounds to soil. <i>Soil Biology and Biochemistry</i> , 2010, 42, 896-903.	8.8	436
132	Large-scale replicated field study of maize rhizosphere identifies heritable microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7368-7373.	7.1	435
133	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019, 10, 2719.	12.8	428
134	Organismal, genetic, and transcriptional variation in the deeply sequenced gut microbiomes of identical twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7503-7508.	7.1	414
135	Bacterial community structures are unique and resilient in full-scale bioenergy systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4158-4163.	7.1	412
136	Global biogeography of highly diverse protistan communities in soil. <i>ISME Journal</i> , 2013, 7, 652-659.	9.8	412
137	Species divergence and the measurement of microbial diversity. <i>FEMS Microbiology Reviews</i> , 2008, 32, 557-578.	8.6	400
138	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <i>Nature Biotechnology</i> , 2017, 35, 1077-1086.	17.5	400
139	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. <i>Nature</i> , 2017, 551, 340-345.	27.8	396
140	Sequencing our way towards understanding global eukaryotic biodiversity. <i>Trends in Ecology and Evolution</i> , 2012, 27, 233-243.	8.7	395
141	Alterations in the Gut Microbiota Associated with HIV-1 Infection. <i>Cell Host and Microbe</i> , 2013, 14, 329-339.	11.0	387
142	Complex Interactions Among Diet, Gastrointestinal Transit, and Gut Microbiota in Humanized Mice. <i>Gastroenterology</i> , 2013, 144, 967-977.	1.3	387
143	Spatial variability in airborne bacterial communities across land-use types and their relationship to the bacterial communities of potential source environments. <i>ISME Journal</i> , 2011, 5, 601-612.	9.8	385
144	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016, 351, 158-162.	12.6	381

#	ARTICLE	IF	CITATIONS
145	Supervised classification of human microbiota. <i>FEMS Microbiology Reviews</i> , 2011, 35, 343-359.	8.6	377
146	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	3.8	376
147	The Macaque Gut Microbiome in Health, Lentiviral Infection, and Chronic Enterocolitis. <i>PLoS Pathogens</i> , 2008, 4, e20.	4.7	371
148	The Human Microbiome Project: A Community Resource for the Healthy Human Microbiome. <i>PLoS Biology</i> , 2012, 10, e1001377.	5.6	369
149	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	12.8	368
150	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. <i>MSystems</i> , 2016, 1, .	3.8	367
151	Global patterns in the biogeography of bacterial taxa. <i>Environmental Microbiology</i> , 2011, 13, 135-144.	3.8	362
152	The amphibian skin-associated microbiome across species, space and life history stages. <i>Molecular Ecology</i> , 2014, 23, 1238-1250.	3.9	360
153	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014, 15, 531.	8.8	355
154	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. <i>Obesity</i> , 2012, 20, 738-747.	3.0	352
155	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013, 23, 1704-1714.	5.5	352
156	Microbes do not follow the elevational diversity patterns of plants and animals. <i>Ecology</i> , 2011, 92, 797-804.	3.2	351
157	PrimerProspector: <i>de novo</i> design and taxonomic analysis of barcoded polymerase chain reaction primers. <i>Bioinformatics</i> , 2011, 27, 1159-1161.	4.1	351
158	Dietary effects on human gut microbiome diversity. <i>British Journal of Nutrition</i> , 2015, 113, S1-S5.	2.3	350
159	The gut microbiota in human energy homeostasis and obesity. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 493-501.	7.1	350
160	Antibiotic-induced microbiome depletion alters metabolic homeostasis by affecting gut signaling and colonic metabolism. <i>Nature Communications</i> , 2018, 9, 2872.	12.8	343
161	Effect of storage conditions on the assessment of bacterial community structure in soil and human-associated samples. <i>FEMS Microbiology Letters</i> , 2010, 307, 80-86.	1.8	341
162	Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. <i>BMC Microbiology</i> , 2010, 10, 206.	3.3	335

#	ARTICLE	IF	CITATIONS
163	Changes through time: integrating microorganisms into the study of succession. <i>Research in Microbiology</i> , 2010, 161, 635-642.	2.1	334
164	Development of the Human Gastrointestinal Microbiota and Insights From High-Throughput Sequencing. <i>Gastroenterology</i> , 2011, 140, 1713-1719.	1.3	329
165	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. <i>ISME Journal</i> , 2012, 6, 1440-1444.	9.8	326
166	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	9.8	325
167	Bacteria from Diverse Habitats Colonize and Compete in the Mouse Gut. <i>Cell</i> , 2014, 159, 253-266.	28.9	324
168	Host variables confound gut microbiota studies of human disease. <i>Nature</i> , 2020, 587, 448-454.	27.8	324
169	A meta-analysis of changes in bacterial and archaeal communities with time. <i>ISME Journal</i> , 2013, 7, 1493-1506.	9.8	322
170	Rethinking "Enterotypes". <i>Cell Host and Microbe</i> , 2014, 16, 433-437.	11.0	321
171	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders (<i>Plethodon cinereus</i>). <i>ISME Journal</i> , 2014, 8, 830-840.	9.8	316
172	Global chemical effects of the microbiome include new bile-acid conjugations. <i>Nature</i> , 2020, 579, 123-129.	27.8	316
173	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317.	3.9	311
174	Simultaneous Amplicon Sequencing to Explore Co-Occurrence Patterns of Bacterial, Archaeal and Eukaryotic Microorganisms in Rumen Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e47879.	2.5	304
175	Bacterial Communities Associated with the Lichen Symbiosis. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1309-1314.	3.1	302
176	The Effects of Captivity on the Mammalian Gut Microbiome. <i>Integrative and Comparative Biology</i> , 2017, 57, 690-704.	2.0	301
177	Structure-based protein function prediction using graph convolutional networks. <i>Nature Communications</i> , 2021, 12, 3168.	12.8	300
178	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019, 4, .	3.8	295
179	Evaluating the Information Content of Shallow Shotgun Metagenomics. <i>MSystems</i> , 2018, 3, .	3.8	293
180	Dietary input of microbes and host genetic variation shape among-population differences in stickleback gut microbiota. <i>ISME Journal</i> , 2015, 9, 2515-2526.	9.8	291

#	ARTICLE	IF	CITATIONS
181	FXR Regulates Intestinal Cancer Stem Cell Proliferation. <i>Cell</i> , 2019, 176, 1098-1112.e18.	28.9	291
182	Individuals' diet diversity influences gut microbial diversity in two freshwater fish (threespine stickleback). <i>ISME Journal</i> , 2019, 13, 1507-1517.	6.4	288
183	Molecular cartography of the human skin surface in 3D. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2120-9.	7.1	288
184	Genetic and environmental control of host-gut microbiota interactions. <i>Genome Research</i> , 2015, 25, 1558-1569.	5.5	288
185	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2587-2594.e7.	28.9	285
186	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. <i>Genome Research</i> , 2010, 20, 1411-1419.	5.5	284
187	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	3.8	284
188	Extreme Dysbiosis of the Microbiome in Critical Illness. <i>MSphere</i> , 2016, 1, .	2.9	283
189	Co-habiting amphibian species harbor unique skin bacterial communities in wild populations. <i>ISME Journal</i> , 2012, 6, 588-596.	9.8	282
190	Characterization of Airborne Microbial Communities at a High-Elevation Site and Their Potential To Act as Atmospheric Ice Nuclei. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5121-5130.	3.1	273
191	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. <i>ELife</i> , 2013, 2, e01104.	6.0	270
192	The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 1204-1208.	2.9	266
193	The Microbiome and Human Biology. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 65-86.	6.2	266
194	Finding the Missing Links among Metabolites, Microbes, and the Host. <i>Immunity</i> , 2014, 40, 824-832.	14.3	256
195	A gut bacterial amyloid promotes α -synuclein aggregation and motor impairment in mice. <i>ELife</i> , 2020, 9, .	6.0	251
196	Short-Term Temporal Variability in Airborne Bacterial and Fungal Populations. <i>Applied and Environmental Microbiology</i> , 2008, 74, 200-207.	3.1	250
197	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012, 30, 513-520.	17.5	250
198	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. <i>Nature Methods</i> , 2010, 7, 813-819.	19.0	249

#	ARTICLE	IF	CITATIONS
199	Bacterial colonization and succession in a newly opened hospital. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	248
200	The human microbiome in evolution. <i>BMC Biology</i> , 2017, 15, 127.	3.8	243
201	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. <i>Microbiome</i> , 2020, 8, 82.	11.1	239
202	Sources of Bacteria in Outdoor Air across Cities in the Midwestern United States. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6350-6356.	3.1	237
203	Genetically dictated change in host mucus carbohydrate landscape exerts a diet-dependent effect on the gut microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17059-17064.	7.1	237
204	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019, 13, 576-587.	9.8	236
205	ConStrains identifies microbial strains in metagenomic datasets. <i>Nature Biotechnology</i> , 2015, 33, 1045-1052.	17.5	235
206	The 'rare biosphere': a reality check. <i>Nature Methods</i> , 2009, 6, 636-637.	19.0	231
207	Postprandial remodeling of the gut microbiota in Burmese pythons. <i>ISME Journal</i> , 2010, 4, 1375-1385.	9.8	229
208	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
209	The Intestinal Metabolome: An Intersection Between Microbiota and Host. <i>Gastroenterology</i> , 2014, 146, 1470-1476.	1.3	227
210	Regulation of myocardial ketone body metabolism by the gut microbiota during nutrient deprivation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11276-11281.	7.1	224
211	Microbial Biogeography of Public Restroom Surfaces. <i>PLoS ONE</i> , 2011, 6, e28132.	2.5	222
212	Pan-genome of the dominant human gut-associated archaeon, <i>Methanobrevibacter smithii</i> , studied in twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4599-4606.	7.1	221
213	Baseline survey of the anatomical microbial ecology of an important food plant: <i>Solanum lycopersicum</i> (tomato). <i>BMC Microbiology</i> , 2013, 13, 114.	3.3	221
214	Improved HF183 Quantitative Real-Time PCR Assay for Characterization of Human Fecal Pollution in Ambient Surface Water Samples. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3086-3094.	3.1	221
215	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. <i>MBio</i> , 2017, 8, .	4.1	219
216	Farm-like indoor microbiota in non-farm homes protects children from asthma development. <i>Nature Medicine</i> , 2019, 25, 1089-1095.	30.7	219

