

Simon Frost

List of Publications by Year in descending order

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Version: 2024-02-01

126
papers

16,303
citations

34105

52
h-index

20358

116
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130
all docs

130
docs citations

130
times ranked

16850
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | HyPhy: hypothesis testing using phylogenies. <i>Bioinformatics</i> , 2005, 21, 676-679. | 4.1 | 2,599 |
| 2 | 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. | 8.9 | 1,965 |
| 3 | Datamonkey: rapid detection of selective pressure on individual sites of codon alignments. <i>Bioinformatics</i> , 2005, 21, 2531-2533. | 4.1 | 1,223 |
| 4 | Datamonkey 2010: a suite of phylogenetic analysis tools for evolutionary biology. <i>Bioinformatics</i> , 2010, 26, 2455-2457. | 4.1 | 1,158 |
| 5 | Automated Phylogenetic Detection of Recombination Using a Genetic Algorithm. <i>Molecular Biology and Evolution</i> , 2006, 23, 1891-1901. | 8.9 | 866 |
| 6 | GARD: a genetic algorithm for recombination detection. <i>Bioinformatics</i> , 2006, 22, 3096-3098. | 4.1 | 750 |
| 7 | Modeling infectious disease dynamics in the complex landscape of global health. <i>Science</i> , 2015, 347, aaa4339. | 12.6 | 492 |
| 8 | A Random Effects Branch-Site Model for Detecting Episodic Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2011, 28, 3033-3043. | 8.9 | 383 |
| 9 | HyPhy 2.5 – A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. <i>Molecular Biology and Evolution</i> , 2020, 37, 295-299. | 8.9 | 342 |
| 10 | 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. | 7.1 | 313 |
| 11 | Evaluation of Respondent-driven Sampling. <i>Epidemiology</i> , 2012, 23, 138-147. | 2.7 | 229 |
| 12 | Adaptation to Different Human Populations by HIV-1 Revealed by Codon-Based Analyses. <i>PLoS Computational Biology</i> , 2006, 2, e62. | 3.2 | 209 |
| 13 | Phylodynamics of Infectious Disease Epidemics. <i>Genetics</i> , 2009, 183, 1421-1430. | 2.9 | 200 |
| 14 | Persistence of Transmitted Drug Resistance among Subjects with Primary Human Immunodeficiency Virus Infection. <i>Journal of Virology</i> , 2008, 82, 5510-5518. | 3.4 | 192 |
| 15 | 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. | 3.4 | 187 |
| 16 | A Genetic Algorithm Approach to Detecting Lineage-Specific Variation in Selection Pressure. <i>Molecular Biology and Evolution</i> , 2005, 22, 478-485. | 8.9 | 178 |
| 17 | Fast hierarchical Bayesian analysis of population structure. <i>Nucleic Acids Research</i> , 2019, 47, 5539-5549. | 14.5 | 173 |
| 18 | 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. | 3.4 | 171 |

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|----|---|------|-----------|
| 19 | 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. | 4.0 | 162 |
| 20 | 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. | 3.4 | 152 |
| 21 | An Evolutionary Model-Based Algorithm for Accurate Phylogenetic Breakpoint Mapping and Subtype Prediction in HIV-1. <i>PLoS Computational Biology</i> , 2009, 5, e1000581. | 3.2 | 151 |
| 22 | 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. | 2.7 | 140 |
| 23 | HIV dynamics and T-cell immunity after three structured treatment interruptions in chronic HIV-1 infection. <i>Aids</i> , 2001, 15, F19-F27. | 2.2 | 135 |
| 24 | Eight challenges in phylodynamic inference. <i>Epidemics</i> , 2015, 10, 88-92. | 3.0 | 131 |
| 25 | 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. | 4.0 | 123 |
| 26 | 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. | 3.6 | 120 |
| 27 | CCL3L1-CCR5 genotype influences durability of immune recovery during antiretroviral therapy of HIV-1-infected individuals. <i>Nature Medicine</i> , 2008, 14, 413-420. | 30.7 | 118 |
| 28 | Syringe possession arrests are associated with receptive syringe sharing in two Mexico-US border cities. <i>Addiction</i> , 2008, 103, 101-108. | 3.3 | 118 |
| 29 | A public health model for the molecular surveillance of HIV transmission in San Diego, California. <i>Aids</i> , 2009, 23, 225-232. | 2.2 | 111 |
| 30 | Immune-driven recombination and loss of control after HIV superinfection. <i>Journal of Experimental Medicine</i> , 2008, 205, 1789-1796. | 8.5 | 106 |
| 31 | 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. | 8.9 | 106 |
| 32 | An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. <i>PLoS Computational Biology</i> , 2007, 3, e231. | 3.2 | 103 |
| 33 | Comparative Study of Methods for Detecting Sequence Compartmentalization in Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2007, 81, 6643-6651. | 3.4 | 97 |
| 34 | Lack of neutralizing antibody response to HIV-1 predisposes to superinfection. <i>Virology</i> , 2006, 355, 1-5. | 2.4 | 94 |
| 35 | Amprenavir-resistant HIV-1 exhibits lopinavir cross-resistance and reduced replication capacity. <i>Aids</i> , 2002, 16, 1009-1017. | 2.2 | 92 |
| 36 | Simple Epidemiological Dynamics Explain Phylogenetic Clustering of HIV from Patients with Recent Infection. <i>PLoS Computational Biology</i> , 2012, 8, e1002552. | 3.2 | 89 |

