

# David W Ussery

## List of Publications by Year in descending order

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216  
papers

19,987  
citations

28190

55  
h-index

11581

135  
g-index

241  
all docs

241  
docs citations

241  
times ranked

24920  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNAmmr: consistent and rapid annotation of ribosomal RNA genes. <i>Nucleic Acids Research</i> , 2007, 35, 3100-3108.	6.5	5,357
2	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1355-1361.	1.8	1,925
3	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	9.4	1,069
4	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	9.4	1,047
5	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
6	Insights from 20 years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , 2015, 15, 141-161.	1.4	580
7	Comparison of 61 Sequenced <i>Escherichia coli</i> Genomes. <i>Microbial Ecology</i> , 2010, 60, 708-720.	1.4	436
8	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> , 2012, 109, E1277-86.	3.3	373
9	Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539.	1.8	241
10	A DNA structural atlas for <i>Escherichia coli</i> 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 2000, 299, 907-930.	2.0	213
11	Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse <i>Escherichia coli</i> genomes. <i>BMC Genomics</i> , 2012, 13, 577.	1.2	205
12	The Complete Genome Sequence and Analysis of the Epsilonproteobacterium <i>Arcobacter butzleri</i> . <i>PLoS ONE</i> , 2007, 2, e1358.	1.1	203
13	On the total number of genes and their length distribution in complete microbial genomes. <i>Trends in Genetics</i> , 2001, 17, 425-428.	2.9	193
14	Machine Learning Methods in Drug Discovery. <i>Molecules</i> , 2020, 25, 5277.	1.7	182
15	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011, 9, e1001088.	2.6	180
16	The <i>Salmonella enterica</i> Pan-genome. <i>Microbial Ecology</i> , 2011, 62, 487-504.	1.4	175
17	Genomic taxonomy of vibrios. <i>BMC Evolutionary Biology</i> , 2009, 9, 258.	3.2	168
18	Ten years of bacterial genome sequencing: comparative-genomics-based discoveries. <i>Functional and Integrative Genomics</i> , 2006, 6, 165-185.	1.4	156

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19	Decoding the epitranscriptional landscape from native RNA sequences. <i>Nucleic Acids Research</i> , 2021, 49, e7-e7.	6.5	149
20	Microbial taxonomy in the post-genomic era: Rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015, 197, 359-370.	1.0	144
21	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> , 2015, 5, 44-61.	1.5	139
22	A Closer Look at Bacteroides: Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut. <i>Microbial Ecology</i> , 2011, 61, 473-485.	1.4	135
23	The chromatin-associated protein H-NS. <i>Biochimie</i> , 1994, 76, 968-980.	1.3	122
24	CMG-Biotools, a Free Workbench for Basic Comparative Microbial Genomics. <i>PLoS ONE</i> , 2013, 8, e60120.	1.1	119
25	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> , 2018, 46, e38-e38.	6.5	116
26	Origin of replication in circular prokaryotic chromosomes. <i>Environmental Microbiology</i> , 2006, 8, 353-361.	1.8	115
27	The genomic code: inferring <i>Vibrionaceae</i> niche specialization. <i>Nature Reviews Microbiology</i> , 2006, 4, 697-704.	13.6	115
28	Molecular analysis of the emergence of pandemic <i>Vibrio parahaemolyticus</i> . <i>BMC Microbiology</i> , 2008, 8, 110.	1.3	114
29	Comparative Genomics of <i>Bifidobacterium</i> , <i>Lactobacillus</i> and Related Probiotic Genera. <i>Microbial Ecology</i> , 2012, 63, 651-673.	1.4	113
30	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> , 2013, 79, 2944-2951.	1.4	110
31	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> , 2003, 51, 15-32.	1.2	106
32	From essential to persistent genes: a functional approach to constructing synthetic life. <i>Trends in Genetics</i> , 2013, 29, 273-279.	2.9	106
33	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	1.4	105
34	The genome of the versatile nitrogen fixer <i>Azorhizobium caulinodans</i> ORS571. <i>BMC Genomics</i> , 2008, 9, 271.	1.2	104
35	Defining the <i>Pseudomonas</i> Genus: Where Do We Draw the Line with <i>Azotobacter</i> ?. <i>Microbial Ecology</i> , 2012, 63, 239-248.	1.4	100
36	Microbial comparative pan-genomics using binomial mixture models. <i>BMC Genomics</i> , 2009, 10, 385.	1.2	94

