

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	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
2	Decoding the epitranscriptional landscape from native RNA sequences. <i>Nucleic Acids Research</i> , 2021, 49, e7-e7.	6.5	149
3	Assessment of Bacterial Load in Polyethylene Terephthalate (PET) Bottled Water Marketed in Kathmandu Valley, Nepal. <i>International Journal of Polymer Science</i> , 2021, 2021, 1-10.	1.2	4
4	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
5	Mash-based analyses of <i>Escherichia coli</i> genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , 2021, 4, 117.	2.0	52
6	Is amplification bias consequential in transposon sequencing (TnSeq) assays? A case study with a <i>Staphylococcus aureus</i> TnSeq library subjected to PCR-based and amplification-free enrichment methods. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
7	Comparative genomics of hepatitis A virus, hepatitis C virus, and hepatitis E virus provides insights into the evolutionary history of <i>Hepatovirus</i> species. <i>MicrobiologyOpen</i> , 2020, 9, e973.	1.2	5
8	Machine Learning Methods in Drug Discovery. <i>Molecules</i> , 2020, 25, 5277.	1.7	182
9	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
10	ProdMX: Rapid query and analysis of protein functional domain based on compressed sparse matrices. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3890-3896.	1.9	0
11	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
12	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
13	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
14	Complete Genome Sequences of Four Isolates of Vancomycin-Resistant <i>Enterococcus faecium</i> with the <i>vanA</i> Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
15	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
16	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
17	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
18	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45

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19	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
20	Draft Genome Sequences of 48 Vancomycin-Resistant <i>Enterococcus faecium</i> Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
21	In silico Selection of Amplification Targets for Rapid Polymorphism Screening in Ebola Virus Outbreaks. <i>Frontiers in Microbiology</i> , 2019, 10, 857.	1.5	0
22	Complete Genome and Plasmid Sequences of <i>Escherichia coli</i> Type Strain ATCC 11775. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
23	Rapid Sequencing of Multiple RNA Viruses in Their Native Form. <i>Frontiers in Microbiology</i> , 2019, 10, 260.	1.5	46
24	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
25	Mechanisms linking preterm birth to onset of cardiovascular disease later in adulthood. <i>European Heart Journal</i> , 2019, 40, 1107-1112.	1.0	64
26	GENE-18. TRANSCRIPTOME-WIDE ANALYSIS USING NANOPORE THIRD GENERATION SEQUENCING IN A RAT GLIOBLASTOMA MODEL: PROOF OF PRINCIPLE. <i>Neuro-Oncology</i> , 2019, 21, vi101-vi101.	0.6	0
27	PATH-05. RAPID SIMULTANEOUS IDH MUTATION AND MGMT METHYLATION STATUS ASSESSMENT IN GLIOMA PATIENTS USING CRISPR-Cas9-TARGETED NANOPORE SEQUENCING. <i>Neuro-Oncology</i> , 2019, 21, vi143-vi144.	0.6	0
28	Genome-Based Comparison of <i>Clostridioides difficile</i> : Average Amino Acid Identity Analysis of Core Genomes. <i>Microbial Ecology</i> , 2018, 76, 801-813.	1.4	6
29	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
30	Genome Sequences of Zika Virus Strains Recovered from Amniotic Fluid, Placenta, and Fetal Brain of a Microcephaly Patient in Thailand, 2017. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
31	Conservation of Two-Component Signal Transduction Systems in <i>E. coli</i> , <i>Salmonella</i> , and Across 100,000 Bacteria of Various Bacterial Phyla. <i>Grand Challenges in Biology and Biotechnology</i> , 2018, , 153-174.	2.4	1
32	Case of Microcephaly after Congenital Infection with Asian Lineage Zika Virus, Thailand. <i>Emerging Infectious Diseases</i> , 2018, 24, 1758-1761.	2.0	75
33	PARP1 Is Up-Regulated in Non-small Cell Lung Cancer Tissues in the Presence of the Cyanobacterial Toxin Microcystin. <i>Frontiers in Microbiology</i> , 2018, 9, 1757.	1.5	76
34	Gender Differences in the Gut Microbiome and How These Affect Cardiovascular Diseases. , 2018, , 89-100.		5
35	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
36	PanViz: interactive visualization of the structure of functionally annotated pangenomes. <i>Bioinformatics</i> , 2017, 33, 1081-1082.	1.8	21

