

# David W Ussery

## List of Publications by Citations

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215  
papers

15,162  
citations

51  
h-index

121  
g-index

239  
ext. papers

18,685  
ext. citations

5.5  
avg. IF

6.29  
L-index

#	Paper	IF	Citations
215	RNAmmr: consistent and rapid annotation of ribosomal RNA genes. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, 3100-8	20.1	3946
214	Multilocus sequence typing of total-genome-sequenced bacteria. <i>Journal of Clinical Microbiology</i> , <b>2012</b> , 50, 1355-61	9.7	1163
213	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 541-7	44.5	964
212	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 221-31	44.5	889
211	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 822-8	44.5	624
210	Insights from 20 years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , <b>2015</b> , 15, 141-61	3.8	391
209	Comparison of 61 sequenced <i>Escherichia coli</i> genomes. <i>Microbial Ecology</i> , <b>2010</b> , 60, 708-20	4.4	360
208	The transcriptional landscape and small RNAs of <i>Salmonella enterica</i> serovar Typhimurium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E1277-86	11.5	294
207	A DNA structural atlas for <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , <b>2000</b> , 299, 907-30	6.5	194
206	On the total number of genes and their length distribution in complete microbial genomes. <i>Trends in Genetics</i> , <b>2001</b> , 17, 425-8	8.5	170
205	The complete genome sequence and analysis of the epsilonproteobacterium <i>Arcobacter butzleri</i> . <i>PLoS ONE</i> , <b>2007</b> , 2, e1358	3.7	155
204	The Genomic Standards Consortium. <i>PLoS Biology</i> , <b>2011</b> , 9, e1001088	9.7	143
203	Benchmarking of methods for genomic taxonomy. <i>Journal of Clinical Microbiology</i> , <b>2014</b> , 52, 1529-39	9.7	141
202	Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse <i>Escherichia coli</i> genomes. <i>BMC Genomics</i> , <b>2012</b> , 13, 577	4.5	137
201	The <i>Salmonella enterica</i> pan-genome. <i>Microbial Ecology</i> , <b>2011</b> , 62, 487-504	4.4	134
200	Genomic taxonomy of <i>Vibrios</i> . <i>BMC Evolutionary Biology</i> , <b>2009</b> , 9, 258	3	132
199	Ten years of bacterial genome sequencing: comparative-genomics-based discoveries. <i>Functional and Integrative Genomics</i> , <b>2006</b> , 6, 165-85	3.8	120