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37	Genomic Characterization of <i>Campylobacter jejuni</i> Strain M1. PLoS ONE, 2010, 5, e12253.	1.1	86
38	RpoD Promoters in <i>Campylobacter jejuni</i> Exhibit a Strong Periodic Signal Instead of a $\sigma^{35}$ Box. Journal of Molecular Biology, 2003, 326, 1361-1372.	2.0	84
39	Meeting report: GenBank microbial genomic taxonomy workshop (12–13 May, 2015). Standards in Genomic Sciences, 2016, 11, .	1.5	81
40	CBS Genome Atlas Database: a dynamic storage for bioinformatic results and sequence data. Bioinformatics, 2004, 20, 3682-3686.	1.8	80
41	Characterization of probiotic <i>Escherichia coli</i> isolates with a novel pan-genome microarray. Genome Biology, 2007, 8, R267.	13.9	80
42	Genome organisation and chromatin structure in <i>Escherichia coli</i> . Biochimie, 2001, 83, 201-212.	1.3	79
43	Genomic variation in <i>Salmonella enterica</i> core genes for epidemiological typing. BMC Genomics, 2012, 13, 88.	1.2	76
44	PARP1 Is Up-Regulated in Non-small Cell Lung Cancer Tissues in the Presence of the Cyanobacterial Toxin Microcystin. Frontiers in Microbiology, 2018, 9, 1757.	1.5	76
45	Case of Microcephaly after Congenital Infection with Asian Lineage Zika Virus, Thailand. Emerging Infectious Diseases, 2018, 24, 1758-1761.	2.0	75
46	Diversity of <i>Pseudomonas</i> Genomes, Including <i>Populus</i> -Associated Isolates, as Revealed by Comparative Genome Analysis. Applied and Environmental Microbiology, 2016, 82, 375-383.	1.4	70
47	LeuO is a global regulator of gene expression in <i>Salmonella enterica</i> serovar Typhimurium. Molecular Microbiology, 2012, 85, 1072-1089.	1.2	68
48	The genome BLAST Atlas—a GeneWiz extension for visualization of whole-genome homology. Molecular BioSystems, 2008, 4, 363.	2.9	67
49	Three views of microbial genomes. Research in Microbiology, 1999, 150, 773-777.	1.0	65
50	The $\sigma^{54}$ regulon (sigmulon) of <i>Pseudomonas putida</i> . Environmental Microbiology, 2003, 5, 1281-1293.	1.8	65
51	Standard operating procedure for computing pangenome trees. Standards in Genomic Sciences, 2010, 2, 135-141.	1.5	64
52	Mechanisms linking preterm birth to onset of cardiovascular disease later in adulthood. European Heart Journal, 2019, 40, 1107-1112.	1.0	64
53	DNA Binding Is Not Sufficient for H-NS-mediated Repression of proU Expression. Journal of Biological Chemistry, 1997, 272, 12083-12090.	1.6	63
54	Metabolic functions of <i>Pseudomonas fluorescens</i> strains from <i>Populus deltoides</i> depend on rhizosphere or endosphere isolation compartment. Frontiers in Microbiology, 2015, 6, 1118.	1.5	60

