

Christophe Fraser

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8329954/publications.pdf>

Version: 2024-02-01

245
papers

35,855
citations

7087

78
h-index

4427

172
g-index

280
all docs

280
docs citations

280
times ranked

37020
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020, 368, .	6.0	2,048
2	Strategies for mitigating an influenza pandemic. <i>Nature</i> , 2006, 442, 448-452.	13.7	1,863
3	Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. <i>Science</i> , 2009, 324, 1557-1561.	6.0	1,665
4	Strategies for containing an emerging influenza pandemic in Southeast Asia. <i>Nature</i> , 2005, 437, 209-214.	13.7	1,592
5	A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. <i>American Journal of Epidemiology</i> , 2013, 178, 1505-1512.	1.6	1,206
6	Transmission Dynamics of the Etiological Agent of SARS in Hong Kong: Impact of Public Health Interventions. <i>Science</i> , 2003, 300, 1961-1966.	6.0	1,004
7	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	13.7	1,001
8	Factors that make an infectious disease outbreak controllable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6146-6151.	3.3	1,000
9	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	13.5	843
10	Epidemiological determinants of spread of causal agent of severe acute respiratory syndrome in Hong Kong. <i>Lancet, The</i> , 2003, 361, 1761-1766.	6.3	840
11	Rapid Pneumococcal Evolution in Response to Clinical Interventions. <i>Science</i> , 2011, 331, 430-434.	6.0	828
12	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021, 592, 277-282.	13.7	802
13	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021, 593, 136-141.	13.7	648
14	Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study. <i>Lancet Infectious Diseases, The</i> , 2022, 22, 35-42.	4.6	612
15	HIV-1 Transmission, by Stage of Infection. <i>Journal of Infectious Diseases</i> , 2008, 198, 687-693.	1.9	575
16	Modeling targeted layered containment of an influenza pandemic in the United States. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4639-4644.	3.3	570
17	Mathematical models of infectious disease transmission. <i>Nature Reviews Microbiology</i> , 2008, 6, 477-487.	13.6	527
18	Recombination and the Nature of Bacterial Speciation. <i>Science</i> , 2007, 315, 476-480.	6.0	512

#	ARTICLE	IF	CITATIONS
19	Household Transmission of 2009 Pandemic Influenza A (H1N1) Virus in the United States. <i>New England Journal of Medicine</i> , 2009, 361, 2619-2627.	13.9	420
20	Epidemiology, transmission dynamics and control of SARS: the 2002–2003 epidemic. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004, 359, 1091-1105.	1.8	412
21	Seasonal infectious disease epidemiology. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 2541-2550.	1.2	409
22	Estimating Individual and Household Reproduction Numbers in an Emerging Epidemic. <i>PLoS ONE</i> , 2007, 2, e758.	1.1	393
23	The Bacterial Species Challenge: Making Sense of Genetic and Ecological Diversity. <i>Science</i> , 2009, 323, 741-746.	6.0	381
24	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	2.9	375
25	Variation in HIV-1 set-point viral load: Epidemiological analysis and an evolutionary hypothesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17441-17446.	3.3	363
26	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
27	HIV Treatment as Prevention: Systematic Comparison of Mathematical Models of the Potential Impact of Antiretroviral Therapy on HIV Incidence in South Africa. <i>PLoS Medicine</i> , 2012, 9, e1001245.	3.9	324
28	Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. <i>Lancet Infectious Diseases</i> , The, 2014, 14, 50-56.	4.6	298
29	The Epidemiology of Severe Acute Respiratory Syndrome in the 2003 Hong Kong Epidemic: An Analysis of All 1755 Patients. <i>Annals of Internal Medicine</i> , 2004, 141, 662.	2.0	293
30	Fuzzy species among recombinogenic bacteria. <i>BMC Biology</i> , 2005, 3, 6.	1.7	283
31	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278
32	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	4.7	269
33	Effect of Universal Testing and Treatment on HIV Incidence – HPTN 071 (PopART). <i>New England Journal of Medicine</i> , 2019, 381, 207-218.	13.9	255
34	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	3.4	232
35	New Strategies for the Elimination of Polio from India. <i>Science</i> , 2006, 314, 1150-1153.	6.0	230
36	Methods for Estimating the Case Fatality Ratio for a Novel, Emerging Infectious Disease. <i>American Journal of Epidemiology</i> , 2005, 162, 479-486.	1.6	224

