

David W Ussery

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.

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	Decoding the epitranscriptional landscape from native RNA sequences. <i>Nucleic Acids Research</i> , 2021 , 49, e7	20.1	68
214	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	2.4	1
213	Mash-based analyses of Escherichia coli genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , 2021 , 4, 117	6.7	20
212	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	6.8	
211	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	7.3	13
210	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
209	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	1.8	4
208	Complete Genome Sequences of Four Isolates of Vancomycin-Resistant Enterococcus faecium with the Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
207	Comparative genomics of hepatitis A virus, hepatitis C virus, and hepatitis E virus provides insights into the evolutionary history of Hepatovirus species. <i>MicrobiologyOpen</i> , 2020 , 9, e973	3.4	1
206	Machine Learning Methods in Drug Discovery. <i>Molecules</i> , 2020 , 25,	4.8	51
205	Two Cases of Vancomycin-Resistant Bacteremia With Development of Daptomycin-Resistant Phenotype and its Detection Using Oxford Nanopore Sequencing. <i>Open Forum Infectious Diseases</i> , 2020 , 7, ofaa180	1	2
204	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> , 2020 , 10,	1.3	5
203	SMARCB1 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	4.8	6
202	Toward unrestricted use of public genomic data. <i>Science</i> , 2019 , 363, 350-352	33.3	25
201	Consent insufficient for data release-Response. <i>Science</i> , 2019 , 364, 446	33.3	4
200	Draft Genome Sequences of 48 Vancomycin-Resistant Enterococcus faecium Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
199	Selection of Amplification Targets for Rapid Polymorphism Screening in Ebola Virus Outbreaks. <i>Frontiers in Microbiology</i> , 2019 , 10, 857	5.7	

198	Complete Genome and Plasmid Sequences of Escherichia coli Type Strain ATCC 11775. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	3
197	Rapid Sequencing of Multiple RNA Viruses in Their Native Form. <i>Frontiers in Microbiology</i> , 2019 , 10, 260	5.7	31
196	Decaffeinated Green Tea Extract Does Not Elicit Hepatotoxic Effects and Modulates the Gut Microbiome in Lean B6C3F ₁ Mice. <i>Nutrients</i> , 2019 , 11,	6.7	7
195	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , 2019 , 75, 103965	4.5	5
194	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	2.8	9
193	Mechanisms linking preterm birth to onset of cardiovascular disease later in adulthood. <i>European Heart Journal</i> , 2019 , 40, 1107-1112	9.5	28
192	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	1	78
191	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	1	78
190	Genome-Based Comparison of Clostridioides difficile: Average Amino Acid Identity Analysis of Core Genomes. <i>Microbial Ecology</i> , 2018 , 76, 801-813	4.4	5
189	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of Saccharomyces cerevisiae CEN.PK113-7D. <i>Nucleic Acids Research</i> , 2018 , 46, e38	20.1	91
188	Case of Microcephaly after Congenital Infection with Asian Lineage Zika Virus, Thailand. <i>Emerging Infectious Diseases</i> , 2018 , 24,	10.2	46
187	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	5.7	37
186	Gender Differences in the Gut Microbiome and How These Affect Cardiovascular Diseases 2018 , 89-100		4
185	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,	1.3	4
184	Conservation of Two-Component Signal Transduction Systems in E. coli, Salmonella, and Across 100,000 Bacteria of Various Bacterial Phyla. <i>Grand Challenges in Biology and Biotechnology</i> , 2018 , 153-174	2.4	
183	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	4.9	23
182	PanViz: interactive visualization of the structure of functionally annotated pangenomes. <i>Bioinformatics</i> , 2017 , 33, 1081-1082	7.2	10
181	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> , 2017 , 10, 14	7.8	23

