

Christophe Fraser

List of Publications by Citations

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257
papers

25,835
citations

76
h-index

158
g-index

280
ext. papers

32,104
ext. citations

11.8
avg, IF

7.19
L-index

#	Paper	IF	Citations
257	Strategies for mitigating an influenza pandemic. <i>Nature</i> , 2006 , 442, 448-52	50.4	1530
256	Pandemic potential of a strain of influenza A (H1N1): early findings. <i>Science</i> , 2009 , 324, 1557-61	33.3	1403
255	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020 , 368,	33.3	1366
254	Strategies for containing an emerging influenza pandemic in Southeast Asia. <i>Nature</i> , 2005 , 437, 209-14	50.4	1323
253	Transmission dynamics of the etiological agent of SARS in Hong Kong: impact of public health interventions. <i>Science</i> , 2003 , 300, 1961-6	33.3	823
252	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, 6146-51	11.5	767
251	Epidemiological determinants of spread of causal agent of severe acute respiratory syndrome in Hong Kong. <i>Lancet, The</i> , 2003 , 361, 1761-6	40	691
250	Rapid pneumococcal evolution in response to clinical interventions. <i>Science</i> , 2011 , 331, 430-4	33.3	680
249	A new framework and software to estimate time-varying reproduction numbers during epidemics. <i>American Journal of Epidemiology</i> , 2013 , 178, 1505-12	3.8	648
248	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021 , 184, 64-75.e11	56.2	518
247	HIV-1 transmission, by stage of infection. <i>Journal of Infectious Diseases</i> , 2008 , 198, 687-93	7	485
246	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, 4639-44	11.5	462
245	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021 , 593, 266-269	50.4	452
244	Recombination and the nature of bacterial speciation. <i>Science</i> , 2007 , 315, 476-80	33.3	407
243	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021 , 592, 277-282	50.4	390
242	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021 , 593, 136-141	50.4	376
241	Mathematical models of infectious disease transmission. <i>Nature Reviews Microbiology</i> , 2008 , 6, 477-87	22.2	373

240	Household transmission of 2009 pandemic influenza A (H1N1) virus in the United States. <i>New England Journal of Medicine</i> , 2009 , 361, 2619-27	59.2	370
239	Seasonal infectious disease epidemiology. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006 , 273, 2541-50	4.4	332
238	The bacterial species challenge: making sense of genetic and ecological diversity. <i>Science</i> , 2009 , 323, 741-6	33.3	322
237	Epidemiology, transmission dynamics and control of SARS: the 2002-2003 epidemic. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004 , 359, 1091-105	5.8	312
236	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, 17441-6	11.5	306
235	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	11.6	284
234	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
233	Estimating individual and household reproduction numbers in an emerging epidemic. <i>PLoS ONE</i> , 2007 , 2, e758	3.7	238
232	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, 662-73	8	235
231	Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. <i>Lancet Infectious Diseases, The</i> , 2014 , 14, 50-56	25.5	231
230	Fuzzy species among recombinogenic bacteria. <i>BMC Biology</i> , 2005 , 3, 6	7.3	223
229	New strategies for the elimination of polio from India. <i>Science</i> , 2006 , 314, 1150-3	33.3	192
228	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> , 2021 ,	25.5	188
227	Reducing the impact of the next influenza pandemic using household-based public health interventions. <i>PLoS Medicine</i> , 2006 , 3, e361	11.6	178
226	Assessing the severity of the novel influenza A/H1N1 pandemic. <i>BMJ, The</i> , 2009 , 339, b2840	5.9	175
225	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	10.6	172
224	After Ebola in West Africa--Unpredictable Risks, Preventable Epidemics. <i>New England Journal of Medicine</i> , 2016 , 375, 587-96	59.2	172
223	Methods for estimating the case fatality ratio for a novel, emerging infectious disease. <i>American Journal of Epidemiology</i> , 2005 , 162, 479-86	3.8	169

