

Philip Hugenholtz

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427
papers

66,225
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254
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472
ext. papers

92,099
ext. citations

12.3
avg, IF

7.89
L-index

#	Paper	IF	Citations
427	Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 5069-72	4.8	7556
426	CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. <i>Genome Research</i> , 2015 , 25, 1043-55	9.7	3441
425	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , 2012 , 6, 610-8	11.9	3287
424	STAMP: statistical analysis of taxonomic and functional profiles. <i>Bioinformatics</i> , 2014 , 30, 3123-4	7.2	1960
423	Impact of culture-independent studies on the emerging phylogenetic view of bacterial diversity. <i>Journal of Bacteriology</i> , 1998 , 180, 4765-74	3.5	1908
422	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004 , 428, 37-43	50.4	1710
421	Defining the core Arabidopsis thaliana root microbiome. <i>Nature</i> , 2012 , 488, 86-90	50.4	1613
420	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
419	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , 2018 , 36, 996-1004	44.5	1369
418	Bellerophon: a program to detect chimeric sequences in multiple sequence alignments. <i>Bioinformatics</i> , 2004 , 20, 2317-9	7.2	1339
417	Comparative metagenomics of microbial communities. <i>Science</i> , 2005 , 308, 554-7	33.3	1211
416	Wrinkles in the rare biosphere: pyrosequencing errors can lead to artificial inflation of diversity estimates. <i>Environmental Microbiology</i> , 2010 , 12, 118-23	5.2	1000
415	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007 , 450, 560-5	50.4	990
414	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008 , 26, 541-7	44.5	964
413	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013 , 31, 533-8	44.5	869
412	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	10.2	829
411	NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. <i>Nucleic Acids Research</i> , 2006 , 34, W394-9	20.1	810

410	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009 , 462, 1056-60	50.4	803
409	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , 2017 , 2, 1533-1542	26.6	764
408	Novel division level bacterial diversity in a Yellowstone hot spring. <i>Journal of Bacteriology</i> , 1998 , 180, 366-76	3.5	754
407	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <i>Nature</i> , 2013 , 500, 567-70	50.4	750
406	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	44.5	648
405	GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. <i>Bioinformatics</i> , 2019 ,	7.2	636
404	Microbial diversity in a hydrocarbon- and chlorinated-solvent-contaminated aquifer undergoing intrinsic bioremediation. <i>Applied and Environmental Microbiology</i> , 1998 , 64, 3869-77	4.8	634
403	CRISPR--a widespread system that provides acquired resistance against phages in bacteria and archaea. <i>Nature Reviews Microbiology</i> , 2008 , 6, 181-6	22.2	630
402	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, 1175-82	4.8	626
401	Emerging pathogenic links between microbiota and the gut-lung axis. <i>Nature Reviews Microbiology</i> , 2017 , 15, 55-63	22.2	579
400	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006 , 24, 1263-9	44.5	541
399	Exploring prokaryotic diversity in the genomic era. <i>Genome Biology</i> , 2002 , 3, REVIEWS0003	18.3	520
398	CRISPR recognition tool (CRT): a tool for automatic detection of clustered regularly interspaced palindromic repeats. <i>BMC Bioinformatics</i> , 2007 , 8, 209	3.6	482
397	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, 11889-94	11.5	464
396	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
395	Experimental factors affecting PCR-based estimates of microbial species richness and evenness. <i>ISME Journal</i> , 2010 , 4, 642-7	11.9	438
394	Accurate phylogenetic classification of variable-length DNA fragments. <i>Nature Methods</i> , 2007 , 4, 63-72	21.6	435
393	Laboratory cultivation of widespread and previously uncultured soil bacteria. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 7210-5	4.8	391

