

Christophe Fraser

List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	A highly virulent variant of HIV-1 circulating in the Netherlands.. <i>Science</i> , 2022 , 375, 540-545	33.3	5
256	Many but small HIV-1 non-B transmission chains in the Netherlands. <i>Aids</i> , 2022 , 36, 83-94	3.5	1
255	Phylogenetic estimation of the viral fitness landscape of HIV-1 set-point viral load.. <i>Virus Evolution</i> , 2022 , 8, veac022	3.7	
254	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , 2022 , 13, 1012	17.4	2
253	Deep-sequence phylogenetics to quantify patterns of HIV transmission in the context of a universal testing and treatment trial - BCPP/ Ya Tsie trial.. <i>ELife</i> , 2022 , 11,	8.9	1
252	Monitoring key epidemiological parameters of SARS-CoV-2 transmission. <i>Nature Medicine</i> , 2021 , 27, 1854-1855	30.9	3
251	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , 2021 , 12, 5861	17.4	11
250	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>IScience</i> , 2021 , 24, 103353	6.1	12
249	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	4.3	1
248	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	11.6	6
247	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021 , 593, 266-269	50.4	452
246	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
245	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021 , 593, 136-141	50.4	376
244	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021 , 372,	33.3	110
243	The epidemiological impact of the NHS COVID-19 app. <i>Nature</i> , 2021 , 594, 408-412	50.4	57
242	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	13.6	5
241	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

240	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
239	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
238	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
237	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
236	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021 , 592, 277-282	50.4	390
235	Time to evaluate COVID-19 contact-tracing apps. <i>Nature Medicine</i> , 2021 , 27, 361-362	50.5	32
234	Age patterns of HIV incidence in eastern and southern Africa: a modelling analysis of observational population-based cohort studies. <i>Lancet HIV,the</i> , 2021 , 8, e429-e439	7.8	6
233	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
232	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	5	0
231	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
230	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. <i>Journal of Infectious Diseases</i> , 2020 , 222, 1670-1680 ⁷		3
229	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020 , 6, veaa004	3.7	3
228	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe, The</i> , 2020 , 1, e99-e100	22.2	127
227	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,	6.2	7
226	Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. <i>Science</i> , 2020 , 368,	33.3	1366
225	High prevalence of integrase mutation L74I in West African HIV-1 subtypes prior to integrase inhibitor treatment. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 1575-1579	5.1	8
224	Systematic selection between age and household structure for models aimed at emerging epidemic predictions. <i>Nature Communications</i> , 2020 , 11, 906	17.4	21
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	1.6	1

222	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	2.7	1
221	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	7.8	26
220	Horizontal gene transfer rate is not the primary determinant of observed antibiotic resistance frequencies in. <i>Science Advances</i> , 2020 , 6, eaaz6137	14.3	10
219	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	4.8	4
218	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020 , 18, e3000878	9.7	5
217	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	4.8	4
216	A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	15
215	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
214	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	5.1	5
213	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> 2020 , 18, e3000878		
212	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> 2020 , 18, e3000878		
211	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> 2020 , 18, e3000878		
210	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> 2020 , 18, e3000878		
209	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> 2020 , 18, e3000878		
208	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> 2020 , 18, e3000878		
207	Synergistic Activity of Mobile Genetic Element Defences in. <i>Genes</i> , 2019 , 10,	4.2	2
206	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. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 746-753	5.1	5
205	On the evolutionary ecology of multidrug resistance in bacteria. <i>PLoS Pathogens</i> , 2019 , 15, e1007763	7.6	30

204	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	3.7	6
203	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
202	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
201	HIV-1 Transmission Patterns in Men Who Have Sex with Men: Insights from Genetic Source Attribution Analysis. <i>AIDS Research and Human Retroviruses</i> , 2019 , 35, 805-813	1.6	2
200	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. <i>ELife</i> , 2019 , 8,	8.9	11
199	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	2.8	3
198	Case-based surveillance of antimicrobial resistance with full susceptibility profiles. <i>JAC-Antimicrobial Resistance</i> , 2019 , 1, dlz070	2.9	10
197	PANGEA-HIV 2: Phylogenetics And Networks for Generalised Epidemics in Africa. <i>Current Opinion in HIV and AIDS</i> , 2019 , 14, 173-180	4.2	14
196	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
195	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	7	13
194	Workup of Human Blood Samples for Deep Sequencing of HIV-1 Genomes. <i>Methods in Molecular Biology</i> , 2018 , 1746, 55-61	1.4	
193	Molecular Epidemiology of HIV-1 Subtype B Reveals Heterogeneous Transmission Risk: Implications for Intervention and Control. <i>Journal of Infectious Diseases</i> , 2018 , 217, 1522-1529	7	18
192	The evolution of subtype B HIV-1 tat in the Netherlands during 1985-2012. <i>Virus Research</i> , 2018 , 250, 51-64	6.4	4
191	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	3	3
190	Transformation Asymmetry and the Evolution of the Bacterial Accessory Genome. <i>Molecular Biology and Evolution</i> , 2018 , 35, 575-581	8.3	10
189	A simple approach to measure transmissibility and forecast incidence. <i>Epidemics</i> , 2018 , 22, 29-35	5.1	41
188	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
187	The evolution of antibiotic resistance in a structured host population. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	25