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|----|---|-----|-----------|
| 37 | A Dirichlet process model for detecting positive selection in protein-coding DNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6263-6268. | 7.1 | 87 |
| 38 | Selection of drug-resistant HIV-1 mutants in response to repeated structured treatment interruptions. Aids, 2002, 16, 895-899. | 2.2 | 85 |
| 39 | Spidermonkey: rapid detection of co-evolving sites using Bayesian graphical models. Bioinformatics, 2008, 24, 1949-1950. | 4.1 | 75 |
| 40 | Detecting Signatures of Selection from DNA Sequences Using Datamonkey. Methods in Molecular Biology, 2009, 537, 163-183. | 0.9 | 71 |
| 41 | Evolution of the interferon alpha gene family in eutherian mammals. Gene, 2007, 397, 38-50. | 2.2 | 68 |
| 42 | Inferring the Source of Transmission with Phylogenetic Data. PLoS Computational Biology, 2013, 9, e1003397. | 3.2 | 65 |
| 43 | Evolutionary Interactions between N-Linked Glycosylation Sites in the HIV-1 Envelope. PLoS Computational Biology, 2007, 3, e11. | 3.2 | 63 |
| 44 | Respondent driven sampling—where we are and where should we be going?: Table 1. Sexually Transmitted Infections, 2012, 88, 397-399. | 1.9 | 62 |
| 45 | Long-Term Persistence of Transmitted HIV Drug Resistance in Male Genital Tract Secretions: Implications for Secondary Transmission. Journal of Infectious Diseases, 2007, 196, 356-360. | 4.0 | 61 |
| 46 | Modelling tree shape and structure in viral phylodynamics. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120208. | 4.0 | 61 |
| 47 | Phylogenetic analysis of GBV-C/hepatitis G virus. Journal of General Virology, 2000, 81, 769-780. | 2.9 | 61 |
| 48 | A Simple Hierarchical Approach to Modeling Distributions of Substitution Rates. Molecular Biology and Evolution, 2005, 22, 223-234. | 8.9 | 59 |
| 49 | Phylogenetic Analysis of Population-Based and Deep Sequencing Data to Identify Coevolving Sites in the nef Gene of HIV-1. Molecular Biology and Evolution, 2010, 27, 819-832. | 8.9 | 59 |
| 50 | Neutral Theory and Rapidly Evolving Viral Pathogens. Molecular Biology and Evolution, 2018, 35, 1348-1354. | 8.9 | 58 |
| 51 | Evolutionary Fingerprinting of Genes. Molecular Biology and Evolution, 2010, 27, 520-536. | 8.9 | 57 |
| 52 | 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. Blood, 2007, 109, 845-846. | 1.4 | 55 |
| 53 | Using Respondent-Driven Sampling in a Hidden Population at Risk of HIV Infection: Who Do HIV-Positive Recruiters Recruit?. Sexually Transmitted Diseases, 2009, 36, 750-756. | 1.7 | 55 |
| 54 | Deep Molecular Characterization of HIV-1 Dynamics under Suppressive HAART. PLoS Pathogens, 2011, 7, e1002314. | 4.7 | 55 |