#	ARTICLE	IF	CITATIONS
217	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection. <i>Microbiome</i> , 2015, 3, 10.	11.1	218
218	Improving saliva shotgun metagenomics by chemical host DNA depletion. <i>Microbiome</i> , 2018, 6, 42.	11.1	218
219	A gut microbiome signature for cirrhosis due to nonalcoholic fatty liver disease. <i>Nature Communications</i> , 2019, 10, 1406.	12.8	218
220	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , 2019, 4, .	3.8	214
221	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
222	Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. <i>Cell</i> , 2020, 183, 666-683.e17.	28.9	211
223	HLA-B27 and Human β 2-Microglobulin Affect the Gut Microbiota of Transgenic Rats. <i>PLoS ONE</i> , 2014, 9, e105684.	2.5	209
224	Composition of Human Skin Microbiota Affects Attractiveness to Malaria Mosquitoes. <i>PLoS ONE</i> , 2011, 6, e28991.	2.5	208
225	The Gut Microbiome, Aging, and Longevity: A Systematic Review. <i>Nutrients</i> , 2020, 12, 3759.	4.1	207
226	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. <i>Cell Host and Microbe</i> , 2015, 18, 296-306.	11.0	204
227	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. <i>MSystems</i> , 2018, 3, .	3.8	204
228	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020, 11, .	4.1	204
229	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, 4651-4655.	7.1	200
230	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. <i>Nature</i> , 2022, 609, 101-108.	27.8	200
231	Lake microbial communities are resilient after a whole-ecosystem disturbance. <i>ISME Journal</i> , 2012, 6, 2153-2167.	9.8	198
232	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <i>ISME Journal</i> , 2013, 7, 50-60.	9.8	198
233	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , 2021, 18, 165-169.	19.0	198
234	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	197

#	ARTICLE	IF	CITATIONS
235	The microbiome quality control project: baseline study design and future directions. <i>Genome Biology</i> , 2015, 16, 276.	8.8	196
236	A unified initiative to harness Earth's microbiomes. <i>Science</i> , 2015, 350, 507-508.	12.6	195
237	Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. <i>Nature Microbiology</i> , 2016, 1, 16177.	13.3	194
238	The sponge microbiome project. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	193
239	Antifungal isolates database of amphibian skin-associated bacteria and function against emerging fungal pathogens. <i>Ecology</i> , 2015, 96, 595-595.	3.2	192
240	Interacting Symbionts and Immunity in the Amphibian Skin Mucosome Predict Disease Risk and Probiotic Effectiveness. <i>PLoS ONE</i> , 2014, 9, e96375.	2.5	191
241	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
242	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 218-230.	4.4	187
243	Microbial Eukaryotes in the Human Microbiome: Ecology, Evolution, and Future Directions. <i>Frontiers in Microbiology</i> , 2011, 2, 153.	3.5	186
244	Immunization with a heat-killed preparation of the environmental bacterium <i>Mycobacterium vaccae</i> promotes stress resilience in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3130-9.	7.1	186
245	Learning representations of microbe-metabolite interactions. <i>Nature Methods</i> , 2019, 16, 1306-1314.	19.0	184
246	Analysis of the Gut Microbiota in the Old Order Amish and Its Relation to the Metabolic Syndrome. <i>PLoS ONE</i> , 2012, 7, e43052.	2.5	183
247	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	8.8	183
248	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011, 9, e1001088.	5.6	180
249	A gut-derived metabolite alters brain activity and anxiety behaviour in mice. <i>Nature</i> , 2022, 602, 647-653.	27.8	179
250	Insights from Characterizing Extinct Human Gut Microbiomes. <i>PLoS ONE</i> , 2012, 7, e51146.	2.5	178
251	DNA extraction for streamlined metagenomics of diverse environmental samples. <i>BioTechniques</i> , 2017, 62, 290-293.	1.8	178
252	The Earth Microbiome Project: Meeting report of the 1st EMP meeting on sample selection and acquisition at Argonne National Laboratory October 6th 2010.. <i>Standards in Genomic Sciences</i> , 2010, 3, 249-253.	1.5	176

#	ARTICLE	IF	CITATIONS
253	Widespread Colonization of the Lung by <i>Tropheryma whippelii</i> in HIV Infection. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1110-1117.	5.6	175
254	Major HLA class II polymorphism influences gut microbiota composition and diversity. Molecular Ecology, 2014, 23, 4831-4845.	3.9	174
255	Fructose stimulated de novo lipogenesis is promoted by inflammation. Nature Metabolism, 2020, 2, 1034-1045.	11.9	174
256	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	9.6	170
257	The Western English Channel contains a persistent microbial seed bank. ISME Journal, 2012, 6, 1089-1093.	9.8	170
258	Diversity, distribution and sources of bacteria in residential kitchens. Environmental Microbiology, 2013, 15, 588-596.	3.8	170
259	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
260	Associations between human milk oligosaccharides and infant body composition in the first 6 mo of life. American Journal of Clinical Nutrition, 2015, 102, 1381-1388.	4.7	169
261	Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. Genome Research, 2012, 22, 2146-2152.	5.5	167
262	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. Applied and Environmental Microbiology, 2015, 81, 6200-6209.	3.1	167
263	RNA Amino Acid Binding: A Stereochemical Era for the Genetic Code. Journal of Molecular Evolution, 2009, 69, 406-429.	1.8	166
264	Tracking down the sources of experimental contamination in microbiome studies. Genome Biology, 2014, 15, 564.	8.8	164
265	Effects of Diet versus Gastric Bypass on Metabolic Function in Diabetes. New England Journal of Medicine, 2020, 383, 721-732.	27.0	164
266	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. Nature Genetics, 2022, 54, 134-142.	21.4	164
267	The microbiome explored: recent insights and future challenges. Nature Reviews Microbiology, 2013, 11, 213-217.	28.6	162
268	Mass spectrometry searches using MASST. Nature Biotechnology, 2020, 38, 23-26.	17.5	160
269	Seasonal restructuring of the ground squirrel gut microbiota over the annual hibernation cycle. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2013, 304, R33-R42.	1.8	159
270	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. Microbiome, 2019, 7, 50.	11.1	158

#	ARTICLE	IF	CITATIONS
271	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. <i>Schizophrenia Research</i> , 2019, 204, 23-29.	2.0	157
272	ORIGINS OF THE GENETIC CODE: The Escaped Triplet Theory. <i>Annual Review of Biochemistry</i> , 2005, 74, 179-198.	11.1	155
273	Open-Source Sequence Clustering Methods Improve the State Of the Art. <i>MSystems</i> , 2016, 1, .	3.8	155
274	Cross-biome comparison of microbial association networks. <i>Frontiers in Microbiology</i> , 2015, 6, 1200.	3.5	154
275	Collecting Fecal Samples for Microbiome Analyses in Epidemiology Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 407-416.	2.5	154
276	The Microbiome in Posttraumatic Stress Disorder and Trauma-Exposed Controls: An Exploratory Study. <i>Psychosomatic Medicine</i> , 2017, 79, 936-946.	2.0	153
277	Overview and systematic review of studies of microbiome in schizophrenia and bipolar disorder. <i>Journal of Psychiatric Research</i> , 2018, 99, 50-61.	3.1	151
278	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. <i>ISME Journal</i> , 2014, 8, 1904-1919.	9.8	150
279	Exercise Is More Effective at Altering Gut Microbial Composition and Producing Stable Changes in Lean Mass in Juvenile versus Adult Male F344 Rats. <i>PLoS ONE</i> , 2015, 10, e0125889.	2.5	150
280	The Microbiota, Immunoregulation, and Mental Health: Implications for Public Health. <i>Current Environmental Health Reports</i> , 2016, 3, 270-286.	6.7	150
281	A Modular Organization of the Human Intestinal Mucosal Microbiota and Its Association with Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2013, 8, e80702.	2.5	147
282	Global chemical analysis of biology by mass spectrometry. <i>Nature Reviews Chemistry</i> , 2017, 1, .	30.2	146
283	Probiotic treatment restores protection against lethal fungal infection lost during amphibian captivity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161553.	2.6	144
284	Biphasic assembly of the murine intestinal microbiota during early development. <i>ISME Journal</i> , 2013, 7, 1112-1115.	9.8	142
285	Biogeography and habitat modelling of high-alpine bacteria. <i>Nature Communications</i> , 2010, 1, 53.	12.8	141
286	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <i>MSystems</i> , 2017, 2, .	3.8	141
287	Tools for the Microbiome: Nano and Beyond. <i>ACS Nano</i> , 2016, 10, 6-37.	14.6	137
288	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , 2010, 11, 210.	9.6	134

#	ARTICLE	IF	CITATIONS
289	Human-Associated Microbial Signatures: Examining Their Predictive Value. <i>Cell Host and Microbe</i> , 2011, 10, 292-296.	11.0	134
290	A large-scale benchmark study of existing algorithms for taxonomy-independent microbial community analysis. <i>Briefings in Bioinformatics</i> , 2012, 13, 107-121.	6.5	133
291	Preserving microbial diversity. <i>Science</i> , 2018, 362, 33-34.	12.6	133
292	Quantifying and Understanding Well-to-Well Contamination in Microbiome Research. <i>MSystems</i> , 2019, 4, .	3.8	132
293	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
294	IL-4R α Blockade by Dupilumab Decreases <i>Staphylococcus aureus</i> Colonization and Increases Microbial Diversity in Atopic Dermatitis. <i>Journal of Investigative Dermatology</i> , 2020, 140, 191-202.e7.	0.7	130
295	Role of the microbiome, probiotics, and "dysbiosis therapy"™ in critical illness. <i>Current Opinion in Critical Care</i> , 2016, 22, 347-353.	3.2	128
296	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. <i>Genome Biology</i> , 2016, 17, 217.	8.8	128
297	MlxS-BE: a MlxS extension defining a minimum information standard for sequence data from the built environment. <i>ISME Journal</i> , 2014, 8, 1-3.	9.8	127
298	Toward a Predictive Understanding of Earth's™ Microbiomes to Address 21st Century Challenges. <i>MBio</i> , 2016, 7, .	4.1	124
299	METTL3 regulates viral m6A RNA modification and host cell innate immune responses during SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 35, 109091.	6.4	124
300	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018, 3, .	3.8	123
301	Gut Microbiota in the First 2 Years of Life and the Association with Body Mass Index at Age 12 in a Norwegian Birth Cohort. <i>MBio</i> , 2018, 9, .	4.1	121
302	The convergence of carbohydrate active gene repertoires in human gut microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15076-15081.	7.1	120
303	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. <i>Genome Research</i> , 2012, 22, 1974-1984.	5.5	120
304	Bacterial Diversity in Two Neonatal Intensive Care Units (NICUs). <i>PLoS ONE</i> , 2013, 8, e54703.	2.5	120
305	Predictive modeling of gingivitis severity and susceptibility via oral microbiota. <i>ISME Journal</i> , 2014, 8, 1768-1780.	9.8	118
306	Effect of preservation method on spider monkey (<i>Ateles geoffroyi</i>) fecal microbiota over 8weeks. <i>Journal of Microbiological Methods</i> , 2015, 113, 16-26.	1.6	118

