Erik M Volz

List of Publications by Year
in descending order

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	Human Immunodeficiency Virus (HIV) Genetic Diversity Informs Stage of HIV-1 Infection Among Patients Receiving Antiretroviral Therapy in Botswana. Journal of Infectious Diseases, 2022, 225, 1330-1338.	4.0	5
2	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. Lancet Infectious Diseases, The, 2022, 22, 35-42.	9.1	612
3	Diagnosis delays in the UK according to pre or postmigration acquisition of HIV. Aids, 2022, 36, 415-422.	2.2	3
4	SARS-CoV-2 genomes from Saudi Arabia implicate nucleocapsid mutations in host response and increased viral load. Nature Communications, 2022, 13, 601.	12.8	40
5	Bayesian Inference of Clonal Expansions in a Dated Phylogeny. Systematic Biology, 2022, 71, 1073-1087.	5.6	8
6	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. Nature Communications, 2022, 13, 1012.	12.8	10
7	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. Lancet, The, 2022, 399, 1303-1312.	13.7	889
8	An early warning system for emerging SARS-CoV-2 variants. Nature Medicine, 2022, 28, 1110-1115.	30.7	47
9	Additive Uncorrelated Relaxed Clock Models for the Dating of Genomic Epidemiology Phylogenies. Molecular Biology and Evolution, 2021, 38, 307-317.	8.9	28
10	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 2021, 184, 64-75.e11.	28.9	843
11	Database of epidemic trends and control measures during the first wave of COVID-19 in mainland China. International Journal of Infectious Diseases, 2021, 102, 463-471.	3.3	12
12	Genomic epidemiology of a densely sampled COVID-19 outbreak in China. Virus Evolution, 2021, 7, veaa102.	4.9	18
13	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. Science, 2021, 371, 708-712.	12.6	335
14	Reduction in mobility and COVID-19 transmission. Nature Communications, 2021, 12, 1090.	12.8	394
15	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. Nature, 2021, 593, 266-269.	27.8	1,001
16	Molecular Evolution of Human Norovirus GII.2 Clusters. Frontiers in Microbiology, 2021, 12, 655567.	3.5	7
17	Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions. Nature Communications, 2021, 12, 2188.	12.8	23
18	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. Lancet Public Health, The, 2021, 6, e335-e345.	10.0	269

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19	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	6.4	375
20	HIV-1 Transmission linkages among persons with incident infection to inform public health surveillance. EClinicalMedicine, 2021, 37, 100968.	7.1	6
21	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. Science, 2021, 373, 889-895.	12.6	142
22	Changing composition of SARS-CoV-2 lineages and rise of Delta variant in England. EClinicalMedicine, 2021, 39, 101064.	7.1	116
23	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	27.8	80
24	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
25	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	12.6	111
26	Genetic clustering analysis for HIV infection among MSM in Nigeria: implications for intervention. Aids, 2020, 34, 227-236.	2.2	5
27	Phylodynamic analysis of HIV-1 subtypes B, C and CRF 02_AG in Senegal. Epidemics, 2020, 30, 100376.	3.0	3
28	Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City region. Genome Research, 2020, 30, 1781-1788.	5.5	66
29	Applications of predictive modelling early in the COVID-19 epidemic. The Lancet Digital Health, 2020, 2, e498-e499.	12.3	34
30	SARS-CoV-2 infection prevalence on repatriation flights from Wuhan City, China. Journal of Travel Medicine, 2020, 27, .	3.0	5
31	Comparison of molecular testing strategies for COVID-19 control: a mathematical modelling study. Lancet Infectious Diseases, The, 2020, 20, 1381-1389.	9.1	171
32	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. Virus Evolution, 2020, 6, veaa082.	4.9	21
33	Host or pathogen-related factors in COVID-19 severity? â€“ Authors' reply. Lancet, The, 2020, 396, 1397.	13.7	3
34	Identification of Hidden Population Structure in Time-Scaled Phylogenies. Systematic Biology, 2020, 69, 884-896.	5.6	26
35	Continuation of emtricitabine/lamivudine within combination antiretroviral therapy following detection of the M184V/I HIVâ€1 resistance mutation. HIV Medicine, 2020, 21, 309-321.	2.2	3
36	Estimates of the severity of coronavirus disease 2019: a model-based analysis. Lancet Infectious Diseases, The, 2020, 20, 669-677.	9.1	3,036

