

# James J Davis

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7389206/publications.pdf>

Version: 2024-02-01

23  
papers

6,762  
citations

430754

18  
h-index

642610

23  
g-index

27  
all docs

27  
docs citations

27  
times ranked

8929  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.6	2,080
2	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017, 45, D535-D542.	6.5	1,445
3	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	9.4	955
4	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020, 48, D606-D612.	6.5	552
5	Using Machine Learning To Predict Antimicrobial MICs and Associated Genomic Features for Nontyphoidal <i>Salmonella</i> . <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	181
6	Antimicrobial Resistance Prediction in PATRIC and RAST. <i>Scientific Reports</i> , 2016, 6, 27930.	1.6	179
7	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, .	3.3	164
8	Signals of Significantly Increased Vaccine Breakthrough, Decreased Hospitalization Rates, and Less Severe Disease in Patients with Coronavirus Disease 2019 Caused by the Omicron Variant of Severe Acute Respiratory Syndrome Coronavirus 2 in Houston, Texas. <i>American Journal of Pathology</i> , 2022, 192, 642-652.	1.9	161
9	PATTyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , 2016, 7, 118.	1.5	153
10	Whole-Genome Sequencing of Human Clinical <i>Klebsiella pneumoniae</i> Isolates Reveals Misidentification and Misunderstandings of <i>Klebsiella pneumoniae</i> , <i>Klebsiella variicola</i> , and <i>Klebsiella quasipneumoniae</i> . <i>MSphere</i> , 2017, 2, .	1.3	139
11	Developing an in silico minimum inhibitory concentration panel test for <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2018, 8, 421.	1.6	136
12	Population Genomic Analysis of 1,777 Extended-Spectrum Beta-Lactamase-Producing <i>Klebsiella pneumoniae</i> Isolates, Houston, Texas: Unexpected Abundance of Clonal Group 307. <i>MBio</i> , 2017, 8, .	1.8	124
13	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, .	1.8	99
14	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , 2019, 20, 1094-1102.	3.2	93
15	Delta Variants of SARS-CoV-2 Cause Significantly Increased Vaccine Breakthrough COVID-19 Cases in Houston, Texas. <i>American Journal of Pathology</i> , 2022, 192, 320-331.	1.9	90
16	Whole-Genome Sequencing of a Human Clinical Isolate of the Novel Species <i>Klebsiella quasivariicola</i> sp. nov. <i>Genome Announcements</i> , 2017, 5, .	0.8	46
17	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.	1.9	42
18	Predicting antimicrobial resistance using conserved genes. <i>PLoS Computational Biology</i> , 2020, 16, e1008319.	1.5	29

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19	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.	1.9	26
20	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	15
21	A Genome-Based Model to Predict the Virulence of <i>Pseudomonas aeruginosa</i> Isolates. <i>MBio</i> , 2020, 11, .	1.8	12
22	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.	0.6	11
23	PlasmidHostFinder: Prediction of Plasmid Hosts Using Random Forest. <i>MSystems</i> , 2022, 7, e0118021.	1.7	8