#	ARTICLE	IF	CITATIONS
307	Changes in microbial ecology after fecal microbiota transplantation for recurrent <i>C. difficile</i> infection affected by underlying inflammatory bowel disease. <i>Microbiome</i> , 2017, 5, 55.	11.1	118
308	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. <i>MSystems</i> , 2017, 2, .	3.8	116
309	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. <i>Microbiome</i> , 2015, 3, 20.	11.1	115
310	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1 month. <i>Microbiome</i> , 2019, 7, 34.	11.1	115
311	Mosquito Microbiome Dynamics, a Background for Prevalence and Seasonality of West Nile Virus. <i>Frontiers in Microbiology</i> , 2017, 8, 526.	3.5	114
312	Fecal Microbiota Transplantation Is Highly Effective in Real-World Practice: Initial Results From the FMT National Registry. <i>Gastroenterology</i> , 2021, 160, 183-192.e3.	1.3	113
313	Comparison of Collection Methods for Fecal Samples in Microbiome Studies. <i>American Journal of Epidemiology</i> , 2017, 185, 115-123.	3.4	112
314	Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017, 7, 15497.	3.3	112
315	Inhibitory bacteria reduce fungi on early life stages of endangered Colorado boreal toads (<i>Anaxyrus boreas</i>). <i>ISME Journal</i> , 2016, 10, 934-944.	9.8	111
316	Three-Dimensional Microbiome and Metabolome Cartography of a Diseased Human Lung. <i>Cell Host and Microbe</i> , 2017, 22, 705-716.e4.	11.0	111
317	Tfap2 transcription factors in zebrafish neural crest development and ectodermal evolution. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 679-691.	1.3	110
318	Geography and Location Are the Primary Drivers of Office Microbiome Composition. <i>MSystems</i> , 2016, 1, .	3.8	110
319	Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity. <i>Nature Microbiology</i> , 2022, 7, 262-276.	13.3	110
320	Spatial and temporal dynamics of the microbial community in the Hanford unconfined aquifer. <i>ISME Journal</i> , 2012, 6, 1665-1676.	9.8	109
321	Variable responses of human and non-human primate gut microbiomes to a Western diet. <i>Microbiome</i> , 2015, 3, 53.	11.1	108
322	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , 2018, 9, 2832.	12.8	108
323	Diet Versus Phylogeny: a Comparison of Gut Microbiota in Captive Colobine Monkey Species. <i>Microbial Ecology</i> , 2018, 75, 515-527.	2.8	106
324	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. <i>Journal of Physiology</i> , 2019, 597, 2361-2378.	2.9	106

#	ARTICLE	IF	CITATIONS
325	High-Throughput Wastewater SARS-CoV-2 Detection Enables Forecasting of Community Infection Dynamics in San Diego County. <i>MSystems</i> , 2021, 6, .	3.8	106
326	Links between environment, diet, and the hunter-gatherer microbiome. <i>Gut Microbes</i> , 2019, 10, 216-227.	9.8	105
327	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 109-114.	6.1	104
328	Anal gas evacuation and colonic microbiota in patients with flatulence: effect of diet. <i>Gut</i> , 2014, 63, 401-408.	12.1	104
329	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. <i>Nature Communications</i> , 2018, 9, 2017.	12.8	103
330	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. <i>ISME Journal</i> , 2012, 6, 1273-1276.	9.8	102
331	Distinct cutaneous bacterial assemblages in a sampling of South American Amerindians and US residents. <i>ISME Journal</i> , 2013, 7, 85-95.	9.8	101
332	Fat and vitamin intakes during pregnancy have stronger relations with a pro-inflammatory maternal microbiota than does carbohydrate intake. <i>Microbiome</i> , 2016, 4, 55.	11.1	101
333	The impact of skin care products on skin chemistry and microbiome dynamics. <i>BMC Biology</i> , 2019, 17, 47.	3.8	101
334	The Ecology of Microbial Communities Associated with <i>Macrocystis pyrifera</i> . <i>PLoS ONE</i> , 2013, 8, e67480.	2.5	100
335	Characterizing microbial communities through space and time. <i>Current Opinion in Biotechnology</i> , 2012, 23, 431-436.	6.6	98
336	Host age, social group, and habitat type influence the gut microbiota of wild ring-tailed lemurs (<i>Lemur catta</i>). <i>American Journal of Primatology</i> , 2016, 78, 883-892.	1.7	98
337	Origin of microbial biomineralization and magnetotaxis during the Archean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2171-2176.	7.1	98
338	Current Concepts, Opportunities, and Challenges of Gut Microbiome-Based Personalized Medicine in Nonalcoholic Fatty Liver Disease. <i>Cell Metabolism</i> , 2021, 33, 21-32.	16.2	98
339	Host and gut microbial tryptophan metabolism and type 2 diabetes: an integrative analysis of host genetics, diet, gut microbiome and circulating metabolites in cohort studies. <i>Gut</i> , 2022, 71, 1095-1105.	12.1	98
340	Toward Effective Probiotics for Autism and Other Neurodevelopmental Disorders. <i>Cell</i> , 2013, 155, 1446-1448.	28.9	97
341	Visualizing omic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa023.	3.2	97
342	Air pollution exposure is associated with the gut microbiome as revealed by shotgun metagenomic sequencing. <i>Environment International</i> , 2020, 138, 105604.	10.0	97

#	ARTICLE	IF	CITATIONS
343	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. <i>MSystems</i> , 2018, 3, .	3.8	96
344	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017, 21, 7-10.	11.0	95
345	Exposure to toxic metals triggers unique responses from the rat gut microbiota. <i>Scientific Reports</i> , 2018, 8, 6578.	3.3	95
346	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. <i>Genome Biology</i> , 2019, 20, 219.	8.8	94
347	Rapid, Large-Scale Wastewater Surveillance and Automated Reporting System Enable Early Detection of Nearly 85% of COVID-19 Cases on a University Campus. <i>MSystems</i> , 2021, 6, e0079321.	3.8	94
348	Microbiome Tools for Forensic Science. <i>Trends in Biotechnology</i> , 2017, 35, 814-823.	9.3	93
349	How biologists conceptualize genes: an empirical study. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2004, 35, 647-673.	1.3	92
350	Phylogenetic and ecological factors impact the gut microbiota of two Neotropical primate species. <i>Oecologia</i> , 2016, 180, 717-733.	2.0	91
351	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016, 1, .	3.8	89
352	Are all horizontal gene transfers created equal? Prospects for mechanism-based studies of HGT patterns. <i>Microbiology (United Kingdom)</i> , 2008, 154, 1-15.	1.8	88
353	Seasonal variation of postmortem microbial communities. <i>Forensic Science, Medicine, and Pathology</i> , 2015, 11, 202-207.	1.4	88
354	Gut microbiome and magnetic resonance spectroscopy study of subjects at ultra-high risk for psychosis may support the membrane hypothesis. <i>European Psychiatry</i> , 2018, 53, 37-45.	0.2	88
355	Vitamin D metabolites and the gut microbiome in older men. <i>Nature Communications</i> , 2020, 11, 5997.	12.8	88
356	Evolutionary rates vary among rRNA structural elements. <i>Nucleic Acids Research</i> , 2007, 35, 3339-3354.	14.5	87
357	Diets high in resistant starch increase plasma levels of trimethylamine- <i>N</i> -oxide, a gut microbiome metabolite associated with CVD risk. <i>British Journal of Nutrition</i> , 2016, 116, 2020-2029.	2.3	86
358	Ten simple rules for writing and sharing computational analyses in Jupyter Notebooks. <i>PLoS Computational Biology</i> , 2019, 15, e1007007.	3.2	86
359	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019, 10, 4643.	12.8	86
360	Ribosomal RNA diversity predicts genome diversity in gut bacteria and their relatives. <i>Nucleic Acids Research</i> , 2010, 38, 3869-3879.	14.5	85

#	ARTICLE	IF	CITATIONS
361	Microbiota at Multiple Body Sites during Pregnancy in a Rural Tanzanian Population and Effects of Moringa-Supplemented Probiotic Yogurt. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4965-4975.	3.1	85
362	Vertebrate Decomposition Is Accelerated by Soil Microbes. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4920-4929.	3.1	84
363	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. <i>MSphere</i> , 2017, 2, .	2.9	84
364	Home chemical and microbial transitions across urbanization. <i>Nature Microbiology</i> , 2020, 5, 108-115.	13.8	83
365	Diversity of Rickettsiales in the Microbiome of the Lone Star Tick, <i>Amblyomma americanum</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 354-359.	3.1	82
366	Which is more important for classifying microbial communities: whoâ€™s there or what they can do?. <i>ISME Journal</i> , 2014, 8, 2357-2359.	9.8	82
367	Patterns of Oral Microbiota Diversity in Adults and Children: A Crowdsourced Population Study. <i>Scientific Reports</i> , 2020, 10, 2133.	3.3	82
368	Context and the human microbiome. <i>Microbiome</i> , 2015, 3, 52.	11.1	81
369	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	3.8	81
370	The Cladistic Basis for the Phylogenetic Diversity (PD) Measure Links Evolutionary Features to Environmental Gradients and Supports Broad Applications of Microbial Ecologyâ€™s â€œPhylogenetic Beta Diversityâ€™ Framework. <i>International Journal of Molecular Sciences</i> , 2009, 10, 4723-4741.	4.1	80
371	Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. <i>Genes</i> , 2018, 9, 104.	2.4	80
372	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. <i>MSystems</i> , 2020, 5, .	3.8	80
373	ReDU: a framework to find and reanalyze public mass spectrometry data. <i>Nature Methods</i> , 2020, 17, 901-904.	19.0	79
374	Auto-deconvolution and molecular networking of gas chromatographyâ€™mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173.	17.5	78
375	Dramatic Differences in Gut Bacterial Densities Correlate with Diet and Habitat in Rainforest Ants. <i>Integrative and Comparative Biology</i> , 2017, 57, 705-722.	2.0	77
376	Using the gut microbiota as a novel tool for examining colobine primate GI health. <i>Global Ecology and Conservation</i> , 2016, 7, 225-237.	2.1	76
377	tRNA Creation by Hairpin Duplication. <i>Journal of Molecular Evolution</i> , 2005, 61, 524-530.	1.8	75
378	Perinatal Bisphenol A Exposure Induces Chronic Inflammation in Rabbit Offspring via Modulation of Gut Bacteria and Their Metabolites. <i>MSystems</i> , 2017, 2, .	3.8	75

