

Simon Frost

List of Publications by Year in descending order

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Version: 2024-02-01

126
papers

16,303
citations

39113

52
h-index

23173

116
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130
all docs

130
docs citations

130
times ranked

18636
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome analysis to determine the rate and patterns of intra-subtype reassortment among influenza type-A viruses in Africa. <i>Virus Evolution</i> , 2022, 8, veac005.	2.2	4
2	Molecular Epidemiology and Evolutionary Dynamics of Human Influenza Type-A Viruses in Africa: A Systematic Review. <i>Microorganisms</i> , 2022, 10, 900.	1.6	2
3	Phylogenetic Characterization of Crimean-Congo Hemorrhagic Fever Virus Detected in African Blue Ticks Feeding on Cattle in a Ugandan Abattoir. <i>Microorganisms</i> , 2021, 9, 438.	1.6	11
4	Molecular epidemiology of dengue in a setting of low reported endemicity: Kupang, East Nusa Tenggara province, Indonesia. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2021, 115, 1304-1316.	0.7	0
5	HyPhy 2.5: A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. <i>Molecular Biology and Evolution</i> , 2020, 37, 295-299.	3.5	342
6	Distinct Dengue Disease Epidemiology, Clinical, and Diagnosis Features in Western, Central, and Eastern Regions of Indonesia, 2017-2019. <i>Frontiers in Medicine</i> , 2020, 7, 582235.	1.2	4
7	Identification of Hidden Population Structure in Time-Scaled Phylogenies. <i>Systematic Biology</i> , 2020, 69, 884-896.	2.7	26
8	Assessment of a multiplex PCR and Nanopore-based method for dengue virus sequencing in Indonesia. <i>Virology Journal</i> , 2020, 17, 24.	1.4	26
9	Cross-Continental Dispersal of Major HIV-1 CRF01_AE Clusters in China. <i>Frontiers in Microbiology</i> , 2020, 11, 61.	1.5	10
10	Disease control across urban-rural gradients. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200775.	1.5	16
11	An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008934.	1.3	6
12	An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934.		0
13	An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934.		0
14	An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934.		0
15	An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934.		0
16	Fast hierarchical Bayesian analysis of population structure. <i>Nucleic Acids Research</i> , 2019, 47, 5539-5549.	6.5	173
17	Genome-Wide Patterns of Gene Expression in a Wild Primate Indicate Species-Specific Mechanisms Associated with Tolerance to Natural Simian Immunodeficiency Virus Infection. <i>Genome Biology and Evolution</i> , 2019, 11, 1630-1643.	1.1	10
18	genieR: An R package for inference of demographic history of phylogenies. <i>Journal of Open Source Software</i> , 2019, 4, 634.	2.0	0

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19	Neutral Theory and Rapidly Evolving Viral Pathogens. <i>Molecular Biology and Evolution</i> , 2018, 35, 1348-1354.	3.5	58
20	The role of venues in structuring HIV, sexually transmitted infections, and risk networks among men who have sex with men. <i>BMC Public Health</i> , 2018, 18, 225.	1.2	8
21	Genotype-Specific Evolution of Hepatitis E Virus. <i>Journal of Virology</i> , 2017, 91, .	1.5	27
22	Modeling and Analyzing Respondent-Driven Sampling as a Counting Process. <i>Biometrics</i> , 2017, 73, 1189-1198.	0.8	9
23	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
24	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	3.5	53
25	The changing molecular epidemiology of HIV in the Philippines. <i>International Journal of Infectious Diseases</i> , 2017, 61, 44-50.	1.5	15
26	Adaptation of avian influenza virus to a swine host. <i>Virus Evolution</i> , 2017, 3, vex007.	2.2	15
27	Biased phylodynamic inferences from analysing clusters of viral sequences. <i>Virus Evolution</i> , 2017, 3, vex020.	2.2	37
28	Assessing Commitment and Reporting Fidelity to a Text Message-Based Participatory Surveillance in Rural Western Uganda. <i>PLoS ONE</i> , 2016, 11, e0155971.	1.1	4
29	Surveys, Serologies, and Sequences Reveal History of Iatrogenic Transmission of HIV-1. <i>Journal of Infectious Diseases</i> , 2016, 214, 341-343.	1.9	1
30	Gillespie.jl: Stochastic Simulation Algorithm in Julia. <i>Journal of Open Source Software</i> , 2016, 1, 42.	2.0	1
31	Assigning and visualizing germline genes in antibody repertoires. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140240.	1.8	20
32	Understanding Drivers of Phylogenetic Clustering in Molecular Epidemiological Studies of HIV. <i>Journal of Infectious Diseases</i> , 2015, 211, 856-858.	1.9	18
33	Genomic Characterization of Two Novel HIV-1 Second-Generation Recombinant Forms Among Men Who Have Sex with Men in Beijing, China. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 342-346.	0.5	14
34	Modeling infectious disease dynamics in the complex landscape of global health. <i>Science</i> , 2015, 347, aaa4339.	6.0	492
35	Genomic Characterization of Two Novel HIV-1 Unique (CRF01_AE/B) Recombinant Forms Among Men Who Have Sex with Men in Beijing, China. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 921-925.	0.5	8
36	Eight challenges in phylodynamic inference. <i>Epidemics</i> , 2015, 10, 88-92.	1.5	131