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37	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
38	Three Complete Genome Sequences of Genotype G Mumps Virus from the 2016 Outbreak in Arkansas, USA. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
39	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. <i>BMC Bioinformatics</i> , 2017, 18, 471.	1.2	20
40	dBBQs: dataBase of Bacterial Quality scores. <i>BMC Bioinformatics</i> , 2017, 18, 483.	1.2	27
41	Insights from Comparative Genomics of the Genus <i>Salmonella</i> . , 2017, , .		2
42	The <i>qacC</i> Gene Has Recently Spread between Rolling Circle Plasmids of <i>Staphylococcus</i> , Indicative of a Novel Gene Transfer Mechanism. <i>Frontiers in Microbiology</i> , 2016, 7, 1528.	1.5	15
43	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	1.4	105
44	Meeting report: GenBank microbial genomic taxonomy workshop (12â€“13 May, 2015). <i>Standards in Genomic Sciences</i> , 2016, 11, .	1.5	81
45	Diversity of <i>Pseudomonas</i> Genomes, Including <i>Populus</i> -Associated Isolates, as Revealed by Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 375-383.	1.4	70
46	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
47	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> , 2015, 6, 1118.	1.5	60
48	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
49	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
50	Insights from 20 years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , 2015, 15, 141-161.	1.4	580
51	<i>Ebolavirus</i> comparative genomics. <i>FEMS Microbiology Reviews</i> , 2015, 39, 764-778.	3.9	54
52	Microbial taxonomy in the post-genomic era: Rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015, 197, 359-370.	1.0	144
53	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
54	Genome Atlases, Potential Applications in Study of Metagenomes. , 2015, , 219-222.		0

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55	Vibrio chromosome-specific families. <i>Frontiers in Microbiology</i> , 2014, 5, 73.	1.5	16
56	Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539.	1.8	241
57	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
58	Quality scores for 32,000 genomes. <i>Standards in Genomic Sciences</i> , 2014, 9, 20.	1.5	36
59	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	26
60	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
61	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	29
62	Sigma factors in a thousand <i>Escherichia coli</i> genomes. <i>Environmental Microbiology</i> , 2013, 15, 3121-3129.	1.8	32
63	From essential to persistent genes: a functional approach to constructing synthetic life. <i>Trends in Genetics</i> , 2013, 29, 273-279.	2.9	106
64	Comparative Genomics. , 2013, , 209-227.		1
65	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
66	Veillonella, Firmicutes: Microbes disguised as Gram negatives. <i>Standards in Genomic Sciences</i> , 2013, 9, 431-448.	1.5	47
67	CMG-Biotools, a Free Workbench for Basic Comparative Microbial Genomics. <i>PLoS ONE</i> , 2013, 8, e60120.	1.1	119
68	Bayesian prediction of microbial oxygen requirement. <i>F1000Research</i> , 2013, 2, 184.	0.8	6
69	Amino Acid Usage Is Asymmetrically Biased in AT- and GC-Rich Microbial Genomes. <i>PLoS ONE</i> , 2013, 8, e69878.	1.1	36
70	Genome Atlases, Potential Applications in Study of Metagenomes. , 2013, , 1-4.		0
71	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
72	Polyclonality of Concurrent Natural Populations of <i>Alteromonas macleodii</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 1360-1374.	1.1	57

