

Nicola Felix MÃ¼ller

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

3,283
citations

840585

11
h-index

940416

16
g-index

34
all docs

34
docs citations

34
times ranked

6031
citing authors

#	ARTICLE	IF	CITATIONS
1	Joint Inference of Migration and Reassortment Patterns for Viruses with Segmented Genomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
2	Phylogenetic analysis of the highly pathogenic avian influenza H5N8 epidemic in France, 2016–2017. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	6
3	Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State. <i>ELife</i> , 2021, 10, .	2.8	13
4	Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	58
5	Characterizing the Countrywide Epidemic Spread of Influenza A(H1N1)pdm09 Virus in Kenya between 2009 and 2018. <i>Viruses</i> , 2021, 13, 1956.	1.5	4
6	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	6.0	217
7	Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17104-17111.	3.3	35
8	Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. <i>PLoS Pathogens</i> , 2020, 16, e1008984.	2.1	17
9	Adaptive Metropolis-coupled MCMC for BEAST 2. <i>PeerJ</i> , 2020, 8, e9473.	0.9	28
10	Bayesian phylodynamics of avian influenza A virus H9N2 in Asia with time-dependent predictors of migration. <i>PLoS Computational Biology</i> , 2019, 15, e1007189.	1.5	22
11	Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations. <i>Virus Evolution</i> , 2019, 5, vez030.	2.2	20
12	Evaluation of two workflows for whole genome sequencing-based typing of influenza A viruses. <i>Journal of Virological Methods</i> , 2019, 266, 30-33.	1.0	9
13	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	1.5	2,484
14	Taming the BEAST—A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	2.7	79
15	MASCOT: parameter and state inference under the marginal structured coalescent approximation. <i>Bioinformatics</i> , 2018, 34, 3843-3848.	1.8	78
16	The Structured Coalescent and Its Approximations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2970-2981.	3.5	98