

# Philip Hugenholtz

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

427  
papers

66,225  
citations

108  
h-index

254  
g-index

472  
ext. papers

92,099  
ext. citations

12.3  
avg, IF

7.89  
L-index

#	Paper	IF	Citations
427	Characterization of the juvenile koala gut microbiome across wild populations.. <i>Environmental Microbiology</i> , <b>2022</b> ,	5.2	2
426	Secreted Toxins From Strains Isolated From Keratinocyte Skin Cancers Mediate Pro-tumorigenic Inflammatory Responses in the Skin.. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 789042	5.7	1
425	Maternal inheritance of the koala gut microbiome and its compositional and functional maturation during juvenile development. <i>Environmental Microbiology</i> , <b>2021</b> ,	5.2	2
424	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , <b>2021</b> , 9, 199	16.6	4
423	Candidatus Eremiobacterota, a metabolically and phylogenetically diverse terrestrial phylum with acid-tolerant adaptations. <i>ISME Journal</i> , <b>2021</b> , 15, 2692-2707	11.9	6
422	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 643682	5.7	9
421	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <i>ISME Journal</i> , <b>2021</b> , 15, 1879-1893	16.6	24
420	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , <b>2021</b> , 372,	33.3	32
419	Critical evaluation of faecal microbiome preservation using metagenomic analysis. <i>ISME Communications</i> , <b>2021</b> , 1,		1
418	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , <b>2021</b> , 15, 2986-3004	11.9	12
417	IFN- $\beta$ therapy prevents severe gastrointestinal graft-versus-host disease. <i>Blood</i> , <b>2021</b> , 138, 722-737	2.2	12
416	Chemosynthetic and photosynthetic bacteria contribute differentially to primary production across a steep desert aridity gradient. <i>ISME Journal</i> , <b>2021</b> , 15, 3339-3356	11.9	9
415	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , <b>2021</b> , 6, 960-970	26.6	36
414	A standardized archaeal taxonomy for the Genome Taxonomy Database. <i>Nature Microbiology</i> , <b>2021</b> , 6, 946-959	26.6	34
413	Persistence and resistance: survival mechanisms of Candidatus Dormibacterota from nutrient-poor Antarctic soils. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 4276-4294	5.2	1
412	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , <b>2021</b> , 1,		4
411	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 105-114	44.5	185

410	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> , <b>2021</b> , 118,	11.5	3
409	Kinetic and Structural Characterization of the First B3 Metallo- $\beta$ -Lactamase with an Active-Site Glutamic Acid. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , 65, e0093621	5.9	1
408	Effects of laboratory domestication on the rodent gut microbiome. <i>ISME Communications</i> , <b>2021</b> , 1,		3
407	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> , <b>2021</b> ,	20.1	41
406	Wastewater monitoring for SARS-CoV-2. <i>Microbiology Australia</i> , <b>2021</b> , 42, 18	0.8	1
405	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> , <b>2021</b> , 80, 573-581	2.4	6
404	Microvolume DNA extraction methods for microscale amplicon and metagenomic studies. <i>ISME Communications</i> , <b>2021</b> , 1,		0
403	Fluconazole resistance in <i>Candida albicans</i> is induced by <i>Pseudomonas aeruginosa</i> quorum sensing. <i>Scientific Reports</i> , <b>2020</b> , 10, 7769	4.9	18
402	Broad spectrum antibiotic-degrading metallo- $\beta$ -lactamases are phylogenetically diverse. <i>Protein and Cell</i> , <b>2020</b> , 11, 613-617	7.2	10
401	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , <b>2020</b> , 7, 188	8.2	30
400	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , <b>2020</b> , 5, 987-994	26.6	64
399	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> , <b>2020</b> , 11, 754-770	8.8	10
398	A complete domain-to-species taxonomy for Bacteria and Archaea. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1079-1086	41.9	328
397	Proposal to reclassify the proteobacterial classes $\alpha$ and $\beta$ , and the phylum $\gamma$ into four phyla reflecting major functional capabilities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 5972-6016	2.2	205
396	Tracking seasonal changes in diversity of pollen allergen exposure: Targeted metabarcoding of a subtropical aerobiome. <i>Science of the Total Environment</i> , <b>2020</b> , 747, 141189	10.2	7
395	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> , <b>2020</b> , 27,	12.9	81
394	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. <i>Nature Communications</i> , <b>2020</b> , 11, 5886	17.4	55
393	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> , <b>2020</b> , 728, 138764	10.2	829