222	Host immunity and synchronized epidemics of syphilis across the United States. <i>Nature</i> , 2005 , 433, 417-24	10.4	164
221	Virulence and pathogenesis of HIV-1 infection: an evolutionary perspective. <i>Science</i> , 2014 , 343, 1243-7	33.3	163
220	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> , 2013 , 2, 23-34	13.6	160
219	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	2.8	155
218	West African Ebola epidemic after one year--slowing but not yet under control. <i>New England Journal of Medicine</i> , 2015 , 372, 584-7	59.2	153
217	Effect of Universal Testing and Treatment on HIV Incidence - HPTN 071 (PopART). <i>New England Journal of Medicine</i> , 2019 , 381, 207-218	59.2	149
216	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> , 2021 , 6, e335-e345	22.4	146
215	The effectiveness of contact tracing in emerging epidemics. <i>PLoS ONE</i> , 2006 , 1, e12	3.7	144
214	Bayesian reconstruction of disease outbreaks by combining epidemiologic and genomic data. <i>PLoS Computational Biology</i> , 2014 , 10, e1003457	5	142
213	Sequences, sequence clusters and bacterial species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 1917-27	5.8	139
212	Hyper-recombination, diversity, and antibiotic resistance in pneumococcus. <i>Science</i> , 2009 , 324, 1454-7	33.3	138
211	A resurgent HIV-1 epidemic among men who have sex with men in the era of potent antiretroviral therapy. <i>Aids</i> , 2008 , 22, 1071-7	3.5	137
210	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, 183-92	3.1	133
209	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing		132
208	Public health. Public health risk from the avian H5N1 influenza epidemic. <i>Science</i> , 2004 , 304, 968-9	33.3	128
207	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , 2020 , 1, e99-e100	22.2	127
206	Potential Biases in Estimating Absolute and Relative Case-Fatality Risks during Outbreaks. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003846	4.8	124
205	Neutral microepidemic evolution of bacterial pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1968-73	11.5	118

204	Assessing the reliability of eBURST using simulated populations with known ancestry. <i>BMC Microbiology</i> , 2007 , 7, 30	4.5	115
203	Genomic Infectious Disease Epidemiology in Partially Sampled and Ongoing Outbreaks. <i>Molecular Biology and Evolution</i> , 2017 , 34, 997-1007	8.3	112
202	Evidence that pneumococcal serotype replacement in Massachusetts following conjugate vaccination is now complete. <i>Epidemics</i> , 2010 , 2, 80-4	5.1	111
201	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021 , 372,	33.3	110
200	Modeling the long-term antibody response of a human papillomavirus (HPV) virus-like particle (VLP) type 16 prophylactic vaccine. <i>Vaccine</i> , 2007 , 25, 4324-33	4.1	103
199	Ebola virus disease among children in West Africa. <i>New England Journal of Medicine</i> , 2015 , 372, 1274-7	59.2	100
198	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	2.5	99
197	No coexistence for free: neutral null models for multistrain pathogens. <i>Epidemics</i> , 2009 , 1, 2-13	5.1	96
196	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016 , 14, e1002394	9.7	95
195	The impact of homologous recombination on the generation of diversity in bacteria. <i>Journal of Theoretical Biology</i> , 2006 , 239, 210-9	2.3	94
194	Within-host and between-host evolutionary rates across the HIV-1 genome. <i>Retrovirology</i> , 2013 , 10, 49	3.6	86
193	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	11.5	81
192	HIV treatment as prevention: debate and commentary--will early infection compromise treatment-as-prevention strategies?. <i>PLoS Medicine</i> , 2012 , 9, e1001232	11.6	81
191	Underwhelming the immune response: effect of slow virus growth on CD8+T-lymphocyte responses. <i>Journal of Virology</i> , 2004 , 78, 2247-54	6.6	81
190	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	3.7	80
189	The role of rapid diagnostics in managing Ebola epidemics. <i>Nature</i> , 2015 , 528, S109-16	50.4	79
188	HIV-1 transmitting couples have similar viral load set-points in Rakai, Uganda. <i>PLoS Pathogens</i> , 2010 , 6, e1000876	7.6	79
187	Epidemiological and genetic analysis of severe acute respiratory syndrome. <i>Lancet Infectious Diseases</i> , 2004 , 4, 672-83	25.5	79