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55	An environmental signature for 323 microbial genomes based on codon adaptation indices. <i>Genome Biology</i> , 2006, 7, R114.	13.9	59
56	Polyclonality of Concurrent Natural Populations of <i>Alteromonas macleodii</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 1360-1374.	1.1	57
57	Complete DNA sequence of the linear mitochondrial genome of the pathogenic yeast <i>Candida parapsilosis</i> . <i>Molecular Genetics and Genomics</i> , 2004, 272, 173-180.	1.0	56
58	Genome update: the 1000th genome – a cautionary tale. <i>Microbiology (United Kingdom)</i> , 2010, 156, 603-608.	0.7	55
59	<i>Ebolavirus</i> comparative genomics. <i>FEMS Microbiology Reviews</i> , 2015, 39, 764-778.	3.9	54
60	Investigations of Oligonucleotide Usage Variance Within and Between Prokaryotes. <i>PLoS Computational Biology</i> , 2008, 4, e1000057.	1.5	53
61	Mash-based analyses of <i>Escherichia coli</i> genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , 2021, 4, 117.	2.0	52
62	[13] Probing DNA structure with psoralen in vitro. <i>Methods in Enzymology</i> , 1992, 212, 242-262.	0.4	50
63	DNA microarray analysis of fim mutations in <i>Escherichia coli</i> . <i>Molecular Genetics and Genomics</i> , 2002, 267, 721-729.	1.0	49
64	On the Origins of a <i>Vibrio</i> Species. <i>Microbial Ecology</i> , 2010, 59, 1-13.	1.4	48
65	Strand misalignments lead to quasipalindrome correction. <i>Trends in Genetics</i> , 2003, 19, 365-369.	2.9	47
66	<i>Veillonella</i> , Firmicutes: Microbes disguised as Gram negatives. <i>Standards in Genomic Sciences</i> , 2013, 9, 431-448.	1.5	47
67	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> , 2015, 2015, 1-17.	0.9	47
68	Chromatin architecture and gene expression in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2004, 5, 252.	13.9	46
69	Complete Genome Sequence of the Commensal <i>Enterococcus faecalis</i> 62, Isolated from a Healthy Norwegian Infant. <i>Journal of Bacteriology</i> , 2011, 193, 2377-2378.	1.0	46
70	Rapid Sequencing of Multiple RNA Viruses in Their Native Form. <i>Frontiers in Microbiology</i> , 2019, 10, 260.	1.5	46
71	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
72	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. <i>BMC Genomics</i> , 2007, 8, 325.	1.2	44

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73	The TNF $\alpha$ receptor TNFRSF1A and genes encoding the amiloride-sensitive sodium channel ENaC as modulators in cystic fibrosis. <i>Human Genetics</i> , 2006, 119, 331-343.	1.8	43
74	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> , 2014, 9, e111788.	1.1	41
75	DNA: Structure and function. <i>Advances in Genome Biology</i> , 1998, 5, 1-141.	0.3	39
76	Analysis of intra-genomic GC content homogeneity within prokaryotes. <i>BMC Genomics</i> , 2010, 11, 464.	1.2	39
77	Environmental influences on the in vivo level of intramolecular triplex DNA in <i>Escherichia coli</i> . <i>Biochemistry</i> , 1993, 32, 6206-6213.	1.2	38
78	Viral Phylogenomics Using an Alignment-Free Method: A Three-Step Approach to Determine Optimal Length of k-mer. <i>Scientific Reports</i> , 2017, 7, 40712.	1.6	38
79	Genome update: sigma factors in 240 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3147-3150.	0.7	37
80	Quality scores for 32,000 genomes. <i>Standards in Genomic Sciences</i> , 2014, 9, 20.	1.5	36
81	Amino Acid Usage Is Asymmetrically Biased in AT- and GC-Rich Microbial Genomes. <i>PLoS ONE</i> , 2013, 8, e69878.	1.1	36
82	Functionality of System Components: Conservation of Protein Function in Protein Feature Space. <i>Genome Research</i> , 2003, 13, 2444-2449.	2.4	35
83	Identification of putative noncoding RNA genes in the <i>Burkholderia cenocepacia</i> J2315 genome. <i>FEMS Microbiology Letters</i> , 2007, 276, 83-92.	0.7	35
84	Reliability and applications of statistical methods based on oligonucleotide frequencies in bacterial and archaeal genomes. <i>BMC Genomics</i> , 2008, 9, 104.	1.2	35
85	Evaluation of potential regulatory elements identified as DNase I hypersensitive sites in the CFTR gene. <i>FEBS Journal</i> , 2002, 269, 553-559.	0.2	34
86	Comparative genomic analysis of two-component regulatory proteins in <i>Pseudomonas syringae</i> . <i>BMC Genomics</i> , 2007, 8, 397.	1.2	33
87	Transcriptomics and adaptive genomics of the asymptomatic bacteriuria <i>Escherichia coli</i> strain 83972. <i>Molecular Genetics and Genomics</i> , 2008, 279, 523-534.	1.0	33
88	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 157-160.	1.0	33
89	Is the pan-genome also a pan-selectome?. <i>F1000Research</i> , 2012, 1, 16.	0.8	33
90	Bias of purine stretches in sequenced chromosomes. <i>Computers &amp; Chemistry</i> , 2002, 26, 531-541.	1.2	32

