

Rob Knight

List of Publications by Year in descending order

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Version: 2024-02-01

766
papers

314,955
citations

¹²
208
h-index

²
528
g-index

893
all docs

893
docs citations

893
times ranked

143458
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	19.0	31,818
2	UCHIME improves sensitivity and speed of chimera detection. Bioinformatics, 2011, 27, 2194-2200.	4.1	13,241
3	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
4	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	17.5	8,049
5	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME Journal, 2012, 6, 1621-1624.	9.8	7,430
6	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4516-4522.	7.1	7,425
7	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. Applied and Environmental Microbiology, 2005, 71, 8228-8235.	3.1	7,007
8	A core gut microbiome in obese and lean twins. Nature, 2009, 457, 480-484.	27.8	6,819
9	Human gut microbiome viewed across age and geography. Nature, 2012, 486, 222-227.	27.8	6,247
10	Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. Science, 2011, 334, 105-108.	12.6	5,253
11	The Human Microbiome Project. Nature, 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. ISME Journal, 2012, 6, 610-618.	9.8	4,581
13	Diversity, stability and resilience of the human gut microbiota. Nature, 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. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11971-11975.	7.1	3,738
15	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nature Methods, 2013, 10, 57-59.	19.0	3,402
16	PyNASt: a flexible tool for aligning sequences to a template alignment. Bioinformatics, 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. Applied and Environmental Microbiology, 2009, 75, 5111-5120.	3.1	3,268
18	Evolution of Mammals and Their Gut Microbes. Science, 2008, 320, 1647-1651.	12.6	3,171

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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

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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

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

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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

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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

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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

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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

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

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