

# Philippe Lemey

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8534364/publications.pdf>

Version: 2024-02-01

293  
papers

30,526  
citations

7568

77  
h-index

6996

154  
g-index

325  
all docs

325  
docs citations

325  
times ranked

31727  
citing authors

#	ARTICLE	IF	CITATIONS
1	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018, 4, vey016.	4.9	2,401
2	RDP3: a flexible and fast computer program for analyzing recombination. <i>Bioinformatics</i> , 2010, 26, 2462-2463.	4.1	1,524
3	Bayesian Phylogeography Finds Its Roots. <i>PLoS Computational Biology</i> , 2009, 5, e1000520.	3.2	1,519
4	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	12.6	1,125
5	Improving the Accuracy of Demographic and Molecular Clock Model Comparison While Accommodating Phylogenetic Uncertainty. <i>Molecular Biology and Evolution</i> , 2012, 29, 2157-2167.	8.9	1,053
6	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	13.3	772
7	Phylogeography Takes a Relaxed Random Walk in Continuous Space and Time. <i>Molecular Biology and Evolution</i> , 2010, 27, 1877-1885.	8.9	580
8	Mapping the Origins and Expansion of the Indo-European Language Family. <i>Science</i> , 2012, 337, 957-960.	12.6	549
9	Accurate Model Selection of Relaxed Molecular Clocks in Bayesian Phylogenetics. <i>Molecular Biology and Evolution</i> , 2012, 30, 239-243.	8.9	538
10	The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014, 346, 56-61.	12.6	515
11	Complete Genomic Sequence of Human Coronavirus OC43: Molecular Clock Analysis Suggests a Relatively Recent Zoonotic Coronavirus Transmission Event. <i>Journal of Virology</i> , 2005, 79, 1595-1604.	3.4	477
12	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
13	SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. <i>Bioinformatics</i> , 2011, 27, 2910-2912.	4.1	451
14	Improving Bayesian Population Dynamics Inference: A Coalescent-Based Model for Multiple Loci. <i>Molecular Biology and Evolution</i> , 2013, 30, 713-724.	8.9	449
15	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015, 523, 217-220.	27.8	445
16	Spread3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2167-2169.	8.9	413
17	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
18	Assessing substitution saturation with DAMBE. , 2009, , 615-630.		340

#	ARTICLE	IF	CITATIONS
19	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020, 370, 564-570.	12.6	331
20	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. <i>PLoS Pathogens</i> , 2014, 10, e1003932.	4.7	330
21	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020, 6, veaa061.	4.9	317
22	Tracing the origin and history of the HIV-2 epidemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6588-6592.	7.1	315
23	Distinguishable Epidemics of Multidrug-Resistant <i>Salmonella</i> Typhimurium DT104 in Different Hosts. <i>Science</i> , 2013, 341, 1514-1517.	12.6	310
24	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	13.3	305
25	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014, 3, e01914.	6.0	299
26	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	12.6	279
27	The HIV-1 reservoir in eight patients on long-term suppressive antiretroviral therapy is stable with few genetic changes over time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4987-96.	7.1	260
28	The Spread of Tomato Yellow Leaf Curl Virus from the Middle East to the World. <i>PLoS Pathogens</i> , 2010, 6, e1001164.	4.7	259
29	Ancient Hybridization and an Irish Origin for the Modern Polar Bear Matriline. <i>Current Biology</i> , 2011, 21, 1251-1258.	3.9	257
30	Phylodynamic Analyses of Rotavirus Genotypes G9 and G12 Underscore Their Potential for Swift Global Spread. <i>Molecular Biology and Evolution</i> , 2010, 27, 2431-2436.	8.9	253
31	Unifying the spatial epidemiology and molecular evolution of emerging epidemics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15066-15071.	7.1	226
32	Evolutionary History of the Closely Related Group 2 Coronaviruses: Porcine Hemagglutinating Encephalomyelitis Virus, Bovine Coronavirus, and Human Coronavirus OC43. <i>Journal of Virology</i> , 2006, 80, 7270-7274.	3.4	212
33	Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox ( <i>Ovibos</i> ) Tj ETQq1 1 0.784314 rgBT /Ove States of America, 2010, 107, 5675-5680.	7.1	208
34	Metagenomic sequencing at the epicenter of the Nigeria 2018 Lassa fever outbreak. <i>Science</i> , 2019, 363, 74-77.	12.6	201
35	Genetic History of Hepatitis C Virus in East Asia. <i>Journal of Virology</i> , 2009, 83, 1071-1082.	3.4	190
36	Geographic and Temporal Trends in the Molecular Epidemiology and Genetic Mechanisms of Transmitted HIV-1 Drug Resistance: An Individual-Patient- and Sequence-Level Meta-Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001810.	8.4	188

