

# David A Rasmussen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2134981/publications.pdf>

Version: 2024-02-01

27  
papers

3,627  
citations

471371

17  
h-index

552653

26  
g-index

37  
all docs

37  
docs citations

37  
times ranked

6482  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Porcine reproductive and respiratory syndrome virus dissemination across pig production systems in the United States. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 667-683.        | 1.3 | 31        |
| 2  | Phylogeographic Approaches to Characterize the Emergence of Plant Pathogens. <i>Phytopathology</i> , 2021, 111, 68-77.   | 1.1 | 8         |
| 3  | Inferring environmental transmission using phylodynamics: a case-study using simulated evolution of an enteric pathogen. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210041. | 1.5 | 2         |
| 4  | HIV-1 molecular diversity in Brazil unveiled by 10 years of sampling by the national genotyping network. <i>Scientific Reports</i> , 2021, 11, 15842.  | 1.6 | 9         |
| 5  | Decomposing the sources of SARS-CoV-2 fitness variation in the United States. <i>Virus Evolution</i> , 2021, 7, veab073.   | 2.2 | 14        |
| 6  | A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.  | 6.0 | 144       |
| 7  | Evolutionary dynamics of Tomato spotted wilt virus within and between alternate plant hosts and thrips. <i>Scientific Reports</i> , 2020, 10, 15797.   | 1.6 | 4         |
| 8  | Aphid Transmission of Potyvirus: The Largest Plant-Infecting RNA Virus Genus. <i>Viruses</i> , 2020, 12, 773.  | 1.5 | 75        |
| 9  | Entry of bunyaviruses into plants and vectors. <i>Advances in Virus Research</i> , 2019, 104, 65-96.   | 0.9 | 23        |
| 10 | Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816.  | 3.5 | 39        |
| 11 | BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.   | 1.5 | 2,484     |
| 12 | Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. <i>ELife</i> , 2019, 8, .   | 2.8 | 18        |
| 13 | Tracking external introductions of HIV using phylodynamics reveals a major source of infections in rural KwaZulu-Natal, South Africa. <i>Virus Evolution</i> , 2018, 4, vey037.              | 2.2 | 22        |
| 14 | MASCOT: parameter and state inference under the marginal structured coalescent approximation. <i>Bioinformatics</i> , 2018, 34, 3843-3848.   | 1.8 | 78        |
| 15 | Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.                             | 3.5 | 53        |
| 16 | The Structured Coalescent and Its Approximations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2970-2981.  | 3.5 | 98        |
| 17 | A51 Dengue virus multi-strain models as hypotheses for serotype interaction. <i>Virus Evolution</i> , 2017, 3, .   | 2.2 | 0         |
| 18 | Phylodynamics on local sexual contact networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005448.  | 1.5 | 16        |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 19 | Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. <i>Infection, Genetics and Evolution</i> , 2016, 46, 200-208.                        | 1.0  | 23        |
| 20 | The effects of a deleterious mutation load on patterns of influenza A/H3N2's antigenic evolution in humans. <i>ELife</i> , 2015, 4, e07361.                                    | 2.8  | 65        |
| 21 | Phylogenetic Inference for Structured Epidemiological Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003570.  | 1.5  | 94        |
| 22 | Prediction is worth a shot. <i>Nature</i> , 2014, 507, 47-48.  | 13.7 | 6         |
| 23 | Reconciling Phylogenetics with Epidemiology: The Case of Dengue Virus in Southern Vietnam. <i>Molecular Biology and Evolution</i> , 2014, 31, 258-271.                         | 3.5  | 42        |
| 24 | Insights into the Early Epidemic Spread of Ebola in Sierra Leone Provided by Viral Sequence Data. <i>PLOS Currents</i> , 2014, 6, .  | 1.4  | 71        |
| 25 | Rates of coalescence for common epidemiological models at equilibrium. <i>Journal of the Royal Society Interface</i> , 2012, 9, 997-1007.                                      | 1.5  | 35        |
| 26 | Inference for Nonlinear Epidemiological Models Using Genealogies and Time Series. <i>PLoS Computational Biology</i> , 2011, 7, e1002136.                                       | 1.5  | 107       |
| 27 | What can you do with 0.1x genome coverage? A case study based on a genome survey of the scuttle fly <i>Megaselia scalaris</i> (Phoridae). <i>BMC Genomics</i> , 2009, 10, 382. | 1.2  | 53        |