392	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <i>ISME Journal</i> , 2012 , 6, 94-103	11.9	385
391	Evolutionary relationships of wild hominids recapitulated by gut microbial communities. <i>PLoS Biology</i> , 2010 , 8, e1000546	9.7	364
390	Cultivation of globally distributed soil bacteria from phylogenetic lineages previously only detected in cultivation-independent surveys. <i>Environmental Microbiology</i> , 2002 , 4, 654-66	5.2	345
389	A renaissance for the pioneering 16S rRNA gene. <i>Current Opinion in Microbiology</i> , 2008 , 11, 442-6	7.9	337
388	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
387	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, D346-54	20.1	331
386	Evolutionary conservation of sequence and secondary structures in CRISPR repeats. <i>Genome Biology</i> , 2007 , 8, R61	18.3	331
385	A complete domain-to-species taxonomy for Bacteria and Archaea. <i>Nature Biotechnology</i> , 2020 , 38, 1079-1086	41.9	328
384	Genomics. Genome project standards in a new era of sequencing. <i>Science</i> , 2009 , 326, 236-7	33.3	326
383	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , 2016 , 4, 36	16.6	322
382	<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 Gemmatimonadetes phyl. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003 , 53, 1155-1163	2.2	314
381	Bacterial community structures of phosphate-removing and non-phosphate-removing activated sludges from sequencing batch reactors. <i>Applied and Environmental Microbiology</i> , 1995 , 61, 1910-6	4.8	308
380	The integrated microbial genomes (IMG) system. <i>Nucleic Acids Research</i> , 2006 , 34, D344-8	20.1	306
379	A bioinformatician's guide to metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008 , 72, 557-78, Table of Contents	13.2	292
378	Multiple lateral transfers of dissimilatory sulfite reductase genes between major lineages of sulfate-reducing prokaryotes. <i>Journal of Bacteriology</i> , 2001 , 183, 6028-35	3.5	280
377	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. <i>Nature Microbiology</i> , 2016 , 1, 16170	26.6	276
376	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, 411-9	4.8	269
375	Fast, accurate error-correction of amplicon pyrosequences using Acacia. <i>Nature Methods</i> , 2012 , 9, 425-6	21.6	268

374	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2008 , 36, D534-8	20.1	268
373	A novel ecological role of the Firmicutes identified in thermophilic microbial fuel cells. <i>ISME Journal</i> , 2008 , 2, 1146-56	11.9	266
372	Quantitative phylogenetic assessment of microbial communities in diverse environments. <i>Science</i> , 2007 , 315, 1126-30	33.3	259
371	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007 , 4, 495-500	21.6	257
370	Identifying microbial diversity in the natural environment: a molecular phylogenetic approach. <i>Trends in Biotechnology</i> , 1996 , 14, 190-7	15.1	251
369	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. <i>ISME Journal</i> , 2014 , 8, 2015-28	11.9	224
368	Shining a light on dark sequencing: characterising errors in Ion Torrent PGM data. <i>PLoS Computational Biology</i> , 2013 , 9, e1003031	5	220
367	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 8102-7	11.5	214
366	Filamentous Chloroflexi (green non-sulfur bacteria) are abundant in wastewater treatment processes with biological nutrient removal. <i>Microbiology (United Kingdom)</i> , 2002 , 148, 2309-2318	2.9	214
365	Unlocking the potential of metagenomics through replicated experimental design. <i>Nature Biotechnology</i> , 2012 , 30, 513-20	44.5	212
364	Proposal to reclassify the proteobacterial classes and , and the phylum into four phyla reflecting major functional capabilities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 5972-6016	2.2	205
363	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. <i>International Journal of Systematic Bacteriology</i> , 1994 , 44, 427-34		197
362	Genome-directed isolation of the key nitrogen fixer <i>Leptospirillum ferro Diazotrophum</i> sp. nov. from an acidophilic microbial community. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 6319-24	4.8	195
361	GroopM: an automated tool for the recovery of population genomes from related metagenomes. <i>PeerJ</i> , 2014 , 2, e603	3.1	193
360	Use of stable-isotope probing, full-cycle rRNA analysis, and fluorescence in situ hybridization-microautoradiography to study a methanol-fed denitrifying microbial community. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 588-96	4.8	192
359	Lineages of acidophilic archaea revealed by community genomic analysis. <i>Science</i> , 2006 , 314, 1933-5	33.3	190
358	Comparative Genomic Analysis of the Class and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017 , 8, 682	5.7	188
357	Chimeric 16S rDNA sequences of diverse origin are accumulating in the public databases. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003 , 53, 289-293	2.2	188

