

Erik M Volz

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

15,694
citations

66343

42
h-index

51608

86
g-index

108
all docs

108
docs citations

108
times ranked

23089
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimates of the severity of coronavirus disease 2019: a model-based analysis. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 669-677.	9.1	3,036
2	Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. <i>Nature</i> , 2020, 584, 257-261.	27.8	2,558
3	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
4	Comparative analysis of the risks of hospitalisation and death associated with SARS-CoV-2 omicron (B.1.1.529) and delta (B.1.617.2) variants in England: a cohort study. <i>Lancet</i> , The, 2022, 399, 1303-1312.	13.7	889
5	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
6	Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 35-42.	9.1	612
7	Reduction in mobility and COVID-19 transmission. <i>Nature Communications</i> , 2021, 12, 1090.	12.8	394
8	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
9	Viral Phylodynamics. <i>PLoS Computational Biology</i> , 2013, 9, e1002947.	3.2	340
10	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
11	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	10.0	269
12	SIR dynamics in random networks with heterogeneous connectivity. <i>Journal of Mathematical Biology</i> , 2008, 56, 293-310.	1.9	259
13	Susceptible–infected–recovered epidemics in dynamic contact networks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 2925-2934.	2.6	220
14	Edge-based compartmental modelling for infectious disease spread. <i>Journal of the Royal Society Interface</i> , 2012, 9, 890-906.	3.4	205
15	Phylodynamics of Infectious Disease Epidemics. <i>Genetics</i> , 2009, 183, 1421-1430.	2.9	200
16	Comparison of molecular testing strategies for COVID-19 control: a mathematical modelling study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1381-1389.	9.1	171
17	Epidemic thresholds in dynamic contact networks. <i>Journal of the Royal Society Interface</i> , 2009, 6, 233-241.	3.4	168
18	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142

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19	Effects of Heterogeneous and Clustered Contact Patterns on Infectious Disease Dynamics. PLoS Computational Biology, 2011, 7, e1002042.	3.2	139
20	Complex Population Dynamics and the Coalescent Under Neutrality. Genetics, 2012, 190, 187-201.	2.9	131
21	Viral phylodynamics and the search for an "effective number of infections"™. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1879-1890.	4.0	123
22	Disease transmission in territorial populations: the small-world network of Serengeti lions. Journal of the Royal Society Interface, 2011, 8, 776-786.	3.4	121
23	Non-pharmaceutical interventions, vaccination, and the SARS-CoV-2 delta variant in England: a mathematical modelling study. Lancet, The, 2021, 398, 1825-1835.	13.7	119
24	Scalable relaxed clock phylogenetic dating. Virus Evolution, 2017, 3, .	4.9	116
25	Changing composition of SARS-CoV-2 lineages and rise of Delta variant in England. EClinicalMedicine, 2021, 39, 101064.	7.1	116
26	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	12.6	111
27	HIV-1 Transmission during Early Infection in Men Who Have Sex with Men: A Phylodynamic Analysis. PLoS Medicine, 2013, 10, e1001568.	8.4	106
28	A Discrete-Choice Approach to Modeling Social Influence on Individual Decision Making. Environment and Planning B: Planning and Design, 2008, 35, 1055-1069.	1.7	101
29	Phylodynamic Inference for Structured Epidemiological Models. PLoS Computational Biology, 2014, 10, e1003570.	3.2	94
30	Simple Epidemiological Dynamics Explain Phylogenetic Clustering of HIV from Patients with Recent Infection. PLoS Computational Biology, 2012, 8, e1002552.	3.2	89
31	Incorporating Disease and Population Structure into Models of SIR Disease in Contact Networks. PLoS ONE, 2013, 8, e69162.	2.5	81
32	Distinguishing epidemic waves from disease spillover in a wildlife population. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 1777-1785.	2.6	80
33	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	27.8	80
34	Modeling the Growth and Decline of Pathogen Effective Population Size Provides Insight into Epidemic Dynamics and Drivers of Antimicrobial Resistance. Systematic Biology, 2018, 67, 719-728.	5.6	78
35	Random networks with tunable degree distribution and clustering. Physical Review E, 2004, 70, 056115.	2.1	69
36	Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City region. Genome Research, 2020, 30, 1781-1788.	5.5	66

