

Denise KÃ¼hnert

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

10,581
citations

186209

28
h-index

254106

43
g-index

58
all docs

58
docs citations

58
times ranked

16869
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection Clusters Based on Integrated Genomic Surveillance, Outbreak Analysis and Contact Tracing in an Urban Setting. <i>Clinical Infectious Diseases</i> , 2022, 74, 1039-1046.	2.9	21
2	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, 8211006.	1.5	1
3	Genomic Surveillance of Vancomycin-Resistant <i>Enterococcus faecium</i> Reveals Spread of a Linear Plasmid Conferring a Nutrient Utilization Advantage. <i>MBio</i> , 2022, 13, e0377121.	1.8	11
4	Stone Age <i>Yersinia pestis</i> 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.	3.3	31
5	The source of the Black Death in fourteenth-century central Eurasia. <i>Nature</i> , 2022, 606, 718-724.	13.7	58
6	Women in the European Virus Bioinformatics Center. <i>Viruses</i> , 2022, 14, 1522.	1.5	1
7	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.	3.2	110
8	Quantifying transmission fitness costs of multi-drug resistant tuberculosis. <i>Epidemics</i> , 2021, 36, 100471.	1.5	13
9	Bayesian phylogenetic analysis of linguistic data using BEAST. <i>Journal of Language Evolution</i> , 2021, 6, 119-135.	0.4	9
10	Ten millennia of hepatitis B virus evolution. <i>Science</i> , 2021, 374, 182-188.	6.0	64
11	Rapid incidence estimation from SARS-CoV-2 genomes reveals decreased case detection in Europe during summer 2020. <i>Nature Communications</i> , 2021, 12, 6009.	5.8	17
12	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.	3.8	44
13	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.	1.8	47
14	Field-based sciences must transform in response to COVID-19. <i>Nature Ecology and Evolution</i> , 2020, 4, 1571-1574.	3.4	22
15	Origin and Health Status of First-Generation Africans from Early Colonial Mexico. <i>Current Biology</i> , 2020, 30, 2078-2091.e11.	1.8	34
16	Emergence of human-adapted <i>Salmonella enterica</i> is linked to the Neolithization process. <i>Nature Ecology and Evolution</i> , 2020, 4, 324-333.	3.4	72
17	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. <i>Annual Review of Microbiology</i> , 2019, 73, 639-666.	2.9	36
18	A58â€¦Epidemic dynamics of ancient disease outbreaks. <i>Virus Evolution</i> , 2019, 5, .	2.2	0

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19	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.	5.8	64
20	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	1.5	2,484
21	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , 2019, 93, .	1.5	13
22	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.	1.9	23
23	Taming the BEASTâ€”A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	2.7	79
24	Neolithic and medieval virus genomes reveal complex evolution of hepatitis B. <i>ELife</i> , 2018, 7, .	2.8	101
25	The relationship between transmission time and clustering methods in <i>Mycobacterium tuberculosis</i> epidemiology. <i>EBioMedicine</i> , 2018, 37, 410-416.	2.7	106
26	Tuberculosis outbreak investigation using phylodynamic analysis. <i>Epidemics</i> , 2018, 25, 47-53.	1.5	19
27	Analysis of 3800-year-old <i>Yersinia pestis</i> genomes suggests Bronze Age origin for bubonic plague. <i>Nature Communications</i> , 2018, 9, 2234.	5.8	123
28	Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. <i>PLoS Pathogens</i> , 2018, 14, e1006895.	2.1	53
29	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.	2.1	11
30	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. <i>Nature Microbiology</i> , 2017, 2, 16245.	5.9	138
31	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	3.5	53
32	Phylodynamics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 2102-2116.	3.5	131
33	Spatiotemporal dynamics of Puumala hantavirus associated with its rodent host, <i>Myodes glareolus</i> . <i>Evolutionary Applications</i> , 2015, 8, 545-559.	1.5	41
34	How well can the exponential-growth coalescent approximate constant-rate birthâ€“death population dynamics?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150420.	1.2	29
35	Phylodynamic analysis of HIV sub-epidemics in Mochudi, Botswana. <i>Epidemics</i> , 2015, 13, 44-55.	1.5	22
36	Phylodynamics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	1.5	51

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37	The contrasting phylodynamics of human influenza B viruses. <i>ELife</i> , 2015, 4, e05055.	2.8	166
38	Efficient Bayesian inference under the structured coalescent. <i>Bioinformatics</i> , 2014, 30, 2272-2279.	1.8	118
39	BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003537.	1.5	5,301
40	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.	1.5	104
41	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
42	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	2.1	83
43	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, 228-233.	3.3	454
44	Phylogenetic and epidemic modeling of rapidly evolving infectious diseases. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1825-1841.	1.0	70