198	The chromatin-associated protein H-NS. <i>Biochimie</i> , <b>1994</b> , 76, 968-80	4.6	111
197	Molecular analysis of the emergence of pandemic <i>Vibrio parahaemolyticus</i> . <i>BMC Microbiology</i> , <b>2008</b> , 8, 110	4.5	99
196	Global regulation of virulence and the stress response by CsrA in the highly adapted human gastric pathogen <i>Helicobacter pylori</i> . <i>Molecular Microbiology</i> , <b>2004</b> , 51, 15-32	4.1	98
195	Origin of replication in circular prokaryotic chromosomes. <i>Environmental Microbiology</i> , <b>2006</b> , 8, 353-61	5.2	93
194	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e38	20.1	91
193	Genome sequencing identifies two nearly unchanged strains of persistent <i>Listeria monocytogenes</i> isolated at two different fish processing plants sampled 6 years apart. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 2944-51	4.8	91
192	Review and phylogenetic analysis of <i>qac</i> genes that reduce susceptibility to quaternary ammonium compounds in <i>Staphylococcus</i> species. <i>European Journal of Microbiology and Immunology</i> , <b>2015</b> , 5, 44-61	4.6	90
191	The genome of the versatile nitrogen fixer <i>Azorhizobium caulinodans</i> ORS571. <i>BMC Genomics</i> , <b>2008</b> , 9, 271	4.5	87
190	The genomic code: inferring Vibrionaceae niche specialization. <i>Nature Reviews Microbiology</i> , <b>2006</b> , 4, 697-704	22.2	87
189	A closer look at bacteroides: phylogenetic relationship and genomic implications of a life in the human gut. <i>Microbial Ecology</i> , <b>2011</b> , 61, 473-85	4.4	86
188	Comparative genomics of <i>Bifidobacterium</i> , <i>Lactobacillus</i> and related probiotic genera. <i>Microbial Ecology</i> , <b>2012</b> , 63, 651-73	4.4	84
187	Defining the <i>Pseudomonas</i> genus: where do we draw the line with <i>Azotobacter</i> ?. <i>Microbial Ecology</i> , <b>2012</b> , 63, 239-48	4.4	80
186	Microbial taxonomy in the post-genomic era: rebuilding from scratch?. <i>Archives of Microbiology</i> , <b>2015</b> , 197, 359-70	3	78
185	From essential to persistent genes: a functional approach to constructing synthetic life. <i>Trends in Genetics</i> , <b>2013</b> , 29, 273-9	8.5	78
184	Natural genetic engineering: intelligence & design in evolution?. <i>Microbial Informatics and Experimentation</i> , <b>2011</b> , 1,		78
183	GENE-18. TRANSCRIPTOME-WIDE ANALYSIS USING NANOPORE THIRD GENERATION SEQUENCING IN A RAT GLIOBLASTOMA MODEL: PROOF OF PRINCIPLE. <i>Neuro-Oncology</i> , <b>2019</b> , 21, vi101-vi101	1	78
182	PATH-05. RAPID SIMULTANEOUS IDH MUTATION AND MGMT METHYLATION STATUS ASSESSMENT IN GLIOMA PATIENTS USING CRISPR-Cas9-TARGETED NANOPORE SEQUENCING. <i>Neuro-Oncology</i> , <b>2019</b> , 21, vi143-vi144	1	78
181	CMG-biotools, a free workbench for basic comparative microbial genomics. <i>PLoS ONE</i> , <b>2013</b> , 8, e60120	3.7	76

180	Microbial comparative pan-genomics using binomial mixture models. <i>BMC Genomics</i> , <b>2009</b> , 10, 385	4.5	75
179	Genomic characterization of <i>Campylobacter jejuni</i> strain M1. <i>PLoS ONE</i> , <b>2010</b> , 5, e12253	3.7	72
178	Characterization of probiotic <i>Escherichia coli</i> isolates with a novel pan-genome microarray. <i>Genome Biology</i> , <b>2007</b> , 8, R267	18.3	71
177	CBS Genome Atlas Database: a dynamic storage for bioinformatic results and sequence data. <i>Bioinformatics</i> , <b>2004</b> , 20, 3682-6	7.2	71
176	Genome organisation and chromatin structure in <i>Escherichia coli</i> . <i>Biochimie</i> , <b>2001</b> , 83, 201-12	4.6	71
175	RpoD promoters in <i>Campylobacter jejuni</i> exhibit a strong periodic signal instead of a -35 box. <i>Journal of Molecular Biology</i> , <b>2003</b> , 326, 1361-72	6.5	70
174	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 2516-26	4.8	69
173	Decoding the epitranscriptional landscape from native RNA sequences. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e7	20.1	68
172	Genomic variation in <i>Salmonella enterica</i> core genes for epidemiological typing. <i>BMC Genomics</i> , <b>2012</b> , 13, 88	4.5	61
171	The genome BLASTatlas-a GeneWiz extension for visualization of whole-genome homology. <i>Molecular BioSystems</i> , <b>2008</b> , 4, 363-71		60
170	The sigma54 regulon (sigmulon) of <i>Pseudomonas putida</i> . <i>Environmental Microbiology</i> , <b>2003</b> , 5, 1281-93	5.2	59
169	DNA binding is not sufficient for H-NS-mediated repression of proU expression. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 12083-90	5.4	56
168	Standard operating procedure for computing pangenome trees. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 135-41		53
167	LeuO is a global regulator of gene expression in <i>Salmonella enterica</i> serovar Typhimurium. <i>Molecular Microbiology</i> , <b>2012</b> , 85, 1072-89	4.1	52
166	Meeting report: GenBank microbial genomic taxonomy workshop (12-13 May, 2015). <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11,		51
165	Three views of microbial genomes. <i>Research in Microbiology</i> , <b>1999</b> , 150, 773-7	4	51
164	Machine Learning Methods in Drug Discovery. <i>Molecules</i> , <b>2020</b> , 25,	4.8	51
163	Diversity of <i>Pseudomonas</i> Genomes, Including Populus-Associated Isolates, as Revealed by Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 375-83	4.8	50