#	ARTICLE	IF	CITATIONS
37	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021, 184, 5189-5200.e7.	28.9	186
38	Evolutionary Dynamics of Human Rotaviruses: Balancing Reassortment with Preferred Genome Constellations. <i>PLoS Pathogens</i> , 2009, 5, e1000634.	4.7	178
39	1970s and "Patient 0"™ HIV-1 genomes illuminate early HIV/AIDS history in North America. <i>Nature</i> , 2016, 539, 98-101.	27.8	177
40	HIV evolutionary dynamics within and among hosts. <i>AIDS Reviews</i> , 2006, 8, 125-40.	1.0	176
41	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. <i>PLoS Biology</i> , 2021, 19, e3001115.	5.6	172
42	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. <i>PLoS Computational Biology</i> , 2007, 3, e29.	3.2	152
43	Ancient papillomavirus-host co-speciation in Felidae. <i>Genome Biology</i> , 2007, 8, R57.	9.6	152
44	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , 2016, 5, e12217.	6.0	146
45	Simultaneously reconstructing viral cross-species transmission history and identifying the underlying constraints. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120196.	4.0	141
46	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 1052-1061.	5.6	139
47	New Insights into Flavivirus Evolution, Taxonomy and Biogeographic History, Extended by Analysis of Canonical and Alternative Coding Sequences. <i>PLoS ONE</i> , 2015, 10, e0117849.	2.5	139
48	Longitudinal Genetic Characterization Reveals That Cell Proliferation Maintains a Persistent HIV Type 1 DNA Pool During Effective HIV Therapy. <i>Journal of Infectious Diseases</i> , 2015, 212, 596-607.	4.0	138
49	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717.	27.8	133
50	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015, 6, 6696.	12.8	128
51	Genetic Variability and Molecular Evolution of the Human Respiratory Syncytial Virus Subgroup B Attachment G Protein. <i>Journal of Virology</i> , 2005, 79, 9157-9167.	3.4	127
52	Phylogenetic Reconstruction Reveals Norovirus GII.4 Epidemic Expansions and their Molecular Determinants. <i>PLoS Pathogens</i> , 2010, 6, e1000884.	4.7	124
53	Phylogenetics and Human-Mediated Dispersal of a Zoonotic Virus. <i>PLoS Pathogens</i> , 2010, 6, e1001166.	4.7	124
54	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016, 32, 3204-3206.	4.1	124

#	ARTICLE	IF	CITATIONS
55	The mode and tempo of hepatitis C virus evolution within and among hosts. <i>BMC Evolutionary Biology</i> , 2011, 11, 131.	3.2	122
56	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110.	12.8	118
57	HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. <i>Cell Host and Microbe</i> , 2019, 26, 347-358.e7.	11.0	117
58	Spatial Dynamics of Human-Origin H1 Influenza A Virus in North American Swine. <i>PLoS Pathogens</i> , 2011, 7, e1002077.	4.7	116
59	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
60	U.S. Human Immunodeficiency Virus Type 1 Epidemic: Date of Origin, Population History, and Characterization of Early Strains. <i>Journal of Virology</i> , 2003, 77, 6359-6366.	3.4	112
61	Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000. <i>Journal of Medical Virology</i> , 2003, 70, 420-429.	5.0	111
62	Single Cell Analysis of Lymph Node Tissue from HIV-1 Infected Patients Reveals that the Majority of CD4+ T-cells Contain One HIV-1 DNA Molecule. <i>PLoS Pathogens</i> , 2013, 9, e1003432.	4.7	110
63	Molecular Evolution and Circulation Patterns of Human Respiratory Syncytial Virus Subgroup A: Positively Selected Sites in the Attachment G Glycoprotein. <i>Journal of Virology</i> , 2004, 78, 4675-4683.	3.4	106
64	Analysing recombination in nucleotide sequences. <i>Molecular Ecology Resources</i> , 2011, 11, 943-955.	4.8	106
65	Virome characterization of game animals in China reveals a spectrum of emerging pathogens. <i>Cell</i> , 2022, 185, 1117-1129.e8.	28.9	106
66	The Molecular Population Genetics of HIV-1 Group O. <i>Genetics</i> , 2004, 167, 1059-1068.	2.9	105
67	Phylogeography and Population Dynamics of Dengue Viruses in the Americas. <i>Molecular Biology and Evolution</i> , 2012, 29, 1533-1543.	8.9	105
68	Measles virus and rinderpest virus divergence dated to the sixth century BCE. <i>Science</i> , 2020, 368, 1367-1370.	12.6	102
69	Genealogical Working Distributions for Bayesian Model Testing with Phylogenetic Uncertainty. <i>Systematic Biology</i> , 2016, 65, 250-264.	5.6	101
70	Make the most of your samples: Bayes factor estimators for high-dimensional models of sequence evolution. <i>BMC Bioinformatics</i> , 2013, 14, 85.	2.6	100
71	Reconstructing the initial global spread of a human influenza pandemic A Bayesian spatial-temporal model for the global spread of H1N1pdm. <i>PLOS Currents</i> , 2009, 1, RRN1031.	1.4	97
72	Virus evolution and transmission in an ever more connected world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142878.	2.6	96

#	ARTICLE	IF	CITATIONS
73	Three roads diverged? Routes to phylogeographic inference. <i>Trends in Ecology and Evolution</i> , 2010, 25, 626-632.	8.7	92
74	Air Travel Is Associated with Intracontinental Spread of Dengue Virus Serotypes 1–3 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2769.	3.0	91
75	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015, 12, 18.	2.0	90
76	Quantifying Differences in the Tempo of Human Immunodeficiency Virus Type 1 Subtype Evolution. <i>Journal of Virology</i> , 2009, 83, 12917-12924.	3.4	87
77	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017, 66, syw054.	5.6	87
78	Distinct Effects of T-705 (Favipiravir) and Ribavirin on Influenza Virus Replication and Viral RNA Synthesis. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6679-6691.	3.2	86
79	The Comparative Genomics of Human Respiratory Syncytial Virus Subgroups A and B: Genetic Variability and Molecular Evolutionary Dynamics. <i>Journal of Virology</i> , 2013, 87, 8213-8226.	3.4	85
80	Recombination Confounds the Early Evolutionary History of Human Immunodeficiency Virus Type 1: Subtype G Is a Circulating Recombinant Form. <i>Journal of Virology</i> , 2007, 81, 8543-8551.	3.4	84
81	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	84
82	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	8.9	81
83	Rates of Viral Evolution Are Linked to Host Geography in Bat Rabies. <i>PLoS Pathogens</i> , 2012, 8, e1002720.	4.7	79
84	The Genealogical Population Dynamics of HIV-1 in a Large Transmission Chain: Bridging within and among Host Evolutionary Rates. <i>PLoS Computational Biology</i> , 2014, 10, e1003505.	3.2	79
85	Genetic Variability among Complete Human Respiratory Syncytial Virus Subgroup A Genomes: Bridging Molecular Evolutionary Dynamics and Epidemiology. <i>PLoS ONE</i> , 2012, 7, e51439.	2.5	78
86	Bayesian evolutionary model testing in the phylogenomics era: matching model complexity with computational efficiency. <i>Bioinformatics</i> , 2013, 29, 1970-1979.	4.1	78
87	Investigating the Origin and Spread of Hepatitis C Virus Genotype 5a. <i>Journal of Virology</i> , 2006, 80, 4220-4226.	3.4	77
88	Molecular dating of human-to-bovid host jumps by <i>Staphylococcus aureus</i> reveals an association with the spread of domestication. <i>Biology Letters</i> , 2012, 8, 829-832.	2.3	77
89	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020, 37, 2641-2654.	8.9	76
90	A counting renaissance: combining stochastic mapping and empirical Bayes to quickly detect amino acid sites under positive selection. <i>Bioinformatics</i> , 2012, 28, 3248-3256.	4.1	75