356	The Genomes On Line Database (GOLD) v.2: a monitor of genome projects worldwide. <i>Nucleic Acids Research</i> , 2006 , 34, D332-4	20.1	187
355	An expanded genomic representation of the phylum cyanobacteria. <i>Genome Biology and Evolution</i> , 2014 , 6, 1031-45	3.9	186
354	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021 , 39, 105-114	44.5	185
353	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. <i>Science</i> , 2017 , 355, 1436-1440	33.3	182
352	An evolving view of methane metabolism in the Archaea. <i>Nature Reviews Microbiology</i> , 2019 , 17, 219-232	22.2	181
351	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
350	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 14793-8	11.5	163
349	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017 , 35, 676-683	44.5	161
348	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016 , 10, 2020-32	11.9	161
347	Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. <i>Nature Methods</i> , 2010 , 7, 807-12	21.6	161
346	Atmospheric trace gases support primary production in Antarctic desert surface soil. <i>Nature</i> , 2017 , 552, 400-403	50.4	159
345	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. <i>Microbiome</i> , 2014 , 2, 11	16.6	158
344	Targeted discovery of glycoside hydrolases from a switchgrass-adapted compost community. <i>PLoS ONE</i> , 2010 , 5, e8812	3.7	154
343	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <i>ISME Journal</i> , 2013 , 7, 50-60	11.9	147
342	Non-sulfate-reducing, syntrophic bacteria affiliated with desulfotomaculum cluster I are widely distributed in methanogenic environments. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 2080-91	4.8	147
341	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
340	Evolutionary conservation of a core root microbiome across plant phyla along a tropical soil chronosequence. <i>Nature Communications</i> , 2017 , 8, 215	17.4	143
339	Characterization of trapped lignin-degrading microbes in tropical forest soil. <i>PLoS ONE</i> , 2011 , 6, e19306	3.7	143

338	Loss of bacterial diversity during antibiotic treatment of intubated patients colonized with <i>Pseudomonas aeruginosa</i> . <i>Journal of Clinical Microbiology</i> , 2007 , 45, 1954-62	9.7	143
337	Multiple displacement amplification compromises quantitative analysis of metagenomes. <i>Nature Methods</i> , 2010 , 7, 943-4	21.6	142
336	Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. <i>Nature</i> , 2014 , 513, 242-5	50.4	137
335	Grinder: a versatile amplicon and shotgun sequence simulator. <i>Nucleic Acids Research</i> , 2012 , 40, e94	20.1	137
334	Functional effects of the microbiota in chronic respiratory disease. <i>Lancet Respiratory Medicine</i> , 2019 , 7, 907-920	35.1	133
333	Discovery of a novel methanogen prevalent in thawing permafrost. <i>Nature Communications</i> , 2014 , 5, 3212	17.4	131
332	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. <i>GigaScience</i> , 2016 , 5, 21	7.6	131
331	Numbers and locations of native bacteria on field-grown wheat roots quantified by fluorescence in situ hybridization (FISH). <i>Environmental Microbiology</i> , 2006 , 8, 871-84	5.2	126
330	Airway dysbiosis: <i>Haemophilus influenzae</i> and <i>Tropheryma</i> in poorly controlled asthma. <i>European Respiratory Journal</i> , 2016 , 47, 792-800	13.6	121
329	Isolation of <i>Succinivibrionaceae</i> implicated in low methane emissions from Tammar wallabies. <i>Science</i> , 2011 , 333, 646-8	33.3	119
328	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008 , 18, 293-7	9.7	119
327	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. <i>ISME Journal</i> , 2012 , 6, 531-41	11.9	118
326	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. <i>Molecular Systems Biology</i> , 2008 , 4, 198	12.2	118
325	<i>Chthoniobacter flavus</i> gen. nov., sp. nov., the first pure-culture representative of subdivision two, <i>Spartobacteria classis</i> nov., of the phylum Verrucomicrobia. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 5875-81	4.8	116
324	ShotgunFunctionalizeR: an R-package for functional comparison of metagenomes. <i>Bioinformatics</i> , 2009 , 25, 2737-8	7.2	114
323	Comparative metagenomic and metatranscriptomic analysis of hindgut paunch microbiota in wood- and dung-feeding higher termites. <i>PLoS ONE</i> , 2013 , 8, e61126	3.7	113
322	Liquid serial dilution is inferior to solid media for isolation of cultures representative of the phylum-level diversity of soil bacteria. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 4363-6	4.8	112
321	The core root microbiome of sugarcane cultivated under varying nitrogen fertilizer application. <i>Environmental Microbiology</i> , 2016 , 18, 1338-51	5.2	111

