

Denise Khnert

List of Publications by Citations

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48
papers

6,370
citations

23
h-index

58
g-index

58
ext. papers

8,997
ext. citations

10.4
avg, IF

5.59
L-index

#	Paper	IF	Citations
48	BEAST 2: a software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2014 , 10, e1003537	5	3659
47	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019 , 15, e1006650	5	1014
46	Birth-death skyline plot reveals temporal changes of epidemic spread in HIV and hepatitis C virus (HCV). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 228-33 ^{11.5}	11.5	295
45	The contrasting phylodynamics of human influenza B viruses. <i>ELife</i> , 2015 , 4, e05055	8.9	129
44	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. <i>Nature Microbiology</i> , 2016 , 2, 16245	26.6	81
43	A58 Epidemic dynamics of ancient disease outbreaks. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
42	Efficient Bayesian inference under the structured coalescent. <i>Bioinformatics</i> , 2014 , 30, 2272-9	7.2	78
41	Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth-death SIR model. <i>Journal of the Royal Society Interface</i> , 2014 , 11, 20131106	4.1	78
40	Analysis of 3800-year-old <i>Yersinia pestis</i> genomes suggests Bronze Age origin for bubonic plague. <i>Nature Communications</i> , 2018 , 9, 2234	17.4	72
39	Phylodynamics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2102-16	8.3	71
38	Influenza A virus migration and persistence in North American wild birds. <i>PLoS Pathogens</i> , 2013 , 9, e1003580	7.0	69
37	The relationship between transmission time and clustering methods in <i>Mycobacterium tuberculosis</i> epidemiology. <i>EBioMedicine</i> , 2018 , 37, 410-416	8.8	61
36	Neolithic and medieval virus genomes reveal complex evolution of hepatitis B. <i>ELife</i> , 2018 , 7,	8.9	59
35	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021 , 22, 642-663	13.4	56
34	Insights into the early epidemic spread of ebola in sierra leone provided by viral sequence data. <i>PLOS Currents</i> , 2014 , 6,		53
33	Phylogenetic and epidemic modeling of rapidly evolving infectious diseases. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 1825-41	4.5	51
32	Phylodynamics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015 , 89, 8871-9	6.6	45

31	Taming the BEAST-A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018 , 67, 170-174	8.4	43
30	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017 , 34, 185-203	8.3	41
29	Emergence of human-adapted <i>Salmonella enterica</i> is linked to the Neolithization process. <i>Nature Ecology and Evolution</i> , 2020 , 4, 324-333	12.3	36
28	In-host evolution of <i>Staphylococcus epidermidis</i> in a pacemaker-associated endocarditis resulting in increased antibiotic tolerance. <i>Nature Communications</i> , 2019 , 10, 1149	17.4	33
27	Spatiotemporal dynamics of Puumala hantavirus associated with its rodent host, <i>Myodes glareolus</i> . <i>Evolutionary Applications</i> , 2015 , 8, 545-59	4.8	33
26	Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. <i>PLoS Pathogens</i> , 2018 , 14, e1006895	7.6	30
25	Ancient Bacterial Genomes Reveal a High Diversity of <i>Treponema pallidum</i> Strains in Early Modern Europe. <i>Current Biology</i> , 2020 , 30, 3788-3803.e10	6.3	21
24	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. <i>Annual Review of Microbiology</i> , 2019 , 73, 639-666	17.5	20
23	How well can the exponential-growth coalescent approximate constant-rate birth-death population dynamics?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015 , 282, 20150420	4.4	19
22	A seventeenth-century <i>Mycobacterium tuberculosis</i> genome supports a Neolithic emergence of the <i>Mycobacterium tuberculosis</i> complex. <i>Genome Biology</i> , 2020 , 21, 201	18.3	17
21	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020 , 30, 2078-2091.e11	6.3	16
20	Tuberculosis outbreak investigation using phylodynamic analysis. <i>Epidemics</i> , 2018 , 25, 47-53	5.1	13
19	Phylodynamic analysis of HIV sub-epidemics in Mochudi, Botswana. <i>Epidemics</i> , 2015 , 13, 44-55	5.1	12
18	BEAST 2.5: An Advanced Software Platform for Bayesian Evolutionary Analysis		12
17	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019 , 220, 233-243	7	11
16	Phenotypic deficits in the HIV-1 envelope are associated with the maturation of a V2-directed broadly neutralizing antibody lineage. <i>PLoS Pathogens</i> , 2018 , 14, e1006825	7.6	9
15	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021 , 374, 182-188	33.3	7
14	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , 2019 , 93,	6.6	6

13	Field-based sciences must transform in response to COVID-19. <i>Nature Ecology and Evolution</i> , 2020 , 4, 1571-1574	12.3	6
12	Characterization of SARS-CoV-2 infection clusters based on integrated genomic surveillance, outbreak analysis and contact tracing in an urban setting. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	6
11	Improved multi-type birth-death phylodynamic inference in BEAST 2		4
10	A seventeenth-century <i>Mycobacterium tuberculosis</i> genome supports a Neolithic emergence of the <i>Mycobacterium tuberculosis</i> complex		4
9	Stone Age genomes shed light on the early evolution, diversity, and ecology of plague.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2116722119	11.5	3
8	Computational Strategies to Combat COVID-19: Useful Tools to Accelerate SARS-CoV-2 and Coronavirus Research		2
7	Rapid incidence estimation from SARS-CoV-2 genomes reveals decreased case detection in Europe during summer 2020. <i>Nature Communications</i> , 2021 , 12, 6009	17.4	2
6	Ancient bacterial genomes reveal a formerly unknown diversity of <i>Treponema pallidum</i> strains in early modern Europe		2
5	The relationship between transmission time and clustering methods in <i>Mycobacterium tuberculosis</i> epidemiology		
4	Origin of modern syphilis and emergence of a contemporary pandemic cluster		1
3	Quantifying transmission fitness costs of multi-drug resistant tuberculosis. <i>Epidemics</i> , 2021 , 36, 100471	5.1	1
2	Genomic Surveillance of Vancomycin-Resistant <i>Enterococcus faecium</i> Reveals Spread of a Linear Plasmid Conferring a Nutrient Utilization Advantage.. <i>MBio</i> , 2022 , e0377121	7.8	1
1	Molecular Epidemiology and Transmission Dynamics of the HIV-1 Epidemic in Ethiopia: Epidemic Decline Coincided With Behavioral Interventions Before ART Scale-Up.. <i>Frontiers in Microbiology</i> , 2022 , 13, 821006	5.7	0