David A Rasmussen

List of Publications by Year
in descending order

27 papers	3,627 citations	471061 17 h-index	552369 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. PLoS Computational Biology, 2019, 15, e1006650.	1.5	2,484
2	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	6.0	144
3	Inference for Nonlinear Epidemiological Models Using Genealogies and Time Series. PLoS Computational Biology, 2011, 7, e1002136.	1.5	107
4	The Structured Coalescent and Its Approximations. Molecular Biology and Evolution, 2017, 34, 2970-2981.	3.5	98
5	Phylodynamic Inference for Structured Epidemiological Models. PLoS Computational Biology, 2014, 10, e1003570.	1.5	94
6	MASCOT: parameter and state inference under the marginal structured coalescent approximation. Bioinformatics, 2018, 34, 3843-3848.	1.8	78
7	Aphid Transmission of Potyvirus: The Largest Plant-Infecting RNA Virus Genus. Viruses, 2020, 12, 773.	1.5	75
8	Insights into the Early Epidemic Spread of Ebola in Sierra Leone Provided by Viral Sequence Data. PLOS Currents, 2014, 6, .	1.4	71
9	The effects of a deleterious mutation load on patterns of influenza A/H3N2's antigenic evolution in humans. ELife, 2015, 4, e07361.	2.8	65
10	What can you do with 0.1Ã— genome coverage? A case study based on a genome survey of the scuttle fly Megaselia scalaris (Phoridae). BMC Genomics, 2009, 10, 382.	1.2	53
11	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203.	3.5	53
12	Reconciling Phylodynamics with Epidemiology: The Case of Dengue Virus in Southern Vietnam. Molecular Biology and Evolution, 2014, 31, 258-271.	3.5	42
13	Estimating Epidemic Incidence and Prevalence from Genomic Data. Molecular Biology and Evolution, 2019, 36, 1804-1816.	3.5	39
14	Rates of coalescence for common epidemiological models at equilibrium. Journal of the Royal Society Interface, 2012, 9, 997-1007.	1.5	35
15	Porcine reproductive and respiratory syndrome virus dissemination across pig production systems in the United States. Transboundary and Emerging Diseases, 2021, 68, 667-683.	1.3	31
16	Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. Infection, Genetics and Evolution, 2016, 46, 200-208.	1.0	23
17	Entry of bunyaviruses into plants and vectors. Advances in Virus Research, 2019, 104, 65-96.	0.9	23
18	Tracking external introductions of HIV using phylodynamics reveals a major source of infections in rural KwaZulu-Natal, South Africa. Virus Evolution, 2018, 4, vey037.	2.2	22

#	Article	IF	Citations
19	Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. ELife, 2019, 8, .	2.8	18
20	Phylodynamics on local sexual contact networks. PLoS Computational Biology, 2017, 13, e1005448.	1.5	16
21	Decomposing the sources of SARS-CoV-2 fitness variation in the United States. Virus Evolution, 2021, 7, veab073.	2.2	14
22	HIV-1 molecular diversity in Brazil unveiled by 10 years of sampling by the national genotyping network. Scientific Reports, 2021, 11, 15842.	1.6	9
23	Phylogeographic Approaches to Characterize the Emergence of Plant Pathogens. Phytopathology, 2021, 111, 68-77.	1.1	8
24	Prediction is worth a shot. Nature, 2014, 507, 47-48.	13.7	6
25	Evolutionary dynamics of Tomato spotted wilt virus within and between alternate plant hosts and thrips. Scientific Reports, 2020, 10, 15797.	1.6	4
26	Inferring environmental transmission using phylodynamics: a case-study using simulated evolution of an enteric pathogen. Journal of the Royal Society Interface, 2021, 18, 20210041.	1.5	2
27	A51 Dengue virus multi-strain models as hypotheses for serotype interaction. Virus Evolution, 2017, 3, .	2.2	0