#	ARTICLE	IF	CITATIONS
91	Inferring Heterogeneous Evolutionary Processes Through Time: from Sequence Substitution to Phylogeography. <i>Systematic Biology</i> , 2014, 63, 493-504.	5.6	75
92	Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , 2011, 1, 423-429.	5.4	74
93	Geographical and Historical Patterns in the Emergences of Novel Highly Pathogenic Avian Influenza (HPAI) H5 and H7 Viruses in Poultry. <i>Frontiers in Veterinary Science</i> , 2018, 5, 84.	2.2	72
94	Circulation of genetically distinct contemporary human coronavirus OC43 strains. <i>Virology</i> , 2005, 337, 85-92.	2.4	71
95	Phylogeography of Dengue Virus Serotype 4, Brazil, 2010–2011. <i>Emerging Infectious Diseases</i> , 2012, 18, 1858-1864.	4.3	68
96	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
97	Molecular Footprint of Drug-Selective Pressure in a Human Immunodeficiency Virus Transmission Chain. <i>Journal of Virology</i> , 2005, 79, 11981-11989.	3.4	67
98	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. <i>PLoS Pathogens</i> , 2016, 12, e1005525.	4.7	65
99	Yellow Fever Virus Maintenance in Trinidad and Its Dispersal throughout the Americas. <i>Journal of Virology</i> , 2010, 84, 9967-9977.	3.4	64
100	Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. <i>Molecular Biology and Evolution</i> , 2017, 34, 2563-2571.	8.9	64
101	Genetic Diversity of Highly Pathogenic Avian Influenza A(H5N8/H5N5) Viruses in Italy, 2016–17. <i>Emerging Infectious Diseases</i> , 2017, 23, 1543-1547.	4.3	62
102	Reconstructing the History of Maize Streak Virus Strain A Dispersal To Reveal Diversification Hot Spots and Its Origin in Southern Africa. <i>Journal of Virology</i> , 2011, 85, 9623-9636.	3.4	61
103	Disentangling the role of Africa in the global spread of H5 highly pathogenic avian influenza. <i>Nature Communications</i> , 2019, 10, 5310.	12.8	61
104	Understanding Past Population Dynamics: Bayesian Coalescent-Based Modeling with Covariates. <i>Systematic Biology</i> , 2016, 65, 1041-1056.	5.6	60
105	Evolutionary trajectory of the VP1 gene of human enterovirus 71 genogroup B and C viruses. <i>Journal of General Virology</i> , 2010, 91, 1949-1958.	2.9	59
106	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015, 1, vev016.	4.9	59
107	Phyldynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	12.8	59
108	The global distribution of Banana bunchy top virus reveals little evidence for frequent recent, human-mediated long distance dispersal events. <i>Virus Evolution</i> , 2015, 1, vev009.	4.9	58

#	ARTICLE	IF	CITATIONS
109	Analysis of the Serotype and Genotype Correlation of VP1 and the 5'UTR Noncoding Region in an Epidemiological Survey of the Human Enterovirus B Species. <i>Journal of Clinical Microbiology</i> , 2004, 42, 963-971.	3.9	57
110	Genomic characterization of novel dolphin papillomaviruses provides indications for recombination within the Papillomaviridae. <i>Virology</i> , 2008, 378, 151-161.	2.4	57
111	Identifying recombinants in human and primate immunodeficiency virus sequence alignments using quartet scanning. <i>BMC Bioinformatics</i> , 2009, 10, 126.	2.6	57
112	Are hepatitis B virus "subgenotypes" defined accurately?. <i>Journal of Clinical Virology</i> , 2010, 47, 356-360.	3.1	57
113	Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. <i>Journal of General Virology</i> , 2012, 93, 889-899.	2.9	56
114	A novel hepatitis B virus species discovered in capuchin monkeys sheds new light on the evolution of primate hepadnaviruses. <i>Journal of Hepatology</i> , 2018, 68, 1114-1122.	3.7	56
115	High GUD Incidence in the Early 20th Century Created a Particularly Permissive Time Window for the Origin and Initial Spread of Epidemic HIV Strains. <i>PLoS ONE</i> , 2010, 5, e9936.	2.5	54
116	Mannan-binding lectin (MBL) gene polymorphisms in ulcerative colitis and Crohn's disease. <i>Genes and Immunity</i> , 2001, 2, 323-328.	4.1	52
117	Phylogenetics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012, 12, 453-460.	2.3	52
118	Landscape attributes governing local transmission of an endemic zoonosis: Rabies virus in domestic dogs. <i>Molecular Ecology</i> , 2018, 27, 773-788.	3.9	50
119	Genomic Analysis of Hepatitis B Virus Reveals Antigen State and Genotype as Sources of Evolutionary Rate Variation. <i>Viruses</i> , 2011, 3, 83-101.	3.3	49
120	Phylogeography of Lassa Virus in Nigeria. <i>Journal of Virology</i> , 2019, 93, .	3.4	49
121	Complete Genome Sequence, Taxonomic Assignment, and Comparative Analysis of the Untranslated Regions of the Modoc Virus, a Flavivirus with No Known Vector. <i>Virology</i> , 2002, 293, 125-140.	2.4	46
122	Isolation and cloning of the raccoon ( <i>Procyon lotor</i> ) papillomavirus type 1 by using degenerate papillomavirus-specific primers. <i>Journal of General Virology</i> , 2005, 86, 2029-2033.	2.9	46
123	Novel hepatitis B virus subgenotype A6 in African-Belgian patients. <i>Journal of Clinical Virology</i> , 2010, 47, 93-96.	3.1	46
124	Bayesian Inference Reveals Host-Specific Contributions to the Epidemic Expansion of Influenza A H5N1. <i>Molecular Biology and Evolution</i> , 2015, 32, msv185.	8.9	46
125	The spread of Type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in North America: A phylogeographic approach. <i>Virology</i> , 2013, 447, 146-154.	2.4	45
126	Differential Infection Patterns and Recent Evolutionary Origins of Equine Hepaciviruses in Donkeys. <i>Journal of Virology</i> , 2017, 91, .	3.4	45