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37	Inferring the Source of Transmission with Phylogenetic Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003397.	3.2	65
38	Bayesian phylodynamic inference with complex models. <i>PLoS Computational Biology</i> , 2018, 14, e1006546.	3.2	64
39	Modelling tree shape and structure in viral phylodynamics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120208.	4.0	61
40	Using Respondent-Driven Sampling in a Hidden Population at Risk of HIV Infection: Who Do HIV-Positive Recruiters Recruit?. <i>Sexually Transmitted Diseases</i> , 2009, 36, 750-756.	1.7	55
41	Sampling through time and phylodynamic inference with coalescent and birth-death models. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140945.	3.4	53
42	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
43	Topology and Dependency Tests in Spatial and Network Autoregressive Models. <i>Geographical Analysis</i> , 2009, 41, 158-180.	3.5	51
44	An early warning system for emerging SARS-CoV-2 variants. <i>Nature Medicine</i> , 2022, 28, 1110-1115.	30.7	47
45	SARS-CoV-2 genomes from Saudi Arabia implicate nucleocapsid mutations in host response and increased viral load. <i>Nature Communications</i> , 2022, 13, 601.	12.8	40
46	Phylodynamic Analysis of Ebola Virus in the 2014 Sierra Leone Epidemic. <i>PLOS Currents</i> , 2014, 6, .	1.4	39
47	Weight matrices for social influence analysis: An investigation of measurement errors and their effect on model identification and estimation quality. <i>Social Networks</i> , 2008, 30, 309-317.	2.1	38
48	Comparison of cluster-based and source-attribution methods for estimating transmission risk using large HIV sequence databases. <i>Epidemics</i> , 2018, 23, 1-10.	3.0	37
49	Phylodynamic Inference across Epidemic Scales. <i>Molecular Biology and Evolution</i> , 2017, 34, 1276-1288.	8.9	36
50	Applications of predictive modelling early in the COVID-19 epidemic. <i>The Lancet Digital Health</i> , 2020, 2, e498-e499.	12.3	34
51	Molecular Epidemiology of HIV-1 Subtype B Reveals Heterogeneous Transmission Risk: Implications for Intervention and Control. <i>Journal of Infectious Diseases</i> , 2018, 217, 1522-1529.	4.0	32
52	Design and methods of a social network isolation study for reducing respiratory infection transmission: The eX-FLU cluster randomized trial. <i>Epidemics</i> , 2016, 15, 38-55.	3.0	31
53	Estimating the contribution of key populations towards the spread of HIV in Dakar, Senegal. <i>Journal of the International AIDS Society</i> , 2018, 21, e25126.	3.0	30
54	Model hierarchies in edge-based compartmental modeling for infectious disease spread. <i>Journal of Mathematical Biology</i> , 2013, 67, 869-899.	1.9	29

