

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. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
2	UCHIME improves sensitivity and speed of chimera detection. <i>Bioinformatics</i> , 2011, 27, 2194-2200.	1.8	13,241
3	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
4	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049
5	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , 2012, 6, 1621-1624.	4.4	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.	3.3	7,425
7	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8228-8235.	1.4	7,007
8	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009, 457, 480-484.	13.7	6,819
9	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	13.7	6,247
10	Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. <i>Science</i> , 2011, 334, 105-108.	6.0	5,253
11	The Human Microbiome Project. <i>Nature</i> , 2007, 449, 804-810.	13.7	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.	4.4	4,581
13	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012, 489, 220-230.	13.7	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.	3.3	3,738
15	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 57-59.	9.0	3,402
16	PyNASt: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , 2010, 26, 266-267.	1.8	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.	1.4	3,268
18	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	6.0	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.	4.9	3,159
20	Soil bacterial and fungal communities across a pH gradient in an arable soil. <i>ISME Journal</i> , 2010, 4, 1340-1351.	4.4	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.	2.4	3,015
22	Gut Microbiota from Twins Discordant for Obesity Modulate Metabolism in Mice. <i>Science</i> , 2013, 341, 1241-1244.	6.0	3,006
23	The Impact of the Gut Microbiota on Human Health: An Integrative View. <i>Cell</i> , 2012, 148, 1258-1270.	13.5	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.	9.4	2,802
25	Bacterial Community Variation in Human Body Habitats Across Space and Time. <i>Science</i> , 2009, 326, 1694-1697.	6.0	2,713
26	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	5.1	2,582
27	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	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.	5.8	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.	1.4	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.	13.5	2,399
31	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172.	4.4	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.	3.3	2,108
33	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
34	Metabolic Syndrome and Altered Gut Microbiota in Mice Lacking Toll-Like Receptor 5. <i>Science</i> , 2010, 328, 228-231.	6.0	1,804
35	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	6.0	1,712
36	The Long-Term Stability of the Human Gut Microbiota. <i>Science</i> , 2013, 341, 1237-1239.	6.0	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.	13.7	1,638
38	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. <i>Cell</i> , 2012, 150, 470-480.	13.5	1,603
39	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	15.2	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.	9.4	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.	3.3	1,461
42	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
43	Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. <i>ISME Journal</i> , 2012, 6, 1007-1017.	4.4	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, .	1.7	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.	0.6	1,344
46	Worlds within worlds: evolution of the vertebrate gut microbiota. <i>Nature Reviews Microbiology</i> , 2008, 6, 776-788.	13.6	1,342
47	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	1.7	1,339
48	UniFrac--an online tool for comparing microbial community diversity in a phylogenetic context. <i>BMC Bioinformatics</i> , 2006, 7, 371.	1.2	1,321
49	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011, 8, 761-763.	9.0	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.	3.8	1,283
51	Error-correcting barcoded primers for pyrosequencing hundreds of samples in multiplex. <i>Nature Methods</i> , 2008, 5, 235-237.	9.0	1,190
52	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
53	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	9.0	1,125
54	Examining the global distribution of dominant archaeal populations in soil. <i>ISME Journal</i> , 2011, 5, 908-917.	4.4	1,112

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55	EMPeror: a tool for visualizing high-throughput microbial community data. <i>GigaScience</i> , 2013, 2, 16.	3.3	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.	4.4	1,025
57	Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. <i>Science</i> , 2013, 339, 548-554.	6.0	1,012
58	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , 2009, 3, 442-453.	4.4	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.	3.3	980
60	Bacterial phylogeny structures soil resistomes across habitats. <i>Nature</i> , 2014, 509, 612-616.	13.7	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.	3.3	943
62	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	13.9	934
63	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	13.7	929
64	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	4.4	928
65	The gut-liver axis and the intersection with the microbiome. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018, 15, 397-411.	8.2	905
66	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	5.1	831
67	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	5.9	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.	2.0	814
69	Microbial community profiling for human microbiome projects: Tools, techniques, and challenges. <i>Genome Research</i> , 2009, 19, 1141-1152.	2.4	805
70	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013, 2, e00458.	2.8	801
71	Defining the human microbiome. <i>Nutrition Reviews</i> , 2012, 70, S38-S44.	2.6	789
72	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	6.0	751