#	ARTICLE	IF	CITATIONS
127	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018, 31, 24-32.	5.4	45
128	Molecular testing of multiple HIV-1 transmissions in a criminal case. <i>Aids</i> , 2005, 19, 1649-1658.	2.2	43
129	On the Biogeography of Centipeda: A Species-Tree Diffusion Approach. <i>Systematic Biology</i> , 2014, 63, 178-191.	5.6	43
130	Genome-Wide Evolutionary Analyses of G1P[8] Strains Isolated Before and After Rotavirus Vaccine Introduction. <i>Genome Biology and Evolution</i> , 2015, 7, 2473-2483.	2.5	43
131	Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5949-5954.	7.1	43
132	A large Finnish echovirus 30 outbreak was preceded by silent circulation of the same genotype. <i>Virus Genes</i> , 2011, 42, 28-36.	1.6	41
133	Complete genome sequence of Montana Myotis leukoencephalitis virus, phylogenetic analysis and comparative study of the 3' untranslated region of flaviviruses with no known vector. <i>Journal of General Virology</i> , 2002, 83, 1875-1885.	2.9	40
134	A genotypic resistance assay for the detection of drug resistance in the human immunodeficiency virus type 1 envelope gene. <i>Journal of Virological Methods</i> , 2005, 123, 25-34.	2.1	39
135	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. <i>Molecular Biology and Evolution</i> , 2019, 36, 1793-1803.	8.9	39
136	Limitations to Contact Tracing And Phylogenetic Analysis in Establishing HIV Type 1 Transmission Networks in Cuba. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 347-356.	1.1	38
137	Impact of CCR5delta32 Host Genetic Background and Disease Progression on HIV-1 Intra-host Evolutionary Processes: Efficient Hypothesis Testing through Hierarchical Phylogenetic Models. <i>Molecular Biology and Evolution</i> , 2011, 28, 1605-1616.	8.9	38
138	Viral Characteristics Associated with the Clinical Nonprogressor Phenotype Are Inherited by Viruses from a Cluster of HIV-1 Elite Controllers. <i>MBio</i> , 2018, 9, .	4.1	37
139	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019, 15, e1007976.	4.7	37
140	Characterization of a Putative Ancestor of Coxsackievirus B5. <i>Journal of Virology</i> , 2010, 84, 9695-9708.	3.4	36
141	A Bayesian statistical analysis of human T-cell lymphotropic virus evolutionary rates. <i>Infection, Genetics and Evolution</i> , 2005, 5, 291-298.	2.3	35
142	Molecular evolutionary analysis and mutational pattern of full-length genomes of hepatitis B virus isolated from Belgian patients with different clinical manifestations. <i>Journal of Medical Virology</i> , 2010, 82, 379-389.	5.0	35
143	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. <i>Bioinformatics</i> , 2017, 33, 1798-1805.	4.1	35
144	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018, 14, e1007392.	4.7	35

