

# 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  | Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020, 368, .  | 12.6 | 2,048     |
| 2  | The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021, 594, 408-412.  | 27.8 | 188       |
| 3  | <scp>treespace</scp>: Statistical exploration of landscapes of phylogenetic trees. <i>Molecular Ecology Resources</i> , 2017, 17, 1385-1392.   | 4.8  | 158       |
| 4  | Mapping Phylogenetic Trees to Reveal Distinct Patterns of Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 2735-2743.   | 8.9  | 121       |
| 5  | OpenABM-Covid19â€”An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. <i>PLoS Computational Biology</i> , 2021, 17, e1009146.  | 3.2  | 118       |
| 6  | Epidemiological changes on the Isle of Wight after the launch of the NHS Test and Trace programme: a preliminary analysis. <i>The Lancet Digital Health</i> , 2020, 2, e658-e666.  | 12.3 | 74        |
| 7  | Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021, 27, 361-362.  | 30.7 | 71        |
| 8  | Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.   | 8.9  | 53        |
| 9  | Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.  | 1.8  | 42        |
| 10 | Genomic Epidemiology Analysis of Infectious Disease Outbreaks Using TransPhylo. <i>Current Protocols</i> , 2021, 1, e60.   | 2.9  | 34        |
| 11 | Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. <i>PLoS ONE</i> , 2017, 12, e0189838.  | 2.5  | 19        |
| 12 | HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098. | 1.1  | 18        |
| 13 | Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 0, 3, 33.   | 1.8  | 18        |
| 14 | Graph-theoretic design and analysis of key predistribution schemes. <i>Designs, Codes, and Cryptography</i> , 2016, 81, 11-34.   | 1.6  | 14        |
| 15 | Estimating Transmission from Genetic and Epidemiological Data: A Metric to Compare Transmission Trees. <i>Statistical Science</i> , 2018, 33, .  | 2.8  | 12        |
| 16 | On the Role of Expander Graphs in Key Predistribution Schemes for Wireless Sensor Networks. <i>Lecture Notes in Computer Science</i> , 2012, , 62-82.  | 1.3  | 8         |
| 17 | Broadcast-Enhanced Key Predistribution Schemes. <i>ACM Transactions on Sensor Networks</i> , 2014, 11, 1-33.   | 3.6  | 7         |