#	ARTICLE	IF	CITATIONS
37	After Ebola in West Africa “Unpredictable Risks, Preventable Epidemics. <i>New England Journal of Medicine</i> , 2016, 375, 587-596.	13.9	216
38	Host immunity and synchronized epidemics of syphilis across the United States. <i>Nature</i> , 2005, 433, 417-421.	13.7	215
39	Virulence and Pathogenesis of HIV-1 Infection: An Evolutionary Perspective. <i>Science</i> , 2014, 343, 1243727.	6.0	215
40	The Effectiveness of Contact Tracing in Emerging Epidemics. <i>PLoS ONE</i> , 2006, 1, e12.	1.1	215
41	Assessing the severity of the novel influenza A/H1N1 pandemic. <i>BMJ: British Medical Journal</i> , 2009, 339, b2840-b2840.	2.4	212
42	Reducing the Impact of the Next Influenza Pandemic Using Household-Based Public Health Interventions. <i>PLoS Medicine</i> , 2006, 3, e361.	3.9	208
43	Bayesian Reconstruction of Disease Outbreaks by Combining Epidemiologic and Genomic Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003457.	1.5	207
44	Health benefits, costs, and cost-effectiveness of earlier eligibility for adult antiretroviral therapy and expanded treatment coverage: a combined analysis of 12 mathematical models. <i>The Lancet Global Health</i> , 2014, 2, e23-e34.	2.9	188
45	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021, 594, 408-412.	13.7	188
46	HPTN 071 (PopART): Rationale and design of a cluster-randomised trial of the population impact of an HIV combination prevention intervention including universal testing and treatment “a study protocol for a cluster randomised trial. <i>Trials</i> , 2014, 15, 57.	0.7	185
47	Genomic infectious disease epidemiology in partially sampled and ongoing outbreaks. <i>Molecular Biology and Evolution</i> , 2017, 34, msw075.	3.5	181
48	Ethics of instantaneous contact tracing using mobile phone apps in the control of the COVID-19 pandemic. <i>Journal of Medical Ethics</i> , 2020, 46, 427-431.	1.0	177
49	West African Ebola Epidemic after One Year “Slowing but Not Yet under Control. <i>New England Journal of Medicine</i> , 2015, 372, 584-587.	13.9	174
50	Potential Biases in Estimating Absolute and Relative Case-Fatality Risks during Outbreaks. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003846.	1.3	170
51	Sequences, sequence clusters and bacterial species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1917-1927.	1.8	167
52	Hyper-Recombination, Diversity, and Antibiotic Resistance in <i>Pneumococcus</i> . <i>Science</i> , 2009, 324, 1454-1457.	6.0	164
53	PUBLIC HEALTH: Enhanced: Public Health Risk from the Avian H5N1 Influenza Epidemic. <i>Science</i> , 2004, 304, 968-969.	6.0	154
54	CD4 Cell Counts of 800 Cells/mm ³ or Greater After 7 Years of Highly Active Antiretroviral Therapy Are Feasible in Most Patients Starting With 350 Cells/mm ³ or Greater. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2007, 45, 183-192.	0.9	153

#	ARTICLE	IF	CITATIONS
55	A resurgent HIV-1 epidemic among men who have sex with men in the era of potent antiretroviral therapy. <i>Aids</i> , 2008, 22, 1071-1077.	1.0	153
56	Neutral microepidemic evolution of bacterial pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1968-1973.	3.3	141
57	Evolution of antibiotic resistance is linked to any genetic mechanism affecting bacterial duration of carriage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1075-1080.	3.3	133
58	No coexistence for free: Neutral null models for multistrain pathogens. <i>Epidemics</i> , 2009, 1, 2-13.	1.5	130
59	Evidence that pneumococcal serotype replacement in Massachusetts following conjugate vaccination is now complete. <i>Epidemics</i> , 2010, 2, 80-84.	1.5	128
60	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016, 14, e1002394.	2.6	127
61	Modeling the long-term antibody response of a human papillomavirus (HPV) virus-like particle (VLP) type 16 prophylactic vaccine. <i>Vaccine</i> , 2007, 25, 4324-4333.	1.7	125
62	Assessing the reliability of eBURST using simulated populations with known ancestry. <i>BMC Microbiology</i> , 2007, 7, 30.	1.3	123
63	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018, 35, 719-733.	3.5	122
64	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	3.4	121
65	Ebola Virus Disease among Children in West Africa. <i>New England Journal of Medicine</i> , 2015, 372, 1274-1277.	13.9	118
66	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
67	Identifying Currents in the Gene Pool for Bacterial Populations Using an Integrative Approach. <i>PLoS Computational Biology</i> , 2009, 5, e1000455.	1.5	112
68	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. <i>Genome Research</i> , 2015, 25, 111-118.	2.4	111
69	Within-host and between-host evolutionary rates across the HIV-1 genome. <i>Retrovirology</i> , 2013, 10, 49.	0.9	110
70	Clinical and public health implications of acute and early HIV detection and treatment: a scoping review. <i>Journal of the International AIDS Society</i> , 2017, 20, 21579.	1.2	107
71	The impact of homologous recombination on the generation of diversity in bacteria. <i>Journal of Theoretical Biology</i> , 2006, 239, 210-219.	0.8	106
72	Sources of HIV infection among men having sex with men and implications for prevention. <i>Science Translational Medicine</i> , 2016, 8, 320ra2.	5.8	106