162	Genome update: the 1000th genome--a cautionary tale. <i>Microbiology (United Kingdom)</i> , <b>2010</b> , 156, 603-608	48
161	Case of Microcephaly after Congenital Infection with Asian Lineage Zika Virus, Thailand. <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24,	10.2 46
160	Investigations of oligonucleotide usage variance within and between prokaryotes. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000057	5 46
159	Probing DNA structure with psoralen in vitro. <i>Methods in Enzymology</i> , <b>1992</b> , 212, 242-62	1.7 44
158	An environmental signature for 323 microbial genomes based on codon adaptation indices. <i>Genome Biology</i> , <b>2006</b> , 7, R114	18.3 43
157	Metabolic functions of <i>Pseudomonas fluorescens</i> strains from <i>Populus deltoides</i> depend on rhizosphere or endosphere isolation compartment. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1118	5.7 42
156	Complete DNA sequence of the linear mitochondrial genome of the pathogenic yeast <i>Candida parapsilosis</i> . <i>Molecular Genetics and Genomics</i> , <b>2004</b> , 272, 173-80	3.1 42
155	DNA microarray analysis of fim mutations in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , <b>2002</b> , 267, 721-9	3.1 42
154	Strand misalignments lead to quasipalindrome correction. <i>Trends in Genetics</i> , <b>2003</b> , 19, 365-9	8.5 42
153	The TNFalpha receptor TNFRSF1A and genes encoding the amiloride-sensitive sodium channel ENaC as modulators in cystic fibrosis. <i>Human Genetics</i> , <b>2006</b> , 119, 331-43	6.3 40
152	Polyclonality of concurrent natural populations of <i>Alteromonas macleodii</i> . <i>Genome Biology and Evolution</i> , <b>2012</b> , 4, 1360-74	3.9 39
151	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. <i>BMC Genomics</i> , <b>2007</b> , 8, 325	4.5 38
150	PARP1 Is Up-Regulated in Non-small Cell Lung Cancer Tissues in the Presence of the Cyanobacterial Toxin Microcystin. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1757	5.7 37
149	On the origins of a <i>Vibrio</i> species. <i>Microbial Ecology</i> , <b>2010</b> , 59, 1-13	4.4 37
148	Complete genome sequence of the commensal <i>Enterococcus faecalis</i> 62, isolated from a healthy Norwegian infant. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2377-8	3.5 36
147	DNA: Structure and function. <i>Advances in Genome Biology</i> , <b>1998</b> , 5, 1-141	36
146	Pan-genome analysis of human gastric pathogen <i>H. pylori</i> : comparative genomics and pathogenomics approaches to identify regions associated with pathogenicity and prediction of potential core therapeutic targets. <i>BioMed Research International</i> , <b>2015</b> , 2015, 139580	3 35
145	Chromatin architecture and gene expression in <i>Escherichia coli</i> . <i>Genome Biology</i> , <b>2004</b> , 5, 252	18.3 35

