Anne Cori

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6436082/publications.pdf

Version: 2024-02-01

66 9,768 35 65 papers citations h-index g-index

77 77 16327

times ranked

citing authors

docs citations

all docs

#	Article	IF	CITATIONS
1	Characterising within-hospital SARS-CoV-2 transmission events using epidemiological and viral genomic data across two pandemic waves. Nature Communications, 2022, 13, 671.	12.8	33
2	Inferring the reproduction number using the renewal equation in heterogeneous epidemics. Journal of the Royal Society Interface, 2022, 19, 20210429.	3.4	9
3	Occupational and community risk of SARS-CoV-2 infection among employees of a long-term care facility: an observational study. Antimicrobial Resistance and Infection Control, 2022, 11, 51.	4.1	8
4	Real-time estimation of the epidemic reproduction number: Scoping review of the applications and challenges., 2022, 1, e0000052.		15
5	A Comparative Analysis of Statistical Methods to Estimate the Reproduction Number in Emerging Epidemics, With Implications for the Current Coronavirus Disease 2019 (COVID-19) Pandemic. Clinical Infectious Diseases, 2021, 73, e215-e223.	5.8	28
6	Reduction in mobility and COVID-19 transmission. Nature Communications, 2021, 12, 1090.	12.8	394
7	Using digital surveillance tools for near real-time mapping of the risk of infectious disease spread. Npj Digital Medicine, 2021, 4, 73.	10.9	23
8	Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions. Nature Communications, 2021, 12, 2188.	12.8	23
9	Cost and cost-effectiveness of a universal HIV testing and treatment intervention in Zambia and South Africa: evidence and projections from the HPTN 071 (PopART) trial. The Lancet Global Health, 2021, 9, e668-e680.	6. 3	18
10	Key epidemiological drivers and impact of interventions in the 2020 SARS-CoV-2 epidemic in England. Science Translational Medicine, 2021, 13, .	12.4	89
11	Age patterns of HIV incidence in eastern and southern Africa: a modelling analysis of observational population-based cohort studies. Lancet HIV,the, 2021, 8, e429-e439.	4.7	40
12	Comparing the responses of the UK, Sweden and Denmark to COVID-19 using counterfactual modelling. Scientific Reports, 2021, 11, 16342.	3.3	26
13	Explosive nosocomial outbreak of SARS-CoV-2 in a rehabilitation clinic: the limits of genomics for outbreak reconstruction. Journal of Hospital Infection, 2021, 117, 124-134.	2.9	29
14	PopART-IBM, a highly efficient stochastic individual-based simulation model of generalised HIV epidemics developed in the context of the HPTN 071 (PopART) trial. PLoS Computational Biology, 2021, 17, e1009301.	3.2	5
15	Data journalism and the COVID-19 pandemic: opportunities and challenges. The Lancet Digital Health, 2021, 3, e619-e621.	12.3	16
16	A Quantitative Framework for Defining the End of an Infectious Disease Outbreak: Application to Ebola Virus Disease. American Journal of Epidemiology, 2021, 190, 642-651.	3.4	17
17	Non-pharmaceutical interventions, vaccination, and the SARS-CoV-2 delta variant in England: a mathematical modelling study. Lancet, The, 2021, 398, 1825-1835.	13.7	119
18	Estimates of the severity of coronavirus disease 2019: a model-based analysis. Lancet Infectious Diseases, The, 2020, 20, 669-677.	9.1	3,036

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19	Estimating the number of undetected COVID-19 cases among travellers from mainland China. Wellcome Open Research, 2020, 5, 143.	1.8	5
20	Reproducible parallel inference and simulation of stochastic state space models using odin, dust, and mostate. Wellcome Open Research, 2020, 5, 288.	1.8	4
21	Real-time Epidemic Forecasting: Challenges and Opportunities. Health Security, 2019, 17, 268-275.	1.8	83
22	Outbreak analytics: a developing data science for informing the response to emerging pathogens. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180276.	4.0	118
23	Bayesian inference of transmission chains using timing of symptoms, pathogen genomes and contact data. PLoS Computational Biology, 2019, 15, e1006930.	3.2	60
24	A simple approach to measure transmissibility and forecast incidence. Epidemics, 2018, 22, 29-35.	3.0	63
25	A graph-based evidence synthesis approach to detecting outbreak clusters: An application to dog rabies. PLoS Computational Biology, 2018, 14, e1006554.	3.2	33
26	outbreaker2: a modular platform for outbreak reconstruction. BMC Bioinformatics, 2018, 19, 363.	2.6	60
27	Outbreak of Ebola virus disease in the Democratic Republic of the Congo, April–May, 2018: an epidemiological study. Lancet, The, 2018, 392, 213-221.	13.7	93
28	When are pathogen genome sequences informative of transmission events?. PLoS Pathogens, 2018, 14, e1006885.	4.7	169
29	Heterogeneities in the case fatality ratio in the West African Ebola outbreak 2013–2016. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160308.	4.0	83
30	Key data for outbreak evaluation: building on the Ebola experience. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160371.	4.0	70
31	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203.	8.9	53
32	Differences in health-related quality of life between HIV-positive and HIV-negative people in Zambia and South Africa: a cross-sectional baseline survey of the HPTN 071 (PopART) trial. The Lancet Global Health, 2017, 5, e1133-e1141.	6.3	37
33	International risk of yellow fever spread from the ongoing outbreak in Brazil, December 2016 to May 2017. Eurosurveillance, 2017, 22, .	7.0	36
34	Impact and Cost-Effectiveness of Point-Of-Care CD4 Testing on the HIV Epidemic in South Africa. PLoS ONE, 2016, 11, e0158303.	2.5	16
35	Evolution of HIV virulence in response to widespread scale up of antiretroviral therapy: a modeling study. Virus Evolution, 2016, 2, vew028.	4.9	21
36	Unraveling the drivers of MERS-CoV transmission. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9081-9086.	7.1	95