#	ARTICLE	IF	CITATIONS
379	Disease-modifying therapies alter gut microbial composition in MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2019, 6, e517.	6.0	75
380	Impacts of the Human Gut Microbiome on Therapeutics. <i>Annual Review of Pharmacology and Toxicology</i> , 2018, 58, 253-270.	9.4	74
381	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	8.0	73
382	Discrete False-Discovery Rate Improves Identification of Differentially Abundant Microbes. <i>MSystems</i> , 2017, 2, .	3.8	73
383	Natural selection is not required to explain universal compositional patterns in rRNA secondary structure categories. <i>Rna</i> , 2006, 12, 1-14.	3.5	72
384	Walls talk: Microbial biogeography of homes spanning urbanization. <i>Science Advances</i> , 2016, 2, e1501061.	10.3	72
385	Our microbial selves: what ecology can teach us. <i>EMBO Reports</i> , 2011, 12, 775-784.	4.5	71
386	Commensal Bacteria and MAMPs Are Necessary for Stress-Induced Increases in IL-1 β and IL-18 but Not IL-6, IL-10 or MCP-1. <i>PLoS ONE</i> , 2012, 7, e50636.	2.5	71
387	Changes in vaginal microbiota following antimicrobial and probiotic therapy. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 27799.	3.5	71
388	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018, 15, 847-848.	19.0	71
389	Microbial Ecology of Atlantic Salmon (<i>Salmo salar</i>) Hatcheries: Impacts of the Built Environment on Fish Mucosal Microbiota. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	71
390	Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. <i>Environmental Science & Technology</i> , 2021, 55, 4899-4913.	10.0	71
391	Patterns in Gut Microbiota Similarity Associated with Degree of Sociality among Sex Classes of a Neotropical Primate. <i>Microbial Ecology</i> , 2017, 74, 250-258.	2.8	70
392	Differential Activation of Hepatic Invariant NKT Cell Subsets Plays a Key Role in Progression of Nonalcoholic Steatohepatitis. <i>Journal of Immunology</i> , 2018, 201, 3017-3035.	0.8	69
393	Interleukin-1 β (IL-1 β) promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. <i>Gut</i> , 2012, 61, 373-384.	12.1	68
394	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	13.3	68
395	Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information. <i>Genome Research</i> , 2020, 30, 898-909.	5.5	68
396	A preliminary survey of lichen associated eukaryotes using pyrosequencing. <i>Lichenologist</i> , 2012, 44, 137-146.	0.8	67

#	ARTICLE	IF	CITATIONS
397	Uncovering the Horseshoe Effect in Microbial Analyses. <i>MSystems</i> , 2017, 2, .	3.8	67
398	Dietary Prebiotics and Bioactive Milk Fractions Improve NREM Sleep, Enhance REM Sleep Rebound and Attenuate the Stress-Induced Decrease in Diurnal Temperature and Gut Microbial Alpha Diversity. <i>Frontiers in Behavioral Neuroscience</i> , 2016, 10, 240.	2.0	67
399	Association Between the Gut Microbiota and Blood Pressure in a Population Cohort of 6953 Individuals. <i>Journal of the American Heart Association</i> , 2020, 9, e016641.	3.7	67
400	Effects of the microalgae <i>Chlamydomonas</i> on gastrointestinal health. <i>Journal of Functional Foods</i> , 2020, 65, 103738.	3.4	66
401	From knotted to nested RNA structures: A variety of computational methods for pseudoknot removal. <i>Rna</i> , 2008, 14, 410-416.	3.5	65
402	The bacterial microbiota in the oral mucosa of rural Amerindians. <i>Microbiology (United Kingdom)</i> , 2010, 156, 3282-3287.	1.8	65
403	Vertebrate Hosts as Islands: Dynamics of Selection, Immigration, Loss, Persistence, and Potential Function of Bacteria on Salamander Skin. <i>Frontiers in Microbiology</i> , 2016, 7, 333.	3.5	65
404	Earth Microbiome Project and Global Systems Biology. <i>MSystems</i> , 2018, 3, .	3.8	65
405	Engineering the microbiome for animal health and conservation. <i>Experimental Biology and Medicine</i> , 2019, 244, 494-504.	2.4	65
406	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	28.9	64
407	Precision medicine in alcoholic and nonalcoholic fatty liver disease via modulating the gut microbiota. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, G1018-G1036.	3.4	64
408	Comparison of Collection Methods for Fecal Samples for Discovery Metabolomics in Epidemiologic Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1483-1490.	2.5	63
409	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
410	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	19.0	63
411	Coupling Targeted and Untargeted Mass Spectrometry for Metabolome-Microbiome-Wide Association Studies of Human Fecal Samples. <i>Analytical Chemistry</i> , 2017, 89, 7549-7559.	6.5	62
412	Intermittent Hypoxia and Hypercapnia Accelerate Atherosclerosis, Partially via Trimethylamine-Oxide. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2017, 57, 581-588.	2.9	62
413	Spatial and temporal variability of the human microbiota. <i>Clinical Microbiology and Infection</i> , 2012, 18, 5-7.	6.0	61
414	The Oral and Skin Microbiomes of Captive Komodo Dragons Are Significantly Shared with Their Habitat. <i>MSystems</i> , 2016, 1, .	3.8	61

#	ARTICLE	IF	CITATIONS
415	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021, 39, 165-168.	17.5	61
416	Abundance of correctly folded RNA motifs in sequence space, calculated on computational grids. <i>Nucleic Acids Research</i> , 2005, 33, 5924-5935.	14.5	60
417	The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , 2011, 5, 1565-1567.	9.8	59
418	Longitudinal survey of microbiome associated with particulate matter in a megacity. <i>Genome Biology</i> , 2020, 21, 55.	8.8	59
419	Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules. <i>Genome Research</i> , 2021, 31, 64-74.	5.5	59
420	The human microbiome: eliminating the biomedical/environmental dichotomy in microbial ecology. <i>Environmental Microbiology</i> , 2007, 9, 3-4.	3.8	58
421	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. <i>MSystems</i> , 2018, 3, .	3.8	58
422	Mortality Risk Profiling of <i>Staphylococcus aureus</i> Bacteremia by Multi-omic Serum Analysis Reveals Early Predictive and Pathogenic Signatures. <i>Cell</i> , 2020, 182, 1311-1327.e14.	28.9	58
423	Advancing analytical algorithms and pipelines for billions of microbial sequences. <i>Current Opinion in Biotechnology</i> , 2012, 23, 64-71.	6.6	57
424	Structural basis for diversity in the SAM clan of riboswitches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6624-6629.	7.1	57
425	Social behaviour and gut microbiota in red-bellied lemurs (<i>Eulemur rubriventer</i>): In search of the role of immunity in the evolution of sociality. <i>Journal of Animal Ecology</i> , 2018, 87, 388-399.	2.8	57
426	Convergence of human and Old World monkey gut microbiomes demonstrates the importance of human ecology over phylogeny. <i>Genome Biology</i> , 2019, 20, 201.	8.8	57
427	Multilevel Research Strategies and Biological Systems. <i>Philosophy of Science</i> , 2014, 81, 811-828.	1.0	56
428	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. <i>MSystems</i> , 2018, 3, .	3.8	56
429	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. <i>PLoS ONE</i> , 2020, 15, e0229001.	2.5	56
430	Size, constant sequences, and optimal selection. <i>Rna</i> , 2005, 11, 1701-1709.	3.5	55
431	pH is a good predictor of the distribution of anoxygenic purple phototrophic bacteria in Arctic soils. <i>Soil Biology and Biochemistry</i> , 2014, 74, 193-200.	8.8	55
432	Lifestyle chemistries from phones for individual profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7645-E7654.	7.1	55

#	ARTICLE	IF	CITATIONS
433	Bacterial community changes in an industrial algae production system. <i>Algal Research</i> , 2018, 31, 147-156.	4.6	55
434	Gut microbiota in wild and captive Guizhou snub-nosed monkeys, <i>Rhinopithecus brelichi</i> . <i>American Journal of Primatology</i> , 2019, 81, e22989.	1.7	55
435	Microbial Diversity in Clinical Microbiome Studies: Sample Size and Statistical Power Considerations. <i>Gastroenterology</i> , 2020, 158, 1524-1528.	1.3	55
436	Insight into the function and evolution of the Wood-Ljungdahl pathway in <i>Actinobacteria</i> . <i>ISME Journal</i> , 2021, 15, 3005-3018.	9.8	55
437	Taxonomic signatures of cause-specific mortality risk in human gut microbiome. <i>Nature Communications</i> , 2021, 12, 2671.	12.8	55
438	How delivery mode and feeding can shape the bacterial community in the infant gut. <i>Cmaj</i> , 2013, 185, 373-374.	2.0	54
439	Impact of ileocecal Resection and Concomitant Antibiotics on the Microbiome of the Murine Jejunum and Colon. <i>PLoS ONE</i> , 2013, 8, e73140.	2.5	54
440	Skin bacteria provide early protection for newly metamorphosed southern leopard frogs (<i>Rana</i>). <i>Conservation Biology</i> , 2015, 187, 91-102.	4.1	54
441	Coprolites reveal ecological interactions lost with the extinction of New Zealand birds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1546-1551.	7.1	54
442	From Sample to Multi-Omics Conclusions in under 48 Hours. <i>MSystems</i> , 2016, 1, .	3.8	53
443	Gut microbiome of mothers delivering prematurely shows reduced diversity and lower relative abundance of <i>Bifidobacterium</i> and <i>Streptococcus</i> . <i>PLoS ONE</i> , 2017, 12, e0184336.	2.5	53
444	Major shifts in gut microbiota during development and its relationship to growth in ostriches. <i>Molecular Ecology</i> , 2019, 28, 2653-2667.	3.9	53
445	Neutrophilic proteolysis in the cystic fibrosis lung correlates with a pathogenic microbiome. <i>Microbiome</i> , 2019, 7, 23.	11.1	53
446	Finding specific RNA motifs: Function in a zeptomole world?. <i>Rna</i> , 2003, 9, 218-230.	3.5	52
447	The murine vaginal microbiota and its perturbation by the human pathogen group B <i>Streptococcus</i> . <i>BMC Microbiology</i> , 2018, 18, 197.	3.3	52
448	Insights and inferences about integron evolution from genomic data. <i>BMC Genomics</i> , 2008, 9, 261.	2.8	51
449	The founding charter of the Genomic Observatories Network. <i>GigaScience</i> , 2014, 3, 2.	6.4	51
450	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. <i>Microbiome</i> , 2016, 4, 11.	11.1	51

