

# Lucie Abeler-Dörner

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8934499/publications.pdf>

Version: 2024-02-01

15  
papers

3,451  
citations

686830

13  
h-index

996533

15  
g-index

25  
all docs

25  
docs citations

25  
times ranked

6166  
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	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021, 27, 361-362.	15.2	71
3	Modeling the effect of exposure notification and non-pharmaceutical interventions on COVID-19 transmission in Washington state. <i>Npj Digital Medicine</i> , 2021, 4, 49.	5.7	59
4	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278
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	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. <i>Journal of Infectious Diseases</i> , 2020, 222, 1670-1680.	1.9	12
10	Phylogenetic and Demographic Characterization of Directed HIV-1 Transmission Using Deep Sequences from High-Risk and General Population Cohorts/Groups in Uganda. <i>Viruses</i> , 2020, 12, 331.	1.5	17
11	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020, 368, .	6.0	2,048
12	Recombination Analysis of Near Full-Length HIV-1 Sequences and the Identification of a Potential New Circulating Recombinant Form from Rakai, Uganda. <i>AIDS Research and Human Retroviruses</i> , 2020, 36, 467-474.	0.5	4
13	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
14	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
15	PANGEA-HIV 2. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 173-180.	1.5	28