#	ARTICLE	IF	CITATIONS
73	Underwhelming the Immune Response: Effect of Slow Virus Growth on CD8 + -T-Lymphocyte Responses. <i>Journal of Virology</i> , 2004, 78, 2247-2254.	1.5	99
74	The role of rapid diagnostics in managing Ebola epidemics. <i>Nature</i> , 2015, 528, S109-S116.	13.7	97
75	Unraveling the drivers of MERS-CoV transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9081-9086.	3.3	95
76	Epidemiological and genetic analysis of severe acute respiratory syndrome. <i>Lancet Infectious Diseases</i> , 2004, 4, 672-683.	4.6	93
77	HPTN 071 (PopART): A Cluster-Randomized Trial of the Population Impact of an HIV Combination Prevention Intervention Including Universal Testing and Treatment: Mathematical Model. <i>PLoS ONE</i> , 2014, 9, e84511.	1.1	91
78	Modelling bacterial speciation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 2039-2044.	1.8	88
79	HIV-1 Transmitting Couples Have Similar Viral Load Set-Points in Rakai, Uganda. <i>PLoS Pathogens</i> , 2010, 6, e1000876.	2.1	88
80	HIV Treatment as Prevention: Debate and Commentaryâ€”Will Early Infection Compromise Treatment-as-Prevention Strategies?. <i>PLoS Medicine</i> , 2012, 9, e1001232.	3.9	88
81	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	1.5	84
82	Seroprevalence of IgG antibodies to SARS-coronavirus in asymptomatic or subclinical population groups. <i>Epidemiology and Infection</i> , 2006, 134, 211-221.	1.0	83
83	What is the mechanism for persistent coexistence of drug-susceptible and drug-resistant strains of <i>Streptococcus pneumoniae</i> ?. <i>Journal of the Royal Society Interface</i> , 2010, 7, 905-919.	1.5	83
84	Influenza Transmission in Households During the 1918 Pandemic. <i>American Journal of Epidemiology</i> , 2011, 174, 505-514.	1.6	83
85	Heterogeneities in the case fatality ratio in the West African Ebola outbreak 2013â€”2016. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160308.	1.8	83
86	Community based distribution of oral HIV self-testing kits in Zambia: a cluster-randomised trial nested in four HPTN 071 (PopART) intervention communities. <i>Lancet HIV</i> , 2019, 6, e81-e92.	2.1	82
87	Phylogenetic Studies of Transmission Dynamics in Generalized HIV Epidemics. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 67, 181-195.	0.9	80
88	Estimating HIV Incidence, Time to Diagnosis, and the Undiagnosed HIV Epidemic Using Routine Surveillance Data. <i>Epidemiology</i> , 2015, 26, 653-660.	1.2	79
89	The Early Transmission Dynamics of H1N1pdm Influenza in the United Kingdom. <i>PLOS Currents</i> , 2009, 1, RRN1130.	1.4	76
90	Studies Needed to Address Public Health Challenges of the 2009 H1N1 Influenza Pandemic: Insights from Modeling. <i>PLoS Medicine</i> , 2010, 7, e1000275.	3.9	75