#	ARTICLE	IF	CITATIONS
451	Human Immunodeficiency Virus Signature Sequences Are Associated with Pulmonary Hypertension. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 607-618.	1.1	50
452	Nucleotides Adjacent to the Ligand-Binding Pocket are Linked to Activity Tuning in the Purine Riboswitch. <i>Journal of Molecular Biology</i> , 2013, 425, 1596-1611.	4.2	50
453	Microbiology of death. <i>Current Biology</i> , 2016, 26, R561-R563.	3.9	50
454	Comparison of Fecal Collection Methods for Microbiota Studies in Bangladesh. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	50
455	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , 2020, 82, 26-41.	13.4	50
456	A Simulated MS/MS Library for Spectrum-to-spectrum Searching in Large Scale Identification of Proteins. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 857-869.	3.8	49
457	Co-Enriching Microflora Associated with Culture Based Methods to Detect Salmonella from Tomato Phyllosphere. <i>PLoS ONE</i> , 2013, 8, e73079.	2.5	49
458	Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. <i>Water Research</i> , 2015, 69, 30-39.	11.3	49
459	Carcass mass has little influence on the structure of gravesoil microbial communities. <i>International Journal of Legal Medicine</i> , 2016, 130, 253-263.	2.2	49
460	Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, <i>Scomber japonicus</i> . <i>MSphere</i> , 2020, 5, .	2.9	49
461	Triplicate PCR reactions for 16S rRNA gene amplicon sequencing are unnecessary. <i>BioTechniques</i> , 2019, 67, 29-32.	1.8	48
462	Stress response, gut microbial diversity and sexual signals correlate with social interactions. <i>Biology Letters</i> , 2016, 12, 20160352.	2.3	47
463	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	8.8	47
464	Gut microbiome in serious mental illnesses: A systematic review and critical evaluation. <i>Schizophrenia Research</i> , 2021, 234, 24-40.	2.0	47
465	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020, 5, .	3.8	47
466	Gut Microbiome Composition Is Predictive of Incident Type 2 Diabetes in a Population Cohort of 5,572 Finnish Adults. <i>Diabetes Care</i> , 2022, 45, 811-818.	8.6	47
467	Bioinformatics Assessment of Î²-Myosin Mutations Reveals Myosin's High Sensitivity to Mutations. <i>Trends in Cardiovascular Medicine</i> , 2008, 18, 141-149.	4.9	46
468	A Microbiome Foundation for the Study of Crohn's Disease. <i>Cell Host and Microbe</i> , 2017, 21, 301-304.	11.0	46

#	ARTICLE	IF	CITATIONS
469	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	6.2	46
470	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	45
471	The Urinary Tract Microbiome in Older Women Exhibits Host Genetic and Environmental Influences. <i>Cell Host and Microbe</i> , 2020, 28, 298-305.e3.	11.0	45
472	Mass Spectrometry-Based Visualization of Molecules Associated with Human Habitats. <i>Analytical Chemistry</i> , 2016, 88, 10775-10784.	6.5	44
473	Environmental radiation alters the gut microbiome of the bank vole <i>Myodes glareolus</i> . <i>ISME Journal</i> , 2018, 12, 2801-2806.	9.8	44
474	Expanding magnetic organelle biogenesis in the domain Bacteria. <i>Microbiome</i> , 2020, 8, 152.	11.1	44
475	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. <i>Brain, Behavior, and Immunity</i> , 2021, 91, 245-256.	4.1	44
476	Bacterial communities of disease vectors sampled across time, space, and species. <i>ISME Journal</i> , 2010, 4, 223-231.	9.8	43
477	Host-Associated and Free-Living Phage Communities Differ Profoundly in Phylogenetic Composition. <i>PLoS ONE</i> , 2011, 6, e16900.	2.5	43
478	Triclosan leads to dysregulation of the metabolic regulator FGF21 exacerbating high fat diet-induced nonalcoholic fatty liver disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31259-31266.	7.1	43
479	Supervised classification of microbiota mitigates mislabeling errors. <i>ISME Journal</i> , 2011, 5, 570-573.	9.8	42
480	Turning Participatory Microbiome Research into Usable Data: Lessons from the American Gut Project. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 46-50.	1.0	42
481	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. <i>Bioinformatics</i> , 2020, 36, 4088-4090.	4.1	42
482	Associations of healthy food choices with gut microbiota profiles. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 605-616.	4.7	42
483	Links between gut microbiome composition and fatty liver disease in a large population sample. <i>Gut Microbes</i> , 2021, 13, 1-22.	9.8	41
484	Prevalence and genetic diversity of <i>Blastocystis</i> in family units living in the United States. <i>Infection, Genetics and Evolution</i> , 2016, 45, 95-97.	2.3	40
485	Metagenomic covariation along densely sampled environmental gradients in the Red Sea. <i>ISME Journal</i> , 2017, 11, 138-151.	9.8	40
486	Niche partitioning of a pathogenic microbiome driven by chemical gradients. <i>Science Advances</i> , 2018, 4, eaau1908.	10.3	40

#	ARTICLE	IF	CITATIONS
487	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. <i>MSystems</i> , 2019, 4, .	3.8	40
488	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. <i>Journal of Forensic Sciences</i> , 2019, 64, 791-798.	1.6	40
489	Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. <i>Microbiome</i> , 2021, 9, 92.	11.1	40
490	BayesFold: Rational 2 ^Δ folds that combine thermodynamic, covariation, and chemical data for aligned RNA sequences. <i>Rna</i> , 2004, 10, 1323-1336.	3.5	39
491	Replenishing our defensive microbes. <i>BioEssays</i> , 2013, 35, 810-817.	2.5	39
492	Experimental Chagas disease-induced perturbations of the fecal microbiome and metabolome. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006344.	3.0	39
493	Altered Gut Microbiota and Host Metabolite Profiles in Women With Human Immunodeficiency Virus. <i>Clinical Infectious Diseases</i> , 2020, 71, 2345-2353.	5.8	38
494	Metagenomics-Based, Strain-Level Analysis of <i>Escherichia coli</i> From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018, 9, 2559.	3.5	37
495	Single-Cell Transcriptomics Reveal a Correlation between Genome Architecture and Gene Family Evolution in Ciliates. <i>MBio</i> , 2019, 10, .	4.1	37
496	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
497	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	4.4	37
498	Stable tRNA-based phylogenies using only 76 nucleotides. <i>Rna</i> , 2010, 16, 1469-1477.	3.5	36
499	Twisted Tales: Insights into Genome Diversity of Ciliates Using Single-Cell ¹⁶ S-Omics. <i>Genome Biology and Evolution</i> , 2018, 10, 1927-1938.	2.5	36
500	Challenges in the construction of knowledge bases for human microbiome-disease associations. <i>Microbiome</i> , 2019, 7, 129.	11.1	36
501	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	3.8	36
502	Simple, recurring RNA binding sites for L-arginine. <i>Rna</i> , 2010, 16, 805-816.	3.5	35
503	Xenobiotics and the Human Gut Microbiome: Metatranscriptomics Reveal the Active Players. <i>Cell Metabolism</i> , 2013, 17, 317-318.	16.2	35
504	Glycan Degradation (GlyDeR) Analysis Predicts Mammalian Gut Microbiota Abundance and Host Diet-Specific Adaptations. <i>MBio</i> , 2014, 5, .	4.1	35

#	ARTICLE	IF	CITATIONS
505	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. <i>GigaScience</i> , 2016, 5, 27.	6.4	35
506	Mass Spectrometry-Based Chemical Cartography of a Cardiac Parasitic Infection. <i>Analytical Chemistry</i> , 2017, 89, 10414-10421.	6.5	35
507	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	3.8	35
508	Development of a Rapid and Sensitive CasRx-Based Diagnostic Assay for SARS-CoV-2. <i>ACS Sensors</i> , 2021, 6, 3957-3966.	7.8	35
509	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. <i>Cell Metabolism</i> , 2022, 34, 719-730.e4.	16.2	35
510	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
511	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	3.8	35
512	The RNA structure alignment ontology. <i>Rna</i> , 2009, 15, 1623-1631.	3.5	34
513	Meeting Report: Fungal ITS Workshop (October 2012). <i>Standards in Genomic Sciences</i> , 2013, 8, 118-123.	1.5	34
514	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018, 8, 3669.	3.3	34
515	Ruminiclostridium 5, Parabacteroides distasonis, and bile acid profile are modulated by prebiotic diet and associate with facilitated sleep/clock realignment after chronic disruption of rhythms. <i>Brain, Behavior, and Immunity</i> , 2021, 97, 150-166.	4.1	34
516	Environmental reservoirs of pathogenic mycobacteria across the Ethiopian biogeographical landscape. <i>PLoS ONE</i> , 2017, 12, e0173811.	2.5	34
517	A population of Pax7-expressing muscle progenitor cells show differential responses to muscle injury dependent on developmental stage and injury extent. <i>Frontiers in Aging Neuroscience</i> , 2015, 7, 161.	3.4	33
518	Benchmarking urine storage and collection conditions for evaluating the female urinary microbiome. <i>Scientific Reports</i> , 2019, 9, 13409.	3.3	33
519	Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. <i>International Journal of Cancer</i> , 2021, 148, 2712-2723.	5.1	33
520	Digitizing mass spectrometry data to explore the chemical diversity and distribution of marine cyanobacteria and algae. <i>ELife</i> , 2017, 6, .	6.0	33
521	Error Minimization and Coding Triplet/Binding Site Associations Are Independent Features of the Canonical Genetic Code. <i>Journal of Molecular Evolution</i> , 2005, 61, 597-607.	1.8	32
522	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018, 67, 1743-1745.	12.1	32

#	ARTICLE	IF	CITATIONS
523	Early life gut microbiota is associated with rapid infant growth in Hispanics from Southern California. <i>Gut Microbes</i> , 2021, 13, 1961203.	9.8	32
524	Dietary factors, gut microbiota, and serum trimethylamine-N-oxide associated with cardiovascular disease in the Hispanic Community Health Study/Study of Latinos. <i>American Journal of Clinical Nutrition</i> , 2021, 113, 1503-1514.	4.7	32
525	Context-aware deconvolution of cell-cell communication with Tensor-cell2cell. <i>Nature Communications</i> , 2022, 13, .	12.8	32
526	Diet and feeding pattern modulate diurnal dynamics of the ileal microbiome and transcriptome. <i>Cell Reports</i> , 2022, 40, 111008.	6.4	32
527	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	28.9	31
528	RNASTAR: An RNA STRUCTURAL ALIGNMENT REPOSITORY that provides insight into the evolution of natural and artificial RNAs. <i>Rna</i> , 2012, 18, 1319-1327.	3.5	30
529	Translating the human microbiome. <i>Nature Biotechnology</i> , 2013, 31, 304-308.	17.5	30
530	Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. <i>Engineering</i> , 2017, 3, 66-70.	6.7	30
531	Ground beef microbiome changes with antimicrobial decontamination interventions and product storage. <i>PLoS ONE</i> , 2019, 14, e0217947.	2.5	30
532	Early-life gut dysbiosis linked to juvenile mortality in ostriches. <i>Microbiome</i> , 2020, 8, 147.	11.1	30
533	Candidate probiotic <i>Lactiplantibacillus plantarum</i> HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. <i>Microbiome</i> , 2021, 9, 151.	11.1	30
534	Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021, 15, 3399-3411.	9.8	30
535	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011, 17, 1204-1212.	3.5	28
536	Effects of field conditions on fecal microbiota. <i>Journal of Microbiological Methods</i> , 2016, 130, 180-188.	1.6	28
537	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018, 9, .	4.1	28
538	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	3.8	28
539	Comparison of Oral Collection Methods for Studies of Microbiota. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 137-143.	2.5	28
540	Type I IFNs and CD8 T cells increase intestinal barrier permeability after chronic viral infection. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	28

