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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.

52 papers	20,731 citations	34 h-index	58 g-index
58 ext. papers	26,110 ext. citations	16 avg, IF	5.87 L-index

#	Paper	IF	Citations
52	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020 , 48, D606-D612	20.1	206
51	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1094-1102	13.4	43
50	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018 , 36, 566-569	44.5	419
49	The essential genome of the crenarchaeal model <i>Sulfolobus islandicus</i> . <i>Nature Communications</i> , 2018 , 9, 4908	17.4	44
48	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017 , 45, D535-D542	20.1	809
47	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , 2016 , 7, 118	5.7	65
46	RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <i>Scientific Reports</i> , 2015 , 5, 8365	4.9	1061
45	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , 2015 , 10, e0126883	3.7	27
44	The repABC Plasmids with Quorum-Regulated Transfer Systems in Members of the Rhizobiales Divide into Two Structurally and Separately Evolving Groups. <i>Genome Biology and Evolution</i> , 2015 , 7, 3337-57	3.9	16
43	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). <i>Nucleic Acids Research</i> , 2014 , 42, D206-14	20.1	2534
42	Quorum-dependent mannopine-inducible conjugative transfer of an <i>Agrobacterium</i> opine-catabolic plasmid. <i>Journal of Bacteriology</i> , 2014 , 196, 1031-44	3.5	12
41	In search of genome annotation consistency: solid gene clusters and how to use them. <i>3 Biotech</i> , 2014 , 4, 331-335	2.8	5
40	Genomes of the class Erysipelotrichia clarify the firmicute origin of the class Mollicutes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013 , 63, 2727-2741	2.2	31
39	SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. <i>PLoS ONE</i> , 2012 , 7, e48053	3.7	121
38	Differences between the normal vaginal bacterial community of baboons and that of humans. <i>American Journal of Primatology</i> , 2011 , 73, 119-26	2.5	22
37	Characterizing the native codon usages of a genome: an axis projection approach. <i>Molecular Biology and Evolution</i> , 2011 , 28, 211-21	8.3	22
36	Similarity of genes horizontally acquired by <i>Escherichia coli</i> and <i>Salmonella enterica</i> is evidence of a supraspecies pangenome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20154-9	11.5	31

35	Modal codon usage: assessing the typical codon usage of a genome. <i>Molecular Biology and Evolution</i> , 2010 , 27, 800-10	8.3	34
34	Heterogeneity of vaginal microbial communities within individuals. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 1181-9	9.7	115
33	Messenger RNA processing in <i>Methanocaldococcus</i> (<i>Methanococcus</i>) <i>jannaschii</i> . <i>Rna</i> , 2009 , 15, 1909-16	5.8	11
32	Protein-coding gene promoters in <i>Methanocaldococcus</i> (<i>Methanococcus</i>) <i>jannaschii</i> . <i>Nucleic Acids Research</i> , 2009 , 37, 3588-601	20.1	13
31	The RAST Server: rapid annotations using subsystems technology. <i>BMC Genomics</i> , 2008 , 9, 75	4.5	7153
30	A whole-genome approach to identifying protein binding sites: promoters in <i>Methanocaldococcus</i> (<i>Methanococcus</i>) <i>jannaschii</i> . <i>Nucleic Acids Research</i> , 2008 , 36, 6948-58	20.1	4
29	Critical evaluation of two primers commonly used for amplification of bacterial 16S rRNA genes. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 2461-70	4.8	937
28	Genomic minimalism in the early diverging intestinal parasite <i>Giardia lamblia</i> . <i>Science</i> , 2007 , 317, 1921-6	33.3	613
27	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. <i>Nucleic Acids Research</i> , 2007 , 35, D347-53	20.1	77
26	Evolution of eukaryotic transcription: insights from the genome of <i>Giardia lamblia</i> . <i>Genome Research</i> , 2004 , 14, 1537-47	9.7	78
25	Shotgun proteomics of <i>Methanococcus jannaschii</i> and insights into methanogenesis. <i>Journal of Proteome Research</i> , 2004 , 3, 538-48	5.6	57
24	Archaeal RecA homologues: different response to DNA-damaging agents in mesophilic and thermophilic Archaea. <i>Extremophiles</i> , 2001 , 5, 265-75	3	19
23	Structural modifications of <i>Methanococcus jannaschii</i> flagellin proteins revealed by proteome analysis. <i>Proteomics</i> , 2001 , 1, 1033-42	4.8	17
22	Similar subunit architecture of archaeal and eukaryal RNA polymerases. <i>FEMS Microbiology Letters</i> , 2001 , 195, 85-90	2.9	12
21	Aminoacyl-tRNA synthetases, the genetic code, and the evolutionary process. <i>Microbiology and Molecular Biology Reviews</i> , 2000 , 64, 202-36	13.2	515
20	Archaeal and bacterial hyperthermophiles: horizontal gene exchange or common ancestry?. <i>Trends in Genetics</i> , 1999 , 15, 298-9	8.5	52
19	The complete genome of the hyperthermophilic bacterium <i>Aquifex aeolicus</i> . <i>Nature</i> , 1998 , 392, 353-8	50.4	988
18	Archaeal genomics: an overview. <i>Cell</i> , 1997 , 89, 991-4	56.2	213

