Nicola Felix Müller

List of Publications by Year
in descending order

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