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73	Non-O1 <i>Vibrio cholerae</i> unlinked to cholera in Haiti. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3206-E3206.	3.3	10
74	Relative entropy differences in bacterial chromosomes, plasmids, phages and genomic islands. BMC Genomics, 2012, 13, 66.	1.2	17
75	Genomic variation in <i>Salmonella enterica</i> core genes for epidemiological typing. BMC Genomics, 2012, 13, 88.	1.2	76
76	Computational genomics-proteomics and Phylogeny analysis of twenty one mycobacterial genomes (Tuberculosis & non Tuberculosis strains). Microbial Informatics and Experimentation, 2012, 2, 7.	7.6	28
77	Analysis of evolutionary patterns of genes in <i>Campylobacter jejuni</i> and <i>C. coli</i> . Microbial Informatics and Experimentation, 2012, 2, 8.	7.6	8
78	<i>Campylobacter fetus</i> subspecies: Comparative genomics and prediction of potential virulence targets. Gene, 2012, 508, 145-156.	1.0	32
79	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. Journal of Clinical Microbiology, 2012, 50, 1355-1361.	1.8	1,925
80	Bayesian prediction of bacterial growth temperature range based on genome sequences. BMC Genomics, 2012, 13, S3.	1.2	24
81	Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse <i>Escherichia coli</i> genomes. BMC Genomics, 2012, 13, 577.	1.2	205
82	LeuO is a global regulator of gene expression in <i>Salmonella enterica</i> serovar Typhimurium. Molecular Microbiology, 2012, 85, 1072-1089.	1.2	68
83	Defining the <i>Pseudomonas</i> Genus: Where Do We Draw the Line with <i>Azotobacter</i> ?. Microbial Ecology, 2012, 63, 239-248.	1.4	100
84	Comparative Genomics of <i>Bifidobacterium</i> , <i>Lactobacillus</i> and Related Probiotic Genera. Microbial Ecology, 2012, 63, 651-673.	1.4	113
85	Two novel methods for using genome sequences to infer taxonomy. Microbiology (United Kingdom), 2012, 158, 1414-1414.	0.7	3
86	Is the pan-genome also a pan-selectome?. F1000Research, 2012, 1, 16.	0.8	33
87	A domain sequence approach to pangenomics: applications to <i>Escherichia coli</i> . F1000Research, 2012, 1, 19.	0.8	8
88	A domain sequence approach to pangenomics: applications to <i>Escherichia coli</i> . F1000Research, 2012, 1, 19.	0.8	12
89	Genome Sequence of <i>Campylobacter jejuni</i> strain 327, a strain isolated from a turkey slaughterhouse. Standards in Genomic Sciences, 2011, 4, 113-122.	1.5	12
90	A Closer Look at <i>Bacteroides</i> : Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut. Microbial Ecology, 2011, 61, 473-485.	1.4	135

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91	The Salmonella enterica Pan-genome. <i>Microbial Ecology</i> , 2011, 62, 487-504.	1.4	175
92	Natural genetic engineering: intelligence & design in evolution?. <i>Microbial Informatics and Experimentation</i> , 2011, 1, .	7.6	0
93	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
94	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
95	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011, 9, e1001088.	2.6	180
96	Standard operating procedure for computing pangenome trees. <i>Standards in Genomic Sciences</i> , 2010, 2, 135-141.	1.5	64
97	On the Origins of a <i>Vibrio</i> Species. <i>Microbial Ecology</i> , 2010, 59, 1-13.	1.4	48
98	Comparison of 61 Sequenced <i>Escherichia coli</i> Genomes. <i>Microbial Ecology</i> , 2010, 60, 708-720.	1.4	436
99	Comparative genomics of green sulfur bacteria. <i>Photosynthesis Research</i> , 2010, 104, 137-152.	1.6	12
100	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
101	Analysis of intra-genomic GC content homogeneity within prokaryotes. <i>BMC Genomics</i> , 2010, 11, 464.	1.2	39
102	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
103	Genomic Characterization of <i>Campylobacter jejuni</i> Strain M1. <i>PLoS ONE</i> , 2010, 5, e12253.	1.1	86
104	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
105	Design of an Enterobacteriaceae Pan-Genome Microarray Chip. <i>Communications in Computer and Information Science</i> , 2010, , 165-179.	0.4	3
106	Genome update: the 1000th genome â€“ a cautionary tale. <i>Microbiology (United Kingdom)</i> , 2010, 156, 603-608.	0.7	55
107	The Genome Atlas Resource. <i>Communications in Computer and Information Science</i> , 2010, , 141-150.	0.4	0
108	Genome Comparison of Bacterial Pathogens. <i>Genome Dynamics</i> , 2009, 6, 1-20.	2.4	10