320	Nitrogen fertilizer dose alters fungal communities in sugarcane soil and rhizosphere. <i>Scientific Reports</i> , 2015 , 5, 8678	4.9	105
319	Reclassification of <i>Sphaerobacter thermophilus</i> from the subclass Sphaerobacteridae in the phylum Actinobacteria to the class Thermomicrobia (emended description) in the phylum Chloroflexi (emended description). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 2049-2051	2.2	105
318	Comparison of DNA extraction methods for microbial community profiling with an application to pediatric bronchoalveolar lavage samples. <i>PLoS ONE</i> , 2012 , 7, e34605	3.7	104
317	Molecular analysis of dimethyl sulphide dehydrogenase from <i>Rhodovulum sulfidophilum</i> : its place in the dimethyl sulphoxide reductase family of microbial molybdopterin-containing enzymes. <i>Molecular Microbiology</i> , 2002 , 44, 1575-87	4.1	104
316	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. <i>Frontiers in Microbiology</i> , 2016 , 7, 211	5.7	102
315	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011 , 5, 122-30	11.9	99
314	The DMSO Reductase Family of Microbial Molybdenum Enzymes; Molecular Properties and Role in the Dissimilatory Reduction of Toxic Elements. <i>Geomicrobiology Journal</i> , 2002 , 19, 3-21	2.5	96
313	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541). <i>Standards in Genomic Sciences</i> , 2009 , 1, 12-20		94
312	Identification of a haloalkaliphilic and thermostable cellulase with improved ionic liquid tolerance. <i>Green Chemistry</i> , 2011 , 13, 2083	10	93
311	Glycoside hydrolase activities of thermophilic bacterial consortia adapted to switchgrass. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 5804-12	4.8	91
310	Design and evaluation of 16S rRNA-targeted oligonucleotide probes for fluorescence in situ hybridization. <i>Methods in Molecular Biology</i> , 2002 , 179, 29-42	1.4	90
309	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, 640-7	10.2	89
308	Environmental distribution and population biology of <i>Candidatus Accumulibacter</i> , a primary agent of biological phosphorus removal. <i>Environmental Microbiology</i> , 2008 , 10, 2692-703	5.2	87
307	Strategies for Enhancing the Effectiveness of Metagenomic-based Enzyme Discovery in Lignocellulolytic Microbial Communities. <i>Bioenergy Research</i> , 2010 , 3, 146-158	3.1	82
306	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,	12.9	81
305	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	1	78
304	Comparative genomics of two ' <i>Candidatus Accumulibacter</i> ' clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013 , 7, 2301-14	11.9	75
303	Genomic analysis of " <i>Elusimicrobium minutum</i> ," the first cultivated representative of the phylum "Elusimicrobia" (formerly termite group 1). <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2841-9	4.8	75