180	dBBQs: dataBase of Bacterial Quality scores. <i>BMC Bioinformatics</i> , 2017 , 18, 483	3.6	7
179	Insights from Comparative Genomics of the Genus Salmonella 2017 ,		2
178	Three Complete Genome Sequences of Genotype G Mumps Virus from the 2016 Outbreak in Arkansas, USA. <i>Genome Announcements</i> , 2017 , 5,		3
177	Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?. <i>BMC Bioinformatics</i> , 2017 , 18, 471	3.6	16
176	Meeting report: GenBank microbial genomic taxonomy workshop (12-13 May, 2015). <i>Standards in Genomic Sciences</i> , 2016 , 11,		51
175	Diversity of Pseudomonas Genomes, Including Populus-Associated Isolates, as Revealed by Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 375-83	4.8	50
174	The Gene Has Recently Spread between Rolling Circle Plasmids of , Indicative of a Novel Gene Transfer Mechanism. <i>Frontiers in Microbiology</i> , 2016 , 7, 1528	5.7	10
173	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 2516-26	4.8	69
172	Insights from 20 years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , 2015 , 15, 141-61	3.8	391
171	Ebolavirus comparative genomics. <i>FEMS Microbiology Reviews</i> , 2015 , 39, 764-78	15.1	34
170	Microbial taxonomy in the post-genomic era: rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015 , 197, 359-70	3	78
169	Review and phylogenetic analysis of qac genes that reduce susceptibility to quaternary ammonium compounds in Staphylococcus species. <i>European Journal of Microbiology and Immunology</i> , 2015 , 5, 44-61	4.6	90
168	Metabolic functions of Pseudomonas fluorescens strains from Populus deltoides depend on rhizosphere or endosphere isolation compartment. <i>Frontiers in Microbiology</i> , 2015 , 6, 1118	5.7	42
167	Pan-genome analysis of human gastric pathogen H. pylori: 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, 139580	3	35
166	Molecular analysis of asymptomatic bacteriuria Escherichia coli strain VR50 reveals adaptation to the urinary tract by gene acquisition. <i>Infection and Immunity</i> , 2015 , 83, 1749-64	3.7	20
165	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> , 2015 , 161, 1762-1779	2.9	10
164	Benchmarking of methods for genomic taxonomy. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 1529-39	9.7	141
163	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624

162	Quality scores for 32,000 genomes. <i>Standards in Genomic Sciences</i> , 2014 , 9, 20		33
161	Genomic standards consortium projects. <i>Standards in Genomic Sciences</i> , 2014 , 9, 599-601		21
160	Vibrio chromosome-specific families. <i>Frontiers in Microbiology</i> , 2014 , 5, 73	5.7	12
159	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	3.7	24
158	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014 , 9, 599-601		23
157	Sigma factors in a thousand <i>E. coli</i> genomes. <i>Environmental Microbiology</i> , 2013 , 15, 3121-9	5.2	27
156	From essential to persistent genes: a functional approach to constructing synthetic life. <i>Trends in Genetics</i> , 2013 , 29, 273-9	8.5	78
155	Comparative Genomics 2013 , 209-227		1
154	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, 2944-51	4.8	91
153	Veillonella, Firmicutes: Microbes disguised as Gram negatives. <i>Standards in Genomic Sciences</i> , 2013 , 9, 431-48		26
152	CMG-biotools, a free workbench for basic comparative microbial genomics. <i>PLoS ONE</i> , 2013 , 8, e60120	3.7	76
151	Bayesian prediction of microbial oxygen requirement. <i>F1000Research</i> , 2013 , 2, 184	3.6	4
150	Amino acid usage is asymmetrically biased in AT- and GC-rich microbial genomes. <i>PLoS ONE</i> , 2013 , 8, e69878	3.7	20
149	LeuO is a global regulator of gene expression in <i>Salmonella enterica</i> serovar Typhimurium. <i>Molecular Microbiology</i> , 2012 , 85, 1072-89	4.1	52
148	Defining the <i>Pseudomonas</i> genus: where do we draw the line with <i>Azotobacter</i> ?. <i>Microbial Ecology</i> , 2012 , 63, 239-48	4.4	80
147	Comparative genomics of <i>Bifidobacterium</i> , <i>Lactobacillus</i> and related probiotic genera. <i>Microbial Ecology</i> , 2012 , 63, 651-73	4.4	84
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; author reply E3207	11.5	10
145	Relative entropy differences in bacterial chromosomes, plasmids, phages and genomic islands. <i>BMC Genomics</i> , 2012 , 13, 66	4.5	14