#	ARTICLE	IF	CITATIONS
91	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
92	SARS-CoV Antibody Prevalence in All Hong Kong Patient Contacts. <i>Emerging Infectious Diseases</i> , 2004, 10, 1653-1656.	2.0	72
93	Exposure Patterns Driving Ebola Transmission in West Africa: A Retrospective Observational Study. <i>PLoS Medicine</i> , 2016, 13, e1002170.	3.9	72
94	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021, 27, 361-362.	15.2	71
95	Key data for outbreak evaluation: building on the Ebola experience. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160371.	1.8	70
96	New insights into the evolutionary rate of HIV-1 at the within-host and epidemiological levels. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3367-3375.	1.2	69
97	Dispersion of the HIV-1 Epidemic in Men Who Have Sex with Men in the Netherlands: A Combined Mathematical Model and Phylogenetic Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001898.	3.9	69
98	Essential epidemiological mechanisms underpinning the transmission dynamics of seasonal influenza. <i>Journal of the Royal Society Interface</i> , 2012, 9, 304-312.	1.5	65
99	Pneumococcal Capsule Synthesis Locus <i>cps</i> as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017, 34, 2537-2554.	3.5	65
100	HIV Treatment as Prevention: Models, Data, and Questions—Towards Evidence-Based Decision-Making. <i>PLoS Medicine</i> , 2012, 9, e1001259.	3.9	64
101	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	2.2	64
102	A simple approach to measure transmissibility and forecast incidence. <i>Epidemics</i> , 2018, 22, 29-35.	1.5	63
103	COVID-19 symptoms at hospital admission vary with age and sex: results from the ISARIC prospective multinational observational study. <i>Infection</i> , 2021, 49, 889-905.	2.3	62
104	Antigen-driven CD4+ T cell and HIV-1 dynamics: Residual viral replication under highly active antiretroviral therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 15167-15172.	3.3	61
105	Recent trends and patterns in HIV-1 transmitted drug resistance in the United Kingdom. <i>HIV Medicine</i> , 2017, 18, 204-213.	1.0	61
106	Ebola Virus Disease among Male and Female Persons in West Africa. <i>New England Journal of Medicine</i> , 2016, 374, 96-98.	13.9	60
107	HIV recombination: what is the impact on antiretroviral therapy?. <i>Journal of the Royal Society Interface</i> , 2005, 2, 489-503.	1.5	59
108	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

#	ARTICLE	IF	CITATIONS
109	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
110	Resurgence of HIV Infection among Men Who Have Sex with Men in Switzerland: Mathematical Modelling Study. <i>PLoS ONE</i> , 2012, 7, e44819.	1.1	58
111	Transmission Characteristics of the 2009 H1N1 Influenza Pandemic: Comparison of 8 Southern Hemisphere Countries. <i>PLoS Pathogens</i> , 2011, 7, e1002225.	2.1	57
112	Integrating Phylodynamics and Epidemiology to Estimate Transmission Diversity in Viral Epidemics. <i>PLoS Computational Biology</i> , 2013, 9, e1002876.	1.5	57
113	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>iScience</i> , 2021, 24, 103353.	1.9	57
114	Historical Zoonoses and Other Changes in Host Tropism of <i>Staphylococcus aureus</i> , Identified by Phylogenetic Analysis of a Population Dataset. <i>PLoS ONE</i> , 2013, 8, e62369.	1.1	55
115	Reduction of the HIV-1-infected T-cell reservoir by immune activation treatment is dose-dependent and restricted by the potency of antiretroviral drugs. <i>Aids</i> , 2000, 14, 659-669.	1.0	54
116	On the evolutionary ecology of multidrug resistance in bacteria. <i>PLoS Pathogens</i> , 2019, 15, e1007763.	2.1	54
117	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGAEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	3.5	53
118	PANGAEA-HIV: phylogenetics for generalised epidemics in Africa. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 259-261.	4.6	51
119	HIV Treatment as Prevention: Optimising the Impact of Expanded HIV Treatment Programmes. <i>PLoS Medicine</i> , 2012, 9, e1001258.	3.9	50
120	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
121	27 years of the HIV epidemic amongst men having sex with men in the Netherlands: An in depth mathematical model-based analysis. <i>Epidemics</i> , 2010, 2, 66-79.	1.5	49
122	IS HIV SHORT-SIGHTED? INSIGHTS FROM A MULTISTRAIN NESTED MODEL. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2769-2782.	1.1	49
123	The evolution of antibiotic resistance in a structured host population. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180040.	1.5	49
124	S-duality in N = 4 supersymmetric gauge theories with arbitrary gauge group. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 1996, 383, 422-428.	1.5	46
125	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. <i>The Lancet Global Health</i> , 2015, 3, e598-e608.	2.9	46
126	A transmission-virulence evolutionary trade-off explains attenuation of HIV-1 in Uganda. <i>ELife</i> , 2016, 5, .	2.8	46

