

Philip Hugenholtz

List of Publications by Year in descending order

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424
papers

103,563
citations

729

120
h-index

250

301
g-index

472
all docs

472
docs citations

472
times ranked

68386
citing authors

#	ARTICLE	IF	CITATIONS
1	Greengenes, a Chimera-Checked 16S rRNA Gene Database and Workbench Compatible with ARB. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5069-5072.	1.4	9,859
2	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
3	The Genomes On Line Database (GOLD) in 2009: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , 2010, 38, D346-D354.	6.5	6,188
4	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
5	STAMP: statistical analysis of taxonomic and functional profiles. <i>Bioinformatics</i> , 2014, 30, 3123-3124.	1.8	3,456
6	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
7	GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. <i>Bioinformatics</i> , 2020, 36, 1925-1927.	1.8	2,524
8	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , 2012, 488, 86-90.	13.7	2,475
9	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239
10	Impact of Culture-Independent Studies on the Emerging Phylogenetic View of Bacterial Diversity. <i>Journal of Bacteriology</i> , 1998, 180, 4765-4774.	1.0	2,165
11	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004, 428, 37-43.	13.7	2,045
12	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
13	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
14	Bellerophon: a program to detect chimeric sequences in multiple sequence alignments. <i>Bioinformatics</i> , 2004, 20, 2317-2319.	1.8	1,443
15	Comparative Metagenomics of Microbial Communities. <i>Science</i> , 2005, 308, 554-557.	6.0	1,432
16	First confirmed detection of SARS-CoV-2 in untreated wastewater in Australia: A proof of concept for the wastewater surveillance of COVID-19 in the community. <i>Science of the Total Environment</i> , 2020, 728, 138764.	3.9	1,393
17	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	13.7	1,181
18	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	9.4	1,176

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19	Wrinkles in the rare biosphere: pyrosequencing errors can lead to artificial inflation of diversity estimates. <i>Environmental Microbiology</i> , 2010, 12, 118-123.	1.8	1,138
20	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	9.4	1,069
21	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <i>Nature</i> , 2013, 500, 567-570.	13.7	1,029
22	Emerging pathogenic links between microbiota and the gut-lung axis. <i>Nature Reviews Microbiology</i> , 2017, 15, 55-63.	13.6	950
23	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	13.7	924
24	NASt: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , 2006, 34, W394-W399.	6.5	918
25	A complete domain-to-species taxonomy for Bacteria and Archaea. <i>Nature Biotechnology</i> , 2020, 38, 1079-1086.	9.4	883
26	Novel Division Level Bacterial Diversity in a Yellowstone Hot Spring. <i>Journal of Bacteriology</i> , 1998, 180, 366-376.	1.0	862
27	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
28	CRISPR – a widespread system that provides acquired resistance against phages in bacteria and archaea. <i>Nature Reviews Microbiology</i> , 2008, 6, 181-186.	13.6	789
29	CRISPR Recognition Tool (CRT): a tool for automatic detection of clustered regularly interspaced palindromic repeats. <i>BMC Bioinformatics</i> , 2007, 8, 209.	1.2	754
30	Identification of Polyphosphate-Accumulating Organisms and Design of 16S rRNA-Directed Probes for Their Detection and Quantitation. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1175-1182.	1.4	691
31	Microbial Diversity in a Hydrocarbon- and Chlorinated-Solvent-Contaminated Aquifer Undergoing Intrinsic Bioremediation. <i>Applied and Environmental Microbiology</i> , 1998, 64, 3869-3877.	1.4	683
32	Exploring prokaryotic diversity in the genomic era. <i>Genome Biology</i> , 2002, 3, reviews0003.1.	13.9	677
33	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
34	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	9.4	634
35	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	9.4	628
36	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

