

Rob Knight

List of Publications by Citations

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

780

papers

206,124

citations

181

h-index

450

g-index

893

ext. papers

258,131

ext. citations

12.9

avg, IF

8.94

L-index

#	Paper	IF	Citations
780	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010 , 7, 335-6	21	22581
779	UCHIME improves sensitivity and speed of chimera detection. <i>Bioinformatics</i> , 2011 , 27, 2194-200	6.9	9252
778	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009 , 457, 480-4	47.5	5365
777	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013 , 31, 814-21	43.2	5180
776	UniFrac: a new phylogenetic method for comparing microbial communities. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8228-35	4.7	5074
775	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , 2012 , 6, 1621-4	11.6	4962
774	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 Suppl 1, 4516-22	11.2	4626
773	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012 , 486, 222-7	47.5	4528
772	Linking long-term dietary patterns with gut microbial enterotypes. <i>Science</i> , 2011 , 334, 105-8	32.2	3856
771	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	43.2	3760
770	The human microbiome project. <i>Nature</i> , 2007 , 449, 804-10	47.5	3525
769	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , 2012 , 6, 610-8	11.6	3243
768	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, 11971-5	11.2	2865
767	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012 , 489, 220-30	47.5	2849
766	PyNAST: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , 2010 , 26, 266-7	6.9	2711
765	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, 5111-20	4.7	2401
764	Evolution of mammals and their gut microbes. <i>Science</i> , 2008 , 320, 1647-51	32.2	2316

763	Gut microbiota from twins discordant for obesity modulate metabolism in mice. <i>Science</i> , 2013 , 341, 1241-1244	32.1	2218
762	Bacterial community variation in human body habitats across space and time. <i>Science</i> , 2009 , 326, 1694-7	32.2	2151
761	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. <i>Genome Research</i> , 2011 , 21, 494-504	9.4	2132
760	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013 , 10, 57-9	21	2122
759	Soil bacterial and fungal communities across a pH gradient in an arable soil. <i>ISME Journal</i> , 2010 , 4, 1340-51	51.6	2106
758	The impact of the gut microbiota on human health: an integrative view. <i>Cell</i> , 2012 , 148, 1258-70	54.6	2067
757	The effect of diet on the human gut microbiome: a metagenomic analysis in humanized gnotobiotic mice. <i>Science Translational Medicine</i> , 2009 , 1, 6ra14	16.9	1964
756	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , 2014 , 15, 382-392	22.9	1800
755	Human genetics shape the gut microbiome. <i>Cell</i> , 2014 , 159, 789-99	54.6	1737
754	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 Suppl 1, 4578-85	11.2	1650
753	Quantitative and qualitative beta diversity measures lead to different insights into factors that structure microbial communities. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 1576-85	4.7	1580
752	Gut Microbiota Regulate Motor Deficits and Neuroinflammation in a Model of Parkinson's Disease. <i>Cell</i> , 2016 , 167, 1469-1480.e12	54.6	1510
751	Metabolic syndrome and altered gut microbiota in mice lacking Toll-like receptor 5. <i>Science</i> , 2010 , 328, 228-31	32.2	1514
750	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016 , 34, 828-837	43.2	1483
749	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011 , 5, 169-72	11.6	1453
748	Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. <i>Science</i> , 2011 , 332, 970-4	32.2	1198
747	The long-term stability of the human gut microbiota. <i>Science</i> , 2013 , 341, 1237-439	32.2	1186
746	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018 , 6, 90	16.1	1134

