

# 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  | The Sequence Read Archive: a decade more of explosive growth. <i>Nucleic Acids Research</i> , 2022, 50, D387-D390.   | 14.5 | 128       |
| 2  | Database resources of the national center for biotechnology information. <i>Nucleic Acids Research</i> , 2022, 50, D20-D26.  | 14.5 | 887       |
| 3  | 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        |
| 4  | 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        |
| 5  | Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.   | 5.4  | 31        |
| 6  | 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        |
| 7  | Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2020, 48, D9-D16.   | 14.5 | 381       |
| 8  | VADR: validation and annotation of virus sequence submissions to GenBank. <i>BMC Bioinformatics</i> , 2020, 21, 211.   | 2.6  | 46        |
| 9  | Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , 2019, 37, 632-639.   | 17.5 | 569       |
| 10 | 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        |
| 11 | Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.  | 17.5 | 414       |
| 12 | 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        |
| 13 | Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2019, 47, D23-D28.  | 14.5 | 502       |
| 14 | 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       |
| 15 | Bacteriophage Taxonomy: An Evolving Discipline. <i>Methods in Molecular Biology</i> , 2018, 1693, 57-71.   | 0.9  | 34        |
| 16 | Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 161-168.   | 28.6 | 590       |
| 17 | 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        |
| 18 | Virus Variation Resource “improved response to emergent viral outbreaks. <i>Nucleic Acids Research</i> , 2017, 45, D482-D490.  | 14.5 | 342       |

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|----|--|------|-----------|
| 19 | 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     |
| 20 | HIV-1, human interaction database: current status and new features. <i>Nucleic Acids Research</i> , 2015, 43, D566-D570.   | 14.5 | 79        |
| 21 | NCBI Viral Genomes Resource. <i>Nucleic Acids Research</i> , 2015, 43, D571-D577.  | 14.5 | 541       |
| 22 | Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.   | 3.3  | 49        |
| 23 | 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        |
| 24 | Virus Variation Resource—recent updates and future directions. <i>Nucleic Acids Research</i> , 2014, 42, D660-D665.  | 14.5 | 43        |
| 25 | Microbial virus genome annotation—Mustering the troops to fight the sequence onslaught. <i>Virology</i> , 2012, 434, 175-180.  | 2.4  | 12        |
| 26 | Quantifying the immunological distinctiveness of emerging SARS-CoV-2 variants in the context of prior regional herd exposure. , 0, , .   |      | 0         |