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37	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
38	Dissecting biological "dark matter" with single-cell genetic analysis of rare and uncultivated TM7 microbes from the human mouth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11889-11894.	3.3	552
39	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
40	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , 2016, 4, 36.	4.9	533
41	Accurate phylogenetic classification of variable-length DNA fragments. <i>Nature Methods</i> , 2007, 4, 63-72.	9.0	524
42	Experimental factors affecting PCR-based estimates of microbial species richness and evenness. <i>ISME Journal</i> , 2010, 4, 642-647.	4.4	523
43	Evolutionary Relationships of Wild Hominids Recapitulated by Gut Microbial Communities. <i>PLoS Biology</i> , 2010, 8, e1000546.	2.6	464
44	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. <i>Nature Microbiology</i> , 2016, 1, 16170.	5.9	459
45	<i>Gemmatimonas aurantiaca</i> gen. nov., sp. nov., a Gram-negative, aerobic, polyphosphate-accumulating micro-organism, the first cultured representative of the new bacterial phylum <i>Gemmatimonadetes</i> phyl. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1155-1163.	0.8	458
46	Laboratory Cultivation of Widespread and Previously Uncultured Soil Bacteria. <i>Applied and Environmental Microbiology</i> , 2003, 69, 7210-7215.	1.4	439
47	Bacterial community structures of phosphate-removing and non-phosphate-removing activated sludges from sequencing batch reactors. <i>Applied and Environmental Microbiology</i> , 1995, 61, 1910-1916.	1.4	429
48	A renaissance for the pioneering 16S rRNA gene. <i>Current Opinion in Microbiology</i> , 2008, 11, 442-446.	2.3	418
49	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
50	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
51	Cultivation of globally distributed soil bacteria from phylogenetic lineages previously only detected in cultivation-independent surveys. <i>Environmental Microbiology</i> , 2002, 4, 654-666.	1.8	408
52	Evolutionary conservation of sequence and secondary structures in CRISPR repeats. <i>Genome Biology</i> , 2007, 8, R61.	13.9	382
53	Genome Project Standards in a New Era of Sequencing. <i>Science</i> , 2009, 326, 236-237.	6.0	382
54	A Bioinformatician's Guide to Metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 557-578.	2.9	361

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55	The integrated microbial genomes (IMG) system. <i>Nucleic Acids Research</i> , 2006, 34, D344-D348.	6.5	355
56	Metagenomics. <i>Nature</i> , 2008, 455, 481-483.	13.7	352
57	An evolving view of methane metabolism in the Archaea. <i>Nature Reviews Microbiology</i> , 2019, 17, 219-232.	13.6	350
58	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. <i>Science</i> , 2017, 355, 1436-1440.	6.0	344
59	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. <i>ISME Journal</i> , 2014, 8, 2015-2028.	4.4	328
60	An Expanded Genomic Representation of the Phylum Cyanobacteria. <i>Genome Biology and Evolution</i> , 2014, 6, 1031-1045.	1.1	326
61	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	9.0	322
62	Fast, accurate error-correction of amplicon pyrosequences using Acacia. <i>Nature Methods</i> , 2012, 9, 425-426.	9.0	322
63	Investigation of Candidate Division TM7, a Recently Recognized Major Lineage of the Domain Bacteria with No Known Pure-Culture Representatives. <i>Applied and Environmental Microbiology</i> , 2001, 67, 411-419.	1.4	311
64	Multiple Lateral Transfers of Dissimilatory Sulfite Reductase Genes between Major Lineages of Sulfate-Reducing Prokaryotes. <i>Journal of Bacteriology</i> , 2001, 183, 6028-6035.	1.0	309
65	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2007, 36, D534-D538.	6.5	309
66	Identifying microbial diversity in the natural environment: A molecular phylogenetic approach. <i>Trends in Biotechnology</i> , 1996, 14, 190-197.	4.9	306
67	Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. <i>Science</i> , 2007, 315, 1126-1130.	6.0	300
68	A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. <i>ISME Journal</i> , 2008, 2, 1146-1156.	4.4	299
69	Atmospheric trace gases support primary production in Antarctic desert surface soil. <i>Nature</i> , 2017, 552, 400-403.	13.7	290
70	Functional effects of the microbiota in chronic respiratory disease. <i>Lancet Respiratory Medicine</i> , the, 2019, 7, 907-920.	5.2	269
71	Filamentous Chloroflexi (green non-sulfur bacteria) are abundant in wastewater treatment processes with biological nutrient removal. The EMBL accession numbers for the sequences reported in this paper are X84472 (strain SBR1029 16S rDNA), X84474 (strain SBR1031 16S rDNA), X84498 (strain SBR1064) Tj E00q1 1 0.784314	10.0	264
72	Shining a Light on Dark Sequencing: Characterising Errors in Ion Torrent PGM Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003031.	1.5	265