302	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, 254-62	4.8	74
301	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, 5512-8	4.8	73
300	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1278-84		72
299	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21). <i>Standards in Genomic Sciences</i> , 2011 , 5, 97-111		72
298	Contrasting life strategies of viruses that infect photo- and heterotrophic bacteria, as revealed by viral tagging. <i>MBio</i> , 2012 , 3,	7.8	72
297	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006 , 22, e359-67	7.2	72
296	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	16.6	71
295	Metatranscriptomic array analysis of 'Candidatus <i>Accumulibacter phosphatis</i> '-enriched enhanced biological phosphorus removal sludge. <i>Environmental Microbiology</i> , 2010 , 12, 1205-17	5.2	67
294	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020 , 5, 987-994	26.6	64
293	A new species of <i>Burkholderia</i> isolated from sugarcane roots promotes plant growth. <i>Microbial Biotechnology</i> , 2014 , 7, 142-54	6.3	63
292	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 200-9		62
291	Microbiomes in respiratory health and disease: An Asia-Pacific perspective. <i>Respirology</i> , 2017 , 22, 240-250	6	61
290	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. <i>PeerJ</i> , 2015 , 3, e740	3.1	61
289	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (Ca. Poseidoniales ord. nov.). <i>ISME Journal</i> , 2019 , 13, 663-675	11.9	61
288	Fixation-free fluorescence in situ hybridization for targeted enrichment of microbial populations. <i>ISME Journal</i> , 2010 , 4, 1352-6	11.9	60
287	Recipient mucosal-associated invariant T cells control GVHD within the colon. <i>Journal of Clinical Investigation</i> , 2018 , 128, 1919-1936	15.9	60
286	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019 , 4, 2192-2203	26.6	57
285	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , 2010 , 2, 87-95		57

284	Back from the dead; the curious tale of the predatory cyanobacterium <i>Vampirovibrio chlorellavorus</i> . <i>PeerJ</i> , 2015 , 3, e968	3.1	57
283	Acute graft-versus-host disease is regulated by an IL-17-sensitive microbiome. <i>Blood</i> , 2017 , 129, 2172-2185		55
282	Focus: Synergistetes. <i>Environmental Microbiology</i> , 2009 , 11, 1327-9	5.2	55
281	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. <i>Nature Communications</i> , 2020 , 11, 5886	17.4	55
280	Crosstalk between sugarcane and a plant-growth promoting Burkholderia species. <i>Scientific Reports</i> , 2016 , 6, 37389	4.9	54
279	Proteome insights into the symbiotic relationship between a captive colony of <i>Nasutitermes corniger</i> and its hindgut microbiome. <i>ISME Journal</i> , 2011 , 5, 161-4	11.9	54
278	Genome analysis of the anaerobic thermohalophilic bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009 , 4, e4192	3.7	54
277	Heterotrophic bacteria in an air-handling system. <i>Applied and Environmental Microbiology</i> , 1992 , 58, 3914-20	4.20	54
276	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , 2010 , 2, 96-106		53
275	<i>Microthrix parvicella</i> is a Novel, Deep Branching Member of the Actinomycetes Subphylum. <i>Systematic and Applied Microbiology</i> , 1995 , 17, 513-518	4.2	52
274	16S rRNA Analysis of Isolates Obtained from Gram-Negative, Filamentous Bacteria Micromanipulated from Activated Sludge. <i>Systematic and Applied Microbiology</i> , 1996 , 19, 334-343	4.2	52
273	Proteogenomic analysis of a thermophilic bacterial consortium adapted to deconstruct switchgrass. <i>PLoS ONE</i> , 2013 , 8, e68465	3.7	51
272	Integrating ecology into biotechnology. <i>Current Opinion in Biotechnology</i> , 2007 , 18, 287-92	11.4	51
271	Genome-Based Microbial Taxonomy Coming of Age. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016 , 8,	10.2	50
270	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <i>Molecular Biology and Evolution</i> , 2016 , 33, 915-27	8.3	50
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268	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , 2010 , 2, 158-67		49
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