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73	Contribution of human hippocampal region to novelty detection. <i>Nature</i> , 1996, 383, 256-259.	13.7	743
74	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016, 22, 250-253.	15.2	736
75	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , 2014, 12, 69.	1.7	723
76	The microbiome of uncontacted Amerindians. <i>Science Advances</i> , 2015, 1, .	4.7	721
77	Gut Microbes and the Brain: Paradigm Shift in Neuroscience. <i>Journal of Neuroscience</i> , 2014, 34, 15490-15496.	1.7	719
78	Microbiota Regulate Intestinal Absorption and Metabolism of Fatty Acids in the Zebrafish. <i>Cell Host and Microbe</i> , 2012, 12, 277-288.	5.1	717
79	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	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.	3.3	709
81	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	13.5	701
82	Meta-analyses of human gut microbes associated with obesity and IBD. <i>FEBS Letters</i> , 2014, 588, 4223-4233.	1.3	697
83	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. <i>Science</i> , 2017, 357, 802-806.	6.0	694
84	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , 2020, 579, 567-574.	13.7	691
85	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	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.	3.3	671
87	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. <i>Trends in Microbiology</i> , 2019, 27, 105-117.	3.5	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.	2.2	649
89	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. <i>Nature Methods</i> , 2010, 7, 668-669.	9.0	647
90	Short pyrosequencing reads suffice for accurate microbial community analysis. <i>Nucleic Acids Research</i> , 2007, 35, e120-e120.	6.5	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.	15.2	629
92	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , 2015, 17, 603-616.	5.1	628
93	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	13.5	625
94	The under-recognized dominance of Verrucomicrobia in soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2011, 43, 1450-1455.	4.2	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.	5.1	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.	9.4	608
97	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
98	Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2012, 13, 47-58.	7.7	601
99	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016, 535, 94-103.	13.7	595
100	Diversity, structure and convergent evolution of the global sponge microbiome. <i>Nature Communications</i> , 2016, 7, 11870.	5.8	594
101	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	4.4	593
102	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	5.9	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.	1.8	574
104	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	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.	1.8	551
106	Conditionally Rare Taxa Disproportionately Contribute to Temporal Changes in Microbial Diversity. <i>MBio</i> , 2014, 5, e01371-14.	1.8	549
107	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <i>ISME Journal</i> , 2012, 6, 94-103.	4.4	537
108	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	0.9	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.	6.5	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.	3.3	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, .	6.0	506
113	Role of the microbiome in human development. <i>Gut</i> , 2019, 68, 1108-1114.	6.1	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.	1.8	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.	1.4	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.	6.0	480
118	Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. <i>Ecology</i> , 2010, 91, 3463-3470.	1.5	475
119	Fast-Find: a novel computational approach to analyzing combinatorial motifs. <i>BMC Bioinformatics</i> , 2006, 7, 1.	1.2	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.	7.2	464
121	Individual diet has sex-dependent effects on vertebrate gut microbiota. <i>Nature Communications</i> , 2014, 5, 4500.	5.8	464
122	Microbiota restoration: natural and supplemented recovery of human microbial communities. <i>Nature Reviews Microbiology</i> , 2011, 9, 27-38.	13.6	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.	5.1	459
124	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	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.	5.8	456
126	Specialized Metabolites from the Microbiome in Health and Disease. <i>Cell Metabolism</i> , 2014, 20, 719-730.	7.2	454