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37	Assessing the use of hospital staff influenza-like absence (ILA) for enhancing hospital preparedness and national surveillance. <i>BMC Infectious Diseases</i> , 2015, 15, 110.	1.3	9
38	Measuring Asymmetry in Time-Stamped Phylogenies. <i>PLoS Computational Biology</i> , 2015, 11, e1004312.	1.5	28
39	Sampling through time and phylodynamic inference with coalescent and birth-death models. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140945.	1.5	53
40	HIV Prevalence and Demographic Determinants of Unprotected Anal Sex and HIV Testing Among Men Who Have Sex with Men in Beirut, Lebanon. <i>Archives of Sexual Behavior</i> , 2014, 43, 779-788.	1.2	29
41	OutbreakTools: A new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014, 7, 28-34.	1.5	37
42	Beyond Bushmeat: Animal Contact, Injury, and Zoonotic Disease Risk in Western Uganda. <i>EcoHealth</i> , 2014, 11, 534-543.	0.9	54
43	Inferring the Source of Transmission with Phylogenetic Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003397.	1.5	65
44	Can Non-lytic CD8+ T Cells Drive HIV-1 Escape?. <i>PLoS Pathogens</i> , 2013, 9, e1003656.	2.1	29
45	Modelling tree shape and structure in viral phylodynamics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120208.	1.8	61
46	Individual and Network Factors Associated With Prevalent Hepatitis C Infection Among Rural Appalachian Injection Drug Users. <i>American Journal of Public Health</i> , 2013, 103, e44-e52.	1.5	140
47	Genetic Imprint of Vaccination on Simian/Human Immunodeficiency Virus Type 1 Transmitted Viral Genomes in Rhesus Macaques. <i>PLoS ONE</i> , 2013, 8, e70814.	1.1	1
48	Respondent Driven Sampling: Determinants of Recruitment and a Method to Improve Point Estimation. <i>PLoS ONE</i> , 2013, 8, e78402.	1.1	27
49	Respondent driven sampling—where we are and where should we be going?: Table 1. <i>Sexually Transmitted Infections</i> , 2012, 88, 397-399.	0.8	62
50	Simple Epidemiological Dynamics Explain Phylogenetic Clustering of HIV from Patients with Recent Infection. <i>PLoS Computational Biology</i> , 2012, 8, e1002552.	1.5	89
51	Mixed Adjuvant Formulations Reveal a New Combination That Elicit Antibody Response Comparable to Freund's Adjuvants. <i>PLoS ONE</i> , 2012, 7, e35083.	1.1	44
52	Evaluation of Respondent-driven Sampling. <i>Epidemiology</i> , 2012, 23, 138-147.	1.2	229
53	A Random Effects Branch-Site Model for Detecting Episodic Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 3033-3043.	3.5	383
54	Transmitted Drug Resistance in the CFAR Network of Integrated Clinical Systems Cohort: Prevalence and Effects on Pre-Therapy CD4 and Viral Load. <i>PLoS ONE</i> , 2011, 6, e21189.	1.1	28