745	UniFrac--an online tool for comparing microbial community diversity in a phylogenetic context. <i>BMC Bioinformatics</i> , 2006 , 7, 371	3.4	1121
744	Host remodeling of the gut microbiome and metabolic changes during pregnancy. <i>Cell</i> , 2012 , 150, 470-80	14.6	1109
743	Global patterns in bacterial diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11436-40	11.2	1081
742	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	47.5	1042
741	High-fat diet determines the composition of the murine gut microbiome independently of obesity. <i>Gastroenterology</i> , 2009 , 137, 1716-24.e1-2	7.9	1032
740	Worlds within worlds: evolution of the vertebrate gut microbiota. <i>Nature Reviews Microbiology</i> , 2008 , 6, 776-88	21.4	1035
739	Error-correcting barcoded primers for pyrosequencing hundreds of samples in multiplex. <i>Nature Methods</i> , 2008 , 5, 235-7	21	997
738	Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. <i>ISME Journal</i> , 2012 , 6, 1007-17	11.6	935
737	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	11.6	856
736	Examining the global distribution of dominant archaeal populations in soil. <i>ISME Journal</i> , 2011 , 5, 908-17	11.6	816
735	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017 , 5, 27	16.1	812
734	Gut microbiomes of Malawian twin pairs discordant for kwashiorkor. <i>Science</i> , 2013 , 339, 548-54	32.2	806
733	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, 17994-9	11.2	786
732	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018 , 24, 392-400	49.4	774
731	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011 , 8, 761-3	11	748
730	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017 , 2,	7.4	721
729	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , 2009 , 3, 442-53	11.6	720
728	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011 , 12, R50	17.7	716

727	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019 , 569, 655-662	47.5	722
726	Analysis of composition of microbiomes: a novel method for studying microbial composition. <i>Microbial Ecology in Health and Disease</i> , 2015 , 26, 27663		702
725	EMPeror: a tool for visualizing high-throughput microbial community data. <i>GigaScience</i> , 2013 , 2, 16	7.3	687
724	Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. <i>MSystems</i> , 2016 , 1,	7.4	675
723	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 Suppl 1, 4592-8	11.2	665
722	Contribution of human hippocampal region to novelty detection. <i>Nature</i> , 1996 , 383, 256-9	47.5	661
721	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012 , 6, 298-308	11.6	645
720	Bacterial phylogeny structures soil resistomes across habitats. <i>Nature</i> , 2014 , 509, 612-6	47.5	643
719	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018 , 16, 410-422	21.4	643
718	Microbial community profiling for human microbiome projects: Tools, techniques, and challenges. <i>Genome Research</i> , 2009 , 19, 1141-52	9.4	636
717	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	43.2	633
716	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013 , 2, e004586	58.6	608
715	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. <i>Nature Methods</i> , 2010 , 7, 668-9	21	587
714	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018 , 15, 962-968	21	579
713	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017 , 550, 61-66	47.5	581
712	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016 , 19, 731-43	22.9	538
711	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014 , 345, 1048-52	32.2	539
710	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016 , 22, 250-3	49.4	534

709	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017 , 2, 17004	25.9	514
708	Short pyrosequencing reads suffice for accurate microbial community analysis. <i>Nucleic Acids Research</i> , 2007 , 35, e120	19.4	505
707	Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. <i>Molecular Ecology</i> , 2012 , 21, 3363-78	5.5	499
706	The microbiome of uncontacted Amerindians. <i>Science Advances</i> , 2015 , 1,	13.9	503
705	Gut microbes and the brain: paradigm shift in neuroscience. <i>Journal of Neuroscience</i> , 2014 , 34, 15490-6	6.4	513
704	Meta-analyses of human gut microbes associated with obesity and IBD. <i>FEBS Letters</i> , 2014 , 588, 4223-33	3.6	502
703	The Earth Microbiome project: successes and aspirations. <i>BMC Biology</i> , 2014 , 12, 69	7	489
702	Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2011 , 13, 47-58	29	481
701	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012 , 1, 7	7.3	472
700	Identifying genetic determinants needed to establish a human gut symbiont in its habitat. <i>Cell Host and Microbe</i> , 2009 , 6, 279-89	22.9	469
699	Microbiota regulate intestinal absorption and metabolism of fatty acids in the zebrafish. <i>Cell Host and Microbe</i> , 2012 , 12, 277-88	22.9	467
698	The gut-liver axis and the intersection with the microbiome. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 397-411	23.6	443
697	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	11.2	445
696	The under-recognized dominance of Verrucomicrobia in soil bacterial communities. <i>Soil Biology and Biochemistry</i> , 2011 , 43, 1450-1455	7.4	437
695	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	43.2	439
694	Defining the human microbiome. <i>Nutrition Reviews</i> , 2012 , 70 Suppl 1, S38-44	6.2	442
693	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016 , 535, 94-103	10.5	434
692	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. <i>Environmental Microbiology</i> , 2010 , 12, 2998-3006	5.1	428