144	Genomic variation in Salmonella enterica core genes for epidemiological typing. <i>BMC Genomics</i> , 2012 , 13, 88	4.5	61
143	Computational genomics-proteomics and Phylogeny analysis of twenty one mycobacterial genomes (Tuberculosis & non Tuberculosis strains). <i>Microbial Informatics and Experimentation</i> , 2012 , 2, 7		21
142	Analysis of evolutionary patterns of genes in Campylobacter jejuni and C. coli. <i>Microbial Informatics and Experimentation</i> , 2012 , 2, 8		7
141	Campylobacter fetus subspecies: comparative genomics and prediction of potential virulence targets. <i>Gene</i> , 2012 , 508, 145-56	3.8	27
140	Multilocus sequence typing of total-genome-sequenced bacteria. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 1355-61	9.7	1163
139	Bayesian prediction of bacterial growth temperature range based on genome sequences. <i>BMC Genomics</i> , 2012 , 13 Suppl 7, S3	4.5	14
138	Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse Escherichia coli genomes. <i>BMC Genomics</i> , 2012 , 13, 577	4.5	137
137	The transcriptional landscape and small RNAs of Salmonella enterica serovar Typhimurium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E1277-86	11.5	294
136	Polyclonality of concurrent natural populations of Alteromonas macleodii. <i>Genome Biology and Evolution</i> , 2012 , 4, 1360-74	3.9	39
135	Is the pan-genome also a pan-selectome?. <i>F1000Research</i> , 2012 , 1, 16	3.6	28
134	A domain sequence approach to pangenomics: applications to Escherichia coli. <i>F1000Research</i> , 2012 , 1, 19	3.6	8
133	A domain sequence approach to pangenomics: applications to Escherichia coli. <i>F1000Research</i> , 2012 , 1, 19	3.6	11
132	Two novel methods for using genome sequences to infer taxonomy. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1414	2.9	3
131	Genome Sequence of Campylobacter jejuni strain 327, a strain isolated from a turkey slaughterhouse. <i>Standards in Genomic Sciences</i> , 2011 , 4, 113-22		12
130	A closer look at bacteroides: phylogenetic relationship and genomic implications of a life in the human gut. <i>Microbial Ecology</i> , 2011 , 61, 473-85	4.4	86
129	The Salmonella enterica pan-genome. <i>Microbial Ecology</i> , 2011 , 62, 487-504	4.4	134
128	Natural genetic engineering: intelligence & design in evolution?. <i>Microbial Informatics and Experimentation</i> , 2011 , 1,		78
127	Complete genome sequence of the commensal Enterococcus faecalis 62, isolated from a healthy Norwegian infant. <i>Journal of Bacteriology</i> , 2011 , 193, 2377-8	3.5	36

126	Genome sequences of two stress-tolerant <i>Campylobacter jejuni</i> poultry strains, 305 and DFVF1099. <i>Journal of Bacteriology</i> , 2011 , 193, 5546-7	3.5	11
125	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011 , 9, e1001088	9.7	143
124	Genomic characterization of <i>Campylobacter jejuni</i> strain M1. <i>PLoS ONE</i> , 2010 , 5, e12253	3.7	72
123	Genomic analysis of two-component signal transduction proteins in basidiomycetes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010 , 18, 63-73	0.9	13
122	Standard operating procedure for computing pangenome trees. <i>Standards in Genomic Sciences</i> , 2010 , 2, 135-41		53
121	On the origins of a <i>Vibrio</i> species. <i>Microbial Ecology</i> , 2010 , 59, 1-13	4.4	37
120	Comparison of 61 sequenced <i>Escherichia coli</i> genomes. <i>Microbial Ecology</i> , 2010 , 60, 708-20	4.4	360
119	Comparative genomics of green sulfur bacteria. <i>Photosynthesis Research</i> , 2010 , 104, 137-52	3.7	11
118	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	23
117	Analysis of intra-genomic GC content homogeneity within prokaryotes. <i>BMC Genomics</i> , 2010 , 11, 464	4.5	32
116	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, 478-83	3.3	6
115	Design of an Enterobacteriaceae Pan-Genome Microarray Chip. <i>Communications in Computer and Information Science</i> , 2010 , 165-179	0.3	3
114	Genome update: the 1000th genome--a cautionary tale. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 603-608		48
113	The Genome Atlas Resource. <i>Communications in Computer and Information Science</i> , 2010 , 141-150	0.3	
112	Genome comparison of bacterial pathogens. <i>Genome Dynamics</i> , 2009 , 6, 1-20		9
111	Genomic taxonomy of <i>Vibrios</i> . <i>BMC Evolutionary Biology</i> , 2009 , 9, 258	3	132
110	Stretches of alternating pyrimidine/purines and purines are respectively linked with pathogenicity and growth temperature in prokaryotes. <i>BMC Genomics</i> , 2009 , 10, 346	4.5	5
109	Microbial comparative pan-genomics using binomial mixture models. <i>BMC Genomics</i> , 2009 , 10, 385	4.5	75