#	ARTICLE	IF	CITATIONS
127	Threshold parameters for a model of epidemic spread among households and workplaces. <i>Journal of the Royal Society Interface</i> , 2009, 6, 979-987.	1.5	44
128	How the Dynamics and Structure of Sexual Contact Networks Shape Pathogen Phylogenies. <i>PLoS Computational Biology</i> , 2013, 9, e1003105.	1.5	43
129	Reproductive numbers, epidemic spread and control in a community of households. <i>Mathematical Biosciences</i> , 2009, 221, 11-25.	0.9	42
130	Estimating the Severity and Subclinical Burden of Middle East Respiratory Syndrome Coronavirus Infection in the Kingdom of Saudi Arabia. <i>American Journal of Epidemiology</i> , 2016, 183, 657-663.	1.6	41
131	Inferring pandemic growth rates from sequence data. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1797-1808.	1.5	40
132	Age patterns of HIV incidence in eastern and southern Africa: a modelling analysis of observational population-based cohort studies. <i>Lancet HIV</i> , 2021, 8, e429-e439.	2.1	40
133	Ethical considerations in global HIV phylogenetic research. <i>Lancet HIV</i> , 2018, 5, e656-e666.	2.1	39
134	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
135	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019, 8, .	2.8	39
136	A highly virulent variant of HIV-1 circulating in the Netherlands. <i>Science</i> , 2022, 375, 540-545.	6.0	39
137	Viral Load Levels Measured at Set-Point Have Risen Over the Last Decade of the HIV Epidemic in the Netherlands. <i>PLoS ONE</i> , 2009, 4, e7365.	1.1	38
138	CD4+ cell dynamics in untreated HIV-1 infection. <i>Aids</i> , 2015, 29, 2435-2446.	1.0	38
139	Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. <i>PLoS Biology</i> , 2017, 15, e2001855.	2.6	38
140	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , 2021, 12, 5861.	5.8	38
141	OutbreakTools: A new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014, 7, 28-34.	1.5	37
142	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. <i>The Lancet Global Health</i> , 2017, 5, e1133-e1141.	2.9	37
143	Quantifying Transmission Heterogeneity Using Both Pathogen Phylogenies and Incidence Time Series. <i>Molecular Biology and Evolution</i> , 2017, 34, 2982-2995.	3.5	37
144	Comparison of cluster-based and source-attribution methods for estimating transmission risk using large HIV sequence databases. <i>Epidemics</i> , 2018, 23, 1-10.	1.5	37

#	ARTICLE	IF	CITATIONS
145	Transmission Selects for HIV-1 Strains of Intermediate Virulence: A Modelling Approach. PLoS Computational Biology, 2011, 7, e1002185.	1.5	36
146	Phylogenetic Inference and Model Assessment with Approximate Bayesian Computation: Influenza as a Case Study. PLoS Computational Biology, 2012, 8, e1002835.	1.5	34
147	The role of antigenic stimulation and cytotoxic T cell activity in regulating the long-term immunopathogenesis of HIV: mechanisms and clinical implications. Proceedings of the Royal Society B: Biological Sciences, 2001, 268, 2085-2095.	1.2	33
148	The relationship between real-time and discrete-generation models of epidemic spread. Mathematical Biosciences, 2008, 216, 63-70.	0.9	33
149	The potential effects of changing HIV treatment policy on tuberculosis outcomes in South Africa. Aids, 2014, 28, S25-S34.	1.0	33
150	Semi-classical quantization in N = 4 supersymmetric Yang-Mills theory and duality. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1997, 402, 106-112.	1.5	32
151	Host population structure and treatment frequency maintain balancing selection on drug resistance. Journal of the Royal Society Interface, 2017, 14, 20170295.	1.5	32
152	Molecular Epidemiology of HIV-1 Subtype B Reveals Heterogeneous Transmission Risk: Implications for Intervention and Control. Journal of Infectious Diseases, 2018, 217, 1522-1529.	1.9	32
153	Systematic selection between age and household structure for models aimed at emerging epidemic predictions. Nature Communications, 2020, 11, 906.	5.8	32
154	Evolutionary epidemiology: preparing for an age of genomic plenty. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120193.	1.8	31
155	Viral dynamics and anti-viral pharmacodynamics: rethinking in vitro measures of drug potency. Trends in Pharmacological Sciences, 2001, 22, 97-100.	4.0	30
156	High Heritability Is Compatible with the Broad Distribution of Set Point Viral Load in HIV Carriers. PLoS Pathogens, 2015, 11, e1004634.	2.1	29
157	An evolutionary model to predict the frequency of antibiotic resistance under seasonal antibiotic use, and an application to <i>Streptococcus pneumoniae</i> . Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170679.	1.2	29
158	PANGEA-HIV 2. Current Opinion in HIV and AIDS, 2019, 14, 173-180.	1.5	28
159	Monitoring key epidemiological parameters of SARS-CoV-2 transmission. Nature Medicine, 2021, 27, 1854-1855.	15.2	28
160	The Osp(8) singleton action from the supermembrane. Nuclear Physics B, 1999, 542, 157-194.	0.9	27
161	A Strong Case for Viral Genetic Factors in HIV Virulence. Viruses, 2011, 3, 204-216.	1.5	27
162	Evolution of HIV-1 within untreated individuals and at the population scale in Uganda. PLoS Pathogens, 2018, 14, e1007167.	2.1	27