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73	GroopM: an automated tool for the recovery of population genomes from related metagenomes. PeerJ, 2014, 2, e603.	0.9	254
74	A korarchaeal genome reveals insights into the evolution of the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8102-8107.	3.3	253
75	Unlocking the potential of metagenomics through replicated experimental design. Nature Biotechnology, 2012, 30, 513-520.	9.4	250
76	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. Nature Microbiology, 2021, 6, 960-970.	5.9	248
77	Evolutionary conservation of a core root microbiome across plant phyla along a tropical soil chronosequence. Nature Communications, 2017, 8, 215.	5.8	244
78	Phylogenetic Positions of Novel Aerobic, Bacteriochlorophyll a-Containing Bacteria and Description of <i>Roseococcus thiosulfatophilus</i> gen. nov., sp. nov., <i>Erythromicrobium ramosum</i> gen. nov., sp. nov., and <i>Erythrobacter litoralis</i> sp. nov.. International Journal of Systematic Bacteriology, 1994, 44, 427-434.	2.8	242
79	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14793-14798.	3.3	234
80	High-resolution phylogenetic microbial community profiling. ISME Journal, 2016, 10, 2020-2032.	4.4	232
81	Genome-Directed Isolation of the Key Nitrogen Fixer <i>Leptospirillum ferro Diazotrophum</i> sp. nov. from an Acidophilic Microbial Community. Applied and Environmental Microbiology, 2005, 71, 6319-6324.	1.4	225
82	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. Microbiome, 2014, 2, 11.	4.9	225
83	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	9.4	222
84	The Genomes On Line Database (GOLD) v.2: a monitor of genome projects worldwide. Nucleic Acids Research, 2006, 34, D332-D334.	6.5	220
85	Lineages of Acidophilic Archaea Revealed by Community Genomic Analysis. Science, 2006, 314, 1933-1935.	6.0	217
86	Use of Stable-Isotope Probing, Full-Cycle rRNA Analysis, and Fluorescence In Situ Hybridization-Microautoradiography To Study a Methanol-Fed Denitrifying Microbial Community. Applied and Environmental Microbiology, 2004, 70, 588-596.	1.4	213
87	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. GigaScience, 2016, 5, 21.	3.3	204
88	Chimeric 16S rDNA sequences of diverse origin are accumulating in the public databases. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 289-293.	0.8	203
89	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. ISME Journal, 2013, 7, 50-60.	4.4	198
90	A standardized archaeal taxonomy for the Genome Taxonomy Database. Nature Microbiology, 2021, 6, 946-959.	5.9	198