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109	Genomic taxonomy of vibrios. BMC Evolutionary Biology, 2009, 9, 258.	3.2	168
110	Stretches of alternating pyrimidine/purines and purines are respectively linked with pathogenicity and growth temperature in prokaryotes. BMC Genomics, 2009, 10, 346.	1.2	6
111	Microbial comparative pan-genomics using binomial mixture models. BMC Genomics, 2009, 10, 385.	1.2	94
112	Analysis of genomic signatures in prokaryotes using multinomial regression and hierarchical clustering. BMC Genomics, 2009, 10, 487.	1.2	17
113	Analysis and prediction of gene splice sites in four Aspergillus genomes. Fungal Genetics and Biology, 2009, 46, S14-S18.	0.9	25
114	Microbial Communities: Core and Pan-Genomics. Computational Biology, 2009, , 213-228.	0.1	2
115	Sequences as Biological Information: Cells Obey the Laws of Chemistry and Physics. Computational Biology, 2009, , 3-17.	0.1	0
116	Methods to Compare Genomes The First Examples. Computational Biology, 2009, , 95-109.	0.1	0
117	Genomic Properties: Length, Base Composition and DNA Structures. Computational Biology, 2009, , 111-135.	0.1	0
118	Word Frequencies and Repeats. Computational Biology, 2009, , 137-150.	0.1	3
119	Expression of Genes and Proteins. Computational Biology, 2009, , 167-187.	0.1	0
120	Evolution of Microbial Communities; or, On the Origins of Bacterial Species. Computational Biology, 2009, , 243-256.	0.1	0
121	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. Standards in Genomic Sciences, 2009, 1, 204-215.	1.5	21
122	Studies on Monitoring and Tracking Genetic Resources: An Executive Summary. Standards in Genomic Sciences, 2009, 1, 78-86.	1.5	8
123	Microbial Genome Sequences: A New Era in Microbiology. Computational Biology, 2009, , 37-51.	0.1	1
124	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. Standards in Genomic Sciences, 2009, 1, 204-215.	1.5	18
125	Of Proteins, Genomes, and Proteomes. Computational Biology, 2009, , 189-210.	0.1	0
126	Metagenomics of Microbial Communities. Computational Biology, 2009, , 229-242.	0.1	0