#	ARTICLE	IF	CITATIONS
163	Quantifying the transmissibility of human influenza and its seasonal variation in temperate regions. PLOS Currents, 2009, 1, RRN1125.	1.4	27
164	The Timing of COVID-19 Transmission. SSRN Electronic Journal, 0, , .	0.4	27
165	Quantification of intrinsic residual viral replication in treated HIV-infected patients. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 15167-15172.	3.3	26
166	Modelling sexual transmission of HIV: testing the assumptions, validating the predictions. Current Opinion in HIV and AIDS, 2010, 5, 269-276.	1.5	26
167	Effect of the Latent Reservoir on the Evolution of HIV at the Within- and Between-Host Levels. PLoS Computational Biology, 2017, 13, e1005228.	1.5	26
168	Adherence to antiretroviral therapy and its impact on clinical outcome in HIV-infected patients. Journal of the Royal Society Interface, 2005, 2, 349-363.	1.5	24
169	Frequency-dependent selection can forecast evolution in Streptococcus pneumoniae. PLoS Biology, 2020, 18, e3000878.	2.6	24
170	Genomic analysis of emerging pathogens: methods, application and future trends. Genome Biology, 2014, 15, 541.	3.8	23
171	High Transmissibility During Early HIV Infection Among Men Who Have Sex With Men—San Francisco, California: Table 1.. Journal of Infectious Diseases, 2015, 211, 1757-1760.	1.9	23
172	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. Scientific Reports, 2016, 6, 39489.	1.6	23
173	From clinical sample to complete genome: Comparing methods for the extraction of HIV-1 RNA for high-throughput deep sequencing. Virus Research, 2017, 239, 10-16.	1.1	23
174	Transformation Asymmetry and the Evolution of the Bacterial Accessory Genome. Molecular Biology and Evolution, 2018, 35, 575-581.	3.5	22
175	How effectively can HIV phylogenies be used to measure heritability?. Evolution, Medicine and Public Health, 2013, 2013, 209-224.	1.1	21
176	HIV-1 drug resistance mutations emerging on darunavir therapy in PI-naïve and -experienced patients in the UK. Journal of Antimicrobial Chemotherapy, 2016, 71, 3487-3494.	1.3	21
177	Evolution of HIV virulence in response to widespread scale up of antiretroviral therapy: a modeling study. Virus Evolution, 2016, 2, vew028.	2.2	21
178	Distinguishing Between Reservoir Exposure and Human-to-Human Transmission for Emerging Pathogens Using Case Onset Data. PLOS Currents, 2014, 6, .	1.4	21
179	Increasing sexual risk behaviour among Dutch men who have sex with men. Aids, 2012, 26, 1840-1843.	1.0	20
180	On the weak coupling spectrum of N = 2 supersymmetric SU(n) gauge theory. Nuclear Physics B, 1997, 490, 217-235.	0.9	19