144	Environmental influences on the in vivo level of intramolecular triplex DNA in Escherichia coli. <i>Biochemistry</i> , <b>1993</b> , 32, 6206-13	3.2	35
143	Ebolavirus comparative genomics. <i>FEMS Microbiology Reviews</i> , <b>2015</b> , 39, 764-78	15.1	34
142	Quality scores for 32,000 genomes. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 20		33
141	Identification of putative noncoding RNA genes in the Burkholderia cenocepacia J2315 genome. <i>FEMS Microbiology Letters</i> , <b>2007</b> , 276, 83-92	2.9	33
140	Analysis of intra-genomic GC content homogeneity within prokaryotes. <i>BMC Genomics</i> , <b>2010</b> , 11, 464	4.5	32
139	Rapid Sequencing of Multiple RNA Viruses in Their Native Form. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 260	5.7	31
138	Toward a standards-compliant genomic and metagenomic publication record. <i>OMICS A Journal of Integrative Biology</i> , <b>2008</b> , 12, 157-60	3.8	31
137	Functionality of system components: conservation of protein function in protein feature space. <i>Genome Research</i> , <b>2003</b> , 13, 2444-9	9.7	31
136	Bias of purine stretches in sequenced chromosomes. <i>Computers &amp; Chemistry</i> , <b>2002</b> , 26, 531-41		31
135	Evaluation of potential regulatory elements identified as DNase I hypersensitive sites in the CFTR gene. <i>FEBS Journal</i> , <b>2002</b> , 269, 553-9		30
134	Genome Update: proteome comparisons. <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 1-4	2.9	30
133	Genome update: sigma factors in 240 bacterial genomes. <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 3147-3150	2.3	29
132	Environmental influences on DNA curvature. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>1999</b> , 16, 811-23	3.6	29
131	Reliability and applications of statistical methods based on oligonucleotide frequencies in bacterial and archaeal genomes. <i>BMC Genomics</i> , <b>2008</b> , 9, 104	4.5	28
130	Is the pan-genome also a pan-selectome?. <i>F1000Research</i> , <b>2012</b> , 1, 16	3.6	28
129	Mechanisms linking preterm birth to onset of cardiovascular disease later in adulthood. <i>European Heart Journal</i> , <b>2019</b> , 40, 1107-1112	9.5	28
128	Sigma factors in a thousand E. coli genomes. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 3121-9	5.2	27
127	Campylobacter fetus subspecies: comparative genomics and prediction of potential virulence targets. <i>Gene</i> , <b>2012</b> , 508, 145-56	3.8	27

126	Comparative genomic analysis of two-component regulatory proteins in <i>Pseudomonas syringae</i> . <i>BMC Genomics</i> , <b>2007</b> , 8, 397	4.5	27
125	Transcriptomics and adaptive genomics of the asymptomatic bacteriuria <i>Escherichia coli</i> strain 83972. <i>Molecular Genetics and Genomics</i> , <b>2008</b> , 279, 523-34	3.1	27
124	Veillonella, Firmicutes: Microbes disguised as Gram negatives. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 431-48		26
123	Genome update: distribution of two-component transduction systems in 250 bacterial genomes. <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 3447-3452	2.9	26
122	Toward unrestricted use of public genomic data. <i>Science</i> , <b>2019</b> , 363, 350-352	33.3	25
121	Global features of the <i>Alcanivorax borkumensis</i> SK2 genome. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 614-25	3.5	25
120	Analysis and prediction of gene splice sites in four <i>Aspergillus</i> genomes. <i>Fungal Genetics and Biology</i> , <b>2009</b> , 46 Suppl 1, S14-8	3.9	24
119	Genome update: DNA repeats in bacterial genomes. <i>Microbiology (United Kingdom)</i> , <b>2004</b> , 150, 3519-3521.9	2.9	24
118	Inheritance and organisation of the mitochondrial genome differ between two <i>Saccharomyces</i> yeasts. <i>Journal of Molecular Biology</i> , <b>2002</b> , 318, 627-36	6.5	24
117	Analysis of DNA structure in vivo using psoralen photobinding: measurement of supercoiling, topological domains, and DNA-protein interactions. <i>Methods in Enzymology</i> , <b>1992</b> , 212, 319-35	1.7	24
116	Comparative genomics to delineate pathogenic potential in non-O157 Shiga toxin-producing <i>Escherichia coli</i> (STEC) from patients with and without haemolytic uremic syndrome (HUS) in Norway. <i>PLoS ONE</i> , <b>2014</b> , 9, e111788	3.7	24
115	Viral Phylogenomics Using an Alignment-Free Method: A Three-Step Approach to Determine Optimal Length of k-mer. <i>Scientific Reports</i> , <b>2017</b> , 7, 40712	4.9	23
114	Integrated omics analyses reveal the details of metabolic adaptation of to lignocellulose-derived growth inhibitors released during the deconstruction of switchgrass. <i>Biotechnology for Biofuels</i> , <b>2017</b> , 10, 14	7.8	23
113	Genomic comparisons of <i>Brucella</i> spp. and closely related bacteria using base compositional and proteome based methods. <i>BMC Evolutionary Biology</i> , <b>2010</b> , 10, 249	3	23
112	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 599-601		23
111	Design of a seven-genome <i>Escherichia coli</i> microarray for comparative genomic profiling. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 7713-21	3.5	22
110	Genome Update: annotation quality in sequenced microbial genomes. <i>Microbiology (United Kingdom)</i> , <b>2004</b> , 150, 2015-2017	2.9	22
109	A classification of possible routes of Darwinian evolution. <i>Journal of Theoretical Biology</i> , <b>2000</b> , 203, 111-6.3	6.3	22