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37	Estimating the number of undetected COVID-19 cases among travellers from mainland China. Wellcome Open Research, 2020, 5, 143.	1.8	5
38	Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. Nature, 2020, 584, 257-261.	27.8	2,558
39	HIV-1 Transmission Patterns in Men Who Have Sex with Men: Insights from Genetic Source Attribution Analysis. AIDS Research and Human Retroviruses, 2019, 35, 805-813.	1.1	8
40	Molecular Epidemiology of HIV-1 Subtype B Reveals Heterogeneous Transmission Risk: Implications for Intervention and Control. Journal of Infectious Diseases, 2018, 217, 1522-1529.	4.0	32
41	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
42	Comparison of cluster-based and source-attribution methods for estimating transmission risk using large HIV sequence databases. Epidemics, 2018, 23, 1-10.	3.0	37
43	Bayesian phylodynamic inference with complex models. PLoS Computational Biology, 2018, 14, e1006546.	3.2	64
44	Determining the Origins of Human Immunodeficiency Virus Type 1 Drug-resistant Minority Variants in People Who Are Recently Infected Using Phylogenetic Reconstruction. Clinical Infectious Diseases, 2018, 69, 1136-1143.	5.8	5
45	Estimating the contribution of key populations towards the spread of <scp>HIV</scp> in Dakar, Senegal. Journal of the International AIDS Society, 2018, 21, e25126.	3.0	30
46	HIV-1 Transmission Clustering and Phylodynamics Highlight the Important Role of Young Men Who Have Sex with Men. AIDS Research and Human Retroviruses, 2018, 34, 879-888.	1.1	27
47	Phylodynamic Inference across Epidemic Scales. Molecular Biology and Evolution, 2017, 34, 1276-1288.	8.9	36
48	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
49	Phylodynamic analysis to inform prevention efforts in mixed HIV epidemics. Virus Evolution, 2017, 3, vex014.	4.9	24
50	Scalable relaxed clock phylogenetic dating. Virus Evolution, 2017, 3, .	4.9	116
51	Share2Quit: Online Social Network Peer Marketing of Tobacco Cessation Systems. Nicotine and Tobacco Research, 2016, 19, ntw187.	2.6	15
52	Design and methods of a social network isolation study for reducing respiratory infection transmission: The eX-FLU cluster randomized trial. Epidemics, 2016, 15, 38-55.	3.0	31
53	Phylodynamic Inference for Structured Epidemiological Models. PLoS Computational Biology, 2014, 10, e1003570.	3.2	94
54	Sampling through time and phylodynamic inference with coalescent and birth–death models. Journal of the Royal Society Interface, 2014, 11, 20140945.	3.4	53