#	ARTICLE	IF	CITATIONS
181	Epidemic growth rate and household reproduction number in communities of households, schools and workplaces. <i>Journal of Mathematical Biology</i> , 2011, 63, 691-734.	0.8	19
182	Case-based surveillance of antimicrobial resistance with full susceptibility profiles. <i>JAC-Antimicrobial Resistance</i> , 2019, 1, dlz070.	0.9	19
183	Horizontal gene transfer rate is not the primary determinant of observed antibiotic resistance frequencies in <i>Streptococcus pneumoniae</i> . <i>Science Advances</i> , 2020, 6, eaaz6137.	4.7	19
184	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. <i>PLoS ONE</i> , 2017, 12, e0189838.	1.1	19
185	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	0.5	18
186	Phylogenetic Methods Inconsistently Predict the Direction of HIV Transmission Among Heterosexual Pairs in the HPTN 052 Cohort. <i>Journal of Infectious Diseases</i> , 2019, 220, 1406-1413.	1.9	18
187	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. <i>The Lancet Global Health</i> , 2021, 9, e668-e680.	2.9	18
188	Estimating the public health impact of the effect of herpes simplex virus suppressive therapy on plasma HIV-1 viral load. <i>Aids</i> , 2009, 23, 1005-1013.	1.0	17
189	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
190	Large Variations in HIV-1 Viral Load Explained by Shifting-Mosaic Metapopulation Dynamics. <i>PLoS Biology</i> , 2016, 14, e1002567.	2.6	17
191	Impact and Cost-Effectiveness of Point-Of-Care CD4 Testing on the HIV Epidemic in South Africa. <i>PLoS ONE</i> , 2016, 11, e0158303.	1.1	16
192	Evaluation of Phylogenetic Methods for Inferring the Direction of Human Immunodeficiency Virus (HIV) Transmission: HIV Prevention Trials Network (HPTN) 052. <i>Clinical Infectious Diseases</i> , 2021, 72, 30-37.	2.9	16
193	Comparative potency of three antiretroviral therapy regimes in primary HIV infection. <i>Aids</i> , 2006, 20, 247-252.	1.0	15
194	Has the Rate of CD4 Cell Count Decline before Initiation of Antiretroviral Therapy Changed over the Course of the Dutch HIV Epidemic among MSM?. <i>PLoS ONE</i> , 2013, 8, e64437.	1.1	14
195	Instantons, three dimensional gauge theories, and monopole moduli spaces. <i>Physical Review D</i> , 1998, 58, .	1.6	13
196	Viral Replication Under Combination Antiretroviral Therapy: A Comparison of Four Different Regimens. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2002, 30, 167-176.	0.9	13
197	Link between the numbers of particles and variants founding new HIV-1 infections depends on the timing of transmission. <i>Virus Evolution</i> , 2019, 5, vey038.	2.2	13
198	Performance of a high-throughput next-generation sequencing method for analysis of HIV drug resistance and viral load. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3510-3516.	1.3	13

#	ARTICLE	IF	CITATIONS
199	A systematic review of reported reassortant viral lineages of influenza A. BMC Infectious Diseases, 2015, 16, 3.	1.3	12
200	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. Journal of Infectious Diseases, 2020, 222, 1670-1680.	1.9	12
201	High prevalence of integrase mutation L74I in West African HIV-1 subtypes prior to integrase inhibitor treatment. Journal of Antimicrobial Chemotherapy, 2020, 75, 1575-1579.	1.3	12
202	Deep-sequence phylogenetics to quantify patterns of HIV transmission in the context of a universal testing and treatment trial "BCPP/Ya Tsie trial. ELife, 2022, 11, .	2.8	12
203	The Effect on Treatment Comparisons of Different Measurement Frequencies in Human Immunodeficiency Virus Observational Databases. American Journal of Epidemiology, 2006, 163, 676-683.	1.6	11
204	Epidemiology, transmission dynamics, and control of SARS: the 2002-2003 epidemic. , 2005, , 61-80.		11
205	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. Nature Communications, 2022, 13, 1012.	5.8	10
206	Interpretation of correlations in setpoint viral load in transmitting couples. Aids, 2010, 24, 2596-2597.	1.0	9
207	Optimizing the Precision of Case Fatality Ratio Estimates Under the Surveillance Pyramid Approach. American Journal of Epidemiology, 2014, 180, 1036-1046.	1.6	9
208	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. Virus Evolution, 2020, 6, veaa004.	2.2	9
209	Bimodal distribution and set point HBV DNA viral loads in chronic infection: retrospective analysis of cohorts from the UK and South Africa. Wellcome Open Research, 2020, 5, 113.	0.9	9
210	The evolution of subtype B HIV-1 tat in the Netherlands during 1985-2012. Virus Research, 2018, 250, 51-64.	1.1	8
211	HIV-1 Transmission Patterns in Men Who Have Sex with Men: Insights from Genetic Source Attribution Analysis. AIDS Research and Human Retroviruses, 2019, 35, 805-813.	0.5	8
212	HIV Treatment-As-Prevention Research: Taking the Right Road at the Crossroads. PLoS Medicine, 2015, 12, e1001800.	3.9	7
213	Virological failure and development of new resistance mutations according to $CD4$ count at combination antiretroviral therapy initiation. HIV Medicine, 2016, 17, 368-372.	1.0	7
214	Virological outcomes of boosted protease inhibitor-based first-line ART in subjects harbouring thymidine analogue-associated mutations as the sole form of transmitted drug resistance. Journal of Antimicrobial Chemotherapy, 2019, 74, 746-753.	1.3	7
215	Antigen-driven T-cell Turnover. Journal of Theoretical Biology, 2002, 219, 177-192.	0.8	6
216	Synergistic Activity of Mobile Genetic Element Defences in Streptococcus pneumoniae. Genes, 2019, 10, 707.	1.0	6

