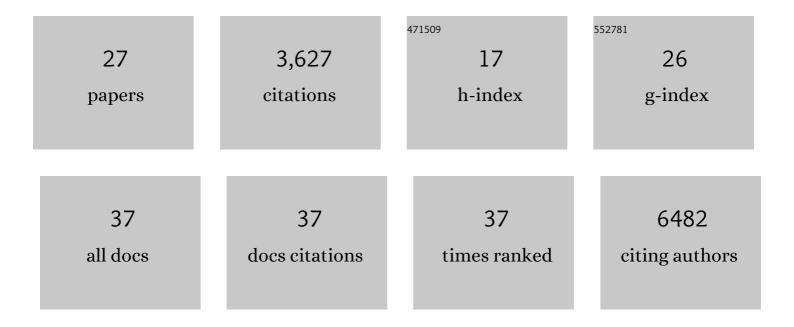
David A Rasmussen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2134981/publications.pdf Version: 2024-02-01



DAVID A RASMUSSEN

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Porcine reproductive and respiratory syndrome virus dissemination across pig production systems in the United States. Transboundary and Emerging Diseases, 2021, 68, 667-683. | 3.0 | 31 |
| 2 | Phylogeographic Approaches to Characterize the Emergence of Plant Pathogens. Phytopathology, 2021, 111, 68-77. | 2.2 | 8 |
| 3 | Inferring environmental transmission using phylodynamics: a case-study using simulated evolution of an enteric pathogen. Journal of the Royal Society Interface, 2021, 18, 20210041. | 3.4 | 2 |
| 4 | HIV-1 molecular diversity in Brazil unveiled by 10Âyears of sampling by the national genotyping network. Scientific Reports, 2021, 11, 15842. | 3.3 | 9 |
| 5 | Decomposing the sources of SARS-CoV-2 fitness variation in the United States. Virus Evolution, 2021, 7, veab073. | 4.9 | 14 |
| 6 | A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431. | 12.6 | 144 |
| 7 | Evolutionary dynamics of Tomato spotted wilt virus within and between alternate plant hosts and thrips. Scientific Reports, 2020, 10, 15797. | 3.3 | 4 |
| 8 | Aphid Transmission of Potyvirus: The Largest Plant-Infecting RNA Virus Genus. Viruses, 2020, 12, 773. | 3.3 | 75 |
| 9 | Entry of bunyaviruses into plants and vectors. Advances in Virus Research, 2019, 104, 65-96. | 2.1 | 23 |
| 10 | Estimating Epidemic Incidence and Prevalence from Genomic Data. Molecular Biology and Evolution, 2019, 36, 1804-1816. | 8.9 | 39 |
| 11 | BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. PLoS Computational Biology, 2019, 15, e1006650. | 3.2 | 2,484 |
| 12 | Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. ELife, 2019, 8, . | 6.0 | 18 |
| 13 | Tracking external introductions of HIV using phylodynamics reveals a major source of infections in rural KwaZulu-Natal, South Africa. Virus Evolution, 2018, 4, vey037. | 4.9 | 22 |
| 14 | MASCOT: parameter and state inference under the marginal structured coalescent approximation. Bioinformatics, 2018, 34, 3843-3848. | 4.1 | 78 |
| 15 | Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203. | 8.9 | 53 |
| 16 | The Structured Coalescent and Its Approximations. Molecular Biology and Evolution, 2017, 34, 2970-2981. | 8.9 | 98 |
| 17 | A51 Dengue virus multi-strain models as hypotheses for serotype interaction. Virus Evolution, 2017, 3, . | 4.9 | 0 |
| 18 | Phylodynamics on local sexual contact networks. PLoS Computational Biology, 2017, 13, e1005448. | 3.2 | 16 |

DAVID A RASMUSSEN

| # | Article | IF | CITATION |
|----|--|------|----------|
| 19 | Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. Infection, Genetics and Evolution, 2016, 46, 200-208. | 2.3 | 23 |
| 20 | The effects of a deleterious mutation load on patterns of influenza A/H3N2's antigenic evolution in humans. ELife, 2015, 4, e07361. | 6.0 | 65 |
| 21 | Phylodynamic Inference for Structured Epidemiological Models. PLoS Computational Biology, 2014, 10, e1003570. | 3.2 | 94 |
| 22 | Prediction is worth a shot. Nature, 2014, 507, 47-48. | 27.8 | 6 |
| 23 | Reconciling Phylodynamics with Epidemiology: The Case of Dengue Virus in Southern Vietnam. Molecular Biology and Evolution, 2014, 31, 258-271. | 8.9 | 42 |
| 24 | Insights into the Early Epidemic Spread of Ebola in Sierra Leone Provided by Viral Sequence Data. PLOS Currents, 2014, 6, . | 1.4 | 71 |
| 25 | Rates of coalescence for common epidemiological models at equilibrium. Journal of the Royal Society Interface, 2012, 9, 997-1007. | 3.4 | 35 |
| 26 | Inference for Nonlinear Epidemiological Models Using Genealogies and Time Series. PLoS Computational Biology, 2011, 7, e1002136. | 3.2 | 107 |
| 27 | What can you do with 0.1× genome coverage? A case study based on a genome survey of the scuttle fly Megaselia scalaris (Phoridae). BMC Genomics, 2009, 10, 382. | 2.8 | 53 |