

Philip Hugenholtz

List of Publications by Year in descending order

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Version: 2024-02-01

424
papers

103,563
citations

735

120
h-index

250

301
g-index

472
all docs

472
docs citations

472
times ranked

68386
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.	14.5	662
2	Characterization of the juvenile koala gut microbiome across wild populations. <i>Environmental Microbiology</i> , 2022, 24, 4209-4219.	3.8	9
3	Changes in the skin microbiome associated with squamous cell carcinoma in transplant recipients. <i>ISME Communications</i> , 2022, 2, .	4.2	6
4	Maternal inheritance of the koala gut microbiome and its compositional and functional maturation during juvenile development. <i>Environmental Microbiology</i> , 2022, 24, 475-493.	3.8	12
5	Chemotaxis shapes the microscale organization of the ocean's microbiome. <i>Nature</i> , 2022, 605, 132-138.	27.8	51
6	Skin Cancer-Associated <i>S. aureus</i> Strains Can Induce DNA Damage in Human Keratinocytes by Downregulating DNA Repair and Promoting Oxidative Stress. <i>Cancers</i> , 2022, 14, 2143.	3.7	8
7	A genome and gene catalog of glacier microbiomes. <i>Nature Biotechnology</i> , 2022, 40, 1341-1348.	17.5	50
8	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	17.5	628
9	<i>Candidatus</i> Eremiobacterota, a metabolically and phylogenetically diverse terrestrial phylum with acid-tolerant adaptations. <i>ISME Journal</i> , 2021, 15, 2692-2707.	9.8	36
10	Interferon Lambda Protects Gastrointestinal Stem Cells from Acute Gvhd. <i>Transplantation and Cellular Therapy</i> , 2021, 27, S78.	1.2	0
11	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.	3.5	25
12	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <i>ISME Journal</i> , 2021, 15, 1879-1892.	9.8	87
13	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , 2021, 372, .	12.6	128
14	Critical evaluation of faecal microbiome preservation using metagenomic analysis. <i>ISME Communications</i> , 2021, 1, .	4.2	8
15	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , 2021, 15, 2986-3004.	9.8	89
16	IFN- γ therapy prevents severe gastrointestinal graft-versus-host disease. <i>Blood</i> , 2021, 138, 722-737.	1.4	21
17	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. <i>ISME Journal</i> , 2021, 15, 3339-3356.	9.8	48
18	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	13.3	248

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19	A standardized archaeal taxonomy for the Genome Taxonomy Database. <i>Nature Microbiology</i> , 2021, 6, 946-959.	13.3	198
20	Persistence and resistance: survival mechanisms of <i>Candidatus</i> Dormibacterota from nutrient-poor Antarctic soils. <i>Environmental Microbiology</i> , 2021, 23, 4276-4294.	3.8	7
21	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , 2021, 1, .	4.2	23
22	Termite gas emissions select for hydrogenotrophic microbial communities in termite mounds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	15
23	Kinetic and Structural Characterization of the First B3 Metallo- β -Lactamase with an Active-Site Glutamic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0093621.	3.2	7
24	Effects of laboratory domestication on the rodent gut microbiome. <i>ISME Communications</i> , 2021, 1, .	4.2	21
25	Wastewater monitoring for SARS-CoV-2. <i>Microbiology Australia</i> , 2021, 42, 18.	0.4	5
26	<i>Streptococcus</i> species enriched in the oral cavity of patients with RA are a source of peptidoglycan-polysaccharide polymers that can induce arthritis in mice. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 573-581.	0.9	24
27	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	11.1	33
28	Secreted Toxins From <i>Staphylococcus aureus</i> Strains Isolated From Keratinocyte Skin Cancers Mediate Pro-tumorigenic Inflammatory Responses in the Skin. <i>Frontiers in Microbiology</i> , 2021, 12, 789042.	3.5	14
29	Microvolume DNA extraction methods for microscale amplicon and metagenomic studies. <i>ISME Communications</i> , 2021, 1, .	4.2	10
30	GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. <i>Bioinformatics</i> , 2020, 36, 1925-1927.	4.1	2,524
31	Tracking seasonal changes in diversity of pollen allergen exposure: Targeted metabarcoding of a subtropical aerobiome. <i>Science of the Total Environment</i> , 2020, 747, 141189.	8.0	23
32	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. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	146
33	Su1204 VARIATIONS OF THE MUCOSA ASSOCIATED MICROBIOTA ALONG THE HUMAN GASTROINTESTINAL TRACT IN HEALTH AND INFLAMMATORY BOWEL DISEASE. <i>Gastroenterology</i> , 2020, 158, S-542.	1.3	1
34	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. <i>Nature Communications</i> , 2020, 11, 5886.	12.8	194
35	Changes in the Gut Microbiome in Chronic Obstructive Pulmonary Disease. , 2020, , .		0
36	Draft Genome Sequence of <i>Limisphaera ngatamarikiensis</i> NGM72.4 ^T , a Moderately Alkaliphilic Thermophile Belonging to the Class <i>Verrucomicrobiae</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2