392	An evolving view of methane metabolism in the Archaea. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 219-232	2.2	181
391	Toward unrestricted use of public genomic data. <i>Science</i> , <b>2019</b> , 363, 350-352	33.3	25
390	IL-23 favours outgrowth of spondyloarthritis-associated pathobionts and suppresses host support for homeostatic microbiota. <i>Annals of the Rheumatic Diseases</i> , <b>2019</b> , 78, 494-503	2.4	26
389	Evaluation of a concatenated protein phylogeny for classification of tailed double-stranded DNA viruses belonging to the order Caudovirales. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1306-1315	26.6	37
388	Functional effects of the microbiota in chronic respiratory disease. <i>Lancet Respiratory Medicine</i> , <b>2019</b> , 7, 907-920	35.1	133
387	Consent insufficient for data release-Response. <i>Science</i> , <b>2019</b> , 364, 446	33.3	4
386	Bacterial fermentation and respiration processes are uncoupled in anoxic permeable sediments. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1014-1023	26.6	34
385	Evolution of photosynthesis and aerobic respiration in the cyanobacteria. <i>Free Radical Biology and Medicine</i> , <b>2019</b> , 140, 200-205	7.8	25
384	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , <b>2019</b> , 42, 15-21	4.2	40
383	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , <b>2019</b> , 4, 2192-2203	26.6	57
382	Faecal inoculations alter the gastrointestinal microbiome and allow dietary expansion in a wild specialist herbivore, the koala. <i>Animal Microbiome</i> , <b>2019</b> , 1, 6	4.1	23
381	Road Map of the Phylum Campylobacterota <b>2019</b> , 1-11		5
380	GTDB-Tk: a toolkit to classify genomes with the Genome Taxonomy Database. <i>Bioinformatics</i> , <b>2019</b> ,	7.2	636
379	Genomic Encyclopedia of Bacteria and Archaea (GEBA) VI: learning from type strains. <i>Microbiology Australia</i> , <b>2019</b> , 40, 125	0.8	2
378	2125. Staphylococcus Species Identification by Fourier Transform Infrared (FTIR) Spectroscopic Techniques: A Cross-Lab Study. <i>Open Forum Infectious Diseases</i> , <b>2019</b> , 6, S720-S720	1	78
377	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , <b>2019</b> , 37, 29-37	44.5	180
376	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (Ca. Poseidoniales ord. nov.). <i>ISME Journal</i> , <b>2019</b> , 13, 663-675	11.9	61
375	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria Nitrosomonas to the Biocide Free Nitrous Acid. <i>Environmental Science &amp; Technology</i> , <b>2018</b> , 52, 5386-5397	10.3	32

374	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> , <b>2018</b> , 124, 855-866	4.7	14
373	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> , <b>2018</b> , 12, 2942-2953	11.9	9
372	A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 996-1004	44.5	1369
371	Recipient mucosal-associated invariant T cells control GVHD within the colon. <i>Journal of Clinical Investigation</i> , <b>2018</b> , 128, 1919-1936	15.9	60
370	A Natural History of Actinic Keratosis and Cutaneous Squamous Cell Carcinoma Microbiomes. <i>MBio</i> , <b>2018</b> , 9,	7.8	14
369	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , <b>2018</b> , 3,	7.6	336
368	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , <b>2018</b> , 8, 8128	4.9	6
367	Microbiomes in respiratory health and disease: An Asia-Pacific perspective. <i>Respirology</i> , <b>2017</b> , 22, 240-250	6	61
366	Acute graft-versus-host disease is regulated by an IL-17-sensitive microbiome. <i>Blood</i> , <b>2017</b> , 129, 2172-2185	15	55
365	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 676-683	44.5	161
364	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. <i>Science</i> , <b>2017</b> , 355, 1436-1440	33.3	182
363	Evolutionary conservation of a core root microbiome across plant phyla along a tropical soil chronosequence. <i>Nature Communications</i> , <b>2017</b> , 8, 215	17.4	143
362	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , <b>2017</b> , 2, 1533-1542	26.6	764
361	Characterization of a highly efficient antibiotic-degrading metallo- $\beta$ -lactamase obtained from an uncultured member of a permafrost community. <i>Metallomics</i> , <b>2017</b> , 9, 1157-1168	4.5	9
360	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 725-731	44.5	648
359	Atmospheric trace gases support primary production in Antarctic desert surface soil. <i>Nature</i> , <b>2017</b> , 552, 400-403	50.4	159
358	Emerging pathogenic links between microbiota and the gut-lung axis. <i>Nature Reviews Microbiology</i> , <b>2017</b> , 15, 55-63	22.2	579
357	Comparative Genomic Analysis of the Class and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 682	5.7	188