#	ARTICLE	IF	CITATIONS
217	Associations between baseline characteristics, CD4 cell count response and virological failure on first-line efavirenz+tenofovir+emtricitabine for HIV. <i>Journal of Virus Eradication</i> , 2019, 5, 204-211.	0.3	6
218	Rates of viral suppression in a cohort of people with stable HIV from two community models of ART delivery versus facility-based HIV care in Lusaka, Zambia: a cluster-randomised, non-inferiority trial nested in the HPTN 071 (PopART) trial. <i>Lancet HIV</i> , 2022, 9, e13-e23.	2.1	6
219	Let it be sexual - selection, aggregation and distortion used to construct a case against sexual transmission. <i>International Journal of STD and AIDS</i> , 2003, 14, 782-784.	0.5	5
220	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.	1.9	5
221	PopART-IBM, a highly efficient stochastic individual-based simulation model of generalised HIV epidemics developed in the context of the HPTN 071 (PopART) trial. <i>PLoS Computational Biology</i> , 2021, 17, e1009301.	1.5	5
222	Bimodal distribution and set point HBV DNA viral loads in chronic infection: retrospective analysis of cohorts from the UK and South Africa. <i>Wellcome Open Research</i> , 2020, 5, 113.	0.9	5
223	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
224	Risk factors and outcomes for the Q151M and T69 insertion HIV-1 resistance mutations in historic UK data. <i>AIDS Research and Therapy</i> , 2018, 15, 11.	0.7	3
225	Continuation of emtricitabine/lamivudine within combination antiretroviral therapy following detection of the M184V/I HIV-1 resistance mutation. <i>HIV Medicine</i> , 2020, 21, 309-321.	1.0	3
226	Many but small HIV-1 non-B transmission chains in the Netherlands. <i>Aids</i> , 2022, 36, 83-94.	1.0	3
227	Improving Post-Release Care Engagement for People Living with HIV Involved in the Criminal Justice System: A Systematic Review. <i>AIDS and Behavior</i> , 2021, , 1.	1.4	3
228	HIV drug resistance in a community-randomized trial of universal testing and treatment: HPTN 071 (PopART). <i>Journal of the International AIDS Society</i> , 2022, 25, .	1.2	3
229	Response to Influenza. <i>Science</i> , 2009, 325, 1072-1073.	6.0	2
230	HIV-1 Sequence Data Coverage in Central East Africa from 1959 to 2013. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 904-908.	0.5	2
231	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load. <i>Virus Evolution</i> , 2022, 8, veac022.	2.2	1
232	Influenza Pandemic Vaccines: Spread Them Thin?. <i>PLoS Medicine</i> , 2007, 4, e228.	3.9	0
233	Exploring Genetic Relatedness, Patterns of Evolutionary Descent, and the Population Genetics of Bacterial Pathogens Using Multilocus Sequence Typing. , 0, , 495-508.		0
234	P14-06. Phase 1 safety and immunogenicity randomised controlled trial of a vaginal gp140 vaccine. <i>Retrovirology</i> , 2009, 6, .	0.9	0

#	ARTICLE	IF	CITATIONS
235	Modelling the between-host evolution of set-point viral load in HIV infection. <i>International Journal of Infectious Diseases</i> , 2010, 14, e79.	1.5	0
236	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , 2018, 1746, 55-61.	0.4	0
237	VIRAL REPLICATION UNDER COMBINATION ANTIRETROVIRAL THERAPY: A COMPARISON OF FOUR DIFFERENT REGIMENS. <i>Infectious Diseases in Clinical Practice</i> , 2002, 11, 267.	0.1	0
238	Multilocus Models of Bacterial Population Genetics. , 0, , 93-104.		0
239	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
240	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
241	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
242	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
243	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
244	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
245	Evaluating whole HIV-1 genome sequence for estimation of incidence and migration in a rural South African community. <i>Wellcome Open Research</i> , 0, 7, 174.	0.9	0