17	A reconstruction of the metabolism of <i>Methanococcus jannaschii</i> from sequence data. <i>Gene</i> , 1997 , 197, GC11-26	3.8	87
16	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , 1997 , 390, 364-70	50.4	1257
15	Lessons from an Archaeal genome: what are we learning from <i>Methanococcus jannaschii</i> ?. <i>Trends in Genetics</i> , 1996 , 12, 377-9	8.5	47
14	Response : <i>Methanococcus</i> Genome. <i>Science</i> , 1996 , 274, 902-903	33.3	
13	Response : <i>Methanococcus</i> Genome. <i>Science</i> , 1996 , 274, 902-903	33.3	
12	fastDNAmL: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. <i>Bioinformatics</i> , 1994 , 10, 41-8	7.2	313
11	The Ribosomal Database Project. <i>Nucleic Acids Research</i> , 1994 , 22, 3485-7	20.1	614
10	The ribosomal database project. <i>Nucleic Acids Research</i> , 1993 , 21, 3021-3	20.1	510
9	Ribosomal RNA: a key to phylogeny. <i>FASEB Journal</i> , 1993 , 7, 113-23	0.9	508
8	A brief note concerning archaebacterial phylogeny. <i>Canadian Journal of Microbiology</i> , 1989 , 35, 119-23	3.2	20
7	Phylogenetic analysis using ribosomal RNA. <i>Methods in Enzymology</i> , 1988 , 164, 793-812	1.7	110
6	Are arguments against archaebacteria valid?. <i>Nature</i> , 1986 , 320, 401-402	50.4	13
5	The Analysis of Natural Microbial Populations by Ribosomal RNA Sequences. <i>Advances in Microbial Ecology</i> , 1986 , 1-55		511
4	Nucleotide sequence of the <i>Dictyostelium discoideum</i> small-subunit ribosomal ribonucleic acid inferred from the gene sequence: evolutionary implications. <i>Biochemistry</i> , 1983 , 22, 5858-5868	3.2	183
3	Secondary structure of the <i>Dictyostelium discoideum</i> small subunit ribosomal RNA. <i>Nucleic Acids Research</i> , 1983 , 11, 8037-49	20.1	40
2	Nucleotide sequence of <i>Dictyostelium discoideum</i> 5.8S ribosomal ribonucleic acid: evolutionary and secondary structural implications. <i>Biochemistry</i> , 1982 , 21, 2335-43	3.2	40
1	Enzymatic and chemical structure mapping of mouse 28S ribosomal ribonucleic acid contacts in 5.8S ribosomal ribonucleic acid. <i>Biochemistry</i> , 1982 , 21, 2320-9	3.2	38