#	ARTICLE	IF	CITATIONS
541	A posteriori dietary patterns better explain variations of the gut microbiome than individual markers in the American Gut Project. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 432-443.	4.7	28
542	Multiple pattern matching: a Markov chain approach. <i>Journal of Mathematical Biology</i> , 2007, 56, 51-92.	1.9	27
543	Avoiding Pandemic Fears in the Subway and Conquering the Platypus. <i>MSystems</i> , 2016, 1, .	3.8	27
544	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	5.1	27
545	Intermittent Hypoxia and Hypercapnia Alter Diurnal Rhythms of Luminal Gut Microbiome and Metabolome. <i>MSystems</i> , 2021, 6, e0011621.	3.8	27
546	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , 2021, 6, e0069121.	3.8	27
547	SnapShot: The Human Microbiome. <i>Cell</i> , 2014, 158, 690-690.e1.	28.9	26
548	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	26
549	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. <i>BMC Evolutionary Biology</i> , 2008, 8, 327.	3.2	25
550	Eggshell Bacterial Load Is Related to Antimicrobial Properties of Feathers Lining Barn Swallow Nests. <i>Microbial Ecology</i> , 2014, 67, 480-487.	2.8	25
551	Wildlife-microbiome interactions and disease: exploring opportunities for disease mitigation across ecological scales. <i>Drug Discovery Today: Disease Models</i> , 2018, 28, 105-115.	1.2	25
552	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 603-616.	1.9	25
553	A comparison of six DNA extraction protocols for 16S, ITS and shotgun metagenomic sequencing of microbial communities. <i>BioTechniques</i> , 2022, 73, 34-46.	1.8	25
554	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	17.5	25
555	Secondary structure information does not improve OTU assignment for partial 16s rRNA sequences. <i>ISME Journal</i> , 2012, 6, 1277-1280.	9.8	24
556	Antibiotic discovery is a walk in the park. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14477-14479.	7.1	24
557	Transcriptional characterization of <i>Vibrio fischeri</i> during colonization of juvenile <i>Euprymna scolopes</i> . <i>Environmental Microbiology</i> , 2017, 19, 1845-1856.	3.8	24
558	Mass Spectrometry Based Molecular 3D-Cartography of Plant Metabolites. <i>Frontiers in Plant Science</i> , 2017, 8, 429.	3.6	24

#	ARTICLE	IF	CITATIONS
559	Exploration of the Germline Genome of the Ciliate <i>Chilodonella uncinata</i> through Single-Cell Omics (Transcriptomics and Genomics). <i>MBio</i> , 2018, 9, .	4.1	24
560	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. <i>MSystems</i> , 2019, 4, .	3.8	24
561	Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2021, 27, 366-379.	3.0	24
562	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. <i>Trends in Microbiology</i> , 2011, 19, 472-482.	7.7	23
563	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. <i>Applied Ontology</i> , 2011, 6, 53-89.	2.0	23
564	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (<i>Oreochromis shiranus</i>) and North African catfish (<i>Clarias gariepinus</i>). <i>MicrobiologyOpen</i> , 2018, 7, e00716.	3.0	23
565	Defining Host Responses during Systemic Bacterial Infection through Construction of a Murine Organ Proteome Atlas. <i>Cell Systems</i> , 2018, 6, 579-592.e4.	6.2	23
566	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. <i>MSystems</i> , 2019, 4, .	3.8	23
567	SitePainter: a tool for exploring biogeographical patterns. <i>Bioinformatics</i> , 2012, 28, 436-438.	4.1	22
568	Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. <i>ACS Synthetic Biology</i> , 2015, 4, 1244-1253.	3.8	22
569	The unifrac significance test is sensitive to tree topology. <i>BMC Bioinformatics</i> , 2015, 16, 211.	2.6	22
570	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. <i>MSystems</i> , 2019, 4, .	3.8	22
571	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021, 6, .	3.8	22
572	Natural and artificial RNAs occupy the same restricted region of sequence space. <i>Rna</i> , 2010, 16, 280-289.	3.5	21
573	Identifying qualitative effects of different grazing types on below-ground communities and function in a long-term field experiment. <i>Environmental Microbiology</i> , 2015, 17, 841-854.	3.8	21
574	Using machine learning to identify major shifts in human gut microbiome protein family abundance in disease. , 2016, , .		21
575	Bacterial density rather than diversity correlates with hatching success across different avian species. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	21
576	Subgingival Microbiota and Longitudinal Glucose Change: The Oral Infections, Glucose Intolerance and Insulin Resistance Study (ORIGINS). <i>Journal of Dental Research</i> , 2019, 98, 1488-1496.	5.2	21

#	ARTICLE	IF	CITATIONS
577	Is there convergence of gut microbes in blood-feeding vertebrates?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180249.	4.0	21
578	The microbiome and prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2022, 25, 159-164.	3.9	21
579	Using all our genomes: Blood-based liquid biopsies for the early detection of cancer. <i>View</i> , 2022, 3, .	5.3	21
580	Ancient human oral plaque preserves a wealth of biological data. <i>Nature Genetics</i> , 2014, 46, 321-323.	21.4	20
581	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , 2020, 5, .	2.9	20
582	Leveling up citizen science. <i>Nature Biotechnology</i> , 2020, 38, 1124-1126.	17.5	20
583	Association of Body Mass Index with Fecal Microbial Diversity and Metabolites in the Northern Finland Birth Cohort. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 2289-2299.	2.5	20
584	Influence of Intermittent Hypoxia/Hypercapnia on Atherosclerosis, Gut Microbiome, and Metabolome. <i>Frontiers in Physiology</i> , 2021, 12, 663950.	2.8	20
585	Vitamin B-12 and the Gastrointestinal Microbiome: A Systematic Review. <i>Advances in Nutrition</i> , 2022, 13, 530-558.	6.4	20
586	Comparison of the vaginal microbial communities in women with recurrent genital HSV receiving acyclovir intravaginal rings. <i>Antiviral Research</i> , 2014, 102, 87-94.	4.1	19
587	Can Your Microbiome Tell You What to Eat?. <i>Cell Metabolism</i> , 2015, 22, 960-961.	16.2	19
588	Associations of the Fecal Microbial Proteome Composition and Proneness to Diet-induced Obesity. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1864-1879.	3.8	19
589	Reproducibility, stability, and accuracy of microbial profiles by fecal sample collection method in three distinct populations. <i>PLoS ONE</i> , 2019, 14, e0224757.	2.5	19
590	A Distinct Microbiome Signature in Posttreatment Lyme Disease Patients. <i>MBio</i> , 2020, 11, .	4.1	19
591	Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. <i>Frontiers in Psychiatry</i> , 2020, 11, 518.	2.6	19
592	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	4.6	19
593	Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , 2021, 6, .	3.8	19
594	Using the nucleotide substitution rate matrix to detect horizontal gene transfer. <i>BMC Bioinformatics</i> , 2006, 7, 476.	2.6	18

#	ARTICLE	IF	CITATIONS
595	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. <i>Standards in Genomic Sciences</i> , 2011, 5, 243-247.	1.5	18
596	The Hospital Microbiome Project: Meeting Report for the 1st Hospital Microbiome Project Workshop on sampling design and building science measurements, Chicago, USA, June 7th-8th 2012. <i>Standards in Genomic Sciences</i> , 2013, 8, 112-117.	1.5	18
597	What Is the Value of a Food and Drug Administration Investigational New Drug Application for Fecal Microbiota Transplantation to Treat <i>Clostridium difficile</i> Infection?. <i>Clinical Gastroenterology and Hepatology</i> , 2014, 12, 289-291.	4.4	18
598	Nutritional Interventions and the Gut Microbiome in Children. <i>Annual Review of Nutrition</i> , 2021, 41, 479-510.	10.1	18
599	Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. <i>Genome Biology</i> , 2021, 22, 336.	8.8	18
600	Satellite remote sensing data can be used to model marine microbial metabolite turnover. <i>ISME Journal</i> , 2015, 9, 166-179.	9.8	17
601	Microbial Skin Inhabitants: Friends Forever. <i>Cell</i> , 2016, 165, 771-772.	28.9	17
602	The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , 2019, 15, e1006213.	3.2	17
603	Three-dimensional culture of oral progenitor cells: Effects on small extracellular vesicles production and proliferative function. <i>Journal of Oral Pathology and Medicine</i> , 2020, 49, 342-349.	2.7	17
604	Coinfection and infection duration shape how pathogens affect the African buffalo gut microbiota. <i>ISME Journal</i> , 2021, 15, 1359-1371.	9.8	17
605	Nonalcoholic Steatohepatitis and HCC in a Hyperphagic Mouse Accelerated by Western Diet. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 891-920.	4.5	17
606	A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. <i>BioTechniques</i> , 2021, 70, 149-159.	1.8	17
607	Association of Loneliness and Wisdom With Gut Microbial Diversity and Composition: An Exploratory Study. <i>Frontiers in Psychiatry</i> , 2021, 12, 648475.	2.6	17
608	Markers of Gut Barrier Function and Microbial Translocation Associate with Lower Gut Microbial Diversity in People with HIV. <i>Viruses</i> , 2021, 13, 1891.	3.3	17
609	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.	3.5	16
610	Enhanced Characterization of Drug Metabolism and the Influence of the Intestinal Microbiome: A Pharmacokinetic, Microbiome, and Untargeted Metabolomics Study. <i>Clinical and Translational Science</i> , 2020, 13, 972-984.	3.1	16
611	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	3.8	16
612	Effects of processed meat and drinking water nitrate on oral and fecal microbial populations in a controlled feeding study. <i>Environmental Research</i> , 2021, 197, 111084.	7.5	16

