

# Chris Wymant

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7108083/publications.pdf>

Version: 2024-02-01

20  
papers

3,320  
citations

623574

14  
h-index

839398

18  
g-index

27  
all docs

27  
docs citations

27  
times ranked

5907  
citing authors

#	ARTICLE	IF	CITATIONS
1	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	6.0	39
2	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	2.2	1
3	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.	2.9	16
4	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021, 27, 361-362.	15.2	71
5	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021, 594, 408-412.	13.7	188
6	OpenABM-Covid19 – An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. <i>PLoS Computational Biology</i> , 2021, 17, e1009146.	1.5	118
7	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	39
8	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.	5.9	74
9	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020, 368, .	6.0	2,048
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.	2.1	59
11	Link between the numbers of particles and variants founding new HIV-1 infections depends on the timing of transmission. <i>Virus Evolution</i> , 2019, 5, vey038.	2.2	13
12	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019, 10, 1411.	5.8	50
13	Airborne in the era of climate change. <i>Science</i> , 2019, 363, 240-240.	6.0	4
14	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , 2018, 1746, 55-61.	0.4	0
15	The evolution of subtype B HIV-1 tat in the Netherlands during 1985–2012. <i>Virus Research</i> , 2018, 250, 51-64.	1.1	8
16	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	2.2	64
17	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	3.5	122
18	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.	0.5	18

#	ARTICLE	IF	CITATIONS
19	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
20	Protein structural robustness to mutations: an in silico investigation. Physical Chemistry Chemical Physics, 2016, 18, 13770-13780.	1.3	24