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127	Bioinformatics for Microbiologists: An Introduction. Computational Biology, 2009, , 19-35.	0.1	0
128	An Overview of Genome Databases. Computational Biology, 2009, , 53-67.	0.1	0
129	The Challenges of Programming: A Brief Introduction. Computational Biology, 2009, , 69-91.	0.1	0
130	Transcriptomics: Translated and Untranslated RNA. Computational Biology, 2009, , 153-166.	0.1	0
131	Transcriptomics and adaptive genomics of the asymptomatic bacteriuria Escherichia coli strain 83972. Molecular Genetics and Genomics, 2008, 279, 523-534.	1.0	33
132	The minimum information about a genome sequence (MIGS) specification. Nature Biotechnology, 2008, 26, 541-547.	9.4	1,069
133	Global features of the <i>Alcanivorax borkumensis</i> SK2 genome. Environmental Microbiology, 2008, 10, 614-625.	1.8	28
134	Reliability and applications of statistical methods based on oligonucleotide frequencies in bacterial and archaeal genomes. BMC Genomics, 2008, 9, 104.	1.2	35
135	The genome of the versatile nitrogen fixer Azorhizobium caulinodans ORS571. BMC Genomics, 2008, 9, 271.	1.2	104
136	Molecular analysis of the emergence of pandemic Vibrio parahaemolyticus. BMC Microbiology, 2008, 8, 110.	1.3	114
137	The genome BLASTatlas—a GeneWiz extension for visualization of whole-genome homology. Molecular BioSystems, 2008, 4, 363.	2.9	67
138	Investigations of Oligonucleotide Usage Variance Within and Between Prokaryotes. PLoS Computational Biology, 2008, 4, e1000057.	1.5	53
139	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. OMICS A Journal of Integrative Biology, 2008, 12, 157-160.	1.0	33
140	RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Research, 2007, 35, 3100-3108.	6.5	5,357
141	Characterization of probiotic Escherichia coli isolates with a novel pan-genome microarray. Genome Biology, 2007, 8, R267.	13.9	80
142	The Importance of Virulence Prediction and Gene Networks in Microbial Risk Assessment. Human and Ecological Risk Assessment (HERA), 2007, 13, 254-268.	1.7	3
143	The Complete Genome Sequence and Analysis of the Epsilonproteobacterium Arcobacter butzleri. PLoS ONE, 2007, 2, e1358.	1.1	203
144	Prediction of highly expressed genes in microbes based on chromatin accessibility. , 2007, 8, 11.		14

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145	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
146	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
147	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. <i>BMC Genomics</i> , 2007, 8, 325.	1.2	44
148	Comparative genomic analysis of two-component regulatory proteins in <i>Pseudomonas syringae</i> . <i>BMC Genomics</i> , 2007, 8, 397.	1.2	33
149	An environmental signature for 323 microbial genomes based on codon adaptation indices. <i>Genome Biology</i> , 2006, 7, R114.	13.9	59
150	Leaner and meaner genomes in <i>Escherichia coli</i> . <i>Genome Biology</i> , 2006, 7, 237.	13.9	4
151	The TNF α receptor TNFRSF1A and genes encoding the amiloride-sensitive sodium channel ENaC as modulators in Cystic Fibrosis. <i>Journal of Cystic Fibrosis</i> , 2006, 5, S5.	0.3	0
152	Origin of replication in circular prokaryotic chromosomes. <i>Environmental Microbiology</i> , 2006, 8, 353-361.	1.8	115
153	The genomic code: inferring <i>Vibrionaceae</i> niche specialization. <i>Nature Reviews Microbiology</i> , 2006, 4, 697-704.	13.6	115
154	The TNF α 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
155	Ten years of bacterial genome sequencing: comparative-genomics-based discoveries. <i>Functional and Integrative Genomics</i> , 2006, 6, 165-185.	1.4	156
156	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
157	Genome update: purine strand bias in 280 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2006, 152, 579-583.	0.7	1
158	Systems biology: in the broadest sense of the word. <i>Environmental Microbiology</i> , 2005, 7, 482-483.	1.8	0
159	Genome update: sigma factors in 240 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3147-3150.	0.7	37
160	Genome update: prediction of membrane proteins in prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3447-3452.	0.7	6
161	Genome update: distribution of two-component transduction systems in 250 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3447-3452.	0.7	27
162	Genome update: prediction of secreted proteins in 225 bacterial proteomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 3447-3452.	0.7	20

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163	Genome Update: Protein secretion systems in 225 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1013-1016.	0.7	7
164	Genome Update: 2D clustering of bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 333-336.	0.7	4
165	Genome Update: proteome comparisons. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1-4.	0.7	32
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