

# Matthew D Hall

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3674690/publications.pdf>

Version: 2024-02-01

28  
papers

2,121  
citations

430874

18  
h-index

501196

28  
g-index

42  
all docs

42  
docs citations

42  
times ranked

4272  
citing authors

#	ARTICLE	IF	CITATIONS
1	Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant. <i>Nature Communications</i> , 2022, 13, 460.	12.8	304
2	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
3	Patientsâ€™™, cliniciansâ€™™ and the research communitiesâ€™™ priorities for treatment research: there is an important mismatch. <i>Research Involvement and Engagement</i> , 2015, 1, 2.	2.9	205
4	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	8.9	122
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	Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set. <i>PLoS Computational Biology</i> , 2015, 11, e1004613.	3.2	89
7	The effects of sampling strategy on the quality of reconstruction of viral population dynamics using Bayesian skyline family coalescent methods: A simulation study. <i>Virus Evolution</i> , 2016, 2, vew003.	4.9	69
8	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. <i>PLoS Pathogens</i> , 2016, 12, e1005525.	4.7	65
9	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	4.9	64
10	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , 2020, 7, e173-e183.	4.7	59
11	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
12	Reconstructing Geographical Movements and Host Species Transitions of Foot-and-Mouth Disease Virus Serotype SAT 2. <i>MBio</i> , 2013, 4, e00591-13.	4.1	50
13	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019, 10, 1411.	12.8	50
14	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	39
15	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019, 8, .	6.0	39
16	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	12.6	39
17	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , 2017, 15, e2001855.	5.6	38
18	Phylogeography of Rift Valley Fever Virus in Africa and the Arabian Peninsula. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005226.	3.0	33

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19	Transmission Trees on a Known Pathogen Phylogeny: Enumeration and Sampling. <i>Molecular Biology and Evolution</i> , 2019, 36, 1333-1343.	8.9	18
20	Phylogenetic Methods Inconsistently Predict the Direction of HIV Transmission Among Heterosexual Pairs in the HPTN 052 Cohort. <i>Journal of Infectious Diseases</i> , 2019, 220, 1406-1413.	4.0	18
21	Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) 052. <i>Clinical Infectious Diseases</i> , 2021, 72, 30-37.	5.8	16
22	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. <i>Epidemics</i> , 2016, 17, 27-34.	3.0	13
23	Number of HIV-1 founder variants is determined by the recency of the source partner infection. <i>Science</i> , 2020, 369, 103-108.	12.6	11
24	Ten months of temporal variation in the clinical journey of hospitalised patients with COVID-19: An observational cohort. <i>ELife</i> , 2021, 10, .	6.0	9
25	The evolution of subtype B HIV-1 tat in the Netherlands during 1985â€“2012. <i>Virus Research</i> , 2018, 250, 51-64.	2.2	8
26	Many but small HIV-1 non-B transmission chains in the Netherlands. <i>Aids</i> , 2022, 36, 83-94.	2.2	3
27	Inferring the Sources of HIV Infection in Africa from Deep-Sequence Data with Semi-Parametric Bayesian Poisson Flow Models. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2022, 71, 517-540.	1.0	2
28	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	4.9	1