186	Identifying currents in the gene pool for bacterial populations using an integrative approach. <i>PLoS Computational Biology</i> , 2009 , 5, e1000455	5	78
185	P14-06. Phase 1 safety and immunogenicity randomised controlled trial of a vaginal gp140 vaccine. <i>Retrovirology</i> , 2009 , 6, P194	3.6	78
184	Modelling bacterial speciation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 2039-44	5.8	78
183	Underwhelming the Immune Response: Effect of Slow Virus Growth on CD8 + -T-Lymphocyte Responses. <i>Journal of Virology</i> , 2004 , 78, 6079-6079	6.6	78
182	Sources of HIV infection among men having sex with men and implications for prevention. <i>Science Translational Medicine</i> , 2016 , 8, 320ra2	17.5	77
181	Genome sequencing defines phylogeny and spread of methicillin-resistant <i>Staphylococcus aureus</i> in a high transmission setting. <i>Genome Research</i> , 2015 , 25, 111-8	9.7	75
180	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	5.4	72
179	Unraveling the drivers of MERS-CoV transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9081-6	11.5	72
178	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1950-1960	12.3	69
177	Studies needed to address public health challenges of the 2009 H1N1 influenza pandemic: insights from modeling. <i>PLoS Medicine</i> , 2010 , 7, e1000275	11.6	69
176	Phylogenetic studies of transmission dynamics in generalized HIV epidemics: an essential tool where the burden is greatest?. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014 , 67, 181-95 ^{3.1}		68
175	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018 , 35, 719-733	8.3	68
174	Seroprevalence of IgG antibodies to SARS-coronavirus in asymptomatic or subclinical population groups. <i>Epidemiology and Infection</i> , 2006 , 134, 211-21	4.3	67
173	Heterogeneities in the case fatality ratio in the West African Ebola outbreak 2013-2016. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	66
172	Estimating HIV Incidence, Time to Diagnosis, and the Undiagnosed HIV Epidemic Using Routine Surveillance Data. <i>Epidemiology</i> , 2015 , 26, 653-60	3.1	64
171	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, 905-19	4.1	64
170	The Early Transmission Dynamics of H1N1pdm Influenza in the United Kingdom. <i>PLOS Currents</i> , 2009 , 1, RRN1130		63
169	SARS-CoV antibody prevalence in all Hong Kong patient contacts. <i>Emerging Infectious Diseases</i> , 2004 , 10, 1653-6	10.2	61

168	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,the</i> , 2019 , 6, e81-e92	7.8	58
167	HIV treatment as prevention: models, data, and questions--towards evidence-based decision-making. <i>PLoS Medicine</i> , 2012 , 9, e1001259	11.6	57
166	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021 , 594, 408-412	50.4	57
165	Influenza transmission in households during the 1918 pandemic. <i>American Journal of Epidemiology</i> , 2011 , 174, 505-14	3.8	56
164	Exposure Patterns Driving Ebola Transmission in West Africa: A Retrospective Observational Study. <i>PLoS Medicine</i> , 2016 , 13, e1002170	11.6	56
163	Heterogeneity in the frequency and characteristics of homologous recombination in pneumococcal evolution. <i>PLoS Genetics</i> , 2014 , 10, e1004300	6	55
162	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, 15167-72	11.5	55
161	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, 3367-75	4.4	54
160	Essential epidemiological mechanisms underpinning the transmission dynamics of seasonal influenza. <i>Journal of the Royal Society Interface</i> , 2012 , 9, 304-12	4.1	54
159	Resurgence of HIV infection among men who have sex with men in Switzerland: mathematical modelling study. <i>PLoS ONE</i> , 2012 , 7, e44819	3.7	54
158	Recent trends and patterns in HIV-1 transmitted drug resistance in the United Kingdom. <i>HIV Medicine</i> , 2017 , 18, 204-213	2.7	53
157	Key data for outbreak evaluation: building on the Ebola experience. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	52
156	HIV recombination: what is the impact on antiretroviral therapy?. <i>Journal of the Royal Society Interface</i> , 2005 , 2, 489-503	4.1	50
155	Ebola Virus Disease among Male and Female Persons in West Africa. <i>New England Journal of Medicine</i> , 2016 , 374, 96-8	59.2	48
154	Integrating phylodynamics and epidemiology to estimate transmission diversity in viral epidemics. <i>PLoS Computational Biology</i> , 2013 , 9, e1002876	5	48
153	The timing of COVID-19 transmission		48
152	Transmission characteristics of the 2009 H1N1 influenza pandemic: comparison of 8 Southern hemisphere countries. <i>PLoS Pathogens</i> , 2011 , 7, e1002225	7.6	47
151	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; discussion e1001898	11.6	45