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91	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. <i>Nature Communications</i> , 2020, 11, 5886.	5.8	194
92	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
93	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. <i>ISME Journal</i> , 2012, 6, 531-541.	4.4	186
94	Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. <i>Nature Methods</i> , 2010, 7, 807-812.	9.0	184
95	Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. <i>Nature</i> , 2014, 513, 242-245.	13.7	183
96	Multiple displacement amplification compromises quantitative analysis of metagenomes. <i>Nature Methods</i> , 2010, 7, 943-944.	9.0	181
97	Grinder: a versatile amplicon and shotgun sequence simulator. <i>Nucleic Acids Research</i> , 2012, 40, e94-e94.	6.5	180
98	Isolation of Succinivibrionaceae Implicated in Low Methane Emissions from Tammar Wallabies. <i>Science</i> , 2011, 333, 646-648.	6.0	179
99	Characterization of Trapped Lignin-Degrading Microbes in Tropical Forest Soil. <i>PLoS ONE</i> , 2011, 6, e19306.	1.1	178
100	Discovery of a novel methanogen prevalent in thawing permafrost. <i>Nature Communications</i> , 2014, 5, 3212.	5.8	170
101	Targeted Discovery of Glycoside Hydrolases from a Switchgrass-Adapted Compost Community. <i>PLoS ONE</i> , 2010, 5, e8812.	1.1	170
102	Loss of Bacterial Diversity during Antibiotic Treatment of Intubated Patients Colonized with <i>Pseudomonas aeruginosa</i> . <i>Journal of Clinical Microbiology</i> , 2007, 45, 1954-1962.	1.8	166
103	Non-Sulfate-Reducing, Syntrophic Bacteria Affiliated with <i>Desulfotomaculum</i> Cluster I Are Widely Distributed in Methanogenic Environments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2080-2091.	1.4	165
104	<i>Chthoniobacter flavus</i> gen. nov., sp. nov., the First Pure-Culture Representative of Subdivision Two, <i>Spartobacteria classis</i> nov., of the Phylum <i>Verrucomicrobia</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 5875-5881.	1.4	162
105	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. <i>Frontiers in Microbiology</i> , 2016, 7, 211.	1.5	161
106	Numbers and locations of native bacteria on field-grown wheat roots quantified by fluorescence in situ hybridization (FISH). <i>Environmental Microbiology</i> , 2006, 8, 871-884.	1.8	160
107	Airway dysbiosis: <i>Haemophilus influenzae</i> and <i>Tropheryma</i> in poorly controlled asthma. <i>European Respiratory Journal</i> , 2016, 47, 792-800.	3.1	159
108	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Ca</i> .) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	4.4	158

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109	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 2015, 3, e740.	0.9	157
110	Nitrogen fertilizer dose alters fungal communities in sugarcane soil and rhizosphere. Scientific Reports, 2015, 5, 8678.	1.6	155
111	Reclassification of Sphaerobacter thermophilus from the subclass Sphaerobacteridae in the phylum Actinobacteria to the class Thermomicrobia (emended description) in the phylum Chloroflexi (emended description). International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 2049-2051.	0.8	151
112	Comparative Metagenomic and Metatranscriptomic Analysis of Hindgut Paunch Microbiota in Wood- and Dung-Feeding Higher Termites. PLoS ONE, 2013, 8, e61126.	1.1	149
113	The core root microbiome of sugarcane cultivated under varying nitrogen fertilizer application. Environmental Microbiology, 2016, 18, 1338-1351.	1.8	149
114	The importance of designating type material for uncultured taxa. Systematic and Applied Microbiology, 2019, 42, 15-21.	1.2	149
115	Detection of SARS-CoV-2 RNA in commercial passenger aircraft and cruise ship wastewater: a surveillance tool for assessing the presence of COVID-19 infected travellers. Journal of Travel Medicine, 2020, 27, .	1.4	146
116	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. Molecular Systems Biology, 2008, 4, 198.	3.2	139
117	Liquid Serial Dilution Is Inferior to Solid Media for Isolation of Cultures Representative of the Phylum-Level Diversity of Soil Bacteria. Applied and Environmental Microbiology, 2004, 70, 4363-4366.	1.4	136
118	A bacterial metapopulation adapts locally to phage predation despite global dispersal. Genome Research, 2008, 18, 293-297.	2.4	135
119	ShotgunFunctionalizeR: an R-package for functional comparison of metagenomes. Bioinformatics, 2009, 25, 2737-2738.	1.8	133
120	Molecular analysis of dimethyl sulphide dehydrogenase from Rhodovulum sulfidophilum: its place in the dimethyl sulphoxide reductase family of microbial molybdopterin-containing enzymes. Molecular Microbiology, 2002, 44, 1575-1587.	1.2	129
121	A rooted phylogeny resolves early bacterial evolution. Science, 2021, 372, .	6.0	128
122	Comparison of DNA Extraction Methods for Microbial Community Profiling with an Application to Pediatric Bronchoalveolar Lavage Samples. PLoS ONE, 2012, 7, e34605.	1.1	126
123	The DMSO Reductase Family of Microbial Molybdenum Enzymes; Molecular Properties and Role in the Dissimilatory Reduction of Toxic Elements. Geomicrobiology Journal, 2002, 19, 3-21.	1.0	125
124	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. Frontiers in Microbiology, 2015, 6, 1469.	1.5	125
125	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. Molecular Biology and Evolution, 2016, 33, 915-927.	3.5	119
126	Design and Evaluation of 16S rRNA-Targeted Oligonucleotide Probes for Fluorescence In Situ Hybridization. , 2002, 179, 029-042.		116