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55	Evaluation of the role of location and distance in recruitment in respondent-driven sampling. <i>International Journal of Health Geographics</i> , 2011, 10, 56.	1.2	29
56	Capture-recapture methods and respondent-driven sampling: their potential and limitations. <i>Sexually Transmitted Infections</i> , 2011, 87, 267-268.	0.8	18
57	Molecular Evolution Analysis of the Human Immunodeficiency Virus Type 1 Envelope in Simian/Human Immunodeficiency Virus-Infected Macaques: Implications for Challenge Dose Selection. <i>Journal of Virology</i> , 2011, 85, 10332-10345.	1.5	15
58	Deep Molecular Characterization of HIV-1 Dynamics under Suppressive HAART. <i>PLoS Pathogens</i> , 2011, 7, e1002314.	2.1	55
59	Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. <i>Bioinformatics</i> , 2010, 26, 2455-2457.	1.8	1,158
60	Evolutionary Fingerprinting of Genes. <i>Molecular Biology and Evolution</i> , 2010, 27, 520-536.	3.5	57
61	Viral phylodynamics and the search for an "effective number of infections"™. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1879-1890.	1.8	123
62	Phylogenetic Analysis of Population-Based and Deep Sequencing Data to Identify Coevolving Sites in the nef Gene of HIV-1. <i>Molecular Biology and Evolution</i> , 2010, 27, 819-832.	3.5	59
63	Epidemiological bridging by injection drug use drives an early HIV epidemic. <i>Epidemics</i> , 2010, 2, 155-164.	1.5	26
64	Rapid social network assessment for predicting HIV and STI risk among men attending bars and clubs in San Diego, California. <i>Sexually Transmitted Infections</i> , 2010, 86, iii17-iii23.	0.8	21
65	Estimating selection pressures on alignments of coding sequences. , 2009, , 419-490.		14
66	An Evolutionary Model-Based Algorithm for Accurate Phylogenetic Breakpoint Mapping and Subtype Prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009, 5, e1000581.	1.5	151
67	Phylodynamics of Infectious Disease Epidemics. <i>Genetics</i> , 2009, 183, 1421-1430.	1.2	200
68	Pleocytosis is associated with disruption of HIV compartmentalization between blood and cerebral spinal fluid viral populations. <i>Virology</i> , 2009, 385, 204-208.	1.1	29
69	Low-level plasma HIVs in patients on prolonged suppressive highly active antiretroviral therapy are produced mostly by cells other than CD4 T-cells. <i>Journal of Medical Virology</i> , 2009, 81, 9-15.	2.5	47
70	Using Respondent-Driven Sampling in a Hidden Population at Risk of HIV Infection: Who Do HIV-Positive Recruiters Recruit?. <i>Sexually Transmitted Diseases</i> , 2009, 36, 750-756.	0.8	55
71	A public health model for the molecular surveillance of HIV transmission in San Diego, California. <i>Aids</i> , 2009, 23, 225-232.	1.0	111
72	Detecting Signatures of Selection from DNA Sequences Using Datamonkey. <i>Methods in Molecular Biology</i> , 2009, 537, 163-183.	0.4	71