#	ARTICLE	IF	CITATIONS
145	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. <i>BMC Genomics</i> , 2018, 19, 617.	2.8	35
146	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	12.8	35
147	Phylogeography Reveals Association between Swine Trade and the Spread of Porcine Epidemic Diarrhea Virus in China and across the World. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	35
148	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
149	HIV-1 compartmentalization in diverse leukocyte populations during antiretroviral therapy. <i>Journal of Leukocyte Biology</i> , 2004, 76, 562-570.	3.3	34
150	Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineages—Application to rabies virus spread in Iran. <i>Molecular Ecology</i> , 2019, 28, 4335-4350.	3.9	34
151	Phylogenetic analysis of hepatitis B virus full-length genomes reveals evidence for a large nosocomial outbreak in Belgium. <i>Journal of Clinical Virology</i> , 2009, 46, 61-68.	3.1	33
152	Phylodynamics of H5N1 avian influenza virus in Indonesia. <i>Molecular Ecology</i> , 2012, 21, 3062-3077.	3.9	33
153	Circulation of HRSV in Belgium: From Multiple Genotype Circulation to Prolonged Circulation of Predominant Genotypes. <i>PLoS ONE</i> , 2013, 8, e60416.	2.5	33
154	Emergence in Japan of an HIV-1 Variant Associated with Transmission among Men Who Have Sex with Men (MSM) in China: First Indication of the International Dissemination of the Chinese MSM Lineage. <i>Journal of Virology</i> , 2013, 87, 5351-5361.	3.4	32
155	A uniquely prevalent nonnucleoside reverse transcriptase inhibitor resistance mutation in Russian subtype A HIV-1 viruses. <i>Aids</i> , 2014, 28, F1-F8.	2.2	32
156	Genesis of avian-origin H7N9 influenza A viruses. <i>Lancet, The</i> , 2013, 381, 1883-1885.	13.7	31
157	The Phylogeography and Spatiotemporal Spread of South-Central Skunk Rabies Virus. <i>PLoS ONE</i> , 2013, 8, e82348.	2.5	31
158	Ecuador Paraiso Escondido Virus, a New Flavivirus Isolated from New World Sand Flies in Ecuador, Is the First Representative of a Novel Clade in the Genus Flavivirus. <i>Journal of Virology</i> , 2015, 89, 11773-11785.	3.4	31
159	Towards a unified classification for human respiratory syncytial virus genotypes. <i>Virus Evolution</i> , 2020, 6, veaa052.	4.9	31
160	A near full-length HIV-1 genome from 1966 recovered from formalin-fixed paraffin-embedded tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12222-12229.	7.1	31
161	Relax, Keep Walking – A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493.	8.9	31
162	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005894.	4.7	31

#	ARTICLE	IF	CITATIONS
163	Analysis of the Evolutionary Relationships of HIV-1 and SIVcpz Sequences Using Bayesian Inference: Implications for the Origin of HIV-1. <i>Molecular Biology and Evolution</i> , 2003, 20, 1986-1996.	8.9	30
164	Assessing phenotypic correlation through the multivariate phylogenetic latent liability model. <i>Annals of Applied Statistics</i> , 2015, 9, 969-991.	1.1	30
165	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018, 4, vey023.	4.9	29
166	Estimation of an <i>in vivo</i> fitness landscape experienced by HIV-1 under drug selective pressure useful for prediction of drug resistance evolution during treatment. <i>Bioinformatics</i> , 2008, 24, 34-41.	4.1	28
167	Evolutionary analysis of HBV antigen genetic diversity in Iranian blood donors: A nationwide study. <i>Journal of Medical Virology</i> , 2014, 86, 144-155.	5.0	28
168	Contribution of Epidemiological Predictors in Unraveling the Phylogeographic History of HIV-1 Subtype C in Brazil. <i>Journal of Virology</i> , 2015, 89, 12341-12348.	3.4	28
169	Combining phylogeography and spatial epidemiology to uncover predictors of H5N1 influenza A virus diffusion. <i>Archives of Virology</i> , 2015, 160, 215-224.	2.1	28
170	Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016, 25, 5994-6008.	3.9	28
171	Genetic analyses reveal structured HIV-1 populations in serially sampled T lymphocytes of patients receiving HAART. <i>Virology</i> , 2006, 348, 35-46.	2.4	27
172	Whole genome analysis of local Kenyan and global sequences unravels the epidemiological and molecular evolutionary dynamics of RSV genotype ON1 strains. <i>Virus Evolution</i> , 2018, 4, vey027.	4.9	27
173	Phylogenetic Reconstruction of a Known HIV-1 CRF04_cpx Transmission Network Using Maximum Likelihood and Bayesian Methods. <i>Journal of Molecular Evolution</i> , 2004, 59, 709-717.	1.8	26
174	Evolutionary Dynamics of Human Retroviruses Investigated Through Full-Genome Scanning. <i>Molecular Biology and Evolution</i> , 2005, 22, 942-951.	8.9	26
175	Estimating the Relative Contribution of dNTP Pool Imbalance and APOBEC3G/3F Editing to HIV Evolution <i>In Vivo</i> . <i>Journal of Computational Biology</i> , 2007, 14, 1105-1114.	1.6	26
176	The recent ancestry of Middle East respiratory syndrome coronavirus in Korea has been shaped by recombination. <i>Scientific Reports</i> , 2016, 6, 18825.	3.3	26
177	Detection of Marburg Virus Disease in Guinea. <i>New England Journal of Medicine</i> , 2022, 386, 2528-2530.	27.0	26
178	Full-genome analysis of a highly divergent simian T-cell lymphotropic virus type 1 strain in <i>Macaca arctoides</i> . <i>Journal of General Virology</i> , 2005, 86, 1953-1959.	2.9	25
179	A Relaxed Directional Random Walk Model for Phylogenetic Trait Evolution. <i>Systematic Biology</i> , 2017, 66, syw093.	5.6	25
180	Mass migration to Europe: an opportunity for elimination of hepatitis B virus?. <i>The Lancet Gastroenterology and Hepatology</i> , 2019, 4, 315-323.	8.1	25

