

# 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

471509

17  
h-index

552781

26  
g-index

37  
all docs

37  
docs citations

37  
times ranked

6482  
citing authors

#	ARTICLE	IF	CITATIONS
1	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	3.2	2,484
2	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
3	Inference for Nonlinear Epidemiological Models Using Genealogies and Time Series. <i>PLoS Computational Biology</i> , 2011, 7, e1002136.	3.2	107
4	The Structured Coalescent and Its Approximations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2970-2981.	8.9	98
5	Phylodynamic Inference for Structured Epidemiological Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003570.	3.2	94
6	MASCOT: parameter and state inference under the marginal structured coalescent approximation. <i>Bioinformatics</i> , 2018, 34, 3843-3848.	4.1	78
7	Aphid Transmission of Potyvirus: The Largest Plant-Infecting RNA Virus Genus. <i>Viruses</i> , 2020, 12, 773.	3.3	75
8	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
9	The effects of a deleterious mutation load on patterns of influenza A/H3N2's antigenic evolution in humans. <i>ELife</i> , 2015, 4, e07361.	6.0	65
10	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.	2.8	53
11	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	8.9	53
12	Reconciling Phylodynamics with Epidemiology: The Case of Dengue Virus in Southern Vietnam. <i>Molecular Biology and Evolution</i> , 2014, 31, 258-271.	8.9	42
13	Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816.	8.9	39
14	Rates of coalescence for common epidemiological models at equilibrium. <i>Journal of the Royal Society Interface</i> , 2012, 9, 997-1007.	3.4	35
15	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.	3.0	31
16	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.	2.3	23
17	Entry of bunyaviruses into plants and vectors. <i>Advances in Virus Research</i> , 2019, 104, 65-96.	2.1	23
18	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.	4.9	22

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19	Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. <i>ELife</i> , 2019, 8, .	6.0	18
20	Phylodynamics on local sexual contact networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005448.	3.2	16
21	Decomposing the sources of SARS-CoV-2 fitness variation in the United States. <i>Virus Evolution</i> , 2021, 7, veab073.	4.9	14
22	HIV-1 molecular diversity in Brazil unveiled by 10 years of sampling by the national genotyping network. <i>Scientific Reports</i> , 2021, 11, 15842.	3.3	9
23	Phylogeographic Approaches to Characterize the Emergence of Plant Pathogens. <i>Phytopathology</i> , 2021, 111, 68-77.	2.2	8
24	Prediction is worth a shot. <i>Nature</i> , 2014, 507, 47-48.	27.8	6
25	Evolutionary dynamics of Tomato spotted wilt virus within and between alternate plant hosts and thrips. <i>Scientific Reports</i> , 2020, 10, 15797.	3.3	4
26	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.	3.4	2
27	A51 Dengue virus multi-strain models as hypotheses for serotype interaction. <i>Virus Evolution</i> , 2017, 3, .	4.9	0