

James J Davis

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.

26
papers

3,338
citations

17
h-index

27
g-index

27
ext. papers

5,458
ext. citations

9.6
avg, IF

4.69
L-index

#	Paper	IF	Citations
26	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
25	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017 , 45, D535-D542	20.1	809
24	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018 , 36, 566-569	44.5	419
23	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020 , 48, D606-D612	20.1	206
22	Antimicrobial Resistance Prediction in PATRIC and RAST. <i>Scientific Reports</i> , 2016 , 6, 27930	4.9	120
21	Using Machine Learning To Predict Antimicrobial MICs and Associated Genomic Features for Nontyphoidal. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	116
20	Developing an in silico minimum inhibitory concentration panel test for <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2018 , 8, 421	4.9	83
19	Population Genomic Analysis of 1,777 Extended-Spectrum Beta-Lactamase-Producing Isolates, Houston, Texas: Unexpected Abundance of Clonal Group 307. <i>MBio</i> , 2017 , 8,	7.8	79
18	Whole-Genome Sequencing of Human Clinical Isolates Reveals Misidentification and Misunderstandings of , , and. <i>MSphere</i> , 2017 , 2,	5	78
17	Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area. <i>MBio</i> , 2020 , 11,	7.8	69
16	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , 2016 , 7, 118	5.7	65
15	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1094-1102	13.4	43
14	Whole-Genome Sequencing of a Human Clinical Isolate of the Novel Species sp. nov. <i>Genome Announcements</i> , 2017 , 5,		32
13	Multiple spillovers from humans and onward transmission of SARS-CoV-2 in white-tailed deer.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	26
12	Sequence Analysis of 20,453 Severe Acute Respiratory Syndrome Coronavirus 2 Genomes From the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern. <i>American Journal of Pathology</i> , 2021 , 191, 983-992	5.8	26
11	Signals of significantly increased vaccine breakthrough, decreased hospitalization rates, and less severe disease in patients with COVID-19 caused by the Omicron variant of SARS-CoV-2 in Houston, Texas.. <i>American Journal of Pathology</i> , 2022 ,	5.8	24
10	Delta Variants of SARS-CoV-2 Cause Significantly Increased Vaccine Breakthrough COVID-19 Cases in Houston, Texas. <i>American Journal of Pathology</i> , 2021 ,	5.8	20

9	Trajectory of Growth of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Variants in Houston, Texas, January through May 2021, Based on 12,476 Genome Sequences. <i>American Journal of Pathology</i> , 2021 , 191, 1754-1773	5.8	17
8	Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area 2020 ,		11
7	Predicting antimicrobial resistance using conserved genes. <i>PLoS Computational Biology</i> , 2020 , 16, e1008319	3.19	10
6	A Genome-Based Model to Predict the Virulence of <i>Pseudomonas aeruginosa</i> Isolates. <i>MBio</i> , 2020 , 11,	7.8	7
5	Using machine learning to predict antimicrobial minimum inhibitory concentrations and associated genomic features for nontyphoidal <i>Salmonella</i>		5
4	Predicting antimicrobial susceptibility from the bacterial genome: A new paradigm for one health resistance monitoring. <i>Journal of Veterinary Pharmacology and Therapeutics</i> , 2021 , 44, 223-237	1.4	5
3	Predicting Antimicrobial Resistance Using Conserved Genes		4
2	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
1	PlasmidHostFinder: Prediction of Plasmid Hosts Using Random Forest.. <i>MSystems</i> , 2022 , e0118021	7.6	1