#	ARTICLE	IF	CITATIONS
181	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020, 37, 1832-1842.	8.9	25
182	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. <i>Nature Communications</i> , 2022, 13, 2314.	12.8	25
183	Plasma Exchange--Associated Immunoglobulin M--Negative Hantavirus Disease after a Camping Holiday in Southern France. <i>Clinical Infectious Diseases</i> , 2004, 38, 1350-1356.	5.8	24
184	The multi-faceted dynamics of HIV-1 transmission in Northern Alberta: A combined analysis of virus genetic and public health data. <i>Infection, Genetics and Evolution</i> , 2017, 52, 100-105.	2.3	24
185	Divergence dating using mixed effects clock modelling: An application to HIV-1. <i>Virus Evolution</i> , 2019, 5, vez036.	4.9	24
186	Genomic Epidemiology of 2015â€“2016 Zika Virus Outbreak in Cape Verde. <i>Emerging Infectious Diseases</i> , 2020, 26, 1084-1090.	4.3	24
187	Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals. <i>Nature Medicine</i> , 2022, 28, 1476-1485.	30.7	24
188	HBV subgenotype misclassification expands quasi-subgenotype A3. <i>Clinical Microbiology and Infection</i> , 2011, 17, 947-949.	6.0	23
189	Molecular characterization of hepatitis B virus strains circulating in Belgian patients coâ€“infected with HIV and HBV: Overt and occult infection. <i>Journal of Medical Virology</i> , 2011, 83, 1876-1884.	5.0	23
190	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019, 220, 233-243.	4.0	23
191	Covering all bases in HIV research: unveiling a hidden world of viral evolution. <i>AIDS Reviews</i> , 2010, 12, 89-102.	1.0	23
192	Genetic Variability of Human Respiratory Coronavirus OC43. <i>Journal of Virology</i> , 2005, 79, 3223-3225.	3.4	22
193	Role of viral evolutionary rate in HIV-1 disease progression in a linked cohort. <i>Retrovirology</i> , 2005, 2, 41.	2.0	22
194	ËBUS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. <i>BMC Bioinformatics</i> , 2014, 15, 133.	2.6	22
195	Simultaneously estimating evolutionary history and repeated traits phylogenetic signal: applications to viral and host phenotypic evolution. <i>Methods in Ecology and Evolution</i> , 2015, 6, 67-82.	5.2	22
196	Enzootic Transmission of Yellow Fever Virus, Venezuela. <i>Emerging Infectious Diseases</i> , 2015, 21, 99-102.	4.3	22
197	The epidemic dynamics of hepatitis C virus subtypes 4a and 4d in Saudi Arabia. <i>Scientific Reports</i> , 2017, 7, 44947.	3.3	22
198	Comparing patterns and scales of plant virus phylogeography: Rice yellow mottle virus in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019, 5, vez023.	4.9	22

#	ARTICLE	IF	CITATIONS
199	Gradients Do Grow on Trees: A Linear-Time $O(N)$ -Dimensional Gradient for Statistical Phylogenetics. <i>Molecular Biology and Evolution</i> , 2020, 37, 3047-3060.	8.9	22
200	Global spatial dynamics and vaccine-induced fitness changes of <i>Bordetella pertussis</i> . <i>Science Translational Medicine</i> , 2022, 14, eabn3253.	12.4	22
201	SlidingBayes: exploring recombination using a sliding window approach based on Bayesian phylogenetic inference. <i>Bioinformatics</i> , 2005, 21, 1274-1275.	4.1	21
202	Proposal for a new subtype of the zoonotic genotype 3 Hepatitis E virus: HEV-3I. <i>Virus Research</i> , 2018, 248, 1-4.	2.2	21
203	Earlier Initiation of Antiretroviral Treatment Coincides With an Initial Control of the HIV-1 Sub-Subtype F1 Outbreak Among Men-Having-Sex-With-Men in Flanders, Belgium. <i>Frontiers in Microbiology</i> , 2019, 10, 613.	3.5	21
204	Genetically Different Highly Pathogenic Avian Influenza A(H5N1) Viruses in West Africa, 2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2132-2136.	4.3	20
205	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. <i>Genome Biology and Evolution</i> , 2017, 9, 3202-3213.	2.5	19
206	Iran's hepatitis elimination programme is under threat. <i>Lancet, The</i> , 2018, 392, 1009.	13.7	19
207	nosoi: A stochastic agent-based transmission chain simulation framework in <code>scpr</code> . <i>Methods in Ecology and Evolution</i> , 2020, 11, 1002-1007.	5.2	19
208	Relaxed Random Walks at Scale. <i>Systematic Biology</i> , 2021, 70, 258-267.	5.6	19
209	A systematic review on global RSV genetic data: Identification of knowledge gaps. <i>Reviews in Medical Virology</i> , 2022, 32, e2284.	8.3	19
210	The epidemic history of hepatitis C among injecting drug users in Flanders, Belgium. <i>Journal of Viral Hepatitis</i> , 2008, 15, 399-408.	2.0	18
211	Dynamic features of the selective pressure on the human immunodeficiency virus type 1 (HIV-1) gp120 CD4-binding site in a group of long term non progressor (LTNP) subjects. <i>Retrovirology</i> , 2009, 6, 4.	2.0	18
212	Graph hierarchies for phylogeography. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120206.	4.0	18
213	High inpatient HIV-1 evolutionary rate is associated with CCR5-to-CXCR4 coreceptor switch. <i>Infection, Genetics and Evolution</i> , 2013, 19, 369-377.	2.3	18
214	Limited evolution of the yellow fever virus 17d in a mouse infection model. <i>Emerging Microbes and Infections</i> , 2019, 8, 1734-1746.	6.5	18
215	Time-measured phylogenies of gag, pol and env sequence data reveal the direction and time interval of HIV-1 transmission. <i>Aids</i> , 2011, 25, 1035-1039.	2.2	16
216	The introduction of fox rabies into Italy (2008–2011) was due to two viral genetic groups with distinct phylogeographic patterns. <i>Infection, Genetics and Evolution</i> , 2013, 17, 202-209.	2.3	16

