

List of Publications by Citations

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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.

30 papers	6,861 citations	20 h-index	32 g-index
32 ext. papers	10,141 ext. citations	10.3 avg, IF	5.06 L-index

#	Paper	IF	Citations
30	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D206-14	20.1	2534
29	RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <i>Scientific Reports</i> , <b>2015</b> , 5, 8365	4.9	1061
28	PATRIC, the bacterial bioinformatics database and analysis resource. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D581-91	20.1	823
27	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D535-D542	20.1	809
26	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 566-569	44.5	419
25	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D606-D612	20.1	206
24	Rickettsia phylogenomics: unwinding the intricacies of obligate intracellular life. <i>PLoS ONE</i> , <b>2008</b> , 3, e20187	3.7	137
23	Antimicrobial Resistance Prediction in PATRIC and RAST. <i>Scientific Reports</i> , <b>2016</b> , 6, 27930	4.9	120
22	A Rickettsia genome overrun by mobile genetic elements provides insight into the acquisition of genes characteristic of an obligate intracellular lifestyle. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 376-94	3.5	115
21	Analysis of ten Brucella genomes reveals evidence for horizontal gene transfer despite a preferred intracellular lifestyle. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 3569-79	3.5	86
20	Developing an in silico minimum inhibitory concentration panel test for Klebsiella pneumoniae. <i>Scientific Reports</i> , <b>2018</b> , 8, 421	4.9	83
19	Comparative phylogenomics and evolution of the Brucellae reveal a path to virulence. <i>Journal of Bacteriology</i> , <b>2014</b> , 196, 920-30	3.5	73
18	Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area. <i>MBio</i> , <b>2020</b> , 11,	7.8	69
17	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 118	5.7	65
16	Predicting tumor cell line response to drug pairs with deep learning. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 486	3.6	51
15	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1094-1102	13.4	43
14	Curation, integration and visualization of bacterial virulence factors in PATRIC. <i>Bioinformatics</i> , <b>2015</b> , 31, 252-8	7.2	37

13	Comparative genomics of early-diverging Brucella strains reveals a novel lipopolysaccharide biosynthesis pathway. <i>MBio</i> , <b>2012</b> , 3, e00246-11	7.8	23
12	Comparative genomics of early-diverging Brucella strains reveals a novel lipopolysaccharide biosynthesis pathway. <i>MBio</i> , <b>2012</b> , 3, e00246-12	7.8	23
11	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , <b>2020</b> , 7, 170	8.2	20
10	Ensemble transfer learning for the prediction of anti-cancer drug response. <i>Scientific Reports</i> , <b>2020</b> , 10, 18040	4.9	15
9	Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area <b>2020</b> ,		11
8	Predicting antimicrobial resistance using conserved genes. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008319	10	
7	Defining the risk of SARS-CoV-2 variants on immune protection.. <i>Nature</i> , <b>2022</b> ,	50.4	7
6	Converting tabular data into images for deep learning with convolutional neural networks. <i>Scientific Reports</i> , <b>2021</b> , 11, 11325	4.9	6
5	Predicting Antimicrobial Resistance Using Conserved Genes		4
4	Enhanced Co-Expression Extrapolation (COXEN) Gene Selection Method for Building Anti-Cancer Drug Response Prediction Models. <i>Genes</i> , <b>2020</b> , 11,	4.2	4
3	Enabling comparative modeling of closely related genomes: example genus Brucella. <i>3 Biotech</i> , <b>2015</b> , 5, 101-105	2.8	3
2	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	2
1	Informatics-Driven Infectious Disease Research. <i>Communications in Computer and Information Science</i> , <b>2013</b> , 3-11	0.3	