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91	Genome Update: proteome comparisons. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1-4.	0.7	32
92	<i>Campylobacter fetus</i> subspecies: Comparative genomics and prediction of potential virulence targets. <i>Gene</i> , 2012, 508, 145-156.	1.0	32
93	Sigma factors in a thousand <i>E. coli</i> genomes. <i>Environmental Microbiology</i> , 2013, 15, 3121-3129.	1.8	32
94	Integrated omics analyses reveal the details of metabolic adaptation of <i>Clostridium thermocellum</i> to lignocellulose-derived growth inhibitors released during the deconstruction of switchgrass. <i>Biotechnology for Biofuels</i> , 2017, 10, 14.	6.2	30
95	Environmental Influences on DNA Curvature. <i>Journal of Biomolecular Structure and Dynamics</i> , 1999, 16, 811-823.	2.0	29
96	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	29
97	Global features of the <i>Alcanivorax borkumensis</i> SK2 genome. <i>Environmental Microbiology</i> , 2008, 10, 614-625.	1.8	28
98	Computational genomics-proteomics and Phylogeny analysis of twenty one mycobacterial genomes (Tuberculosis & non Tuberculosis strains). <i>Microbial Informatics and Experimentation</i> , 2012, 2, 7.	7.6	28
99	[18] Analysis of DNA structure in vivo using psoralen photobinding: Measurement of supercoiling, topological domains, and DNA-protein interactions. <i>Methods in Enzymology</i> , 1992, 212, 319-335.	0.4	27
100	A Classification of Possible Routes of Darwinian Evolution. <i>Journal of Theoretical Biology</i> , 2000, 203, 111-116.	0.8	27
101	Inheritance and organisation of the mitochondrial genome differ between two <i>Saccharomyces</i> yeasts. <i>Journal of Molecular Biology</i> , 2002, 318, 627-636.	2.0	27
102	Genome update: distribution of two-component transduction systems in 250 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3447-3452.	0.7	27
103	dBBQs: dataBase of Bacterial Quality scores. <i>BMC Bioinformatics</i> , 2017, 18, 483.	1.2	27
104	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	26
105	Genome Update: DNA repeats in bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3519-3521.	0.7	25
106	Analysis and prediction of gene splice sites in four <i>Aspergillus</i> genomes. <i>Fungal Genetics and Biology</i> , 2009, 46, S14-S18.	0.9	25
107	Formation of a Combined H-DNA/Open TATA Box Structure in the Promoter Sequence of the Human Na,K-ATPase $\alpha$ 2 Gene. <i>Journal of Biological Chemistry</i> , 1996, 271, 13441-13447.	1.6	24
108	Design of a Seven-Genome <i>Escherichia coli</i> Microarray for Comparative Genomic Profiling. <i>Journal of Bacteriology</i> , 2006, 188, 7713-7721.	1.0	24