#	ARTICLE	IF	CITATIONS
217	Disentangling the impact of within-host evolution and transmission dynamics on the tempo of HIV-1 evolution. <i>Aids</i> , 2015, 29, 1549-1556.	2.2	16
218	Accurate quantification of within- and between-host HBV evolutionary rates requires explicit transmission chain modelling. <i>Virus Evolution</i> , 2017, 3, vex028.	4.9	16
219	Phylogenetic Factor Analysis. <i>Systematic Biology</i> , 2018, 67, 384-399.	5.6	16
220	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019, 5, vez009.	4.9	16
221	Phylogenetic classification of TT virus groups based on the N22 region is unreliable. <i>Virus Research</i> , 2002, 85, 47-59.	2.2	15
222	Evidence for a Complex Mosaic Genome Pattern in a Full-length Hepatitis C Virus Sequence. <i>Evolutionary Bioinformatics</i> , 2008, 4, EBO.S1038.	1.2	15
223	Molecular characterization of hepatitis B virus (HBV) strains circulating in the northern coast of the Persian Gulf and its comparison with worldwide distribution of HBV subgenotype D1. <i>Journal of Medical Virology</i> , 2014, 86, 745-757.	5.0	15
224	Advances in Visualization Tools for Phylogenomic and Phylodynamic Studies of Viral Diseases. <i>Frontiers in Public Health</i> , 2019, 7, 208.	2.7	15
225	In Search of Covariates of HIV-1 Subtype B Spread in the United States—A Cautionary Tale of Large-Scale Bayesian Phylogeography. <i>Viruses</i> , 2020, 12, 182.	3.3	15
226	Evaluating predictive markers for viral rebound and safety assessment in blood and lumbar fluid during HIV-1 treatment interruption. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1311-1320.	3.0	15
227	Massive Parallelization Boosts Big Bayesian Multidimensional Scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021, 30, 11-24.	1.7	15
228	Hamiltonian Monte Carlo sampling to estimate past population dynamics using the skygrid coalescent model in a Bayesian phylogenetics framework. <i>Wellcome Open Research</i> , 2020, 5, 53.	1.8	15
229	Bayesian Phylogeographic Analysis Incorporating Predictors and Individual Travel Histories in BEAST. <i>Current Protocols</i> , 2021, 1, e98.	2.9	14
230	Increasing importance of European lineages in seeding the hepatitis C virus subtype 1a epidemic in Spain. <i>Eurosurveillance</i> , 2019, 24, .	7.0	14
231	Exploring full-genome sequences for phylogenetic support of HIV-1 transmission events. <i>Aids</i> , 2005, 19, 1551-1552.	2.2	13
232	The evolution of human immunodeficiency virus type-1 (HIV-1) envelope molecular properties and coreceptor use at all stages of infection in an HIV-1 donor–recipient pair. <i>Virology</i> , 2012, 422, 70-80.	2.4	13
233	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016, 8, 12.	3.3	13
234	Identifying predictors of time-inhomogeneous viral evolutionary processes. <i>Virus Evolution</i> , 2016, 2, vew023.	4.9	13

#	ARTICLE	IF	CITATIONS
235	A Novel Series of Indole Alkaloid Derivatives Inhibit Dengue and Zika Virus Infection by Interference with the Viral Replication Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0234920.	3.2	13
236	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020, 9, .	6.0	13
237	Cycloraphan yolk proteins and lepidopteran minor yolk proteins originate from two unrelated lipase families. <i>Insect Molecular Biology</i> , 2004, 13, 615-623.	2.0	12
238	Genetic variation in mother-child acute seroconverter pairs from Zambia. <i>Aids</i> , 2008, 22, 817-824.	2.2	12
239	Estimating the individualized HIV-1 genetic barrier to resistance using a nelfinavir fitness landscape. <i>BMC Bioinformatics</i> , 2010, 11, 409.	2.6	12
240	Complete nucleotide sequence and evolutionary analysis of a Gorilla foamy virus. <i>Journal of General Virology</i> , 2011, 92, 582-586.	2.9	11
241	Phylogenetic analysis of two genotype 3 Hepatitis E viruses from wild boar, Italy. <i>Virus Genes</i> , 2018, 54, 812-817.	1.6	11
242	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019, 1910, 691-722.	0.9	11
243	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference - Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020, 36, 2098-2104.	4.1	11
244	Markov-Modulated Continuous-Time Markov Chains to Identify Site- and Branch-Specific Evolutionary Variation in BEAST. <i>Systematic Biology</i> , 2021, 70, 181-189.	5.6	11
245	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021, 7, veab036.	4.9	11
246	Genome Sequence of Ruloma Virus, a Novel Paramyxovirus Clustering Basally to Members of the Genus <i>Jeilongvirus</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	11
247	A Comprehensive Molecular Epidemiological Analysis of SARS-CoV-2 Infection in Cyprus from April 2020 to January 2021: Evidence of a Highly Polyphyletic and Evolving Epidemic. <i>Viruses</i> , 2021, 13, 1098.	3.3	11
248	Site stripping based on likelihood ratio reduction is a useful tool to evaluate the impact of non-clock-like behavior on viral phylogenetic reconstructions. <i>FEMS Immunology and Medical Microbiology</i> , 2003, 39, 125-132.	2.7	10
249	Phylogenetic analysis using protein sequences. , 2009, , 313-342.		10
250	On Hepatitis C Virus Evolution: The Interaction between Virus and Host towards Treatment Outcome. <i>PLoS ONE</i> , 2013, 8, e62393.	2.5	10
251	Reassortment compatibility between PB1, PB2, and HA genes of the two influenza B virus lineages in mammalian cells. <i>Scientific Reports</i> , 2016, 6, 27480.	3.3	10
252	Inferring Phenotypic Trait Evolution on Large Trees With Many Incomplete Measurements. <i>Journal of the American Statistical Association</i> , 2022, 117, 678-692.	3.1	10