108	Genomic standards consortium projects. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 599-601		21
107	Computational genomics-proteomics and Phylogeny analysis of twenty one mycobacterial genomes (Tuberculosis & non Tuberculosis strains). <i>Microbial Informatics and Experimentation</i> , <b>2012</b> , 2, 7		21
106	Extracytoplasmic function sigma factors in <i>Pseudomonas syringae</i> . <i>Trends in Microbiology</i> , <b>2005</b> , 13, 565-624		21
105	Formation of a combined H-DNA/open TATA box structure in the promoter sequence of the human Na,K-ATPase alpha2 gene. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 13441-7	5.4	21
104	Molecular analysis of asymptomatic bacteriuria <i>Escherichia coli</i> strain VR50 reveals adaptation to the urinary tract by gene acquisition. <i>Infection and Immunity</i> , <b>2015</b> , 83, 1749-64	3.7	20
103	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 204-15		20
102	Amino acid usage is asymmetrically biased in AT- and GC-rich microbial genomes. <i>PLoS ONE</i> , <b>2013</b> , 8, e69878	3.7	20
101	Mash-based analyses of <i>Escherichia coli</i> genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , <b>2021</b> , 4, 117	6.7	20
100	Genome update: prediction of secreted proteins in 225 bacterial proteomes. <i>Microbiology (United Kingdom)</i> , <b>2005</b> , 151, 1725-1727	2.9	19
99	The plasmid genome database. <i>Microbiology (United Kingdom)</i> , <b>2003</b> , 149, 3043-3045	2.9	18
98	PanFunPro: PAN-genome analysis based on FUNctional PROfiles. <i>F1000Research</i> , 2, 265	3.6	17
97	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 471	3.6	16
96	Genome Update: AT content in sequenced prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , <b>2004</b> , 150, 749-752	2.9	15
95	Relative entropy differences in bacterial chromosomes, plasmids, phages and genomic islands. <i>BMC Genomics</i> , <b>2012</b> , 13, 66	4.5	14
94	Bayesian prediction of bacterial growth temperature range based on genome sequences. <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 7, S3	4.5	14
93	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 204-215		14
92	A novel Cas9-targeted long-read assay for simultaneous detection of IDH1/2 mutations and clinically relevant MGMT methylation in fresh biopsies of diffuse glioma. <i>Acta Neuropathologica Communications</i> , <b>2020</b> , 8, 87	7.3	13
91	Genomic analysis of two-component signal transduction proteins in basidiomycetes. <i>Journal of Molecular Microbiology and Biotechnology</i> , <b>2010</b> , 18, 63-73	0.9	13



