

# Philip Hugenholtz

## List of Publications by Year in descending order

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Version: 2024-02-01

424  
papers

103,563  
citations

867

120  
h-index

293

301  
g-index

472  
all docs

472  
docs citations

472  
times ranked

75057  
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	Characterization of the juvenile koala gut microbiome across wild populations. <i>Environmental Microbiology</i> , 2022, 24, 4209-4219.	1.8	9
3	Changes in the skin microbiome associated with squamous cell carcinoma in transplant recipients. <i>ISME Communications</i> , 2022, 2, .	1.7	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.	1.8	12
5	Chemotaxis shapes the microscale organization of the ocean's microbiome. <i>Nature</i> , 2022, 605, 132-138.	13.7	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.	1.7	8
7	A genome and gene catalog of glacier microbiomes. <i>Nature Biotechnology</i> , 2022, 40, 1341-1348.	9.4	50
8	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	9.4	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.	4.4	36
10	Interferon Lambda Protects Gastrointestinal Stem Cells from Acute GVHD. <i>Transplantation and Cellular Therapy</i> , 2021, 27, S78.	0.6	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.	1.5	25
12	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <i>ISME Journal</i> , 2021, 15, 1879-1892.	4.4	87
13	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , 2021, 372, .	6.0	128
14	Critical evaluation of faecal microbiome preservation using metagenomic analysis. <i>ISME Communications</i> , 2021, 1, .	1.7	8
15	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
16	IFN- $\lambda$ therapy prevents severe gastrointestinal graft-versus-host disease. <i>Blood</i> , 2021, 138, 722-737.	0.6	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.	4.4	48
18	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	5.9	248