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73	Parsing Social Network Survey Data from Hidden Populations Using Stochastic Context-Free Grammars. <i>PLoS ONE</i> , 2009, 4, e6777.	1.1	14
74	Estimating selection pressures on HIV-1 using phylogenetic likelihood models. <i>Statistics in Medicine</i> , 2008, 27, 4779-4789.	0.8	19
75	CCL3L1-CCR5 genotype influences durability of immune recovery during antiretroviral therapy of HIV-1-infected individuals. <i>Nature Medicine</i> , 2008, 14, 413-420.	15.2	118
76	Syringe possession arrests are associated with receptive syringe sharing in two Mexico-US border cities. <i>Addiction</i> , 2008, 103, 101-108.	1.7	118
77	Immune-driven recombination and loss of control after HIV superinfection. <i>Journal of Experimental Medicine</i> , 2008, 205, 1789-1796.	4.2	106
78	Persistence of Transmitted Drug Resistance among Subjects with Primary Human Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2008, 82, 5510-5518.	1.5	192
79	High-Risk Sexual and Drug Using Behaviors Among Male Injection Drug Users Who Have Sex With Men in 2 Mexico-US Border Cities. <i>Sexually Transmitted Diseases</i> , 2008, 35, 243-249.	0.8	44
80	A Maximum Likelihood Method for Detecting Directional Evolution in Protein Sequences and Its Application to Influenza A Virus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1809-1824.	3.5	106
81	Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models. <i>Bioinformatics</i> , 2008, 24, 1949-1950.	1.8	75
82	Sexual networks and the transmission of drug-resistant HIV. <i>Current Opinion in Infectious Diseases</i> , 2008, 21, 644-652.	1.3	8
83	Herpes Simplex Virus Type 2 Acquisition During Recent HIV Infection Does Not Influence Plasma HIV Levels. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2008, 47, 592-596.	0.9	11
84	Antibody responses in primary HIV-1 infection. <i>Current Opinion in HIV and AIDS</i> , 2008, 3, 45-51.	1.5	18
85	Using sexual affiliation networks to describe the sexual structure of a population. <i>Sexually Transmitted Infections</i> , 2007, 83, i37-i42.	0.8	46
86	Adaptation to Human Populations Is Revealed by Within-Host Polymorphisms in HIV-1 and Hepatitis C Virus. <i>PLoS Pathogens</i> , 2007, 3, e45.	2.1	51
87	Evolutionary Interactions between N-Linked Glycosylation Sites in the HIV-1 Envelope. <i>PLoS Computational Biology</i> , 2007, 3, e11.	1.5	63
88	An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. <i>PLoS Computational Biology</i> , 2007, 3, e231.	1.5	103
89	Herpes Simplex Virus Type 2 Infection Does Not Influence Viral Dynamics during Early HIV-1 Infection. <i>Journal of Infectious Diseases</i> , 2007, 195, 1270-1277.	1.9	21
90	Comparative Study of Methods for Detecting Sequence Compartmentalization in Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2007, 81, 6643-6651.	1.5	97

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91	Long-Term Persistence of Transmitted HIV Drug Resistance in Male Genital Tract Secretions: Implications for Secondary Transmission. <i>Journal of Infectious Diseases</i> , 2007, 196, 356-360.	1.9	61
92	Mapping Protease Inhibitor Resistance to Human Immunodeficiency Virus Type 1 Sequence Polymorphisms within Patients. <i>Journal of Virology</i> , 2007, 81, 13598-13607.	1.5	20
93	Hepatitis C virus and alanine aminotransferase kinetics following B-lymphocyte depletion with rituximab: evidence for a significant role of humoral immunity in the control of viremia in chronic HCV liver disease. <i>Blood</i> , 2007, 109, 845-846.	0.6	55
94	Evolution of the interferon alpha gene family in eutherian mammals. <i>Gene</i> , 2007, 397, 38-50.	1.0	68
95	Computational analysis and identification of amino acid sites in dengue E proteins relevant to development of diagnostics and vaccines. <i>Virus Genes</i> , 2007, 35, 175-186.	0.7	34
96	Respondent-Driven Sampling of Injection Drug Users in Two U.S.-Mexico Border Cities: Recruitment Dynamics and Impact on Estimates of HIV and Syphilis Prevalence. <i>Journal of Urban Health</i> , 2006, 83, 83-97.	1.8	120
97	Lack of neutralizing antibody response to HIV-1 predisposes to superinfection. <i>Virology</i> , 2006, 355, 1-5.	1.1	94
98	Evolutionary Model Selection with a Genetic Algorithm: A Case Study Using Stem RNA. <i>Molecular Biology and Evolution</i> , 2006, 24, 159-170.	3.5	17
99	Adaptation to Different Human Populations by HIV-1 Revealed by Codon-Based Analyses. <i>PLoS Computational Biology</i> , 2006, 2, e62.	1.5	209
100	A Dirichlet process model for detecting positive selection in protein-coding DNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6263-6268.	3.3	87
101	GARD: a genetic algorithm for recombination detection. <i>Bioinformatics</i> , 2006, 22, 3096-3098.	1.8	750
102	Automated Phylogenetic Detection of Recombination Using a Genetic Algorithm. <i>Molecular Biology and Evolution</i> , 2006, 23, 1891-1901.	3.5	866
103	Characteristics of Recently HIV-Infected Men Who Use the Internet to Find Male Sex Partners and Sexual Practices With Those Partners. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2006, 43, 582-587.	0.9	21
104	A Simple Hierarchical Approach to Modeling Distributions of Substitution Rates. <i>Molecular Biology and Evolution</i> , 2005, 22, 223-234.	3.5	59
105	Datamonkey: rapid detection of selective pressure on individual sites of codon alignments. <i>Bioinformatics</i> , 2005, 21, 2531-2533.	1.8	1,223
106	Characterization of Human Immunodeficiency Virus Type 1 (HIV-1) Envelope Variation and Neutralizing Antibody Responses during Transmission of HIV-1 Subtype B. <i>Journal of Virology</i> , 2005, 79, 6523-6527.	1.5	171
107	A Genetic Algorithm Approach to Detecting Lineage-Specific Variation in Selection Pressure. <i>Molecular Biology and Evolution</i> , 2005, 22, 478-485.	3.5	178
108	Phenotypic Hypersusceptibility to Multiple Protease Inhibitors and Low Replicative Capacity in Patients Who Are Chronically Infected with Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2005, 79, 5907-5913.	1.5	14