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109	Genomic comparisons of <i>Brucella</i> spp. and closely related bacteria using base compositional and proteome based methods. <i>BMC Evolutionary Biology</i> , 2010, 10, 249.	3.2	24
110	Bayesian prediction of bacterial growth temperature range based on genome sequences. <i>BMC Genomics</i> , 2012, 13, S3.	1.2	24
111	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> , 2015, 83, 1749-1764.	1.0	24
112	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> , 2020, 8, 87.	2.4	24
113	Genome Update: annotation quality in sequenced microbial genomes. <i>Microbiology (United Kingdom)</i> , 2004, 150, 2015-2017.	0.7	22
114	Extracytoplasmic function sigma factors in <i>Pseudomonas syringae</i> . <i>Trends in Microbiology</i> , 2005, 13, 565-568.	3.5	22
115	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. <i>Standards in Genomic Sciences</i> , 2009, 1, 204-215.	1.5	21
116	PanViz: interactive visualization of the structure of functionally annotated pangenomes. <i>Bioinformatics</i> , 2017, 33, 1081-1082.	1.8	21
117	Genome update: prediction of secreted proteins in 225 bacterial proteomes. <i>Microbiology (United Kingdom)</i> , 2017, 151, 1074-1082.	0.7	20
118	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. <i>BMC Bioinformatics</i> , 2017, 18, 471.	1.2	20
119	The Plasmid Genome Database. <i>Microbiology (United Kingdom)</i> , 2003, 149, 3043-3045.	0.7	18
120	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. <i>Standards in Genomic Sciences</i> , 2009, 1, 204-215.	1.5	18
121	Analysis of genomic signatures in prokaryotes using multinomial regression and hierarchical clustering. <i>BMC Genomics</i> , 2009, 10, 487.	1.2	17
122	Relative entropy differences in bacterial chromosomes, plasmids, phages and genomic islands. <i>BMC Genomics</i> , 2012, 13, 66.	1.2	17
123	Decaffeinated Green Tea Extract Does Not Elicit Hepatotoxic Effects and Modulates the Gut Microbiome in Lean B6C3F1 Mice. <i>Nutrients</i> , 2019, 11, 776.	1.7	17
124	PanFunPro: PAN-genome analysis based on FUNctional PROfiles. <i>F1000Research</i> , 0, 2, 265.	0.8	17
125	Genome Update: AT content in sequenced prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2004, 150, 749-752.	0.7	16
126	<i>Vibrio</i> chromosome-specific families. <i>Frontiers in Microbiology</i> , 2014, 5, 73.	1.5	16