186	Evolution of HIV-1 within untreated individuals and at the population scale in Uganda. <i>PLoS Pathogens</i> , 2018 , 14, e1007167	7.6	15
185	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
184	Ethical considerations in global HIV phylogenetic research. <i>Lancet HIV,the</i> , 2018 , 5, e656-e666	7.8	22
183	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2018 , 35, 719-733	8.3	68
182	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
181	Genomic Infectious Disease Epidemiology in Partially Sampled and Ongoing Outbreaks. <i>Molecular Biology and Evolution</i> , 2017 , 34, 997-1007	8.3	112
180	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
179	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
178	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
177	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
176	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	1.6	13
175	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
174	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
173	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1950-1960	12.3	69
172	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
171	Host population structure and treatment frequency maintain balancing selection on drug resistance. <i>Journal of the Royal Society Interface</i> , 2017 , 14,	4.1	18
170	An evolutionary model to predict the frequency of antibiotic resistance under seasonal antibiotic use, and an application to. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	17
169	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

168	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
167	Quantifying Transmission Heterogeneity Using Both Pathogen Phylogenies and Incidence Time Series. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2982-2995	8.3	24
166	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
165	Effect of the Latent Reservoir on the Evolution of HIV at the Within- and Between-Host Levels. <i>PLoS Computational Biology</i> , 2017 , 13, e1005228	5	14
164	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. <i>PLoS ONE</i> , 2017 , 12, e0189838	3.7	14
163	HIV-1 Sequence Data Coverage in Central East Africa from 1959 to 2013. <i>AIDS Research and Human Retroviruses</i> , 2016 , 32, 904-8	1.6	2
162	Virological failure and development of new resistance mutations according to CD4 count at combination antiretroviral therapy initiation. <i>HIV Medicine</i> , 2016 , 17, 368-72	2.7	5
161	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
160	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
159	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
158	A systematic review of reported reassortant viral lineages of influenza A. <i>BMC Infectious Diseases</i> , 2016 , 16, 3	4	10
157	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016 , 14, e1002394	9.7	95
156	Large Variations in HIV-1 Viral Load Explained by Shifting-Mosaic Metapopulation Dynamics. <i>PLoS Biology</i> , 2016 , 14, e1002567	9.7	11
155	Exposure Patterns Driving Ebola Transmission in West Africa: A Retrospective Observational Study. <i>PLoS Medicine</i> , 2016 , 13, e1002170	11.6	56
154	A transmission-virulence evolutionary trade-off explains attenuation of HIV-1 in Uganda. <i>ELife</i> , 2016 , 5,	8.9	33
153	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
152	Impact and Cost-Effectiveness of Point-Of-Care CD4 Testing on the HIV Epidemic in South Africa. <i>PLoS ONE</i> , 2016 , 11, e0158303	3.7	14
151	Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic. <i>Scientific Reports</i> , 2016 , 6, 39489	4.9	20

