Matthew D Hall

List of Publications by Year
in descending order

28 papers	2,121 citations	430754 18 h-index	501076 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. Nature Communications, 2022, 13, 460.	5.8	304
2	SARS-CoV-2 within-host diversity and transmission. Science, 2021, 372, .	6.0	278
3	Patients', clinicians' and the research communities' priorities for treatment research: there is an important mismatch. Research Involvement and Engagement, 2015, 1, 2.	1.1	205
4	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. Molecular Biology and Evolution, 2018, 35, 719-733.	3.5	122
5	OpenABM-Covid19—An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. PLoS Computational Biology, 2021, 17, e1009146.	1.5	118
6	Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set. PLoS Computational Biology, 2015, 11, e1004613.	1.5	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. Virus Evolution, 2016, 2, vew003.	2.2	69
8	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. PLoS Pathogens, 2016, 12, e1005525.	2.1	65
9	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. Virus Evolution, 2018, 4, vey007.	2.2	64
10	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. Lancet HIV,the, 2020, 7, e173-e183.	2.1	59
11	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203.	3.5	53
12	Reconstructing Geographical Movements and Host Species Transitions of Foot-and-Mouth Disease Virus Serotype SAT 2. MBio, 2013, 4, e00591-13.	1.8	50
13	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. Nature Communications, 2019, 10, 1411.	5.8	50
14	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. Journal of Clinical Microbiology, 2020, 58, .	1.8	39
15	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. ELife, 2019, 8, .	2.8	39
16	A highly virulent variant of HIV-1 circulating in the Netherlands. Science, 2022, 375, 540-545.	6.0	39
17	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. PLoS Biology, 2017, 15, e2001855.	2.6	38
18	Phylogeography of Rift Valley Fever Virus in Africa and the Arabian Peninsula. PLoS Neglected Tropical Diseases, 2017, 11, e0005226.	1.3	33

#	ARTICLE	IF	CITATIONS
19	Transmission Trees on a Known Pathogen Phylogeny: Enumeration and Sampling. Molecular Biology and Evolution, 2019, 36, 1333-1343.	3.5	18
20	Phylogenetic Methods Inconsistently Predict the Direction of HIV Transmission Among Heterosexual Pairs in the HPTN 052 Cohort. Journal of Infectious Diseases, 2019, 220, 1406-1413.	1.9	18
21	Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) 052. Clinical Infectious Diseases, 2021, 72, 30-37.	2.9	16
22	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. Epidemics, 2016, 17, 27-34.	1.5	13
23	Number of HIV-1 founder variants is determined by the recency of the source partner infection. Science, 2020, 369, 103-108.	6.0	11
24	Ten months of temporal variation in the clinical journey of hospitalised patients with COVID-19: An observational cohort. ELife, 2021, 10, .	2.8	9
25	The evolution of subtype B HIV-1 tat in the Netherlands during 1985â€"2012. Virus Research, 2018, 250, 51-64.	1.1	8
26	Many but small HIV-1 non-B transmission chains in the Netherlands. Aids, 2022, 36, 83-94.	1.0	3
27	Inferring the Sources of HIV Infection in Africa from Deep-Sequence Data with Semi-Parametric Bayesian Poisson Flow Models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2022, 71, 517-540.	0.5	2
28	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. Virus Evolution, 2022, 8, veac022.	2.2	1