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109	HyPhy: hypothesis testing using phylogenies. <i>Bioinformatics</i> , 2005, 21, 676-679.	1.8	2,599
110	Neutralizing antibody responses drive the evolution of human immunodeficiency virus type 1 envelope during recent HIV infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18514-18519.	3.3	313
111	Not So Different After All: A Comparison of Methods for Detecting Amino Acid Sites Under Selection. <i>Molecular Biology and Evolution</i> , 2005, 22, 1208-1222.	3.5	1,965
112	An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. <i>PLoS Computational Biology</i> , 2005, preprint, e231.	1.5	0
113	Genetic Basis of Hypersusceptibility to Protease Inhibitors and Low Replicative Capacity of Human Immunodeficiency Virus Type 1 Strains in Primary Infection. <i>Journal of Virology</i> , 2004, 78, 2242-2246.	1.5	23
114	Viral kinetics and hepatitis C. <i>Hepatology</i> , 2003, 38, 1588-1588.	3.6	3
115	Transmission Fitness of Drug-Resistant Human Immunodeficiency Virus and the Prevalence of Resistance in the Antiretroviral-Treated Population. <i>Journal of Infectious Diseases</i> , 2003, 187, 683-686.	1.9	162
116	Human Immunodeficiency Virus-1 RNA Levels in Cerebrospinal Fluid Exhibit a Set Point in Clinically Stable Patients Not Receiving Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2003, 187, 1818-1821.	1.9	12
117	Viral Dynamics during Structured Treatment Interruptions of Chronic Human Immunodeficiency Virus Type 1 Infection. <i>Journal of Virology</i> , 2002, 76, 968-979.	1.5	52
118	Viral Evolution during Structured Treatment Interruptions in Chronically Human Immunodeficiency Virus-Infected Individuals. <i>Journal of Virology</i> , 2002, 76, 12344-12348.	1.5	26
119	Selection of drug-resistant HIV-1 mutants in response to repeated structured treatment interruptions. <i>Aids</i> , 2002, 16, 895-899.	1.0	85
120	Amprenavir-resistant HIV-1 exhibits lopinavir cross-resistance and reduced replication capacity. <i>Aids</i> , 2002, 16, 1009-1017.	1.0	92
121	Dynamics and evolution of HIV-1 during structured treatment interruptions. <i>AIDS Reviews</i> , 2002, 4, 119-27.	0.5	8
122	HIV dynamics and T-cell immunity after three structured treatment interruptions in chronic HIV-1 infection. <i>Aids</i> , 2001, 15, F19-F27.	1.0	135
123	Evolution of Lamivudine Resistance in Human Immunodeficiency Virus Type 1-Infected Individuals: the Relative Roles of Drift and Selection. <i>Journal of Virology</i> , 2000, 74, 6262-6268.	1.5	152
124	Phylogenetic analysis of GBV-C/hepatitis G virus. <i>Journal of General Virology</i> , 2000, 81, 769-780.	1.3	61
125	Evolution of Envelope Sequences of Human Immunodeficiency Virus Type 1 in Cellular Reservoirs in the Setting of Potent Antiviral Therapy. <i>Journal of Virology</i> , 1999, 73, 9404-9412.	1.5	187
126	The Role of Viral Genetic Variability in HIV-Associated Neurocognitive Disorder. , 0, , 201-218.		0