691	Conducting a microbiome study. <i>Cell</i> , 2014 , 158, 250-262	54.6	429
690	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. <i>Nucleic Acids Research</i> , 2008 , 36, e120	19.4	419
689	Forensic identification using skin bacterial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6477-81	11.2	418
688	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. <i>Science</i> , 2017 , 357, 802-806	32.2	419
687	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, 7059-66	4.7	402
686	The ecology of the phyllosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. <i>Environmental Microbiology</i> , 2010 , 12, 2885-93	5.1	398
685	Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. <i>Movement Disorders</i> , 2017 , 32, 739-749	6.8	393
684	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014 , 2, e545	3.1	391
683	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <i>ISME Journal</i> , 2012 , 6, 94-103	11.6	378
682	Genetic control of obesity and gut microbiota composition in response to high-fat, high-sucrose diet in mice. <i>Cell Metabolism</i> , 2013 , 17, 141-52	23.8	378
681	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	16.9	380
680	Advancing our understanding of the human microbiome using QIIME. <i>Methods in Enzymology</i> , 2013 , 531, 371-444	1.6	368
679	Using QIIME to analyze 16S rRNA gene sequences from microbial communities. <i>Current Protocols in Bioinformatics</i> , 2011 , Chapter 10, Unit 10.7.	23	368
678	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	25.9	371
677	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019 , 177, 1600-1618.e17	54.6	364
676	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016 , 10, 1669-81	11.6	359
675	Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. <i>Ecology</i> , 2010 , 91, 3463-70; discussion 3503-14	4.5	360
674	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, 7503-8	11.2	361

673	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , 2015 , 17, 603-162.9	358
672	Microbiota restoration: natural and supplemented recovery of human microbial communities. <i>Nature Reviews Microbiology</i> , 2011 , 9, 27-38	21.4 358
671	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	4.8 352
670	Conditionally rare taxa disproportionately contribute to temporal changes in microbial diversity. <i>MBio</i> , 2014 , 5, e01371-14	7.6 351
669	Geographic distance and pH drive bacterial distribution in alkaline lake sediments across Tibetan Plateau. <i>Environmental Microbiology</i> , 2012 , 14, 2457-66	5.1 351
668	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , 2018 , 24, 1532-1535	49.4 342
667	The macaque gut microbiome in health, lentiviral infection, and chronic enterocolitis. <i>PLoS Pathogens</i> , 2008 , 4, e20	7.4 329
666	Specialized metabolites from the microbiome in health and disease. <i>Cell Metabolism</i> , 2014 , 20, 719-730	23.8 327
665	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. <i>Trends in Microbiology</i> , 2019 , 27, 105-117	12 328
664	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, 4158-63	11.2 324
663	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.4 327
662	Reconstructing the microbial diversity and function of pre-agricultural tallgrass prairie soils in the United States. <i>Science</i> , 2013 , 342, 621-4	32.2 321
661	Transient inability to manage proteobacteria promotes chronic gut inflammation in TLR5-deficient mice. <i>Cell Host and Microbe</i> , 2012 , 12, 139-52	22.9 325
660	Individual diet has sex-dependent effects on vertebrate gut microbiota. <i>Nature Communications</i> , 2014 , 5, 4500	16.9 320
659	Sequencing our way towards understanding global eukaryotic biodiversity. <i>Trends in Ecology and Evolution</i> , 2012 , 27, 233-43	10.6 319
658	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	7.4 312
657	Diversity, structure and convergent evolution of the global sponge microbiome. <i>Nature Communications</i> , 2016 , 7, 11870	16.9 312
656	Using QIIME to analyze 16S rRNA gene sequences from microbial communities. <i>Current Protocols in Microbiology</i> , 2012 , Chapter 1, Unit 1E.5.	7 300