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127	Subsistence strategies in traditional societies distinguish gut microbiomes. <i>Nature Communications</i> , 2015, 6, 6505.	5.8	449
128	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	6.0	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.	1.5	446
130	Microbial endocrinology: the interplay between the microbiota and the endocrine system. <i>FEMS Microbiology Reviews</i> , 2015, 39, 509-521.	3.9	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.	4.2	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.	3.3	435
133	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019, 10, 2719.	5.8	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.	3.3	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.	3.3	412
136	Global biogeography of highly diverse protistan communities in soil. <i>ISME Journal</i> , 2013, 7, 652-659.	4.4	412
137	Species divergence and the measurement of microbial diversity. <i>FEMS Microbiology Reviews</i> , 2008, 32, 557-578.	3.9	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.	9.4	400
139	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. <i>Nature</i> , 2017, 551, 340-345.	13.7	396
140	Sequencing our way towards understanding global eukaryotic biodiversity. <i>Trends in Ecology and Evolution</i> , 2012, 27, 233-243.	4.2	395
141	Alterations in the Gut Microbiota Associated with HIV-1 Infection. <i>Cell Host and Microbe</i> , 2013, 14, 329-339.	5.1	387
142	Complex Interactions Among Diet, Gastrointestinal Transit, and Gut Microbiota in Humanized Mice. <i>Gastroenterology</i> , 2013, 144, 967-977.	0.6	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.	4.4	385
144	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016, 351, 158-162.	6.0	381

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145	Supervised classification of human microbiota. <i>FEMS Microbiology Reviews</i> , 2011, 35, 343-359.	3.9	377
146	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	1.7	376
147	The Macaque Gut Microbiome in Health, Lentiviral Infection, and Chronic Enterocolitis. <i>PLoS Pathogens</i> , 2008, 4, e20.	2.1	371
148	The Human Microbiome Project: A Community Resource for the Healthy Human Microbiome. <i>PLoS Biology</i> , 2012, 10, e1001377.	2.6	369
149	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
150	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. <i>MSystems</i> , 2016, 1, .	1.7	367
151	Global patterns in the biogeography of bacterial taxa. <i>Environmental Microbiology</i> , 2011, 13, 135-144.	1.8	362
152	The amphibian skin-associated microbiome across species, space and life history stages. <i>Molecular Ecology</i> , 2014, 23, 1238-1250.	2.0	360
153	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014, 15, 531.	3.8	355
154	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. <i>Obesity</i> , 2012, 20, 738-747.	1.5	352
155	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013, 23, 1704-1714.	2.4	352
156	Microbes do not follow the elevational diversity patterns of plants and animals. <i>Ecology</i> , 2011, 92, 797-804.	1.5	351
157	PrimerProspector: <i>de novo</i> design and taxonomic analysis of barcoded polymerase chain reaction primers. <i>Bioinformatics</i> , 2011, 27, 1159-1161.	1.8	351
158	Dietary effects on human gut microbiome diversity. <i>British Journal of Nutrition</i> , 2015, 113, S1-S5.	1.2	350
159	The gut microbiota in human energy homeostasis and obesity. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 493-501.	3.1	350
160	Antibiotic-induced microbiome depletion alters metabolic homeostasis by affecting gut signaling and colonic metabolism. <i>Nature Communications</i> , 2018, 9, 2872.	5.8	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.	0.7	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.	1.3	335

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163	Changes through time: integrating microorganisms into the study of succession. <i>Research in Microbiology</i> , 2010, 161, 635-642.	1.0	334
164	Development of the Human Gastrointestinal Microbiota and Insights From High-Throughput Sequencing. <i>Gastroenterology</i> , 2011, 140, 1713-1719.	0.6	329
165	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. <i>ISME Journal</i> , 2012, 6, 1440-1444.	4.4	326
166	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	4.4	325
167	Bacteria from Diverse Habitats Colonize and Compete in the Mouse Gut. <i>Cell</i> , 2014, 159, 253-266.	13.5	324
168	Host variables confound gut microbiota studies of human disease. <i>Nature</i> , 2020, 587, 448-454.	13.7	324
169	A meta-analysis of changes in bacterial and archaeal communities with time. <i>ISME Journal</i> , 2013, 7, 1493-1506.	4.4	322
170	Rethinking "Enterotypes". <i>Cell Host and Microbe</i> , 2014, 16, 433-437.	5.1	321
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