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37	Fluconazole resistance in <i>Candida albicans</i> is induced by <i>Pseudomonas aeruginosa</i> quorum sensing. <i>Scientific Reports</i> , 2020, 10, 7769.	3.3	33
38	Broad spectrum antibiotic-degrading metallo- β -lactamases are phylogenetically diverse. <i>Protein and Cell</i> , 2020, 11, 613-617.	11.0	21
39	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , 2020, 7, 188.	5.3	56
40	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	13.3	115
41	Continuous pre- and post-transplant exposure to a disease-associated gut microbiome promotes hyper-acute graft-versus-host disease in wild-type mice. <i>Gut Microbes</i> , 2020, 11, 754-770.	9.8	17
42	A complete domain-to-species taxonomy for Bacteria and Archaea. <i>Nature Biotechnology</i> , 2020, 38, 1079-1086.	17.5	883
43	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.	8.0	1,393
44	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.	1.7	830
45	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , 2019, 42, 15-21.	2.8	149
46	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019, 4, 2192-2203.	13.3	95
47	Faecal inoculations alter the gastrointestinal microbiome and allow dietary expansion in a wild specialist herbivore, the koala. <i>Animal Microbiome</i> , 2019, 1, 6.	3.8	39
48	An evolving view of methane metabolism in the Archaea. <i>Nature Reviews Microbiology</i> , 2019, 17, 219-232.	28.6	350
49	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	45
50	IL-23 favours outgrowth of spondyloarthritis-associated pathobionts and suppresses host support for homeostatic microbiota. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 494-503.	0.9	36
51	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.	13.3	69
52	Functional effects of the microbiota in chronic respiratory disease. <i>Lancet Respiratory Medicine</i> , the, 2019, 7, 907-920.	10.7	269
53	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	12.6	5
54	Bacterial fermentation and respiration processes are uncoupled in anoxic permeable sediments. <i>Nature Microbiology</i> , 2019, 4, 1014-1023.	13.3	76

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55	Evolution of photosynthesis and aerobic respiration in the cyanobacteria. <i>Free Radical Biology and Medicine</i> , 2019, 140, 200-205.	2.9	48
56	2125. <i>Staphylococcus</i> Species Identification by Fourier Transform Infrared (FTIR) Spectroscopic Techniques: A Cross-Lab Study. <i>Open Forum Infectious Diseases</i> , 2019, 6, S720-S720.	0.9	0
57	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
58	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (<i>Ca</i> .) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	9.8	158
59	Genomic Encyclopedia of Bacteria and Archaea (GEBA) VI: learning from type strains. <i>Microbiology Australia</i> , 2019, 40, 125.	0.4	3
60	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. <i>Environmental Science & Technology</i> , 2018, 52, 5386-5397.	10.0	52
61	Beneficial changes in rumen bacterial community profile in sheep and dairy calves as a result of feeding the probiotic <i>Bacillus amyloliquefaciens</i> H57. <i>Journal of Applied Microbiology</i> , 2018, 124, 855-866.	3.1	34
62	A Natural History of Actinic Keratosis and Cutaneous Squamous Cell Carcinoma Microbiomes. <i>MBio</i> , 2018, 9, .	4.1	37
63	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
64	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	3.3	11
65	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.	9.8	24
66	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018, 36, 996-1004.	17.5	2,615
67	Recipient mucosal-associated invariant T cells control GVHD within the colon. <i>Journal of Clinical Investigation</i> , 2018, 128, 1919-1936.	8.2	78
68	Microbiomes in respiratory health and disease: An Asia-Pacific perspective. <i>Respirology</i> , 2017, 22, 240-250.	2.3	88
69	Acute graft-versus-host disease is regulated by an IL-17-sensitive microbiome. <i>Blood</i> , 2017, 129, 2172-2185.	1.4	63
70	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	17.5	222
71	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. <i>Science</i> , 2017, 355, 1436-1440.	12.6	344
72	Evolutionary conservation of a core root microbiome across plant phyla along a tropical soil chronosequence. <i>Nature Communications</i> , 2017, 8, 215.	12.8	244