150	Evolution of HIV virulence in response to widespread scale up of antiretroviral therapy: a modeling study. <i>Virus Evolution</i> , 2016 , 2, vew028	3.7	13
149	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
148	After Ebola in West Africa--Unpredictable Risks, Preventable Epidemics. <i>New England Journal of Medicine</i> , 2016 , 375, 587-96	59.2	172
147	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
146	HIV treatment-as-prevention research: taking the right road at the crossroads. <i>PLoS Medicine</i> , 2015 , 12, e1001800	11.6	6
145	High heritability is compatible with the broad distribution of set point viral load in HIV carriers. <i>PLoS Pathogens</i> , 2015 , 11, e1004634	7.6	18
144	PANGEA-HIV: phylogenetics for generalised epidemics in Africa. <i>Lancet Infectious Diseases</i> , 2015 , 15, 259-61	25.5	39
143	Ebola virus disease among children in West Africa. <i>New England Journal of Medicine</i> , 2015 , 372, 1274-7	59.2	100
142	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
141	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
140	The role of rapid diagnostics in managing Ebola epidemics. <i>Nature</i> , 2015 , 528, S109-16	50.4	79
139	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
138	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
137	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
136	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
135	Potential Biases in Estimating Absolute and Relative Case-Fatality Risks during Outbreaks. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003846	4.8	124
134	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
133	OutbreakTools: a new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014 , 7, 28-34	5.1	32

132	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
131	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
130	Bayesian reconstruction of disease outbreaks by combining epidemiologic and genomic data. <i>PLoS Computational Biology</i> , 2014 , 10, e1003457	5	142
129	Heterogeneity in the frequency and characteristics of homologous recombination in pneumococcal evolution. <i>PLoS Genetics</i> , 2014 , 10, e1004300	6	55
128	Optimizing the precision of case fatality ratio estimates under the surveillance pyramid approach. <i>American Journal of Epidemiology</i> , 2014 , 180, 1036-46	3.8	9
127	Genomic analysis of emerging pathogens: methods, application and future trends. <i>Genome Biology</i> , 2014 , 15, 541	18.3	18
126	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
125	Virulence and pathogenesis of HIV-1 infection: an evolutionary perspective. <i>Science</i> , 2014 , 343, 1243727 ^{33.3}		163
124	Distinguishing Between Reservoir Exposure and Human-to-Human Transmission for Emerging Pathogens Using Case Onset Data. <i>PLOS Currents</i> , 2014 , 6,		18
123	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
122	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
121	Within-host and between-host evolutionary rates across the HIV-1 genome. <i>Retrovirology</i> , 2013 , 10, 49	3.6	86
120	How the dynamics and structure of sexual contact networks shape pathogen phylogenies. <i>PLoS Computational Biology</i> , 2013 , 9, e1003105	5	35
119	Integrating phylodynamics and epidemiology to estimate transmission diversity in viral epidemics. <i>PLoS Computational Biology</i> , 2013 , 9, e1002876	5	48
118	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
117	How effectively can HIV phylogenies be used to measure heritability?. <i>Evolution, Medicine and Public Health</i> , 2013 , 2013, 209-24	3	16
116	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
115	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

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	3.7	40
113	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	3.7	12
112	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
111	HIV treatment as prevention: optimising the impact of expanded HIV treatment programmes. <i>PLoS Medicine</i> , 2012 , 9, e1001258	11.6	45
110	Phylogenetic inference and model assessment with approximate bayesian computation: influenza as a case study. <i>PLoS Computational Biology</i> , 2012 , 8, e1002835	5	27
109	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
108	HIV treatment as prevention: models, data, and questions--towards evidence-based decision-making. <i>PLoS Medicine</i> , 2012 , 9, e1001259	11.6	57
107	Inferring pandemic growth rates from sequence data. <i>Journal of the Royal Society Interface</i> , 2012 , 9, 1797-808	3.0	30
106	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
105	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
104	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
103	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
102	Rapid pneumococcal evolution in response to clinical interventions. <i>Science</i> , 2011 , 331, 430-4	33.3	680
101	Epidemic growth rate and household reproduction number in communities of households, schools and workplaces. <i>Journal of Mathematical Biology</i> , 2011 , 63, 691-734	2	17
100	Influenza transmission in households during the 1918 pandemic. <i>American Journal of Epidemiology</i> , 2011 , 174, 505-14	3.8	56
99	A strong case for viral genetic factors in HIV virulence. <i>Viruses</i> , 2011 , 3, 204-16	6.2	21
98	Transmission selects for HIV-1 strains of intermediate virulence: a modelling approach. <i>PLoS Computational Biology</i> , 2011 , 7, e1002185	5	30
97	Transmission characteristics of the 2009 H1N1 influenza pandemic: comparison of 8 Southern hemisphere countries. <i>PLoS Pathogens</i> , 2011 , 7, e1002225	7.6	47

96	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
95	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
94	HIV-1 transmitting couples have similar viral load set-points in Rakai, Uganda. <i>PLoS Pathogens</i> , 2010 , 6, e1000876	7.6	79
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