#	ARTICLE	IF	CITATIONS
613	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	5.5	16
614	Menopause Is Associated with an Altered Gut Microbiome and Estrobolome, with Implications for Adverse Cardiometabolic Risk in the Hispanic Community Health Study/Study of Latinos. <i>MSystems</i> , 2022, 7, .	3.8	16
615	TopiaryExplorer: visualizing large phylogenetic trees with environmental metadata. <i>Bioinformatics</i> , 2011, 27, 3067-3069.	4.1	15
616	Parallel Mapping of Antibiotic Resistance Alleles in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2016, 11, e0146916.	2.5	15
617	Key challenges in proteomics and proteoinformatics. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2005, 24, 34-40.	0.8	14
618	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 43.	5.3	14
619	The Microbiome and Its Potential for Pharmacology. <i>Handbook of Experimental Pharmacology</i> , 2019, 260, 301-326.	1.8	14
620	Fecal Microbiome Composition Does Not Predict Diet-Induced TMAO Production in Healthy Adults. <i>Journal of the American Heart Association</i> , 2021, 10, e021934.	3.7	14
621	Analysis of SARS-CoV-2 RNA Persistence across Indoor Surface Materials Reveals Best Practices for Environmental Monitoring Programs. <i>MSystems</i> , 2021, 6, e0113621.	3.8	14
622	DivergentSet, a Tool for Picking Non-redundant Sequences from Large Sequence Collections. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1520-1532.	3.8	13
623	RNA structure prediction from evolutionary patterns of nucleotide composition. <i>Nucleic Acids Research</i> , 2009, 37, 1378-1386.	14.5	13
624	<i>Euphorbia</i> plant latex is inhabited by diverse microbial communities. <i>American Journal of Botany</i> , 2015, 102, 1966-1977.	1.7	13
625	The emergence of microbiome centres. <i>Nature Microbiology</i> , 2020, 5, 2-3.	13.3	13
626	Two hundred and fifty-four metagenome-assembled bacterial genomes from the bank vole gut microbiota. <i>Scientific Data</i> , 2020, 7, 312.	5.3	13
627	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. <i>Microbiome</i> , 2021, 9, 25.	11.1	13
628	Impacts of the Marine Hatchery Built Environment, Water and Feed on Mucosal Microbiome Colonization Across Ontogeny in Yellowtail Kingfish, <i>Seriola lalandi</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	13
629	The oral microbiome and breast cancer and non-malignant breast disease, and its relationship with the fecal microbiome in the Ghana Breast Health Study. <i>International Journal of Cancer</i> , 0, , .	5.1	13
630	From molecules to dynamic biological communities. <i>Biology and Philosophy</i> , 2013, 28, 241-259.	1.4	12

#	ARTICLE	IF	CITATIONS
631	Trait-like vulnerability of higher-order cognition and ability to maintain wakefulness during combined sleep restriction and circadian misalignment. <i>Sleep</i> , 2019, 42, .	1.1	12
632	The Southern Bluefin Tuna Mucosal Microbiome Is Influenced by Husbandry Method, Net Pen Location, and Anti-parasite Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 2015.	3.5	12
633	Metabolome-Informed Microbiome Analysis Refines Metadata Classifications and Reveals Unexpected Medication Transfer in Captive Cheetahs. <i>MSystems</i> , 2020, 5, .	3.8	12
634	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. <i>MSphere</i> , 2021, 6, e0045521.	2.9	12
635	Skin inflammation activates intestinal stromal fibroblasts and promotes colitis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	12
636	Cancer's second genome: Microbial cancer diagnostics and redefining clonal evolution as a multispecies process. <i>BioEssays</i> , 2022, 44, e2100252.	2.5	12
637	The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction. <i>Scientific Reports</i> , 2022, 12, 5077.	3.3	12
638	Reports of the death of the gene are greatly exaggerated. <i>Biology and Philosophy</i> , 2007, 22, 293-306.	1.4	11
639	Activating and inhibiting connections in biological network dynamics. <i>Biology Direct</i> , 2008, 3, 49.	4.6	11
640	Nucleotides that are essential but not conserved; a sufficient L-tryptophan site in RNA. <i>Rna</i> , 2010, 16, 1915-1924.	3.5	11
641	Docent. , 2018, , .		11
642	Red Sea SAR11 and <i>Prochlorococcus</i> Single-Cell Genomes Reflect Globally Distributed Pangenomes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	11
643	Handwashing and Detergent Treatment Greatly Reduce SARS-CoV-2 Viral Load on Halloween Candy Handled by COVID-19 Patients. <i>MSystems</i> , 2020, 5, .	3.8	11
644	Differing salivary microbiome diversity, community and diurnal rhythmicity in association with affective state and peripheral inflammation in adults. <i>Brain, Behavior, and Immunity</i> , 2020, 87, 591-602.	4.1	11
645	Individuals with substance use disorders have a distinct oral microbiome pattern. <i>Brain, Behavior, & Immunity - Health</i> , 2021, 15, 100271.	2.5	11
646	Ancient Diet: Gut Microbiota, Immunity, and Health. <i>Yale Journal of Biology and Medicine</i> , 2018, 91, 177-184.	0.2	11
647	Redrawing therapeutic boundaries: microbiota and cancer. <i>Trends in Cancer</i> , 2022, 8, 87-97.	7.4	11
648	Clean room microbiome complexity impacts planetary protection bioburden. <i>Microbiome</i> , 2021, 9, 238.	11.1	11

#	ARTICLE	IF	CITATIONS
649	CD8 T cells drive anorexia, dysbiosis, and blooms of a commensal with immunosuppressive potential after viral infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24998-25007.	7.1	10
650	The effect of legume supplementation on the gut microbiota in rural Malawian infants aged 6 to 12 months. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 884-892.	4.7	10
651	Pigs, Unlike Mice, Have Two Distinct Colonic Stem Cell Populations Similar to Humans That Respond to High-Calorie Diet prior to Insulin Resistance. <i>Cancer Prevention Research</i> , 2017, 10, 442-450.	1.5	10
652	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	10
653	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 14, 35-53.	4.5	10
654	Nitrite Generating and Depleting Capacity of the Oral Microbiome and Cardiometabolic Risk: Results from ORIGINS. <i>Journal of the American Heart Association</i> , 2022, 11, e023038.	3.7	10
655	Does protein structure influence trypsin miscleavage?. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2005, 24, 58-66.	0.8	9
656	Occurrence of the aminoacyl-tRNA synthetases in high-molecular weight complexes correlates with the size of substrate amino acids. <i>FEBS Letters</i> , 2005, 579, 3467-3472.	2.8	9
657	Short Course in the Microbiome. <i>Journal of Circulating Biomarkers</i> , 2015, 4, 8.	1.3	9
658	Plant Selenium Hyperaccumulation Affects Rhizosphere: Enhanced Species Richness and Altered Species Composition. <i>Phytobiomes Journal</i> , 2018, 2, 82-91.	2.7	9
659	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	3.8	9
660	Effects of Immunization With the Soil-Derived Bacterium <i>Mycobacterium vaccae</i> on Stress Coping Behaviors and Cognitive Performance in a "Two Hit" Stressor Model. <i>Frontiers in Physiology</i> , 2020, 11, 524833.	2.8	9
661	Severe acute respiratory coronavirus virus 2 (SARS-CoV-2) screening among symptom-free healthcare workers. <i>Infection Control and Hospital Epidemiology</i> , 2022, 43, 657-660.	1.8	9
662	Intratumoral bacteria generate a new class of therapeutically relevant tumor antigens in melanoma. <i>Cancer Cell</i> , 2021, 39, 601-603.	16.8	9
663	Reduced Gut Microbiome Diversity in People With HIV Who Have Distal Neuropathic Pain. <i>Journal of Pain</i> , 2022, 23, 318-325.	1.4	9
664	The Gut Microbiome Modifies the Association Between a Mediterranean Diet and Diabetes in USA Hispanic/ Latino Population. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e924-e934.	3.6	9
665	Comparison of methods for estimating the nucleotide substitution matrix. <i>BMC Bioinformatics</i> , 2008, 9, 511.	2.6	8
666	Boulder ALignment Editor (ALE): a web-based RNA alignment tool. <i>Bioinformatics</i> , 2011, 27, 1706-1707.	4.1	8

#	ARTICLE	IF	CITATIONS
667	Technology and Techniques for Microbial Ecology via DNA Sequencing. <i>Annals of the American Thoracic Society</i> , 2014, 11, S16-S20.	3.2	8
668	Why Microbiome Treatments Could Pay Off Soon. <i>Nature</i> , 2015, 518, S5-S5.	27.8	8
669	Faecal transplants. <i>BMJ, The</i> , 2015, 351, h5149.	6.0	8
670	The pediatric intestinal mucosal microbiome remains altered after clinical resolution of inflammatory and ischemic disease. <i>Surgery</i> , 2016, 160, 350-358.	1.9	8
671	Hopanoid-producing bacteria in the Red Sea include the major marine nitrite oxidizers. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	8
672	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 322.	5.3	8
673	The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. <i>MSystems</i> , 2021, 6, e0100621.	3.8	8
674	Salivary bacterial signatures in depression-obesity comorbidity are associated with neurotransmitters and neuroactive dipeptides. <i>BMC Microbiology</i> , 2022, 22, 75.	3.3	8
675	Meeting report: GSC M5 roundtable at the 13th International Society for Microbial Ecology meeting in Seattle, WA, USA August 22-27, 2010. <i>Standards in Genomic Sciences</i> , 2010, 3, 235-239.	1.5	7
676	Using microbiome tools for estimating the postmortem interval. , 2020, , 171-191.		7
677	Absence of <i>CCR2</i> reduces spontaneous intestinal tumorigenesis in the <i>Apc^{Min/+}</i> mouse model. <i>International Journal of Cancer</i> , 2021, 148, 2594-2607.	5.1	7
678	Predicting fungal infection rate and severity with skin-associated microbial communities on amphibians. <i>Molecular Ecology</i> , 2022, 31, 2140-2156.	3.9	7
679	Early microbial markers of periodontal and cardiometabolic diseases in ORIGINS. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 30.	6.4	7
680	Pathological rate matrices: from primates to pathogens. <i>BMC Bioinformatics</i> , 2008, 9, 550.	2.6	6
681	Estimate of the abundance of cardiomyopathic mutations in the β -myosin gene. <i>International Journal of Cardiology</i> , 2010, 144, 124-126.	1.7	6
682	Crystal ball “ 2013. <i>Microbial Biotechnology</i> , 2013, 6, 3-16.	4.2	6
683	Intestinal adaptation in proximal and distal segments: Two epithelial responses diverge after intestinal separation. <i>Surgery</i> , 2017, 161, 1016-1027.	1.9	6
684	Expanding our Understanding of the Role of the Microbiome in Health and Disease. <i>Archives of Medical Research</i> , 2017, 48, 663-665.	3.3	6