150	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	5.1	45
149	HIV treatment as prevention: optimising the impact of expanded HIV treatment programmes. <i>PLoS Medicine</i> , 2012 , 9, e1001258	11.6	45
148	Threshold parameters for a model of epidemic spread among households and workplaces. <i>Journal of the Royal Society Interface</i> , 2009 , 6, 979-87	4.1	43
147	Pneumococcal Capsule Synthesis Locus cps as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2537-2554	8.3	42
146	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, 659-69	3.5	42
145	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017 , 34, 185-203	8.3	41
144	A simple approach to measure transmissibility and forecast incidence. <i>Epidemics</i> , 2018 , 22, 29-35	5.1	41
143	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	3.7	40
142	Reproductive numbers, epidemic spread and control in a community of households. <i>Mathematical Biosciences</i> , 2009 , 221, 11-25	3.9	40
141	PANGEA-HIV: phylogenetics for generalised epidemics in Africa. <i>Lancet Infectious Diseases, The</i> , 2015 , 15, 259-61	25.5	39
140	Is HIV short-sighted? Insights from a multistrain nested model. <i>Evolution; International Journal of Organic Evolution</i> , 2013 , 67, 2769-82	3.8	39
139	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, e598-608	13.6	38
138	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	4.2	38
137	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018 , 4, vey007	3.7	38
136	How the dynamics and structure of sexual contact networks shape pathogen phylogenies. <i>PLoS Computational Biology</i> , 2013 , 9, e1003105	5	35
135	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	3.7	35
134	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	14.4	34
133	The role of antigenic stimulation and cytotoxic T cell activity in regulating the long-term immunopathogenesis of HIV: mechanisms and clinical implications. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001 , 268, 2085-95	4.4	33

132	A transmission-virulence evolutionary trade-off explains attenuation of HIV-1 in Uganda. <i>ELife</i> , 2016 , 5,	8.9	33
131	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, 657-63	3.8	32
130	OutbreakTools: a new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014 , 7, 28-34	5.1	32
129	The potential effects of changing HIV treatment policy on tuberculosis outcomes in South Africa: results from three tuberculosis-HIV transmission models. <i>Aids</i> , 2014 , 28 Suppl 1, S25-34	3.5	32
128	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021 , 27, 361-362	50.5	32
127	Semi-classical quantization in N = 4 supersymmetric Yang-Mills theory and duality. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 1997 , 402, 106-112	4.2	31
126	On the evolutionary ecology of multidrug resistance in bacteria. <i>PLoS Pathogens</i> , 2019 , 15, e1007763	7.6	30
125	Transmission selects for HIV-1 strains of intermediate virulence: a modelling approach. <i>PLoS Computational Biology</i> , 2011 , 7, e1002185	5	30
124	Inferring pandemic growth rates from sequence data. <i>Journal of the Royal Society Interface</i> , 2012 , 9, 1797-808	4.8	30
123	The relationship between real-time and discrete-generation models of epidemic spread. <i>Mathematical Biosciences</i> , 2008 , 216, 63-70	3.9	29
122	Within-host genomics of SARS-CoV-2		29
121	CD4+ cell dynamics in untreated HIV-1 infection: overall rates, and effects of age, viral load, sex and calendar time. <i>Aids</i> , 2015 , 29, 2435-46	3.5	28
120	Evolutionary epidemiology: preparing for an age of genomic plenty. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120193	5.8	28
119	OpenABM-Covid19-An agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing. <i>PLoS Computational Biology</i> , 2021 , 17, e1009146	5	28
118	Phylodynamic inference and model assessment with approximate bayesian computation: influenza as a case study. <i>PLoS Computational Biology</i> , 2012 , 8, e1002835	5	27
117	Viral dynamics and anti-viral pharmacodynamics: rethinking in vitro measures of drug potency. <i>Trends in Pharmacological Sciences</i> , 2001 , 22, 97-100	13.2	27
116	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	15.7	27
115	Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis. <i>Nature Communications</i> , 2019 , 10, 1411	17.4	26