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|----|---|-----|-----------|
| 55 | Beyond Bushmeat: Animal Contact, Injury, and Zoonotic Disease Risk in Western Uganda. <i>EcoHealth</i> , 2014, 11, 534-543. | 2.0 | 54 |
| 56 | Sampling through time and phylodynamic inference with coalescent and birth-death models. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140945. | 3.4 | 53 |
| 57 | Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203. | 8.9 | 53 |
| 58 | Viral Dynamics during Structured Treatment Interruptions of Chronic Human Immunodeficiency Virus Type 1 Infection. <i>Journal of Virology</i> , 2002, 76, 968-979. | 3.4 | 52 |
| 59 | Adaptation to Human Populations Is Revealed by Within-Host Polymorphisms in HIV-1 and Hepatitis C Virus. <i>PLoS Pathogens</i> , 2007, 3, e45. | 4.7 | 51 |
| 60 | 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. | 5.0 | 47 |
| 61 | Using sexual affiliation networks to describe the sexual structure of a population. <i>Sexually Transmitted Infections</i> , 2007, 83, i37-i42. | 1.9 | 46 |
| 62 | 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. | 1.7 | 44 |
| 63 | Mixed Adjuvant Formulations Reveal a New Combination That Elicit Antibody Response Comparable to Freund's Adjuvants. <i>PLoS ONE</i> , 2012, 7, e35083. | 2.5 | 44 |
| 64 | OutbreakTools: A new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014, 7, 28-34. | 3.0 | 37 |
| 65 | Biased phylodynamic inferences from analysing clusters of viral sequences. <i>Virus Evolution</i> , 2017, 3, vex020. | 4.9 | 37 |
| 66 | 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. | 1.6 | 34 |
| 67 | Pleocytosis is associated with disruption of HIV compartmentalization between blood and cerebral spinal fluid viral populations. <i>Virology</i> , 2009, 385, 204-208. | 2.4 | 29 |
| 68 | Evaluation of the role of location and distance in recruitment in respondent-driven sampling. <i>International Journal of Health Geographics</i> , 2011, 10, 56. | 2.5 | 29 |
| 69 | Can Non-lytic CD8+ T Cells Drive HIV-1 Escape?. <i>PLoS Pathogens</i> , 2013, 9, e1003656. | 4.7 | 29 |
| 70 | 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. | 1.9 | 29 |
| 71 | 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. | 2.5 | 28 |
| 72 | Measuring Asymmetry in Time-Stamped Phylogenies. <i>PLoS Computational Biology</i> , 2015, 11, e1004312. | 3.2 | 28 |

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|----|--|-----|-----------|
| 73 | Respondent Driven Sampling: Determinants of Recruitment and a Method to Improve Point Estimation. PLoS ONE, 2013, 8, e78402. | 2.5 | 27 |
| 74 | Genotype-Specific Evolution of Hepatitis E Virus. Journal of Virology, 2017, 91, . | 3.4 | 27 |
| 75 | Viral Evolution during Structured Treatment Interruptions in Chronically Human Immunodeficiency Virus-Infected Individuals. Journal of Virology, 2002, 76, 12344-12348. | 3.4 | 26 |
| 76 | Epidemiological bridging by injection drug use drives an early HIV epidemic. Epidemics, 2010, 2, 155-164. | 3.0 | 26 |
| 77 | Identification of Hidden Population Structure in Time-Scaled Phylogenies. Systematic Biology, 2020, 69, 884-896. | 5.6 | 26 |
| 78 | Assessment of a multiplex PCR and Nanopore-based method for dengue virus sequencing in Indonesia. Virology Journal, 2020, 17, 24. | 3.4 | 26 |
| 79 | Genetic Basis of Hypersusceptibility to Protease Inhibitors and Low Replicative Capacity of Human Immunodeficiency Virus Type 1 Strains in Primary Infection. Journal of Virology, 2004, 78, 2242-2246. | 3.4 | 23 |
| 80 | Herpes Simplex Virus Type 2 Infection Does Not Influence Viral Dynamics during Early HIV-1 Infection. Journal of Infectious Diseases, 2007, 195, 1270-1277. | 4.0 | 21 |
| 81 | Rapid social network assessment for predicting HIV and STI risk among men attending bars and clubs in San Diego, California. Sexually Transmitted Infections, 2010, 86, iii17-iii23. | 1.9 | 21 |
| 82 | Characteristics of Recently HIV-Infected Men Who Use the Internet to Find Male Sex Partners and Sexual Practices With Those Partners. Journal of Acquired Immune Deficiency Syndromes (1999), 2006, 43, 582-587. | 2.1 | 21 |
| 83 | Mapping Protease Inhibitor Resistance to Human Immunodeficiency Virus Type 1 Sequence Polymorphisms within Patients. Journal of Virology, 2007, 81, 13598-13607. | 3.4 | 20 |
| 84 | Assigning and visualizing germline genes in antibody repertoires. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140240. | 4.0 | 20 |
| 85 | Estimating selection pressures on HIV-1 using phylogenetic likelihood models. Statistics in Medicine, 2008, 27, 4779-4789. | 1.6 | 19 |
| 86 | Antibody responses in primary HIV-1 infection. Current Opinion in HIV and AIDS, 2008, 3, 45-51. | 3.8 | 18 |
| 87 | Capture-recapture methods and respondent-driven sampling: their potential and limitations. Sexually Transmitted Infections, 2011, 87, 267-268. | 1.9 | 18 |
| 88 | Understanding Drivers of Phylogenetic Clustering in Molecular Epidemiological Studies of HIV. Journal of Infectious Diseases, 2015, 211, 856-858. | 4.0 | 18 |
| 89 | HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. AIDS Research and Human Retroviruses, 2017, 33, 1083-1098. | 1.1 | 18 |
| 90 | Evolutionary Model Selection with a Genetic Algorithm: A Case Study Using Stem RNA. Molecular Biology and Evolution, 2006, 24, 159-170. | 8.9 | 17 |