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73	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , 2017, 2, 1533-1542.	13.3	1,465
74	Characterization of a highly efficient antibiotic-degrading metallo- β -lactamase obtained from an uncultured member of a permafrost community. <i>Metallomics</i> , 2017, 9, 1157-1168.	2.4	17
75	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
76	Atmospheric trace gases support primary production in Antarctic desert surface soil. <i>Nature</i> , 2017, 552, 400-403.	27.8	290
77	Emerging pathogenic links between microbiota and the gut–lung axis. <i>Nature Reviews Microbiology</i> , 2017, 15, 55-63.	28.6	950
78	DIETARY FIBRE AND MICROBIAL METABOLITES PROTECT AGAINST CIGARETTE SMOKE-INDUCED LUNG PATHOLOGY IN MICE. <i>Respirology</i> , 2017, 22, 4-5.	2.3	2
79	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	3.5	409
80	A microfluidics-based in situ chemotaxis assay to study the behaviour of aquatic microbial communities. <i>Nature Microbiology</i> , 2017, 2, 1344-1349.	13.3	60
81	Gene and genome-centric analyses of koala and wombat fecal microbiomes point to metabolic specialization for digestion. <i>PeerJ</i> , 2017, 5, e4075.	2.0	24
82	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. <i>Frontiers in Microbiology</i> , 2016, 7, 211.	3.5	161
83	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , 2016, 4, 36.	11.1	533
84	The core root microbiome of sugarcane cultivated under varying nitrogen fertilizer application. <i>Environmental Microbiology</i> , 2016, 18, 1338-1351.	3.8	149
85	<i>Candidatus</i> <i>Adiutrix intracellularis</i> TM , an endosymbiont of termite gut flagellates, is the first representative of a deep-branching clade of <i>Deltaproteobacteria</i> and a putative homoacetogen. <i>Environmental Microbiology</i> , 2016, 18, 2548-2564.	3.8	50
86	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. <i>GigaScience</i> , 2016, 5, 21.	6.4	204
87	Anode potential influences the structure and function of anodic electrode and electrolyte-associated microbiomes. <i>Scientific Reports</i> , 2016, 6, 39114.	3.3	57
88	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. <i>Scientific Data</i> , 2016, 3, 160050.	5.3	47
89	Crosstalk between sugarcane and a plant-growth promoting <i>Burkholderia</i> species. <i>Scientific Reports</i> , 2016, 6, 37389.	3.3	92
90	Near complete genome sequence of the animal feed probiotic, <i>Bacillus amyloliquefaciens</i> H57. <i>Standards in Genomic Sciences</i> , 2016, 11, 60.	1.5	16

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91	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. <i>Nature Microbiology</i> , 2016, 1, 16170.	13.3	459
92	Airway dysbiosis: <i>Haemophilus influenzae</i> and <i>Tropheryma</i> in poorly controlled asthma. <i>European Respiratory Journal</i> , 2016, 47, 792-800.	6.7	159
93	Genome-Based Microbial Taxonomy Coming of Age. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018085.	5.5	69
94	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	9.8	232
95	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.	8.9	119
96	Amino Acid and Peptide Utilization Profiles of the Fluoroacetate-Degrading Bacterium <i>Synergistetes</i> Strain MFA1 Under Varying Conditions. <i>Microbial Ecology</i> , 2016, 71, 494-504.	2.8	16
97	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. <i>PeerJ</i> , 2016, 4, e2486.	2.0	64
98	Do You Kiss Your Mother with That Mouth? An Authentic Large-Scale Undergraduate Research Experience in Mapping the Human Oral Microbiome. <i>Journal of Microbiology and Biology Education</i> , 2015, 16, 50-60.	1.0	31
99	Evaluating DNA Extraction Methods for Community Profiling of Pig Hindgut Microbial Community. <i>PLoS ONE</i> , 2015, 10, e0142720.	2.5	8
100	Draft Genome Sequences of <i>Anaerolinea thermolimosa</i> IMO-1, <i>Bellilinea caldifistulae</i> GOMI-1, <i>Leptolinea tardivitalis</i> YMTK-2, <i>Levilinea saccharolytica</i> KIBI-1, <i>Longilinea arvoryzae</i> KOMI-1, Previously Described as Members of the Class <i>Anaerolineae</i> (<i>Chloroflexi</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	14
101	Link scientific publications using linked data. , 2015, , .		2
102	Nitrogen fertilizer dose alters fungal communities in sugarcane soil and rhizosphere. <i>Scientific Reports</i> , 2015, 5, 8678.	3.3	155
103	CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. <i>Genome Research</i> , 2015, 25, 1043-1055.	5.5	7,539
104	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.	11.1	110
105	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains. <i>Standards in Genomic Sciences</i> , 2015, 10, 26.	1.5	74
106	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. <i>Frontiers in Microbiology</i> , 2015, 6, 1469.	3.5	125
107	Comparative genomics of non-pseudomonal bacterial species colonising paediatric cystic fibrosis patients. <i>PeerJ</i> , 2015, 3, e1223.	2.0	35
108	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. <i>PeerJ</i> , 2015, 3, e740.	2.0	157

