

David A Rasmussen

List of Publications by Year in descending order

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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	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
2	Phylogeographic Approaches to Characterize the Emergence of Plant Pathogens. <i>Phytopathology</i> , 2021, 111, 68-77.	2.2	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.	3.4	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.	3.3	9
5	Decomposing the sources of SARS-CoV-2 fitness variation in the United States. <i>Virus Evolution</i> , 2021, 7, veab073.	4.9	14
6	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
7	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
8	Aphid Transmission of Potyvirus: The Largest Plant-Infecting RNA Virus Genus. <i>Viruses</i> , 2020, 12, 773.	3.3	75
9	Entry of bunyaviruses into plants and vectors. <i>Advances in Virus Research</i> , 2019, 104, 65-96.	2.1	23
10	Estimating Epidemic Incidence and Prevalence from Genomic Data. <i>Molecular Biology and Evolution</i> , 2019, 36, 1804-1816.	8.9	39
11	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	3.2	2,484
12	Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. <i>ELife</i> , 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. <i>Virus Evolution</i> , 2018, 4, vey037.	4.9	22
14	MASCOT: parameter and state inference under the marginal structured coalescent approximation. <i>Bioinformatics</i> , 2018, 34, 3843-3848.	4.1	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.	8.9	53
16	The Structured Coalescent and Its Approximations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2970-2981.	8.9	98
17	A51 Dengue virus multi-strain models as hypotheses for serotype interaction. <i>Virus Evolution</i> , 2017, 3, .	4.9	0
18	Phylodynamics on local sexual contact networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005448.	3.2	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.	2.3	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.	6.0	65
21	Phylogenetic Inference for Structured Epidemiological Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003570.	3.2	94
22	Prediction is worth a shot. <i>Nature</i> , 2014, 507, 47-48.	27.8	6
23	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
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.	3.4	35
26	Inference for Nonlinear Epidemiological Models Using Genealogies and Time Series. <i>PLoS Computational Biology</i> , 2011, 7, e1002136.	3.2	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.	2.8	53