

# J Rodney Brister

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3472783/publications.pdf>

Version: 2024-02-01

26  
papers

9,896  
citations

304743

22  
h-index

580821

25  
g-index

28  
all docs

28  
docs citations

28  
times ranked

17979  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. <i>Nucleic Acids Research</i> , 2016, 44, D733-D745.	14.5	4,739
2	Database resources of the national center for biotechnology information. <i>Nucleic Acids Research</i> , 2022, 50, D20-D26.	14.5	887
3	Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 161-168.	28.6	590
4	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , 2019, 37, 632-639.	17.5	569
5	NCBI Viral Genomes Resource. <i>Nucleic Acids Research</i> , 2015, 43, D571-D577.	14.5	541
6	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2019, 47, D23-D28.	14.5	502
7	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
8	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2020, 48, D9-D16.	14.5	381
9	Virus Variation Resource “improved response to emergent viral outbreaks. <i>Nucleic Acids Research</i> , 2017, 45, D482-D490.	14.5	342
10	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	2.1	172
11	The Sequence Read Archive: a decade more of explosive growth. <i>Nucleic Acids Research</i> , 2022, 50, D387-D390.	14.5	128
12	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	5.6	89
13	Nomenclature- and Database-Compatible Names for the Two Ebola Virus Variants that Emerged in Guinea and the Democratic Republic of the Congo in 2014. <i>Viruses</i> , 2014, 6, 4760-4799.	3.3	83
14	HIV-1, human interaction database: current status and new features. <i>Nucleic Acids Research</i> , 2015, 43, D566-D570.	14.5	79
15	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	2.1	57
16	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.	3.3	49
17	VADR: validation and annotation of virus sequence submissions to GenBank. <i>BMC Bioinformatics</i> , 2020, 21, 211.	2.6	46
18	STAT: a fast, scalable, MinHash-based k-mer tool to assess Sequence Read Archive next-generation sequence submissions. <i>Genome Biology</i> , 2021, 22, 270.	8.8	45

#	ARTICLE	IF	CITATIONS
19	Virus Variation Resource“recent updates and future directions. <i>Nucleic Acids Research</i> , 2014, 42, D660-D665.	14.5	43
20	Bacteriophage Taxonomy: An Evolving Discipline. <i>Methods in Molecular Biology</i> , 2018, 1693, 57-71.	0.9	34
21	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.	5.4	31
22	The Phylogeny and Pathogenesis of Sacbrood Virus (SBV) Infection in European Honey Bees, <i>Apis mellifera</i> . <i>Viruses</i> , 2019, 11, 61.	3.3	28
23	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , 2021, 166, 3239-3244.	2.1	24
24	Microbial virus genome annotation“Mustering the troops to fight the sequence onslaught. <i>Virology</i> , 2012, 434, 175-180.	2.4	12
25	Strengthening the Interaction of the Virology Community with the International Committee on Taxonomy of Viruses (ICTV) by Linking Virus Names and Their Abbreviations to Virus Species. <i>Systematic Biology</i> , 2019, 68, 828-839.	5.6	11
26	Quantifying the immunological distinctiveness of emerging SARS-CoV-2 variants in the context of prior regional herd exposure. , 0, , .		0