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109	Back from the dead; the curious tale of the predatory cyanobacterium <i>Vampirovibrio chlorellavorus</i> . PeerJ, 2015, 3, e968.	2.0	104
110	GroopM: an automated tool for the recovery of population genomes from related metagenomes. PeerJ, 2014, 2, e603.	2.0	254
111	Yeast as a Biofertilizer Alters Plant Growth and Morphology. Crop Science, 2014, 54, 785-790.	1.8	35
112	An Expanded Genomic Representation of the Phylum Cyanobacteria. Genome Biology and Evolution, 2014, 6, 1031-1045.	2.5	326
113	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
114	Genome Sequence of Enterotoxigenic Escherichia coli Strain B2C. Genome Announcements, 2014, 2, .	0.8	6
115	Single Clinical Isolates from Acute Uncomplicated Urinary Tract Infections Are Representative of Dominant <i>In Situ</i> Populations. MBio, 2014, 5, e01064-13.	4.1	45
116	Effects of sample treatments on genome recovery via single-cell genomics. ISME Journal, 2014, 8, 2546-2549.	9.8	29
117	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. ISME Journal, 2014, 8, 2015-2028.	9.8	328
118	A new species of <i>Burkholderia</i> isolated from sugarcane roots promotes plant growth. Microbial Biotechnology, 2014, 7, 142-154.	4.2	91
119	STAMP: statistical analysis of taxonomic and functional profiles. Bioinformatics, 2014, 30, 3123-3124.	4.1	3,456
120	Discovery of a novel methanogen prevalent in thawing permafrost. Nature Communications, 2014, 5, 3212.	12.8	170
121	Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. Nature, 2014, 513, 242-245.	27.8	183
122	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. Microbiome, 2014, 2, 11.	11.1	225
123	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. Standards in Genomic Sciences, 2014, 9, 10.	1.5	76
124	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3T) from an African solfataric spring. Standards in Genomic Sciences, 2014, 9, 1105-1117.	1.5	7
125	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279T), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . Standards in Genomic Sciences, 2014, 9, 1076-1088.	1.5	22
126	JTD special edition 'Hot Topics in COPD'-The microbiome in COPD. Journal of Thoracic Disease, 2014, 6, 1525-31.	1.4	18

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127	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <i>Nature</i> , 2013, 500, 567-570.	27.8	1,029
128	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
129	Comparative genomics of two <i>Candidatus</i> Accumulibacter™ clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	9.8	101
130	In-Solution Fluorescence In Situ Hybridization and Fluorescence-Activated Cell Sorting for Single Cell and Population Genome Recovery. <i>Methods in Enzymology</i> , 2013, 531, 3-19.	1.0	18
131	Metagenomics and Community Profiling: Culture-Independent Techniques in the Clinical Laboratory. <i>Clinical Microbiology Newsletter</i> , 2013, 35, 1-9.	0.7	6
132	Longitudinal Holistic Profiling of the Lung Transplant Microbiome. <i>Journal of Heart and Lung Transplantation</i> , 2013, 32, S10-S11.	0.6	3
133	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	17.5	1,176
134	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <i>ISME Journal</i> , 2013, 7, 50-60.	9.8	198
135	From deep sequencing to viral tagging: Recent advances in viral metagenomics. <i>BioEssays</i> , 2013, 35, 436-442.	2.5	38
136	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.	5.6	114
137	Shining a Light on Dark Sequencing: Characterising Errors in Ion Torrent PGM Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003031.	3.2	265
138	Comparative Metagenomic and Metatranscriptomic Analysis of Hindgut Paunch Microbiota in Wood- and Dung-Feeding Higher Termites. <i>PLoS ONE</i> , 2013, 8, e61126.	2.5	149
139	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2T) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013, 8, 15-25.	1.5	8
140	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437T). <i>Standards in Genomic Sciences</i> , 2013, 8, 26-36.	1.5	12
141	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5T). <i>Standards in Genomic Sciences</i> , 2013, 8, 37-46.	1.5	11
142	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGAT). <i>Standards in Genomic Sciences</i> , 2013, 8, 47-57.	1.5	11
143	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (HT), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 228-238.	1.5	11
144	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701T) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 57-70.	1.5	8

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145	Genome sequence of <i>Frateuria aurantia</i> type strain (KondÅ´ 67T), a xanthomonade isolated from <i>Lilium auratum</i> Lindl.. Standards in Genomic Sciences, 2013, 9, 83-92.	1.5	3
146	Prokaryotic Super Program Advisory Committee DOE Joint Genome Institute, Walnut Creek, CA, March 27, 2013. Standards in Genomic Sciences, 2013, 8, 561-570.	1.5	5
147	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. Standards in Genomic Sciences, 2013, 9, 1278-1284.	1.5	79
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