Manon Ragonnet-Cronin

List of Publications by Year
in descending order

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	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. Nature, 2021, 593, 266-269.	27.8	1,001
2	Reduction in mobility and COVID-19 transmission. Nature Communications, 2021, 12, 1090.	12.8	394
3	Automated analysis of phylogenetic clusters. BMC Bioinformatics, 2013, 14, 317.	2.6	305
4	Comparison of molecular testing strategies for COVID-19 control: a mathematical modelling study. Lancet Infectious Diseases, The, 2020, 20, 1381-1389.	9.1	171
5	HIV-1 Modulates the tRNA Pool to Improve Translation Efficiency. Molecular Biology and Evolution, 2011, 28, 1827-1834.	8.9	94
6	Longitudinal Phylogenetic Surveillance Identifies Distinct Patterns of Cluster Dynamics. Journal of Acquired Immune Deficiency Syndromes (1999), 2010, 55, 102-108.	2.1	79
7	Phylogenetic analyses reveal HIV-1 infections between men misclassified as heterosexual transmissions. Aids, 2014, 28, 1967-1975.	2.2	69
8	Transmission of Non-B HIV Subtypes in the United Kingdom Is Increasingly Driven by Large Non-Heterosexual Transmission Clusters. Journal of Infectious Diseases, 2016, 213, 1410-1418.	4.0	67
9	Identifying Transmission Clusters with Cluster Picker and HIV-TRACE. AIDS Research and Human Retroviruses, 2017, 33, 211-218.	1.1	66
10	Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City region. Genome Research, 2020, 30, 1781-1788.	5.5	66
11	HIV transmission networks among transgender women in Los Angeles County, CA, USA: a phylogenetic analysis of surveillance data. Lancet HIV,the, 2019, 6, e164-e172.	4.7	57
12	Genetic Diversity as a Marker for Timing Infection in HIV-Infected Patients: Evaluation of a 6-Month Window and Comparison With BED. Journal of Infectious Diseases, 2012, 206, 756-764.	4.0	50
13	Recent and Rapid Transmission of HIV Among People Who Inject Drugs in Scotland Revealed Through Phylogenetic Analysis. Journal of Infectious Diseases, 2018, 217, 1875-1882.	4.0	50
14	FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences. Bioinformatics, 2019, 35, 1852-1861.	4.1	45
15	Non-disclosed men who have sex with men in UK HIV transmission networks: phylogenetic analysis of surveillance data. Lancet HIV,the, 2018, 5, e309-e316.	4.7	38
16	Analysis of the history and spread of HIV-1 in Uganda using phylodynamics. Journal of General Virology, 2015, 96, 1890-1898.	2.9	34
17	Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions. Nature Communications, 2021, 12, 2188.	12.8	23
18	Genomic epidemiology of a densely sampled COVID-19 outbreak in China. Virus Evolution, 2021, 7, veaa102.	4.9	18

#	Article	IF	Citations
19	Lack of Effectiveness of Antiretroviral Therapy in Preventing HIV Infection in Serodiscordant Couples in Uganda: An Observational Study. PLoS ONE, 2015, 10, e0132182.	2.5	14
20	Database of epidemic trends and control measures during the first wave of COVID-19 in mainland China. International Journal of Infectious Diseases, 2021, 102, 463-471.	3.3	12
21	Detailed phylogenetic analysis of primate T-lymphotropic virus type 1 (PTLV-1) sequences from orangutans (Pongo pygmaeus) reveals new insights into the evolutionary history of PTLV-1 in Asia. Infection, Genetics and Evolution, 2016, 43, 434-450.	2.3	11
22	Understanding disclosed and cryptic HIV transmission risk via genetic analysis. Current Opinion in HIV and AIDS, 2019, 14, 205-212.	3.8	11
23	Forecasting HIV-1 Genetic Cluster Growth in Illinois,United States. Journal of Acquired Immune Deficiency Syndromes (1999), 2022, 89, 49-55.	2.1	7
24	Consent and criminalisation concerns over phylogenetic analysis of surveillance data â€" Authors' reply. Lancet HIV,the, 2019, 6, e420-e421.	4.7	6
25	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. Journal of Infectious Diseases, 2020, 222, S410-S419.	4.0	6
26	Adaptive Evolution of HIV at HLA Epitopes Is Associated with Ethnicity in Canada. PLoS ONE, 2012, 7, e36933.	2.5	5
27	Hepatitis C virus genotype 1 and 2 recombinant genomes and the phylogeographic history of the 2k/1b lineage. Virus Evolution, 2019, 5, vez041.	4.9	5
28	SARS-CoV-2 infection prevalence on repatriation flights from Wuhan City, China. Journal of Travel Medicine, 2020, 27, .	3.0	5
29	Sorting by Race/Ethnicity Across HIV Genetic Transmission Networks in Three Major Metropolitan Areas in the United States. AIDS Research and Human Retroviruses, 2021, 37, 784-792.	1.1	5
30	Human Immunodeficiency Virus (HIV) Genetic Diversity Informs Stage of HIV-1 Infection Among Patients Receiving Antiretroviral Therapy in Botswana. Journal of Infectious Diseases, 2022, 225, 1330-1338.	4.0	5
31	Bayesian inference reveals ancient origin of simian foamy virus in orangutans. Infection, Genetics and Evolution, 2017, 51, 54-66.	2.3	4
32	HIV coâ€infection is associated with increased transmission risk in patients with chronic hepatitis C virus. Journal of Viral Hepatitis, 2019, 26, 1351-1354.	2.0	3
33	Diagnosis delays in the UK according to pre or postmigration acquisition of HIV. Aids, 2022, 36, 415-422.	2.2	3
34	Interplay Between Geography and HIV Transmission Clusters in Los Angeles County. Open Forum Infectious Diseases, 2021, 8, ofab211.	0.9	2