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37	After Ebola in West Africa — Unpredictable Risks, Preventable Epidemics. New England Journal of Medicine, 2016, 375, 587-596.	27.0	216
38	Ebola Virus Disease among Male and Female Persons in West Africa. New England Journal of Medicine, 2016, 374, 96-98.	27.0	60
39	The Incidence Patterns Model to Estimate the Distribution of New HIV Infections in Sub-Saharan Africa: Development and Validation of a Mathematical Model. PLoS Medicine, 2016, 13, e1002121.	8.4	16
40	Exposure Patterns Driving Ebola Transmission in West Africa: A Retrospective Observational Study. PLoS Medicine, 2016, 13, e1002170.	8.4	72
41	How Can Viral Dynamics Models Inform Endpoint Measures in Clinical Trials of Therapies for Acute Viral Infections?. PLoS ONE, 2016, 11, e0158237.	2.5	24
42	CD4+ cell dynamics in untreated HIV-1 infection. Aids, 2015, 29, 2435-2446.	2.2	38
43	Dispersion of the HIV-1 Epidemic in Men Who Have Sex with Men in the Netherlands: A Combined Mathematical Model and Phylogenetic Analysis. PLoS Medicine, 2015, 12, e1001898.	8.4	69
44	The role of rapid diagnostics in managing Ebola epidemics. Nature, 2015, 528, S109-S116.	27.8	97
45	Assessment of epidemic projections using recent HIV survey data in South Africa: a validation analysis of ten mathematical models of HIV epidemiology in the antiretroviral therapy era. The Lancet Global Health, 2015, 3, e598-e608.	6.3	46
46	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. Genome Research, 2015, 25, 111-118.	5.5	111
47	West African Ebola Epidemic after One Year — Slowing but Not Yet under Control. New England Journal of Medicine, 2015, 372, 584-587.	27.0	174
48	HIV Treatment-As-Prevention Research: Taking the Right Road at the Crossroads. PLoS Medicine, 2015, 12, e1001800.	8.4	7
49	Ebola Virus Disease among Children in West Africa. New England Journal of Medicine, 2015, 372, 1274-1277.	27.0	118
50	A New Method for Estimating the Coverage of Mass Vaccination Campaigns Against Poliomyelitis From Surveillance Data. American Journal of Epidemiology, 2015, 182, 961-970.	3.4	9
51	Potential Biases in Estimating Absolute and Relative Case-Fatality Risks during Outbreaks. PLoS Neglected Tropical Diseases, 2015, 9, e0003846.	3.0	170
52	Bayesian Reconstruction of Disease Outbreaks by Combining Epidemiologic and Genomic Data. PLoS Computational Biology, 2014, 10, e1003457.	3.2	207
53	OutbreakTools: A new platform for disease outbreak analysis using the R software. Epidemics, 2014, 7, 28-34.	3.0	37
54	Ebola Virus Disease in West Africa â€" The First 9 Months of the Epidemic and Forward Projections. New England Journal of Medicine, 2014, 371, 1481-1495.	27.0	1,367

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55	Health benefits, costs, and cost-effectiveness of earlier eligibility for adult antiretroviral therapy and expanded treatment coverage: a combined analysis of 12 mathematical models. The Lancet Global Health, 2014, 2, e23-e34.	6.3	188
56	The potential effects of changing HIV treatment policy on tuberculosis outcomes in South Africa. Aids, 2014, 28, S25-S34.	2.2	33
57	Estimating HIV incidence from case-report data. Aids, 2014, 28, S489-S496.	2.2	9
58	HPTN 071 (PopART): A Cluster-Randomized Trial of the Population Impact of an HIV Combination Prevention Intervention Including Universal Testing and Treatment: Mathematical Model. PLoS ONE, 2014, 9, e84511.	2.5	91
59	How effectively can HIV phylogenies be used to measure heritability?. Evolution, Medicine and Public Health, 2013, 2013, 209-224.	2.5	21
60	A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, 2013, 178, 1505-1512.	3.4	1,206
61	Estimating influenza latency and infectious period durations using viral excretion data. Epidemics, 2012, 4, 132-138.	3.0	58
62	Age distribution of cases and deaths during the 1889 influenza pandemic. Vaccine, 2011, 29, B6-B10.	3.8	15
63	Transmission parameters of the A/H1N1 (2009) influenza virus pandemic: a review. Influenza and Other Respiratory Viruses, 2011, 5, 306-316.	3.4	125
64	Transmissibility and geographic spread of the 1889 influenza pandemic. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8778-8781.	7.1	105
65	Temporal Variability and Social Heterogeneity in Disease Transmission: The Case of SARS in Hong Kong. PLoS Computational Biology, 2009, 5, e1000471.	3.2	22
66	Reconstruction of transmission chains of SARS-CoV-2 amidst multiple outbreaks in a geriatric acute-care hospital: a combined retrospective epidemiological and genomic study. ELife, 0, 11 , .	6.0	8