#	ARTICLE	IF	CITATIONS
685	Tracking Human Gut Microbiome Changes Resulting from a Colonoscopy. <i>Methods of Information in Medicine</i> , 2017, 56, 442-447.	1.2	6
686	Evaluating Organism-Wide Changes in the Metabolome and Microbiome following a Single Dose of Antibiotic. <i>MSystems</i> , 2020, 5, .	3.8	6
687	Organ-level protein networks as a reference for the host effects of the microbiome. <i>Genome Research</i> , 2020, 30, 276-286.	5.5	6
688	Reply to: Examining microbeâ€“metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 40-41.	19.0	6
689	A Prebiotic Diet Alters the Fecal Microbiome and Improves Sleep in Response to Sleep Disruption in Rats. <i>Frontiers in Neuroscience</i> , 2022, 16, .	2.8	6
690	Consent insufficient for data releaseâ€“Response. <i>Science</i> , 2019, 364, 446-446.	12.6	5
691	Voices in methods development. <i>Nature Methods</i> , 2019, 16, 945-951.	19.0	5
692	Identifying the effect of vancomycin on health careâ€“associated methicillin-resistant <i>Staphylococcus aureus</i> strains using bacteriological and physiological media. <i>GigaScience</i> , 2021, 10, .	6.4	5
693	A semiparametric model for betweenâ€“subject attributes: Applications to betaâ€“diversity of microbiome data. <i>Biometrics</i> , 2022, 78, 950-962.	1.4	5
694	Impact of Vaginal Estrogen on the Urobiome in Postmenopausal Women With Recurrent Urinary Tract Infection. <i>Female Pelvic Medicine and Reconstructive Surgery</i> , 2022, 28, 20-26.	1.1	5
695	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. <i>MSystems</i> , 2021, 6, e0039421.	3.8	5
696	Genomic Mutations Within the Host Microbiome: Adaptive Evolution or Purifying Selection. <i>Engineering</i> , 2023, 20, 96-102.	6.7	5
697	SARS-CoV-2 Distribution in Residential Housing Suggests Contact Deposition and Correlates with <i>Rothia</i> sp.. <i>MSystems</i> , 2022, 7, e0141121.	3.8	5
698	A Lightweight, Scalable Grid Computing Framework for Parallel Bioinformatics Applications. , 0, , .		4
699	Let researchers try new paths. <i>Nature</i> , 2016, 538, 451-453.	27.8	4
700	Fecal Microbiome in Epidemiologic Studiesâ€“Response. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 870-871.	2.5	4
701	Multiplex growth rate phenotyping of synthetic mutants in selection to engineer glucose and xylose coâ€“utilization in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2017, 114, 885-893.	3.3	4
702	Microbiome and Metagenome Analyses of a Closed Habitat during Human Occupation. <i>MSystems</i> , 2020, 5, .	3.8	4

#	ARTICLE	IF	CITATIONS
703	Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data. <i>Biometrics</i> , 2022, 78, 1155-1167.	1.4	4
704	Challenges in Determining the Role of Microbiome Evolution in Barrett's Esophagus and Progression to Esophageal Adenocarcinoma. <i>Microorganisms</i> , 2021, 9, 2003.	3.6	4
705	Comparison of fecal and oral collection methods for studies of the human microbiota in two Iranian cohorts. <i>BMC Microbiology</i> , 2021, 21, 324.	3.3	4
706	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. <i>MSystems</i> , 2022, 7, e0005022.	3.8	4
707	Multiomomic Analyses of Nascent Preterm Infant Microbiomes Differentiation Suggest Opportunities for Targeted Intervention. <i>Advanced Biology</i> , 2022, 6, .	2.5	4
708	Implementation of Practical Surface SARS-CoV-2 Surveillance in School Settings. <i>MSystems</i> , 2022, 7, .	3.8	4
709	MotifCluster: an interactive online tool for clustering and visualizing sequences using shared motifs. <i>Genome Biology</i> , 2008, 9, R128.	9.6	3
710	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. <i>Nature Precedings</i> , 2009, , .	0.1	3
711	Ensemble dispatching on an IBM Blue Gene/L for a bioinformatics knowledge environment. , 2009, , .		3
712	CodonExplorer: an online tool for analyzing codon usage and sequence composition, scaling from genes to genomes. <i>Bioinformatics</i> , 2009, 25, 1331-1332.	4.1	3
713	Ribosomal RNA, the lens into life. <i>Rna</i> , 2015, 21, 692-694.	3.5	3
714	Reply to Wang and Chen: An ancient origin of magnetotactic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5019-E5020.	7.1	3
715	Microbe-Metabolite Associations Linked to the Rebounding Murine Gut Microbiome Postcolonization with Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>MSystems</i> , 2020, 5, .	3.8	3
716	Reference Data Based Insights Expand Understanding of Human Metabolomes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
717	TaskSpaces: A Software Framework for Parallel Bioinformatics on Computational Grids. , 0, , 651-670.		3
718	Porting and optimizing UniFrac for GPUs. , 2020, , .		3
719	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. <i>MSystems</i> , 2022, 7, e0137821.	3.8	3
720	The impact of maternal asthma on the preterm infants' gut metabolome and microbiome (MAP study). <i>Scientific Reports</i> , 2022, 12, 6437.	3.3	3

#	ARTICLE	IF	CITATIONS
721	Diurnal and eating-associated microbial patterns revealed via high-frequency saliva sampling. <i>Genome Research</i> , 2022, 32, 1112-1123.	5.5	3
722	The molecular impact of life in an indoor environment. <i>Science Advances</i> , 2022, 8, .	10.3	3
723	Nematode contamination in sandpits of registered pre-school facilities in Bloemfontein. <i>The Southern African Journal of Epidemiology & Infection: Official Journal of the Sexually Transmitted Diseases, Infectious Diseases and Epidemiological Societies of Southern Africa</i> , 2006, 21, 173-177.	0.2	2
724	Authors' reply to Mawer and Wilcox and Mullish and Williams. <i>BMJ</i> , The, 2015, 351, h6132-h6132.	6.0	2
725	An <i>Elegans</i> (t) Screen for Drug-Microbe Interactions. <i>Cell Host and Microbe</i> , 2017, 21, 555-556.	11.0	2
726	OP31 Meta-omics reveals microbiome-driven proteolysis as a contributing factor to the severity of ulcerative colitis disease activity. <i>Journal of Crohn's and Colitis</i> , 2020, 14, S030-S031.	1.3	2
727	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	3.2	2
728	CodonExplorer: An Interactive Online Database for the Analysis of Codon Usage and Sequence Composition. <i>Methods in Molecular Biology</i> , 2009, 537, 207-232.	0.9	2
729	Impact of exclusive enteral nutrition on the gut microbiome of children with medical complexity. <i>Journal of Parenteral and Enteral Nutrition</i> , 2023, 47, 77-86.	2.6	2
730	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	3.8	2
731	Artificial Selection: Finding Function amongst Randomized Sequences. , 0, , 783-806.		1
732	Database-Driven Grid Computing and Distributed Web Applications: A Comparison. , 0, , 247-266.		1
733	Systems Biology: Understanding Function from Genes to Networks. <i>Current Proteomics</i> , 2009, 6, 93-103.	0.3	1
734	Life Through A Microbial Lens. <i>Metascience</i> , 2009, 18, 179-205.	0.3	1
735	Reply to Putignani et al.: Vagina as a major source of natural inoculum for the newborn. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, .	7.1	1
736	Meeting report of the RNA Ontology Consortium January 8-9, 2011. <i>Standards in Genomic Sciences</i> , 2011, 4, 252-256.	1.5	1
737	New Insight into the Diversity of Life's Building Blocks: Evenness, Not Variance. <i>Astrobiology</i> , 2011, 11, 197-198.	3.0	1
738	Conceptualizing a Genomics Software Institute (GSI). <i>Standards in Genomic Sciences</i> , 2012, 6, 136-144.	1.5	1

#	ARTICLE	IF	CITATIONS
739	Culturing: Looking it up in our gut. <i>Nature Microbiology</i> , 2016, 1, 16169.	13.3	1
740	Integrated Approaches to Analyze Big Data in the Perinatal/Neonatal Space. <i>Breastfeeding Medicine</i> , 2018, 13, S-5-S-6.	1.7	1
741	Neighborhoods to Nucleotides—Advances and Gaps for an Obesity Disparities Systems Epidemiology Model. <i>Current Epidemiology Reports</i> , 2019, 6, 476-485.	2.4	1
742	Expanding the scope and scale of microbiome research. <i>Genome Biology</i> , 2019, 20, 191.	8.8	1
743	Reduced Independence in Daily Living Is Associated with the Gut Microbiome in People with HIV and HCV. <i>MSystems</i> , 2020, 5, .	3.8	1
744	Host DNA Depletion in Saliva Samples for Improved Shotgun Metagenomics. <i>Methods in Molecular Biology</i> , 2021, 2327, 87-92.	0.9	1
745	Microbiota as in farm homes protect children from asthma. , 2018, , .		1
746	Enabling microbiome research on personal devices. , 2021, , .		1
747	Sentinel Cards Provide Practical SARS-CoV-2 Monitoring in School Settings. <i>MSystems</i> , 2022, 7, .	3.8	1
748	Meeting report for the 1st skin microbiota workshop, boulder, CO October 15-16 2012. <i>Standards in Genomic Sciences</i> , 2014, 9, .	1.5	0
749	Why Microbiome Treatments Could Pay Off Soon. <i>Scientific American</i> , 2015, 312, S5-S5.	1.0	0
750	0213 Trait-like Vulnerability Of Higher-order Cognition To Sleep Loss And Circadian Misalignment. <i>Sleep</i> , 2018, 41, A83-A84.	1.1	0
751	Reply to Sun et al., “Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy” <i>MBio</i> , 2019, 10, .	4.1	0
752	Diet and the Gut Microbiome in 10-18-Month-Old Children Living in Urban Slums of Mumbai, India (OR01-08-19). <i>Current Developments in Nutrition</i> , 2019, 3, nzz040.OR01-08-19.	0.3	0
753	Early-Career Scientists Shaping the World. <i>MSystems</i> , 2019, 4, .	3.8	0
754	Reply to Moossavi and Azad, “Quantifying and Interpreting the Association between Early-Life Gut Microbiota Composition and Childhood Obesity” <i>MBio</i> , 2019, 10, .	4.1	0
755	48: Oral probiotic versus placebo and the maternal microbiome during pregnancy: A randomized controlled trial. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, S41-S42.	1.3	0
756	Accelerating Key Bioinformatics Tasks 100-fold by Improving Memory Access. , 2021, , .		0

#	ARTICLE	IF	CITATIONS
757	Hibernation alters the gut microbial community in ground squirrels. FASEB Journal, 2012, 26, 1155.6.	0.5	0
758	Microbiome/Metabolic Syndrome/Diabetes and CVD. FASEB Journal, 2015, 29, 222.3.	0.5	0
759	Three Dimensional Cartography of Microbiome and Metabolome Data onto Radiological Images of the Human Lung. SSRN Electronic Journal, 0, , .	0.4	0
760	Targeted Activation of Enteric Neurons Shapes the Gut Environment of Mice. SSRN Electronic Journal, 0, , .	0.4	0
761	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
762	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
763	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0