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| 91 | Disease control across urban-rural gradients. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200775. | 3.4 | 16 |
| 92 | 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. | 3.4 | 15 |
| 93 | The changing molecular epidemiology of HIV in the Philippines. <i>International Journal of Infectious Diseases</i> , 2017, 61, 44-50. | 3.3 | 15 |
| 94 | Adaptation of avian influenza virus to a swine host. <i>Virus Evolution</i> , 2017, 3, vex007. | 4.9 | 15 |
| 95 | 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. | 3.4 | 14 |
| 96 | Estimating selection pressures on alignments of coding sequences. , 2009, , 419-490. | | 14 |
| 97 | 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. | 1.1 | 14 |
| 98 | Parsing Social Network Survey Data from Hidden Populations Using Stochastic Context-Free Grammars. <i>PLoS ONE</i> , 2009, 4, e6777. | 2.5 | 14 |
| 99 | 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. | 4.0 | 12 |
| 100 | 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. | 2.1 | 11 |
| 101 | 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. | 3.6 | 11 |
| 102 | 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. | 2.5 | 10 |
| 103 | Cross-Continental Dispersal of Major HIV-1 CRF01_AE Clusters in China. <i>Frontiers in Microbiology</i> , 2020, 11, 61. | 3.5 | 10 |
| 104 | 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. | 2.9 | 9 |
| 105 | Modeling and Analyzing Respondent-Driven Sampling as a Counting Process. <i>Biometrics</i> , 2017, 73, 1189-1198. | 1.4 | 9 |
| 106 | Sexual networks and the transmission of drug-resistant HIV. <i>Current Opinion in Infectious Diseases</i> , 2008, 21, 644-652. | 3.1 | 8 |
| 107 | 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. | 1.1 | 8 |
| 108 | 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. | 2.9 | 8 |

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|-----|---|-----|-----------|
| 109 | Dynamics and evolution of HIV-1 during structured treatment interruptions. <i>AIDS Reviews</i> , 2002, 4, 119-27. | 1.0 | 8 |
| 110 | An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008934. | 3.0 | 6 |
| 111 | Assessing Commitment and Reporting Fidelity to a Text Message-Based Participatory Surveillance in Rural Western Uganda. <i>PLoS ONE</i> , 2016, 11, e0155971. | 2.5 | 4 |
| 112 | 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. | 2.6 | 4 |
| 113 | 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. | 4.9 | 4 |
| 114 | Viral kinetics and hepatitis C. <i>Hepatology</i> , 2003, 38, 1588-1588. | 7.3 | 3 |
| 115 | Molecular Epidemiology and Evolutionary Dynamics of Human Influenza Type-A Viruses in Africa: A Systematic Review. <i>Microorganisms</i> , 2022, 10, 900. | 3.6 | 2 |
| 116 | Genetic Imprint of Vaccination on Simian/Human Immunodeficiency Virus Type 1 Transmitted Viral Genomes in Rhesus Macaques. <i>PLoS ONE</i> , 2013, 8, e70814. | 2.5 | 1 |
| 117 | Surveys, Serologies, and Sequences Reveal History of Iatrogenic Transmission of HIV-1. <i>Journal of Infectious Diseases</i> , 2016, 214, 341-343. | 4.0 | 1 |
| 118 | Gillespie.jl: Stochastic Simulation Algorithm in Julia. <i>Journal of Open Source Software</i> , 2016, 1, 42. | 4.6 | 1 |
| 119 | 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. | 1.8 | 0 |
| 120 | An Evolutionary-Network Model Reveals Stratified Interactions in the V3 Loop of the HIV-1 Envelope. <i>PLoS Computational Biology</i> , 2005, preprint, e231. | 3.2 | 0 |
| 121 | The Role of Viral Genetic Variability in HIV-Associated Neurocognitive Disorder. , 0, , 201-218. | | 0 |
| 122 | genieR: An R package for inference of demographic history of phylogenies. <i>Journal of Open Source Software</i> , 2019, 4, 634. | 4.6 | 0 |
| 123 | An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934. | | 0 |
| 124 | An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934. | | 0 |
| 125 | An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934. | | 0 |
| 126 | An investigation into the epidemiology of chikungunya virus across neglected regions of Indonesia. , 2020, 14, e0008934. | | 0 |