

Manon Ragonnet-Cronin

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

3,205
citations

471509

17
h-index

377865

34
g-index

40
all docs

40
docs citations

40
times ranked

6858
citing authors

#	ARTICLE	IF	CITATIONS
1	Human Immunodeficiency Virus (HIV) Genetic Diversity Informs Stage of HIV-1 Infection Among Patients Receiving Antiretroviral Therapy in Botswana. <i>Journal of Infectious Diseases</i> , 2022, 225, 1330-1338.	4.0	5
2	Forecasting HIV-1 Genetic Cluster Growth in Illinois,United States. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2022, 89, 49-55.	2.1	7
3	Diagnosis delays in the UK according to pre or postmigration acquisition of HIV. <i>Aids</i> , 2022, 36, 415-422.	2.2	3
4	Database of epidemic trends and control measures during the first wave of COVID-19 in mainland China. <i>International Journal of Infectious Diseases</i> , 2021, 102, 463-471.	3.3	12
5	Genomic epidemiology of a densely sampled COVID-19 outbreak in China. <i>Virus Evolution</i> , 2021, 7, veaa102.	4.9	18
6	Sorting by Race/Ethnicity Across HIV Genetic Transmission Networks in Three Major Metropolitan Areas in the United States. <i>AIDS Research and Human Retroviruses</i> , 2021, 37, 784-792.	1.1	5
7	Reduction in mobility and COVID-19 transmission. <i>Nature Communications</i> , 2021, 12, 1090.	12.8	394
8	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
9	Interplay Between Geography and HIV Transmission Clusters in Los Angeles County. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab211.	0.9	2
10	Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions. <i>Nature Communications</i> , 2021, 12, 2188.	12.8	23
11	Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City region. <i>Genome Research</i> , 2020, 30, 1781-1788.	5.5	66
12	From Hospital to the Community: Redesigning the Human Immunodeficiency Virus (HIV) Clinical Service Model to Respond to an Outbreak of HIV Among People Who Inject Drugs. <i>Journal of Infectious Diseases</i> , 2020, 222, S410-S419.	4.0	6
13	SARS-CoV-2 infection prevalence on repatriation flights from Wuhan City, China. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	5
14	Comparison of molecular testing strategies for COVID-19 control: a mathematical modelling study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1381-1389.	9.1	171
15	Hepatitis C virus genotype 1 and 2 recombinant genomes and the phylogeographic history of the 2k/1b lineage. <i>Virus Evolution</i> , 2019, 5, vez041.	4.9	5
16	Consent and criminalisation concerns over phylogenetic analysis of surveillance data “ Authors' reply. <i>Lancet HIV</i> ,the, 2019, 6, e420-e421.	4.7	6
17	HIV coinfection is associated with increased transmission risk in patients with chronic hepatitis C virus. <i>Journal of Viral Hepatitis</i> , 2019, 26, 1351-1354.	2.0	3
18	HIV transmission networks among transgender women in Los Angeles County, CA, USA: a phylogenetic analysis of surveillance data. <i>Lancet HIV</i> ,the, 2019, 6, e164-e172.	4.7	57

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19	Understanding disclosed and cryptic HIV transmission risk via genetic analysis. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 205-212.	3.8	11
20	FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences. <i>Bioinformatics</i> , 2019, 35, 1852-1861.	4.1	45
21	Recent and Rapid Transmission of HIV Among People Who Inject Drugs in Scotland Revealed Through Phylogenetic Analysis. <i>Journal of Infectious Diseases</i> , 2018, 217, 1875-1882.	4.0	50
22	Non-disclosed men who have sex with men in UK HIV transmission networks: phylogenetic analysis of surveillance data. <i>Lancet HIV</i> , 2018, 5, e309-e316.	4.7	38
23	Bayesian inference reveals ancient origin of simian foamy virus in orangutans. <i>Infection, Genetics and Evolution</i> , 2017, 51, 54-66.	2.3	4
24	Identifying Transmission Clusters with Cluster Picker and HIV-TRACE. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 211-218.	1.1	66
25	Detailed phylogenetic analysis of primate T-lymphotropic virus type 1 (PTLV-1) sequences from orangutans (<i>Pongo pygmaeus</i>) reveals new insights into the evolutionary history of PTLV-1 in Asia. <i>Infection, Genetics and Evolution</i> , 2016, 43, 434-450.	2.3	11
26	Transmission of Non-B HIV Subtypes in the United Kingdom Is Increasingly Driven by Large Non-Heterosexual Transmission Clusters. <i>Journal of Infectious Diseases</i> , 2016, 213, 1410-1418.	4.0	67
27	Analysis of the history and spread of HIV-1 in Uganda using phylodynamics. <i>Journal of General Virology</i> , 2015, 96, 1890-1898.	2.9	34
28	Lack of Effectiveness of Antiretroviral Therapy in Preventing HIV Infection in Serodiscordant Couples in Uganda: An Observational Study. <i>PLoS ONE</i> , 2015, 10, e0132182.	2.5	14
29	Phylogenetic analyses reveal HIV-1 infections between men misclassified as heterosexual transmissions. <i>Aids</i> , 2014, 28, 1967-1975.	2.2	69
30	Automated analysis of phylogenetic clusters. <i>BMC Bioinformatics</i> , 2013, 14, 317.	2.6	305
31	Genetic Diversity as a Marker for Timing Infection in HIV-Infected Patients: Evaluation of a 6-Month Window and Comparison With BED. <i>Journal of Infectious Diseases</i> , 2012, 206, 756-764.	4.0	50
32	Adaptive Evolution of HIV at HLA Epitopes Is Associated with Ethnicity in Canada. <i>PLoS ONE</i> , 2012, 7, e36933.	2.5	5
33	HIV-1 Modulates the tRNA Pool to Improve Translation Efficiency. <i>Molecular Biology and Evolution</i> , 2011, 28, 1827-1834.	8.9	94
34	Longitudinal Phylogenetic Surveillance Identifies Distinct Patterns of Cluster Dynamics. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2010, 55, 102-108.	2.1	79