655	Species divergence and the measurement of microbial diversity. <i>FEMS Microbiology Reviews</i> , 2008 , 32, 557-78	14.6	298
654	Global biogeography of highly diverse protistan communities in soil. <i>ISME Journal</i> , 2013 , 7, 652-9	11.6	297
653	Subsistence strategies in traditional societies distinguish gut microbiomes. <i>Nature Communications</i> , 2015 , 6, 6505	16.9	298
652	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, 601-12	11.6	286
651	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013 , 23, 1704-14	9.4	288
650	Alterations in the gut microbiota associated with HIV-1 infection. <i>Cell Host and Microbe</i> , 2013 , 14, 329-39	22.9	284
649	Responses of gut microbiota to diet composition and weight loss in lean and obese mice. <i>Obesity</i> , 2012 , 20, 738-47	7.8	282
648	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019 , 4, 396-403	25.9	276
647	Complex interactions among diet, gastrointestinal transit, and gut microbiota in humanized mice. <i>Gastroenterology</i> , 2013 , 144, 967-77	7.9	284
646	Global patterns in the biogeography of bacterial taxa. <i>Environmental Microbiology</i> , 2011 , 13, 135-144	5.1	277
645	Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. <i>BMC Microbiology</i> , 2010 , 10, 206	4.4	279
644	Fast-Find: a novel computational approach to analyzing combinatorial motifs. <i>BMC Bioinformatics</i> , 2006 , 7, 1	3.4	276
643	Development of the human gastrointestinal microbiota and insights from high-throughput sequencing. <i>Gastroenterology</i> , 2011 , 140, 1713-9	7.9	275
642	Supervised classification of human microbiota. <i>FEMS Microbiology Reviews</i> , 2011 , 35, 343-59	14.6	273
641	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018 , 360, 795-800	32.2	270
640	PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. <i>Bioinformatics</i> , 2011 , 27, 1159-61	6.9	270
639	Effect of storage conditions on the assessment of bacterial community structure in soil and human-associated samples. <i>FEMS Microbiology Letters</i> , 2010 , 307, 80-6	2.8	269
638	The Human Microbiome Project: a community resource for the healthy human microbiome. <i>PLoS Biology</i> , 2012 , 10, e1001377	9.5	261

637	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014 , 8, 1464-75	11.6	259
636	Microbes do not follow the elevational diversity patterns of plants and animals. <i>Ecology</i> , 2011 , 92, 797-804	11.4	253
635	Microbial endocrinology: the interplay between the microbiota and the endocrine system. <i>FEMS Microbiology Reviews</i> , 2015 , 39, 509-21	14.6	255
634	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014 , 15, 531	17.7	252
633	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016 , 351, 158-62	32.2	251
632	Dietary effects on human gut microbiome diversity. <i>British Journal of Nutrition</i> , 2015 , 113 Suppl, S1-5	3.4	251
631	The gut microbiota in human energy homeostasis and obesity. <i>Trends in Endocrinology and Metabolism</i> , 2015 , 26, 493-501	8.5	253
630	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. <i>MSystems</i> , 2016 , 1,	7.4	249
629	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. <i>ISME Journal</i> , 2012 , 6, 1440-4	11.6	243
628	A meta-analysis of changes in bacterial and archaeal communities with time. <i>ISME Journal</i> , 2013 , 7, 1493-506	11.6	236
627	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	11.2	234
626	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <i>Nature Biotechnology</i> , 2017 , 35, 1077-1086	43.2	232
625	Rethinking "enterotypes". <i>Cell Host and Microbe</i> , 2014 , 16, 433-7	22.9	234
624	Bacterial communities associated with the lichen symbiosis. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 1309-14	4.7	232
623	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. <i>Genome Research</i> , 2010 , 20, 1411-9	9.4	233
622	Changes through time: integrating microorganisms into the study of succession. <i>Research in Microbiology</i> , 2010 , 161, 635-42	3.9	228
621	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, 5121-30	4.7	229
620	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	3.6	227

619	Bacteria from diverse habitats colonize and compete in the mouse gut. <i>Cell</i> , 2014 , 159, 253-66	54.6	223
618	Role of the microbiome in human development. <i>Gut</i> , 2019 , 68, 1108-1114	18.6	215
617	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. <i>Nature</i> , 2017 , 551, 340-345	47.5	215
616	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018 , 15, 796-798	21	216
615	The amphibian skin-associated microbiome across species, space and life history stages. <i>Molecular Ecology</i> , 2014 , 23, 1238-50	5.5	216
614	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	11.2	213
613	Short-term temporal variability in airborne bacterial and fungal populations. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 200-7	4.7	210
612	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012 , 30, 513-20	43.2	209
611	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , 2020 , 579, 567-574	47.5	211
610	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019 , 10, 2719	16.9	210
609	The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites. <i>Journal of Allergy and Clinical Immunology</i> , 2012 , 129, 1204-8	4.1	202
608	The 'rare biosphere': a reality check. <i>Nature Methods</i> , 2009 , 6, 636-7	21	201
607	Genetic and environmental control of host-gut microbiota interactions. <i>Genome Research</i> , 2015 , 25, 1558-69	9.4	197
606	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders (<i>Plethodon cinereus</i>). <i>ISME Journal</i> , 2014 , 8, 830-40	11.6	194
605	Finding the missing links among metabolites, microbes, and the host. <i>Immunity</i> , 2014 , 40, 824-32	31.5	194
604	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. <i>Nature Methods</i> , 2010 , 7, 813-9	21	192
603	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, 11276-81	11.2	190
602	Sources of bacteria in outdoor air across cities in the midwestern United States. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6350-6	4.7	190