356	Gene and genome-centric analyses of koala and wombat fecal microbiomes point to metabolic specialization for digestion. <i>PeerJ</i> , <b>2017</b> , 5, e4075	3.1	16
355	A microfluidics-based in situ chemotaxis assay to study the behaviour of aquatic microbial communities. <i>Nature Microbiology</i> , <b>2017</b> , 2, 1344-1349	26.6	37
354	Amino Acid and Peptide Utilization Profiles of the Fluoroacetate-Degrading Bacterium <i>Synergistetes</i> Strain MFA1 Under Varying Conditions. <i>Microbial Ecology</i> , <b>2016</b> , 71, 494-504	4.4	9
353	Crosstalk between sugarcane and a plant-growth promoting <i>Burkholderia</i> species. <i>Scientific Reports</i> , <b>2016</b> , 6, 37389	4.9	54
352	Near complete genome sequence of the animal feed probiotic, <i>Bacillus amyloliquefaciens</i> H57. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 60		7
351	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16170	26.6	276
350	Airway dysbiosis: <i>Haemophilus influenzae</i> and <i>Tropheryma</i> in poorly controlled asthma. <i>European Respiratory Journal</i> , <b>2016</b> , 47, 792-800	13.6	121
349	Genome-Based Microbial Taxonomy Coming of Age. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2016</b> , 8,	10.2	50
348	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , <b>2016</b> , 10, 2020-32	11.9	161
347	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 915-27	8.3	50
346	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. <i>PeerJ</i> , <b>2016</b> , 4, e2486	3.1	41
345	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 211	5.7	102
344	Genomic characterization of the uncultured <i>Bacteroidales</i> family S24-7 inhabiting the guts of homeothermic animals. <i>Microbiome</i> , <b>2016</b> , 4, 36	16.6	322
343	The core root microbiome of sugarcanes cultivated under varying nitrogen fertilizer application. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 1338-51	5.2	111
342	' <i>Candidatus</i> <i>Adiutrix intracellularis</i> ', an endosymbiont of termite gut flagellates, is the first representative of a deep-branching clade of Deltaproteobacteria and a putative homoacetogen. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 2548-64	5.2	24
341	Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. <i>GigaScience</i> , <b>2016</b> , 5, 21	7.6	131
340	Anode potential influences the structure and function of anodic electrode and electrolyte-associated microbiomes. <i>Scientific Reports</i> , <b>2016</b> , 6, 39114	4.9	44
339	A catalogue of 136 microbial draft genomes from Red Sea metagenomes. <i>Scientific Data</i> , <b>2016</b> , 3, 160058.2		34

338	Link scientific publications using linked data <b>2015</b> ,		1
337	Nitrogen fertilizer dose alters fungal communities in sugarcane soil and rhizosphere. <i>Scientific Reports</i> , <b>2015</b> , 5, 8678	4.9	105
336	CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. <i>Genome Research</i> , <b>2015</b> , 25, 1043-55	9.7	3441
335	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> , <b>2015</b> , 3, 5	16.6	71
334	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> , <b>2015</b> , 10, 26		48
333	Blastobacter <b>2015</b> , 1-11		
332	Blastomonas <b>2015</b> , 1-7		
331	Anaerobaculum <b>2015</b> , 1-7		
330	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> , <b>2015</b> , 16, 50-60	1.3	14
329	Evaluating DNA Extraction Methods for Community Profiling of Pig Hindgut Microbial Community. <i>PLoS ONE</i> , <b>2015</b> , 10, e0142720	3.7	7
328	Draft Genome Sequences of Anaerolinea thermolimosa IMO-1, Bellilinea caldifistulae GOMI-1, Leptolinea tardivitalis YMTK-2, Levilinea saccharolytica KIBI-1, Longilinea arvoryzae KOME-1, Previously Described as Members of the Class Anaerolineae (Chloroflexi). <i>Genome Announcements</i> , <b>2015</b> , 3,		13
327	Comparative genomics of non-pseudomonal bacterial species colonising paediatric cystic fibrosis patients. <i>PeerJ</i> , <b>2015</b> , 3, e1223	3.1	18
326	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. <i>PeerJ</i> , <b>2015</b> , 3, e740	3.1	61
325	Back from the dead; the curious tale of the predatory cyanobacterium Vampirovibrio chlorellavorus. <i>PeerJ</i> , <b>2015</b> , 3, e968	3.1	57
324	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1469	5.7	48
323	A new species of Burkholderia isolated from sugarcane roots promotes plant growth. <i>Microbial Biotechnology</i> , <b>2014</b> , 7, 142-54	6.3	63
322	STAMP: statistical analysis of taxonomic and functional profiles. <i>Bioinformatics</i> , <b>2014</b> , 30, 3123-4	7.2	1960
321	Discovery of a novel methanogen prevalent in thawing permafrost. <i>Nature Communications</i> , <b>2014</b> , 5, 3212	17.4	131