108	Analysis of genomic signatures in prokaryotes using multinomial regression and hierarchical clustering. <i>BMC Genomics</i> , 2009 , 10, 487	4.5	13
107	Analysis and prediction of gene splice sites in four <i>Aspergillus</i> genomes. <i>Fungal Genetics and Biology</i> , 2009 , 46 Suppl 1, S14-8	3.9	24
106	Microbial Communities: Core and Pan-Genomics. <i>Computational Biology</i> , 2009 , 213-228	0.7	2
105	Sequences as Biological Information: Cells Obey the Laws of Chemistry and Physics. <i>Computational Biology</i> , 2009 , 3-17	0.7	
104	Methods to Compare Genomes The First Examples. <i>Computational Biology</i> , 2009 , 95-109	0.7	
103	Genomic Properties: Length, Base Composition and DNA Structures. <i>Computational Biology</i> , 2009 , 111-135		
102	Word Frequencies and Repeats. <i>Computational Biology</i> , 2009 , 137-150	0.7	2
101	Expression of Genes and Proteins. <i>Computational Biology</i> , 2009 , 167-187	0.7	
100	Evolution of Microbial Communities; or, On the Origins of Bacterial Species. <i>Computational Biology</i> , 2009 , 243-256	0.7	
99	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. <i>Standards in Genomic Sciences</i> , 2009 , 1, 204-15		20
98	Studies on monitoring and tracking genetic resources: an executive summary. <i>Standards in Genomic Sciences</i> , 2009 , 1, 78-86		6
97	Of Proteins, Genomes, and Proteomes. <i>Computational Biology</i> , 2009 , 189-210	0.7	
96	Metagenomics of Microbial Communities. <i>Computational Biology</i> , 2009 , 229-242	0.7	
95	Bioinformatics for Microbiologists: An Introduction. <i>Computational Biology</i> , 2009 , 19-35	0.7	
94	An Overview of Genome Databases. <i>Computational Biology</i> , 2009 , 53-67	0.7	
93	The Challenges of Programming: A Brief Introduction. <i>Computational Biology</i> , 2009 , 69-91	0.7	
92	Transcriptomics: Translated and Untranslated RNA. <i>Computational Biology</i> , 2009 , 153-166	0.7	
91	GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes. <i>Standards in Genomic Sciences</i> , 2009 , 1, 204-215		14

90	Microbial Genome Sequences: A New Era in Microbiology. <i>Computational Biology</i> , 2009 , 37-51	0.7	1
89	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008 , 26, 541-7	44.5	964
88	Global features of the <i>Alcanivorax borkumensis</i> SK2 genome. <i>Environmental Microbiology</i> , 2008 , 10, 614-25	3.5	25
87	Reliability and applications of statistical methods based on oligonucleotide frequencies in bacterial and archaeal genomes. <i>BMC Genomics</i> , 2008 , 9, 104	4.5	28
86	The genome of the versatile nitrogen fixer <i>Azorhizobium caulinodans</i> ORS571. <i>BMC Genomics</i> , 2008 , 9, 271	4.5	87
85	Molecular analysis of the emergence of pandemic <i>Vibrio parahaemolyticus</i> . <i>BMC Microbiology</i> , 2008 , 8, 110	4.5	99
84	The genome BLASTatlas-a GeneWiz extension for visualization of whole-genome homology. <i>Molecular BioSystems</i> , 2008 , 4, 363-71		60
83	Investigations of oligonucleotide usage variance within and between prokaryotes. <i>PLoS Computational Biology</i> , 2008 , 4, e1000057	5	46
82	Toward a standards-compliant genomic and metagenomic publication record. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 157-60	3.8	31
81	Transcriptomics and adaptive genomics of the asymptomatic bacteriuria <i>Escherichia coli</i> strain 83972. <i>Molecular Genetics and Genomics</i> , 2008 , 279, 523-34	3.1	27
80	The Importance of Virulence Prediction and Gene Networks in Microbial Risk Assessment. <i>Human and Ecological Risk Assessment (HERA)</i> , 2007 , 13, 254-268	4.9	2
79	The complete genome sequence and analysis of the epsilonproteobacterium <i>Arcobacter butzleri</i> . <i>PLoS ONE</i> , 2007 , 2, e1358	3.7	155
78	Prediction of highly expressed genes in microbes based on chromatin accessibility. <i>BMC Molecular Biology</i> , 2007 , 8, 11	4.5	11
77	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007 , 25, 221-31	44.5	889
76	Identification of putative noncoding RNA genes in the <i>Burkholderia cenocepacia</i> J2315 genome. <i>FEMS Microbiology Letters</i> , 2007 , 276, 83-92	2.9	33
75	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. <i>BMC Genomics</i> , 2007 , 8, 325	4.5	38
74	Comparative genomic analysis of two-component regulatory proteins in <i>Pseudomonas syringae</i> . <i>BMC Genomics</i> , 2007 , 8, 397	4.5	27
73	RNAmmer: consistent and rapid annotation of ribosomal RNA genes. <i>Nucleic Acids Research</i> , 2007 , 35, 3100-8	20.1	3946

