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List of Publications by Year in descending order

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54
papers

47,304
citations

76196

40
h-index

143772

57
g-index

78
all docs

78
docs citations

78
times ranked

40018
citing authors

#	ARTICLE	IF	CITATIONS
1	GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalized and complete genome-based taxonomy. <i>Nucleic Acids Research</i> , 2022, 50, D785-D794.	6.5	662
2	Chemotaxis shapes the microscale organization of the ocean's microbiome. <i>Nature</i> , 2022, 605, 132-138.	13.7	51
3	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	9.4	628
4	Evidence for non-methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i> . <i>Environmental Microbiology</i> , 2021, 23, 340-357.	1.8	19
5	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 643682.	1.5	25
6	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <i>ISME Journal</i> , 2021, 15, 1879-1892.	4.4	87
7	Critical evaluation of faecal microbiome preservation using metagenomic analysis. <i>ISME Communications</i> , 2021, 1, .	1.7	8
8	A standardized archaeal taxonomy for the Genome Taxonomy Database. <i>Nature Microbiology</i> , 2021, 6, 946-959.	5.9	198
9	Diverse sediment microbiota shape methane emission temperature sensitivity in Arctic lakes. <i>Nature Communications</i> , 2021, 12, 5815.	5.8	15
10	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	4.9	33
11	GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. <i>Bioinformatics</i> , 2020, 36, 1925-1927.	1.8	2,524
12	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
13	Lateral Gene Transfer Drives Metabolic Flexibility in the Anaerobic Methane-Oxidizing Archaeal Family <i>Methanoperedenaceae</i> . <i>MBio</i> , 2020, 11, .	1.8	51
14	A complete domain-to-species taxonomy for Bacteria and Archaea. <i>Nature Biotechnology</i> , 2020, 38, 1079-1086.	9.4	883
15	Proposal to reclassify the proteobacterial classes Deltaproteobacteria and Oligoflexia, and the phylum Thermodesulfobacteria into four phyla reflecting major functional capabilities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5972-6016.	0.8	830
16	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , 2019, 42, 15-21.	1.2	149
17	An evolving view of methane metabolism in the Archaea. <i>Nature Reviews Microbiology</i> , 2019, 17, 219-232.	13.6	350
18	Evaluation of a concatenated protein phylogeny for classification of tailed double-stranded DNA viruses belonging to the order Caudovirales. <i>Nature Microbiology</i> , 2019, 4, 1306-1315.	5.9	69

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19	AnnoTree: visualization and exploration of a functionally annotated microbial tree of life. <i>Nucleic Acids Research</i> , 2019, 47, 4442-4448.	6.5	220
20	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Candidatus</i> Thaumarchaeota). <i>ISME Journal</i> , 2019, 13, 1000-1010.	4.4	158
21	Culture- and metagenomics-enabled analyses of the <i>Methanosphaera</i> genus reveals their monophyletic origin and differentiation according to genome size. <i>ISME Journal</i> , 2018, 12, 2942-2953.	4.4	24
22	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018, 36, 996-1004.	9.4	2,615
23	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. <i>Science</i> , 2017, 355, 1436-1440.	6.0	344
24	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , 2017, 2, 1533-1542.	5.9	1,465
25	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
26	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	1.5	409
27	Genome-Centric Analysis of Microbial Populations Enriched by Hydraulic Fracture Fluid Additives in a Coal Bed Methane Production Well. <i>Frontiers in Microbiology</i> , 2016, 7, 731.	1.5	67
28	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. <i>Scientific Data</i> , 2016, 3, 160050.	2.4	47
29	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. <i>Nature Microbiology</i> , 2016, 1, 16170.	5.9	459
30	Genome-Based Microbial Taxonomy Coming of Age. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018085.	2.3	69
31	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <i>Molecular Biology and Evolution</i> , 2016, 33, 915-927.	3.5	119
32	CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. <i>Genome Research</i> , 2015, 25, 1043-1055.	2.4	7,539
33	A molecular survey of Australian and North American termite genera indicates that vertical inheritance is the primary force shaping termite gut microbiomes. <i>Microbiome</i> , 2015, 3, 5.	4.9	110
34	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. <i>Science</i> , 2015, 350, 434-438.	6.0	677
35	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. <i>Frontiers in Microbiology</i> , 2015, 6, 1469.	1.5	125
36	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. <i>PeerJ</i> , 2015, 3, e740.	0.9	157

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37	Back from the dead; the curious tale of the predatory cyanobacterium <i>Vampirovibrio chlorellavorus</i> . PeerJ, 2015, 3, e968.	0.9	104
38	GroopM: an automated tool for the recovery of population genomes from related metagenomes. PeerJ, 2014, 2, e603.	0.9	254
39	An Expanded Genomic Representation of the Phylum Cyanobacteria. Genome Biology and Evolution, 2014, 6, 1031-1045.	1.1	326
40	STAMP: statistical analysis of taxonomic and functional profiles. Bioinformatics, 2014, 30, 3123-3124.	1.8	3,456
41	Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. ISME Journal, 2013, 7, 173-183.	4.4	41
42	GenGIS 2: Geospatial Analysis of Traditional and Genetic Biodiversity, with New Gradient Algorithms and an Extensible Plugin Framework. PLoS ONE, 2013, 8, e69885.	1.1	118
43	Measuring Community Similarity with Phylogenetic Networks. Molecular Biology and Evolution, 2012, 29, 3947-3958.	3.5	21
44	Rapid identification of high-confidence taxonomic assignments for metagenomic data. Nucleic Acids Research, 2012, 40, e111-e111.	6.5	57
45	Classifying short genomic fragments from novel lineages using composition and homology. BMC Bioinformatics, 2011, 12, 328.	1.2	64
46	Is local colour normalization good enough for local appearance-based classification?. Machine Vision and Applications, 2010, 21, 789-796.	1.7	1
47	Identifying biologically relevant differences between metagenomic communities. Bioinformatics, 2010, 26, 715-721.	1.8	916
48	GenGIS: A geospatial information system for genomic data. Genome Research, 2009, 19, 1896-1904.	2.4	119
49	Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology, 2009, 75, 7537-7541.	1.4	18,390
50	Quantitative visualizations of hierarchically organized data in a geographic context. , 2009, , .		5
51	Tracking the evolution and geographic spread of Influenza A. PLOS Currents, 2009, 1, RRN1014.	1.4	10
52	SeqMonitor: Influenza Analysis Pipeline and Visualization. PLOS Currents, 2009, 1, RRN1040.	1.4	3
53	Hive: A distributed system for vision processing. , 2008, , .		15
54	Evaluation of Background Subtraction Algorithms with Post-Processing. , 2008, , .		142