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19	A standardized archaeal taxonomy for the Genome Taxonomy Database. <i>Nature Microbiology</i> , 2021, 6, 946-959.	5.9	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.	1.8	7
21	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , 2021, 1, .	1.7	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, .	3.3	15
23	Kinetic and Structural Characterization of the First B3 Metallo- $\beta$ -Lactamase with an Active-Site Glutamic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0093621.	1.4	7
24	Effects of laboratory domestication on the rodent gut microbiome. <i>ISME Communications</i> , 2021, 1, .	1.7	21
25	Wastewater monitoring for SARS-CoV-2. <i>Microbiology Australia</i> , 2021, 42, 18.	0.1	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.	0.5	24
27	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
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.	1.5	14
29	Microvolume DNA extraction methods for microscale amplicon and metagenomic studies. <i>ISME Communications</i> , 2021, 1, .	1.7	10
30	GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. <i>Bioinformatics</i> , 2020, 36, 1925-1927.	1.8	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.	3.9	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, .	1.4	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.	0.6	1
34	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. <i>Nature Communications</i> , 2020, 11, 5886.	5.8	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 <sup>T</sup> , a Moderately Alkaliphilic Thermophile Belonging to the Class <i>Verrucomicrobiae</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	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.	1.6	33
38	Broad spectrum antibiotic-degrading metallo- $\beta$ -lactamases are phylogenetically diverse. <i>Protein and Cell</i> , 2020, 11, 613-617.	4.8	21
39	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , 2020, 7, 188.	2.4	56
40	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	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.	4.3	17
42	A complete domain-to-species taxonomy for Bacteria and Archaea. <i>Nature Biotechnology</i> , 2020, 38, 1079-1086.	9.4	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.	3.9	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.	0.8	830
45	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , 2019, 42, 15-21.	1.2	149
46	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019, 4, 2192-2203.	5.9	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.	1.5	39
48	An evolving view of methane metabolism in the Archaea. <i>Nature Reviews Microbiology</i> , 2019, 17, 219-232.	13.6	350
49	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	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.	0.5	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.	5.9	69
52	Functional effects of the microbiota in chronic respiratory disease. <i>Lancet Respiratory Medicine</i> , 2019, 7, 907-920.	5.2	269
53	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
54	Bacterial fermentation and respiration processes are uncoupled in anoxic permeable sediments. <i>Nature Microbiology</i> , 2019, 4, 1014-1023.	5.9	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.	1.3	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.	0.4	0
57	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	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	4.9	158
59	Genomic Encyclopedia of Bacteria and Archaea (GEBA) VI: learning from type strains. <i>Microbiology Australia</i> , 2019, 40, 125.	0.1	3
60	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5386-5397.	4.6	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.	1.4	34
62	A Natural History of Actinic Keratosis and Cutaneous Squamous Cell Carcinoma Microbiomes. <i>MBio</i> , 2018, 9, .	1.8	37
63	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
64	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	1.6	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.	4.4	24
66	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
67	Recipient mucosal-associated invariant T cells control GVHD within the colon. <i>Journal of Clinical Investigation</i> , 2018, 128, 1919-1936.	3.9	78
68	Microbiomes in respiratory health and disease: An Asia-Pacific perspective. <i>Respirology</i> , 2017, 22, 240-250.	1.3	88
69	Acute graft-versus-host disease is regulated by an IL-17-sensitive microbiome. <i>Blood</i> , 2017, 129, 2172-2185.	0.6	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.	9.4	222
71	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. <i>Science</i> , 2017, 355, 1436-1440.	6.0	344
72	Evolutionary conservation of a core root microbiome across plant phyla along a tropical soil chronosequence. <i>Nature Communications</i> , 2017, 8, 215.	5.8	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.	5.9	1,465
74	Characterization of a highly efficient antibiotic-degrading metallo- $\beta$ -lactamase obtained from an uncultured member of a permafrost community. <i>Metallomics</i> , 2017, 9, 1157-1168.	1.0	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.	9.4	1,512
76	Atmospheric trace gases support primary production in Antarctic desert surface soil. <i>Nature</i> , 2017, 552, 400-403.	13.7	290
77	Emerging pathogenic links between microbiota and the gut-lung axis. <i>Nature Reviews Microbiology</i> , 2017, 15, 55-63.	13.6	950
78	DIETARY FIBRE AND MICROBIAL METABOLITES PROTECT AGAINST CIGARETTE SMOKE-INDUCED LUNG PATHOLOGY IN MICE. <i>Respirology</i> , 2017, 22, 4-5.	1.3	2
79	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	1.5	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.	5.9	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.	0.9	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.	1.5	161
83	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , 2016, 4, 36.	4.9	533
84	The core root microbiome of sugarcane cultivated under varying nitrogen fertilizer application. <i>Environmental Microbiology</i> , 2016, 18, 1338-1351.	1.8	149
85	<i>Candidatus</i> <i>Adiutrix intracellularis</i> <sup>TM</sup> , 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.	1.8	50
86	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. <i>GigaScience</i> , 2016, 5, 21.	3.3	204
87	Anode potential influences the structure and function of anodic electrode and electrolyte-associated microbiomes. <i>Scientific Reports</i> , 2016, 6, 39114.	1.6	57
88	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. <i>Scientific Data</i> , 2016, 3, 160050.	2.4	47
89	Crosstalk between sugarcane and a plant-growth promoting Burkholderia species. <i>Scientific Reports</i> , 2016, 6, 37389.	1.6	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.	5.9	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.	3.1	159
93	Genome-Based Microbial Taxonomy Coming of Age. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018085.	2.3	69
94	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	4.4	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.	3.5	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.	1.4	16
97	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. <i>PeerJ</i> , 2016, 4, e2486.	0.9	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.	0.5	31
99	Evaluating DNA Extraction Methods for Community Profiling of Pig Hindgut Microbial Community. <i>PLoS ONE</i> , 2015, 10, e0142720.	1.1	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.	1.6	155
103	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
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.	4.9	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.	1.5	125
107	Comparative genomics of non-pseudomonal bacterial species colonising paediatric cystic fibrosis patients. <i>PeerJ</i> , 2015, 3, e1223.	0.9	35
108	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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109	Back from the dead; the curious tale of the predatory cyanobacterium <i>Vampirovibrio chlorellavorus</i> . PeerJ, 2015, 3, e968.	0.9	104
110	GroopM: an automated tool for the recovery of population genomes from related metagenomes. PeerJ, 2014, 2, e603.	0.9	254
111	Yeast as a Biofertilizer Alters Plant Growth and Morphology. Crop Science, 2014, 54, 785-790.	0.8	35
112	An Expanded Genomic Representation of the Phylum Cyanobacteria. Genome Biology and Evolution, 2014, 6, 1031-1045.	1.1	326
113	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	2.6	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.	1.8	45
116	Effects of sample treatments on genome recovery via single-cell genomics. ISME Journal, 2014, 8, 2546-2549.	4.4	29
117	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. ISME Journal, 2014, 8, 2015-2028.	4.4	328
118	A new species of <i>Burkholderia</i> isolated from sugarcane roots promotes plant growth. Microbial Biotechnology, 2014, 7, 142-154.	2.0	91
119	STAMP: statistical analysis of taxonomic and functional profiles. Bioinformatics, 2014, 30, 3123-3124.	1.8	3,456
120	Discovery of a novel methanogen prevalent in thawing permafrost. Nature Communications, 2014, 5, 3212.	5.8	170
121	Viral tagging reveals discrete populations in Synechococcus viral genome sequence space. Nature, 2014, 513, 242-245.	13.7	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.	4.9	225
123	Complete genome sequence of Planctomyces brasiliensis type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of Gimesia gen. nov., Planctopirus gen. nov. and Rubinisphaera 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 Thermotoga thermarum 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 Methanoplanus limicola type strain (DSM 2279T), reclassification of Methanoplanus petrolearius as Methanolacinia petrolearia and emended descriptions of the genera Methanoplanus and Methanolacinia. 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.	0.6	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.	13.7	1,029
128	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239
129	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
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.	0.4	18
131	Metagenomics and Community Profiling: Culture-Independent Techniques in the Clinical Laboratory. <i>Clinical Microbiology Newsletter</i> , 2013, 35, 1-9.	0.4	6
132	Longitudinal Holistic Profiling of the Lung Transplant Microbiome. <i>Journal of Heart and Lung Transplantation</i> , 2013, 32, S10-S11.	0.3	3
133	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
134	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <i>ISME Journal</i> , 2013, 7, 50-60.	4.4	198
135	From deep sequencing to viral tagging: Recent advances in viral metagenomics. <i>BioEssays</i> , 2013, 35, 436-442.	1.2	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.	2.5	114
137	Shining a Light on Dark Sequencing: Characterising Errors in Ion Torrent PGM Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003031.	1.5	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.	1.1	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
148	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1T), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeræ</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeræ</i> comb. nov., and emendation of the genus <i>Treponema</i> . Standards in Genomic Sciences, 2013, 8, 88-105.	1.5	44
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