72	Characterization of probiotic Escherichia coli isolates with a novel pan-genome microarray. <i>Genome Biology</i> , 2007 , 8, R267	18.3	71
71	Design of a seven-genome Escherichia coli microarray for comparative genomic profiling. <i>Journal of Bacteriology</i> , 2006 , 188, 7713-21	3.5	22
70	Genome update: purine strand bias in 280 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 579-583	2.9	1
69	An environmental signature for 323 microbial genomes based on codon adaptation indices. <i>Genome Biology</i> , 2006 , 7, R114	18.3	43
68	Leaner and meaner genomes in Escherichia coli. <i>Genome Biology</i> , 2006 , 7, 237	18.3	2
67	Origin of replication in circular prokaryotic chromosomes. <i>Environmental Microbiology</i> , 2006 , 8, 353-61	5.2	93
66	The genomic code: inferring Vibrionaceae niche specialization. <i>Nature Reviews Microbiology</i> , 2006 , 4, 697-704	22.2	87
65	The TNFalpha receptor TNFRSF1A and genes encoding the amiloride-sensitive sodium channel ENaC as modulators in cystic fibrosis. <i>Human Genetics</i> , 2006 , 119, 331-43	6.3	40
64	Ten years of bacterial genome sequencing: comparative-genomics-based discoveries. <i>Functional and Integrative Genomics</i> , 2006 , 6, 165-85	3.8	120
63	Extracytoplasmic function sigma factors in Pseudomonas syringae. <i>Trends in Microbiology</i> , 2005 , 13, 565-82	2.4	21
62	DNA Bendability and Nucleosome Positioning in Transcriptional Regulation 2005 , 189-202		1
61	Crystal ball. Systems biology: in the broadest sense of the word. <i>Environmental Microbiology</i> , 2005 , 7, 482-3	5.2	
60	Genome update: sigma factors in 240 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 3147-3150	2.9	29
59	Genome update: prediction of membrane proteins in prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 2119-2121	2.9	6
58	Genome update: distribution of two-component transduction systems in 250 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 3447-3452	2.9	26
57	Genome update: prediction of secreted proteins in 225 bacterial proteomes. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 1725-1727	2.9	19
56	Genome Update: Protein secretion systems in 225 bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 1013-1016	2.9	6
55	Genome update: 2D clustering of bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 333-336	2.9	3

54	Genome Update: proteome comparisons. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 1-4	2.9	30
53	Genome update: base skews in 200+ bacterial chromosomes. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 633-637	2.9	1
52	Genome Update: AT content in sequenced prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 749-752	2.9	15
51	Genome update: DNA repeats in bacterial genomes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 3519-3521	2.9	24
50	Genome update: tRNAs in sequenced microbial genomes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 1603-1605	2.9	1
49	Genome update: correlation of bacterial genomic properties. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 3899-903	2.9	3
48	Genome update: 161 prokaryotic genomes sequenced, and counting. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 261-263	2.9	6
47	Genome update: chromosome atlases. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 3091-3	2.9	9
46	Genome update: alignment of bacterial chromosomes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 2491-2493	2.9	3
45	Genome update: rRNAs in sequenced microbial genomes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 1113-1115	2.9	4
44	CBS Genome Atlas Database: a dynamic storage for bioinformatic results and sequence data. <i>Bioinformatics</i> , 2004 , 20, 3682-6	7.2	71
43	Genome update: Length distributions of sequenced prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 513-516	2.9	9
42	Genome update: promoter profiles. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 2791-2793	2.9	6
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