#	ARTICLE	IF	CITATIONS
253	Large-scale inference of correlation among mixed-type biological traits with phylogenetic multivariate probit models. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	10
254	Phylogenetic relationships of the HA and NA genes between vaccine and seasonal influenza A(H3N2) strains in Korea. <i>PLoS ONE</i> , 2017, 12, e0172059.	2.5	10
255	Introduction to recombination detection. , 2009, , 493-518.		9
256	Rivers and landscape ecology of a plant virus, Rice yellow mottle virus along the Niger Valley. <i>Virus Evolution</i> , 2021, 7, .	4.9	9
257	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017â€“2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	3.0	9
258	A comparative study of HIV-1 clade C env evolution in a Zambian infant with an infected rhesus macaque during disease progression. <i>Aids</i> , 2009, 23, 1817-1828.	2.2	8
259	Genomic population structure associated with repeated escape of <i>Salmonella enterica</i> ATCC14028s from the laboratory into nature. <i>PLoS Genetics</i> , 2021, 17, e1009820.	3.5	8
260	Accommodating sampling location uncertainty in continuous phylogeography. <i>Virus Evolution</i> , 2022, 8, .	4.9	8
261	HIV-1 evolution in patients undergoing immunotherapy with Tat, Rev, and Nef expressing dendritic cells followed by treatment interruption. <i>Aids</i> , 2013, 27, 2679-2689.	2.2	7
262	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015, 63, 38-41.	3.1	7
263	Low Postseroconversion CD4 + T-cell Level Is Associated with Faster Disease Progression and Higher Viral Evolutionary Rate in HIV-2 Infection. <i>MBio</i> , 2019, 10, .	4.1	7
264	HIV-1 p24Gag adaptation to modern and archaic HLA-allele frequency differences in ethnic groups contributes to viral subtype diversification. <i>Virus Evolution</i> , 2020, 6, veaa085.	4.9	7
265	Efficient Bayesian inference of general Gaussian models on large phylogenetic trees. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	7
266	Molecular clock analysis. , 2009, , 362-380.		6
267	A21â€“HIV-1 sub-subtype F1 outbreak among MSM in Belgium. <i>Virus Evolution</i> , 2017, 3, .	4.9	6
268	Quantifying rates of HIV-1 flow between risk groups and geographic locations in Kenya: A country-wide phylogenetic study. <i>Virus Evolution</i> , 2022, 8, veac016.	4.9	6
269	Emergency of Primary NNRTI Resistance Mutations without Antiretroviral Selective Pressure in a HAART-Treated Child. <i>PLoS ONE</i> , 2009, 4, e4806.	2.5	5
270	HCV genotype distribution in Flanders and Brussels (Belgium): unravelling the spread of an uncommon HCV genotype 5a cluster. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2010, 29, 1427-1434.	2.9	5



#	ARTICLE	IF	CITATIONS
271	Synonymous and nonsynonymous distances help untangle convergent evolution and recombination. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 375-89.	0.6	5
272	Determinants of dengue virus dispersal in the Americas. <i>Virus Evolution</i> , 2020, 6, veaa074.	4.9	5
273	The phylodynamics of SARS-CoV-2 during 2020 in Finland. <i>Communications Medicine</i> , 2022, 2, .	4.2	5
274	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. <i>Statistics in Medicine</i> , 2018, 37, 195-206.	1.6	4
275	<i>In Vivo</i> Therapy with M2e-Specific IgG Selects for an Influenza A Virus Mutant with Delayed Matrix Protein 2 Expression. <i>MBio</i> , 2021, 12, e0074521.	4.1	4
276	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021, 13, 1842.	3.3	4
277	Bayesian codon substitution modelling to identify sources of pathogen evolutionary rate variation. <i>Microbial Genomics</i> , 2016, 2, e000057.	2.0	4
278	Generalized linear models for identifying predictors of the evolutionary diffusion of viruses. <i>AMIA Summits on Translational Science Proceedings</i> , 2014, 2014, 23-8.	0.4	4
279	Reconstruction of the origin and dispersal of the worldwide dominant Hepatitis B Virus subgenotype D1. <i>Virus Evolution</i> , 2022, 8, .	4.9	4
280	High Frequency of HIV-1 Dual Infections in Cameroon, West Central Africa. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2011, 57, e25-e27.	2.1	3
281	Air conditioning system usage and SARS-CoV-2 transmission dynamics in Iran. <i>Medical Hypotheses</i> , 2020, 143, 110164.	1.5	3
282	Phycova " a tool for exploring covariates of pathogen spread. <i>Virus Evolution</i> , 2022, 8, veac015.	4.9	3
283	The role of high-risk geographies in the perpetuation of the HIV epidemic in rural South Africa: A spatial molecular epidemiology study. <i>PLOS Global Public Health</i> , 2022, 2, e0000105.	1.6	3
284	The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022, 14, 973.	3.3	3
285	Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. <i>International Journal of Infectious Diseases</i> , 2019, 79, 9-10.	3.3	2
286	Sequence databases and database searching. , 0, , 33-67.		1
287	High-throughput HIV sequencing: evolution in 2D. <i>Future Virology</i> , 2011, 6, 417-420.	1.8	1
288	International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology. <i>Infection, Genetics and Evolution</i> , 2013, 19, 335-336.	2.3	1

#	ARTICLE	IF	CITATIONS
289	OP3-8 Evolutionary analysis of Hepatitis B virus full-length genomes reveals evidence for a large nosocomial outbreak in Belgium. <i>Journal of Clinical Virology</i> , 2009, 46, S8.	3.1	0
290	A63 Quantifying the dynamics of evolutionary rates through time. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
291	A4 An amplicon-based approach for universal amplification, sequencing, and assembly of full-length HIV-1 samples from the DRC. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
292	Phylogeographic Insights into the Origins and Epidemic History of the Human Immunodeficiency Virus Type 2. , 2013, , 1-9.		0
293	HIV-2, Phylogeographic Insights into the Origins and Epidemic History. , 2018, , 970-978.		0