

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

687363

13
h-index

996975

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.	12.6	39
2	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021, 27, 361-362.	30.7	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.	10.9	59
4	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
5	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021, 594, 408-412.	27.8	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.	3.2	118
7	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
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.	12.3	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.	4.0	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.	3.3	17
11	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020, 368, .	12.6	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.	1.1	4
13	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV</i> , the, 2020, 7, e173-e183.	4.7	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.	12.8	50
15	PANGEA-HIV 2. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 173-180.	3.8	28