114	Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda. <i>Lancet HIV,the</i> , 2020 , 7, e173-e183	7.8	26
113	Modeling the combined effect of digital exposure notification and non-pharmaceutical interventions on the COVID-19 epidemic in Washington state		26
112	The evolution of antibiotic resistance in a structured host population. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	25
111	Quantifying Transmission Heterogeneity Using Both Pathogen Phylogenies and Incidence Time Series. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2982-2995	8.3	24
110	Modelling sexual transmission of HIV: testing the assumptions, validating the predictions. <i>Current Opinion in HIV and AIDS</i> , 2010 , 5, 269-76	4.2	24
109	The Osp(8 4) singleton action from the supermembrane. <i>Nuclear Physics B</i> , 1999 , 542, 157-194	2.8	24
108	Quantification of intrinsic residual viral replication in treated HIV-infected patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 15167-72	11.5	22
107	OpenABM-Covid19 - an agent-based model for non-pharmaceutical interventions against COVID-19 including contact tracing		22
106	Early analysis of a potential link between viral load and the N501Y mutation in the SARS-COV-2 spike protein		22
105	Ethical considerations in global HIV phylogenetic research. <i>Lancet HIV,the</i> , 2018 , 5, e656-e666	7.8	22
104	Systematic selection between age and household structure for models aimed at emerging epidemic predictions. <i>Nature Communications</i> , 2020 , 11, 906	17.4	21
103	From clinical sample to complete genome: Comparing methods for the extraction of HIV-1 RNA for high-throughput deep sequencing. <i>Virus Research</i> , 2017 , 239, 10-16	6.4	21
102	A strong case for viral genetic factors in HIV virulence. <i>Viruses</i> , 2011 , 3, 204-16	6.2	21
101	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	9.7	21
100	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	13.6	20
99	Comparison of cluster-based and source-attribution methods for estimating transmission risk using large HIV sequence databases. <i>Epidemics</i> , 2018 , 23, 1-10	5.1	20
98	Increasing sexual risk behaviour among Dutch men who have sex with men: mathematical models versus prospective cohort data. <i>Aids</i> , 2012 , 26, 1840-3	3.5	20
97	Adherence to antiretroviral therapy and its impact on clinical outcome in HIV-infected patients. <i>Journal of the Royal Society Interface</i> , 2005 , 2, 349-63	4.1	20

96	Quantifying the transmissibility of human influenza and its seasonal variation in temperate regions. <i>PLOS Currents</i> , 2009 , 1, RRN1125		20
95	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	5.8	20
94	HIV-1 drug resistance mutations emerging on darunavir therapy in PI-naive and -experienced patients in the UK. <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 3487-3494	5.1	20
93	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. <i>Scientific Reports</i> , 2016 , 6, 39489	4.9	20
92	High Transmissibility During Early HIV Infection Among Men Who Have Sex With Men-San Francisco, California. <i>Journal of Infectious Diseases</i> , 2015 , 211, 1757-60	7	19
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6 Frequency-dependent selection can forecast evolution in *Streptococcus pneumoniae* **2020**, 18, e3000878

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