90	Analysis of genomic signatures in prokaryotes using multinomial regression and hierarchical clustering. <i>BMC Genomics</i> , <b>2009</b> , 10, 487	4.5	13
89	Vibrio chromosome-specific families. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 73	5.7	12
88	Genome Sequence of Campylobacter jejuni strain 327, a strain isolated from a turkey slaughterhouse. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 113-22		12
87	Decoding the Epitranscriptional Landscape from Native RNA Sequences		12
86	Genome sequences of two stress-tolerant Campylobacter jejuni poultry strains, 305 and DFVF1099. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5546-7	3.5	11
85	Comparative genomics of green sulfur bacteria. <i>Photosynthesis Research</i> , <b>2010</b> , 104, 137-52	3.7	11
84	Prediction of highly expressed genes in microbes based on chromatin accessibility. <i>BMC Molecular Biology</i> , <b>2007</b> , 8, 11	4.5	11
83	A domain sequence approach to pangenomics: applications to Escherichia coli. <i>F1000Research</i> , <b>2012</b> , 1, 19	3.6	11
82	PanViz: interactive visualization of the structure of functionally annotated pangenomes. <i>Bioinformatics</i> , <b>2017</b> , 33, 1081-1082	7.2	10
81	Non-O1 Vibrio cholerae unlinked to cholera in Haiti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E3206; author reply E3207	11.5	10
80	DNA Structure: A-, B- and Z-DNA Helix Families <b>2002</b> ,		10
79	Unique and conserved genome regions in Vibrio harveyi and related species in comparison with the shrimp pathogen Vibrio harveyi CAIM 1792. <i>Microbiology (United Kingdom)</i> , <b>2015</b> , 161, 1762-1779	2.9	10
78	The Gene Has Recently Spread between Rolling Circle Plasmids of , Indicative of a Novel Gene Transfer Mechanism. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1528	5.7	10
77	An assessment of Oxford Nanopore sequencing for human gut metagenome profiling: A pilot study of head and neck cancer patients. <i>Journal of Microbiological Methods</i> , <b>2019</b> , 166, 105739	2.8	9
76	Genome comparison of bacterial pathogens. <i>Genome Dynamics</i> , <b>2009</b> , 6, 1-20		9
75	Genome update: chromosome atlases. <i>Microbiology (United Kingdom)</i> , <b>2004</b> , 150, 3091-3	2.9	9
74	Genome update: Length distributions of sequenced prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , <b>2004</b> , 150, 513-516	2.9	9
73	The Atlas visualization of genomewide information. <i>Methods in Microbiology</i> , <b>2002</b> , 49-63	2.8	9

72	Visualization of pathogenicity regions in bacteria. <i>Genetica</i> , <b>2000</b> , 108, 47-51	1.5	9
71	Comparative Genomics of <i>Pseudomonas aeruginosa</i> PAO1 and <i>Pseudomonas putida</i> KT2440: Orthologs, Codon Usage, Repetitive Extragenic Palindromic Elements, and Oligonucleotide Motif Signatures. <i>Journal of Genome Science and Technology</i> , <b>2002</b> , 1, 175-187		9
70	Analysis of two large functionally uncharacterized regions in the <i>Methanopyrus kandleri</i> AV19 genome. <i>BMC Genomics</i> , <b>2003</b> , 4, 12	4.5	8
69	A domain sequence approach to pangenomics: applications to <i>Escherichia coli</i> . <i>F1000Research</i> , <b>2012</b> , 1, 19	3.6	8
68	Decaffeinated Green Tea Extract Does Not Elicit Hepatotoxic Effects and Modulates the Gut Microbiome in Lean B6C3F <sub>1</sub> Mice. <i>Nutrients</i> , <b>2019</b> , 11,	6.7	7
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