320	Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. <i>Nature</i> , <b>2014</b> , 513, 242-5	50.4	137
319	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. <i>Microbiome</i> , <b>2014</b> , 2, 11	16.6	158
318	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305(T)), 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> , <b>2014</b> , 9, 10		39
317	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3(T)) from an African solfataric spring. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 1105-17		4
316	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279(T)), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 1076-88		10
315	GroopM: an automated tool for the recovery of population genomes from related metagenomes. <i>PeerJ</i> , <b>2014</b> , 2, e603	3.1	193
314	Yeast as a Biofertilizer Alters Plant Growth and Morphology. <i>Crop Science</i> , <b>2014</b> , 54, 785-790	2.4	18
313	An expanded genomic representation of the phylum cyanobacteria. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 1031-45	3.9	186
312	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001920	9.7	146
311	Genome Sequence of Enterotoxigenic <i>Escherichia coli</i> Strain B2C. <i>Genome Announcements</i> , <b>2014</b> , 2,		5
310	Single clinical isolates from acute uncomplicated urinary tract infections are representative of dominant in situ populations. <i>MBio</i> , <b>2014</b> , 5, e01064-13	7.8	27
309	Effects of sample treatments on genome recovery via single-cell genomics. <i>ISME Journal</i> , <b>2014</b> , 8, 2546-2559	11.9	25
308	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. <i>ISME Journal</i> , <b>2014</b> , 8, 2015-28	11.9	224
307	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 1278-84		72
306	JTD special edition 'Hot Topics in COPD'-The microbiome in COPD. <i>Journal of Thoracic Disease</i> , <b>2014</b> , 6, 1525-31	2.6	16
305	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <i>Nature</i> , <b>2013</b> , 500, 567-70	50.4	750
304	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , <b>2013</b> , 499, 431-7	50.4	1484
303	Comparative genomics of two 'Candidatus <i>Accumulibacter</i> ' clades performing biological phosphorus removal. <i>ISME Journal</i> , <b>2013</b> , 7, 2301-14	11.9	75



302	In-solution fluorescence in situ hybridization and fluorescence-activated cell sorting for single cell and population genome recovery. <i>Methods in Enzymology</i> , <b>2013</b> , 531, 3-19	1.7	16
301	Metagenomics and Community Profiling: Culture-Independent Techniques in the Clinical Laboratory. <i>Clinical Microbiology Newsletter</i> , <b>2013</b> , 35, 1-9	1.1	5
300	Longitudinal Holistic Profiling of the Lung Transplant Microbiome. <i>Journal of Heart and Lung Transplantation</i> , <b>2013</b> , 32, S10-S11	5.8	3
299	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 533-8	44.5	869
298	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <i>ISME Journal</i> , <b>2013</b> , 7, 50-60	11.9	147
297	From deep sequencing to viral tagging: recent advances in viral metagenomics. <i>BioEssays</i> , <b>2013</b> , 35, 436-42	4.2	34
296	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> , <b>2013</b> , 187, 640-7	10.2	89
295	Shining a light on dark sequencing: characterising errors in Ion Torrent PGM data. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003031	5	220
294	Comparative metagenomic and metatranscriptomic analysis of hindgut paunch microbiota in wood- and dung-feeding higher termites. <i>PLoS ONE</i> , <b>2013</b> , 8, e61126	3.7	113
293	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2(T)) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 15-25		5
292	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437(T)). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 26-36		6
291	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5(T)). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 37-46		4
290	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGA(T)). <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 47-57		10
289	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (H(T)), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 228-38		8
288	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701(T)) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 57-70		4
287	Genome sequence of <i>Frateuria aurantia</i> type strain (Kond7(T)), a xanthomonade isolated from <i>Lilium auratum</i> Lindl. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 83-92		1
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285	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1(T)), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeriae</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeriae</i> comb. nov., and emendation of the genus <i>Treponema</i> . <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 88-105		24

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244	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 154-62	15
243	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 173-82	9
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