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127	The qacC Gene Has Recently Spread between Rolling Circle Plasmids of Staphylococcus, Indicative of a Novel Gene Transfer Mechanism. <i>Frontiers in Microbiology</i> , 2016, 7, 1528.	1.5	15
128	Prediction of highly expressed genes in microbes based on chromatin accessibility. , 2007, 8, 11.		14
129	Genomic Analysis of Two-Component Signal Transduction Proteins in Basidiomycetes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010, 18, 63-73.	1.0	14
130	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> , 2019, 166, 105739.	0.7	13
131	Comparative genomics of green sulfur bacteria. <i>Photosynthesis Research</i> , 2010, 104, 137-152.	1.6	12
132	Genome Sequence of <i>Campylobacter jejuni</i> strain 327, a strain isolated from a turkey slaughterhouse. <i>Standards in Genomic Sciences</i> , 2011, 4, 113-122.	1.5	12
133	Genome Sequences of Two Stress-Tolerant <i>Campylobacter jejuni</i> Poultry Strains, 305 and DFVF1099. <i>Journal of Bacteriology</i> , 2011, 193, 5546-5547.	1.0	12
134	Unique and conserved genome regions in <i>Vibrio harveyi</i> and related species in comparison with the shrimp pathogen <i>Vibrio harveyi</i> CAIM 1792. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1762-1779.	0.7	12
135	A domain sequence approach to pangenomics: applications to <i>Escherichia coli</i> . <i>F1000Research</i> , 2012, 1, 19.	0.8	12
136	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103965.	1.0	11
137	Two Cases of Vancomycin-Resistant <i>Enterococcus faecium</i> Bacteremia With Development of Daptomycin-Resistant Phenotype and its Detection Using Oxford Nanopore Sequencing. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa180.	0.4	11
138	Report of the 2019 NIST-FDA workshop on standards for next generation sequencing detection of viral adventitious agents in biologics and biomanufacturing. <i>Biologicals</i> , 2020, 64, 76-82.	0.5	11
139	Comparative Genomics of Four <i>Pseudomonas</i> Species. , 2004, , 139-164.		11
140	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> , 2002, 1, 175-187.	0.7	11
141	The first three waves of the Covid-19 pandemic hint at a limited genetic repertoire for SARS-CoV-2. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	11
142	Design and construction of a circular intensity differential scattering instrument. <i>Review of Scientific Instruments</i> , 1984, 55, 1574-1579.	0.6	10
143	Visualization of pathogenicity regions in bacteria. <i>Genetica</i> , 2000, 108, 47-51.	0.5	10
144	Genome Update: length distributions of sequenced prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2010, 160, 1057-1066.	0.7	10

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145	Genome Comparison of Bacterial Pathogens. <i>Genome Dynamics</i> , 2009, 6, 1-20.	2.4	10
146	Non-O1 <i>Vibrio cholerae</i> unlinked to cholera in Haiti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3206-E3206.	3.3	10
147	The Atlas visualization of genomewide information. <i>Methods in Microbiology</i> , 2002, , 49-63.	0.4	9
148	Analysis of two large functionally uncharacterized regions in the <i>Methanopyrus kandleri</i> AV19 genome. <i>BMC Genomics</i> , 2003, 4, 12.	1.2	9
149	Genome Update: Chromosome Atlases. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3091-3093.	0.7	9
150	Differences in two-component signal transduction proteins among the genus <i>Brucella</i> : Implications for host preference and pathogenesis. <i>Veterinary Microbiology</i> , 2010, 144, 478-483.	0.8	9
151	SMARC-B1 deficient sinonasal carcinoma metastasis to the brain with next generation sequencing data: a case report of perineural invasion progressing to leptomeningeal invasion. <i>BMC Cancer</i> , 2019, 19, 827.	1.1	9
152	Two SARS-CoV-2 Genome Sequences of Isolates from Rural U.S. Patients Harboring the D614G Mutation, Obtained Using Nanopore Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	9
153	Appendix Estimation of superhelical density in Vivo from analysis of the level of cruciforms existing in living cells. <i>Journal of Molecular Biology</i> , 1991, 221, 122-129.	2.0	8
154	Genome Update: 161 prokaryotic genomes sequenced, and counting. <i>Microbiology (United Kingdom)</i> , 2004, 150, 261-263.	0.7	8
155	Studies on Monitoring and Tracking Genetic Resources: An Executive Summary. <i>Standards in Genomic Sciences</i> , 2009, 1, 78-86.	1.5	8
156	Analysis of evolutionary patterns of genes in <i>Campylobacter jejuni</i> and <i>C. coli</i> . <i>Microbial Informatics and Experimentation</i> , 2012, 2, 8.	7.6	8
157	A domain sequence approach to pangenomics: applications to <i>Escherichia coli</i> . <i>F1000Research</i> , 2012, 1, 19.	0.8	8
158	Genome Update: Protein secretion systems in 225 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1013-1016.	0.7	7
159	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
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