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55	Phylodynamic Analysis of Ebola Virus in the 2014 Sierra Leone Epidemic. PLOS Currents, 2014, 6, .	1.4	39
56	Model hierarchies in edge-based compartmental modeling for infectious disease spread. Journal of Mathematical Biology, 2013, 67, 869-899.	1.9	29
57	Detectable signals of episodic risk effects on acute HIV transmission: Strategies for analyzing transmission systems using genetic data. Epidemics, 2013, 5, 44-55.	3.0	12
58	Inferring the Source of Transmission with Phylogenetic Data. PLoS Computational Biology, 2013, 9, e1003397.	3.2	65
59	HIV-1 Transmission during Early Infection in Men Who Have Sex with Men: A Phylodynamic Analysis. PLoS Medicine, 2013, 10, e1001568.	8.4	106
60	Viral Phylodynamics. PLoS Computational Biology, 2013, 9, e1002947.	3.2	340
61	Modelling tree shape and structure in viral phylodynamics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120208.	4.0	61
62	Acute-Stage Transmission of HIV. Epidemiology, 2013, 24, 516-521.	2.7	13
63	Incorporating Disease and Population Structure into Models of SIR Disease in Contact Networks. PLoS ONE, 2013, 8, e69162.	2.5	81
64	Share2Quit: Web-Based Peer-Driven Referrals for Smoking Cessation. JMIR Research Protocols, 2013, 2, e37.	1.0	19
65	Web-based peer-driven chain referrals for smoking cessation. Studies in Health Technology and Informatics, 2013, 192, 357-61.	0.3	8
66	Simple Epidemiological Dynamics Explain Phylogenetic Clustering of HIV from Patients with Recent Infection. PLoS Computational Biology, 2012, 8, e1002552.	3.2	89
67	Edge-based compartmental modelling for infectious disease spread. Journal of the Royal Society Interface, 2012, 9, 890-906.	3.4	205
68	Complex Population Dynamics and the Coalescent Under Neutrality. Genetics, 2012, 190, 187-201.	2.9	131
69	Episodic HIV Risk Behavior Can Greatly Amplify HIV Prevalence and the Fraction of Transmissions from Acute HIV Infection. Statistical Communications in Infectious Diseases, 2012, 4, .	0.2	24
70	Heterogeneity in Number and Type of Sexual Contacts in a Gay Urban Cohort. Statistical Communications in Infectious Diseases, 2012, 4, .	0.2	15
71	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
72	Effects of Heterogeneous and Clustered Contact Patterns on Infectious Disease Dynamics. PLoS Computational Biology, 2011, 7, e1002042.	3.2	139

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73	Viral phylodynamics and the search for an â€˜effective number of infectionsâ€™. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 1879-1890.	4.0	123
74	Epidemiological bridging by injection drug use drives an early HIV epidemic. Epidemics, 2010, 2, 155-164.	3.0	26
75	Topology, Dependency Tests and Estimation Bias in Network Autoregressive Models. Advances in Spatial Science, 2010, , 29-57.	0.6	4
76	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
77	Phylodynamics of Infectious Disease Epidemics. Genetics, 2009, 183, 1421-1430.	2.9	200
78	Topology and Dependency Tests in Spatial and Network Autoregressive Models. Geographical Analysis, 2009, 41, 158-180.	3.5	51
79	Epidemic thresholds in dynamic contact networks. Journal of the Royal Society Interface, 2009, 6, 233-241.	3.4	168
80	Using Respondent-Driven Sampling in a Hidden Population at Risk of HIV Infection: Who Do HIV-Positive Recruiters Recruit?. Sexually Transmitted Diseases, 2009, 36, 750-756.	1.7	55
81	SIR dynamics in random networks with heterogeneous connectivity. Journal of Mathematical Biology, 2008, 56, 293-310.	1.9	259
82	Weight matrices for social influence analysis: An investigation of measurement errors and their effect on model identification and estimation quality. Social Networks, 2008, 30, 309-317.	2.1	38
83	Susceptible-infected-recovered epidemics in populations with heterogeneous contact rates. European Physical Journal B, 2008, 63, 381-386.	1.5	8
84	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
85	Susceptibleâ€"infectedâ€"recovered epidemics in dynamic contact networks. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 2925-2934.	2.6	220
86	Random networks with tunable degree distribution and clustering. Physical Review E, 2004, 70, 056115.	2.1	69
87	Evaluating whole HIV-1 genome sequence for estimation of incidence and migration in a rural South African community. Wellcome Open Research, 0, 7, 174.	1.8	0