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55	Additive Uncorrelated Relaxed Clock Models for the Dating of Genomic Epidemiology Phylogenies. <i>Molecular Biology and Evolution</i> , 2021, 38, 307-317.	8.9	28
56	HIV-1 Transmission Clustering and Phylodynamics Highlight the Important Role of Young Men Who Have Sex with Men. <i>AIDS Research and Human Retroviruses</i> , 2018, 34, 879-888.	1.1	27
57	Epidemiological bridging by injection drug use drives an early HIV epidemic. <i>Epidemics</i> , 2010, 2, 155-164.	3.0	26
58	Identification of Hidden Population Structure in Time-Scaled Phylogenies. <i>Systematic Biology</i> , 2020, 69, 884-896.	5.6	26
59	Episodic HIV Risk Behavior Can Greatly Amplify HIV Prevalence and the Fraction of Transmissions from Acute HIV Infection. <i>Statistical Communications in Infectious Diseases</i> , 2012, 4, .	0.2	24
60	Phylogenetic analysis to inform prevention efforts in mixed HIV epidemics. <i>Virus Evolution</i> , 2017, 3, vex014.	4.9	24
61	Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions. <i>Nature Communications</i> , 2021, 12, 2188.	12.8	23
62	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. <i>Virus Evolution</i> , 2020, 6, veaa082.	4.9	21
63	Share2Quit: Web-Based Peer-Driven Referrals for Smoking Cessation. <i>JMIR Research Protocols</i> , 2013, 2, e37.	1.0	19
64	Genomic epidemiology of a densely sampled COVID-19 outbreak in China. <i>Virus Evolution</i> , 2021, 7, veaa102.	4.9	18
65	Heterogeneity in Number and Type of Sexual Contacts in a Gay Urban Cohort. <i>Statistical Communications in Infectious Diseases</i> , 2012, 4, .	0.2	15
66	Share2Quit: Online Social Network Peer Marketing of Tobacco Cessation Systems. <i>Nicotine and Tobacco Research</i> , 2016, 19, ntw187.	2.6	15
67	Acute-Stage Transmission of HIV. <i>Epidemiology</i> , 2013, 24, 516-521.	2.7	13
68	Detectable signals of episodic risk effects on acute HIV transmission: Strategies for analyzing transmission systems using genetic data. <i>Epidemics</i> , 2013, 5, 44-55.	3.0	12
69	Database of epidemic trends and control measures during the first wave of COVID-19 in mainland China. <i>International Journal of Infectious Diseases</i> , 2021, 102, 463-471.	3.3	12
70	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
71	Susceptible-infected-recovered epidemics in populations with heterogeneous contact rates. <i>European Physical Journal B</i> , 2008, 63, 381-386.	1.5	8
72	HIV-1 Transmission Patterns in Men Who Have Sex with Men: Insights from Genetic Source Attribution Analysis. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 805-813.	1.1	8

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73	Web-based peer-driven chain referrals for smoking cessation. <i>Studies in Health Technology and Informatics</i> , 2013, 192, 357-61.	0.3	8
74	Bayesian Inference of Clonal Expansions in a Dated Phylogeny. <i>Systematic Biology</i> , 2022, 71, 1073-1087.	5.6	8
75	Molecular Evolution of Human Norovirus GII.2 Clusters. <i>Frontiers in Microbiology</i> , 2021, 12, 655567.	3.5	7
76	HIV-1 Transmission linkages among persons with incident infection to inform public health surveillance. <i>EClinicalMedicine</i> , 2021, 37, 100968.	7.1	6
77	Determining the Origins of Human Immunodeficiency Virus Type 1 Drug-resistant Minority Variants in People Who Are Recently Infected Using Phylogenetic Reconstruction. <i>Clinical Infectious Diseases</i> , 2018, 69, 1136-1143.	5.8	5
78	Genetic clustering analysis for HIV infection among MSM in Nigeria: implications for intervention. <i>Aids</i> , 2020, 34, 227-236.	2.2	5
79	SARS-CoV-2 infection prevalence on repatriation flights from Wuhan City, China. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	5
80	Human Immunodeficiency Virus (HIV) Genetic Diversity Informs Stage of HIV-1 Infection Among Patients Receiving Antiretroviral Therapy in Botswana. <i>Journal of Infectious Diseases</i> , 2022, 225, 1330-1338.	4.0	5
81	Estimating the number of undetected COVID-19 cases among travellers from mainland China. <i>Wellcome Open Research</i> , 2020, 5, 143.	1.8	5
82	Topology, Dependency Tests and Estimation Bias in Network Autoregressive Models. <i>Advances in Spatial Science</i> , 2010, , 29-57.	0.6	4
83	Phylogenetic analysis of HIV-1 subtypes B, C and CRF 02_AG in Senegal. <i>Epidemics</i> , 2020, 30, 100376.	3.0	3
84	Host or pathogen-related factors in COVID-19 severity? " Authors' reply. <i>Lancet, The</i> , 2020, 396, 1397.	13.7	3
85	Continuation of emtricitabine/lamivudine within combination antiretroviral therapy following detection of the M184V/I HIV resistance mutation. <i>HIV Medicine</i> , 2020, 21, 309-321.	2.2	3
86	Diagnosis delays in the UK according to pre or postmigration acquisition of HIV. <i>Aids</i> , 2022, 36, 415-422.	2.2	3
87	Evaluating whole HIV-1 genome sequence for estimation of incidence and migration in a rural South African community. <i>Wellcome Open Research</i> , 0, 7, 174.	1.8	0