

Michelle Kendall

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1122389/publications.pdf>

Version: 2024-02-01

17
papers

3,333
citations

687363

13
h-index

940533

16
g-index

25
all docs

25
docs citations

25
times ranked

5985
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Epidemiology Analysis of Infectious Disease Outbreaks Using TransPhylo. Current Protocols, 2021, 1, e60.	2.9	34
2	Time to evaluate COVID-19 contact-tracing apps. Nature Medicine, 2021, 27, 361-362.	30.7	71
3	The epidemiological impact of the NHS COVID-19 app. Nature, 2021, 594, 408-412.	27.8	188
4	OpenABM-Covid19â€”An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. PLoS Computational Biology, 2021, 17, e1009146.	3.2	118
5	Epidemiological changes on the Isle of Wight after the launch of the NHS Test and Trace programme: a preliminary analysis. The Lancet Digital Health, 2020, 2, e658-e666.	12.3	74
6	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. Science, 2020, 368, .	12.6	2,048
7	Estimating Transmission from Genetic and Epidemiological Data: A Metric to Compare Transmission Trees. Statistical Science, 2018, 33, .	2.8	12
8	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. Wellcome Open Research, 2018, 3, 33.	1.8	42
9	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. AIDS Research and Human Retroviruses, 2017, 33, 1083-1098.	1.1	18
10	<scp>treespace</scp>: Statistical exploration of landscapes of phylogenetic trees. Molecular Ecology Resources, 2017, 17, 1385-1392.	4.8	158
11	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
12	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. PLoS ONE, 2017, 12, e0189838.	2.5	19
13	Graph-theoretic design and analysis of key predistribution schemes. Designs, Codes, and Cryptography, 2016, 81, 11-34.	1.6	14
14	Mapping Phylogenetic Trees to Reveal Distinct Patterns of Evolution. Molecular Biology and Evolution, 2016, 33, 2735-2743.	8.9	121
15	Broadcast-Enhanced Key Predistribution Schemes. ACM Transactions on Sensor Networks, 2014, 11, 1-33.	3.6	7
16	On the Role of Expander Graphs in Key Predistribution Schemes for Wireless Sensor Networks. Lecture Notes in Computer Science, 2012, , 62-82.	1.3	8
17	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. Wellcome Open Research, 0, 3, 33.	1.8	18