601	Co-habiting amphibian species harbor unique skin bacterial communities in wild populations. <i>ISME Journal</i> , 2012 , 6, 588-96	11.6	186
600	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , 2010 , 3, 243-8		186
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132	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort		4
131	EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets		4
130	Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules		4
129	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	16.2	4
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126	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019 , 6, 43	8	3
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111	CodonExplorer: an online tool for analyzing codon usage and sequence composition, scaling from genes to genomes. <i>Bioinformatics</i> , 2009 , 25, 1331-2	6.9	3
110	Earth Microbiome Project (EMP) high throughput (HTP) DNA extraction protocol v1		3
109	A lightweight, scalable grid computing framework for parallel bioinformatics applications		3
108	Dramatic differences in gut bacterial densities help to explain the relationship between diet and habitat in rainforest ants		3
107	Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree		3
106	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment 2020 ,		3
105	Reference data based insights expand understanding of human metabolomes		3
104	Evaluating the information content of shallow shotgun metagenomics		3
103	Quantifying and understanding well-to-well contamination in microbiome research		3
102	Skin inflammation activates intestinal stromal fibroblasts and promotes colitis. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.4	3
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91	Automated, miniaturized, and scalable screening of healthcare workers, first responders, and students for SARS-CoV-2 in San Diego County		2
90	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment		2
89	Comparison of heat-inactivated and infectious SARS-CoV-2 across indoor surface materials shows comparable RT-qPCR viral signal intensity and persistence 2021 ,		2
88	Individuals with substance use disorders have a distinct oral microbiome pattern. <i>Brain, Behavior, & Immunity - Health</i> , 2021 , 15, 100271	5	2
87	Systems Analysis Reveals Ageing-Related Perturbations in Retinoids and Sex Hormones in Alzheimer's and Parkinson's Diseases. <i>Biomedicine</i> , 2021 , 9,	4.6	2
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82	Ensemble dispatching on an IBM Blue Gene/L for a bioinformatics knowledge environment 2009 ,		2
81	EMP DNA Extraction Protocol v1		2
80	EMP Sample Submission Guide v1		2

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78	Clean room microbiome complexity impacts planetary protection bioburden. <i>Microbiome</i> , 2021 , 9, 238	16.1	2
77	Links between gut microbiome composition and fatty liver disease in a large population sample		2
76	SARS-CoV-2 Screening Among Symptom-Free Healthcare Workers 2020 ,		2
75	Links between environment, diet, and the hunter-gatherer microbiome		2
74	Chemical Impacts of the Microbiome Across Scales Reveal Novel Conjugated Bile Acids		2
73	Metabolome-informed microbiome analysis refines metadata classifications and reveals unexpected medication transfer in captive cheetahs		2
72	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
71	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
70	Species abundance information improves sequence taxonomy classification accuracy		2
69	Integrated Approaches to Analyze Big Data in the Perinatal/Neonatal Space. <i>Breastfeeding Medicine</i> , 2018 , 13, S5-S6	2	1
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65	Meeting report of the RNA Ontology Consortium January 8-9, 2011. <i>Standards in Genomic Sciences</i> , 2011 , 4, 252-6		1
64	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, E160-E160	11.2	1
63	Using microbiome tools for estimating the postmortem interval 2020 , 171-191		1
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61	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	11.2	1
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56	A semiparametric model for between-subject attributes: Applications to beta-diversity of microbiome data. <i>Biometrics</i> , 2021 ,	1.7	1
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