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127	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21T). <i>Standards in Genomic Sciences</i> , 2011, 5, 97-111.	1.5	115
128	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
129	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011, 5, 122-130.	4.4	114
130	Reestablishment of Recipient-associated Microbiota in the Lung Allograft Is Linked to Reduced Risk of Bronchiolitis Obliterans Syndrome. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 640-647.	2.5	114
131	Identification of a haloalkaliphilic and thermostable cellulase with improved ionic liquid tolerance. <i>Green Chemistry</i> , 2011, 13, 2083.	4.6	111
132	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
133	Back from the dead; the curious tale of the predatory cyanobacterium <i>Vampirovibrio chlorellavorus</i> . <i>PeerJ</i> , 2015, 3, e968.	0.9	104
134	Environmental distribution and population biology of <i>Candidatus</i> <i>Accumulibacter</i> , a primary agent of biological phosphorus removal. <i>Environmental Microbiology</i> , 2008, 10, 2692-2703.	1.8	102
135	Extremely Acidophilic Protists from Acid Mine Drainage Host Rickettsiales -Lineage Endosymbionts That Have Intervening Sequences in Their 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5512-5518.	1.4	101
136	Comparative genomics of two <i>Candidatus</i> <i>Accumulibacter</i> ™ clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	4.4	101
137	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
138	Strategies for Enhancing the Effectiveness of Metagenomic-based Enzyme Discovery in Lignocellulolytic Microbial Communities. <i>Bioenergy Research</i> , 2010, 3, 146-158.	2.2	100
139	Glycoside Hydrolase Activities of Thermophilic Bacterial Consortia Adapted to Switchgrass. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5804-5812.	1.4	99
140	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6T). <i>Standards in Genomic Sciences</i> , 2011, 4, 200-209.	1.5	96
141	Genomic Analysis of <i>Elusimicrobium minutum</i> , the First Cultivated Representative of the Phylum <i>Elusimicrobia</i> (Formerly Termite Group 1). <i>Applied and Environmental Microbiology</i> , 2009, 75, 2841-2849.	1.4	95
142	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019, 4, 2192-2203.	5.9	95
143	Crosstalk between sugarcane and a plant-growth promoting <i>Burkholderia</i> species. <i>Scientific Reports</i> , 2016, 6, 37389.	1.6	92
144	A new species of <i>Burkholderia</i> isolated from sugarcane roots promotes plant growth. <i>Microbial Biotechnology</i> , 2014, 7, 142-154.	2.0	91

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145	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , 2021, 15, 2986-3004.	4.4	89
146	Microbiomes in respiratory health and disease: An Asia-Pacific perspective. <i>Respirology</i> , 2017, 22, 240-250.	1.3	88
147	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <i>ISME Journal</i> , 2021, 15, 1879-1892.	4.4	87
148	Contrasting Life Strategies of Viruses that Infect Photo- and Heterotrophic Bacteria, as Revealed by Viral Tagging. <i>MBio</i> , 2012, 3, .	1.8	86
149	Isolation and molecular identification of planctomycete bacteria from postlarvae of the giant tiger prawn, <i>Penaeus monodon</i> . <i>Applied and Environmental Microbiology</i> , 1997, 63, 254-262.	1.4	84
150	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006, 22, e359-e367.	1.8	81
151	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. <i>Standards in Genomic Sciences</i> , 2013, 9, 1278-1284.	1.5	79
152	Recipient mucosal-associated invariant T cells control GVHD within the colon. <i>Journal of Clinical Investigation</i> , 2018, 128, 1919-1936.	3.9	78
153	“ <i>Microthrix parvicella</i> ” is a Novel, Deep Branching Member of the Actinomycetes Subphylum. <i>Systematic and Applied Microbiology</i> , 1995, 17, 513-518.	1.2	76
154	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014, 9, 10.	1.5	76
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