

# Andrew Rambaut

## List of Publications by Year in descending order

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255  
papers

109,097  
citations

872

117  
h-index

642

256  
g-index

294  
all docs

294  
docs citations

294  
times ranked

79021  
citing authors

#	ARTICLE	IF	CITATIONS
1	BEAST: Bayesian evolutionary analysis by sampling trees. <i>BMC Evolutionary Biology</i> , 2007, 7, 214.	3.2	11,072
2	Bayesian Phylogenetics with BEAUti and the BEAST 1.7. <i>Molecular Biology and Evolution</i> , 2012, 29, 1969-1973.	8.9	9,040
3	Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. <i>Systematic Biology</i> , 2018, 67, 901-904.	5.6	6,726
4	Relaxed Phylogenetics and Dating with Confidence. <i>PLoS Biology</i> , 2006, 4, e88.	5.6	5,566
5	BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003537.	3.2	5,301
6	The proximal origin of SARS-CoV-2. <i>Nature Medicine</i> , 2020, 26, 450-452.	30.7	3,871
7	Bayesian Coalescent Inference of Past Population Dynamics from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2005, 22, 1185-1192.	8.9	2,782
8	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021, 19, 409-424.	28.6	2,650
9	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	3.2	2,484
10	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018, 4, vey016.	4.9	2,401
11	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020, 5, 1403-1407.	13.3	2,291
12	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	27.8	1,870
13	Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. <i>Science</i> , 2009, 324, 1557-1561.	12.6	1,665
14	Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , 2016, 2, vew007.	4.9	1,638
15	Bayesian Phylogeography Finds Its Roots. <i>PLoS Computational Biology</i> , 2009, 5, e1000520.	3.2	1,519
16	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	27.8	1,210
17	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	27.8	1,179
18	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

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19	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	12.6	1,083
20	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
21	Seq-Gen: an application for the Monte Carlo simulation of DNA sequence evolution along phylogenetic trees. <i>Bioinformatics</i> , 1997, 13, 235-238.	4.1	1,011
22	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
23	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
24	The genomic and epidemiological dynamics of human influenza A virus. <i>Nature</i> , 2008, 453, 615-619.	27.8	824
25	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. <i>Cell</i> , 2022, 185, 467-484.e15.	28.9	788
26	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	4.9	774
27	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
28	Choosing Appropriate Substitution Models for the Phylogenetic Analysis of Protein-Coding Sequences. <i>Molecular Biology and Evolution</i> , 2006, 23, 7-9.	8.9	695
29	Rise and Fall of the Beringian Steppe Bison. <i>Science</i> , 2004, 306, 1561-1565.	12.6	601
30	Rates of Molecular Evolution in RNA Viruses: A Quantitative Phylogenetic Analysis. <i>Journal of Molecular Evolution</i> , 2002, 54, 156-165.	1.8	596
31	Phylogeography Takes a Relaxed Random Walk in Continuous Space and Time. <i>Molecular Biology and Evolution</i> , 2010, 27, 1877-1885.	8.9	580
32	BEAGLE: An Application Programming Interface and High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2012, 61, 170-173.	5.6	555
33	Persistent HIV-1 replication maintains the tissue reservoir during therapy. <i>Nature</i> , 2016, 530, 51-56.	27.8	550
34	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	28.9	541
35	Evolutionary analysis of the dynamics of viral infectious disease. <i>Nature Reviews Genetics</i> , 2009, 10, 540-550.	16.3	526
36	The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014, 346, 56-61.	12.6	515

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37	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	27.8	515
38	Comparative analysis by independent contrasts (CAIC): an Apple Macintosh application for analysing comparative data. <i>Bioinformatics</i> , 1995, 11, 247-251.	4.1	472
39	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. <i>Nature Medicine</i> , 2022, 28, 1785-1790.	30.7	456
40	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
41	SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. <i>Bioinformatics</i> , 2011, 27, 2910-2912.	4.1	451
42	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
43	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015, 523, 217-220.	27.8	445
44	The causes and consequences of HIV evolution. <i>Nature Reviews Genetics</i> , 2004, 5, 52-61.	16.3	444
45	Inferring confidence sets of possibly misspecified gene trees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 137-142.	2.6	441
46	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013, 502, 241-244.	27.8	429
47	SpredD3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2167-2169.	8.9	413
48	Correlating viral phenotypes with phylogeny: Accounting for phylogenetic uncertainty. <i>Infection, Genetics and Evolution</i> , 2008, 8, 239-246.	2.3	408
49	The Epidemic Behavior of the Hepatitis C Virus. <i>Science</i> , 2001, 292, 2323-2325.	12.6	405
50	Many-core algorithms for statistical phylogenetics. <i>Bioinformatics</i> , 2009, 25, 1370-1376.	4.1	380
51	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.	6.4	375
52	Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , 2003, 18, 481-488.	8.7	371
53	Complete mitochondrial genome sequences of two extinct moas clarify ratite evolution. <i>Nature</i> , 2001, 409, 704-707.	27.8	369
54	Recent human-to-poultry host jump, adaptation, and pandemic spread of <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19545-19550.	7.1	363

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55	Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , 2016, 354, 213-217.	12.6	362
56	Phylogenetic evidence for recombination in dengue virus. <i>Molecular Biology and Evolution</i> , 1999, 16, 405-409.	8.9	356
57	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
58	An Integrated Framework for the Inference of Viral Population History From Reconstructed Genealogies. <i>Genetics</i> , 2000, 155, 1429-1437.	2.9	346
59	Clinical features and virological analysis of a case of Middle East respiratory syndrome coronavirus infection. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 745-751.	9.1	343
60	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
61	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020, 370, 564-570.	12.6	331
62	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
63	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	28.9	330
64	Episodic Sexual Transmission of HIV Revealed by Molecular Phylodynamics. <i>PLoS Medicine</i> , 2008, 5, e50.	8.4	326
65	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	27.8	323
66	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020, 6, veaa061.	4.9	317
67	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	13.3	305
68	The emergence of HIV/AIDS in the Americas and beyond. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18566-18570.	7.1	301
69	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014, 3, e01914.	6.0	299
70	Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. <i>Lancet Infectious Diseases</i> , The, 2014, 14, 50-56.	9.1	298
71	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
72	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet</i> , The, 2013, 382, 1993-2002.	13.7	282

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73	Estimating divergence dates from molecular sequences. <i>Molecular Biology and Evolution</i> , 1998, 15, 442-448.	8.9	280
74	Using Time-Structured Data to Estimate Evolutionary Rates of Double-Stranded DNA Viruses. <i>Molecular Biology and Evolution</i> , 2010, 27, 2038-2051.	8.9	279
75	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	28.9	275
76	Rapid SARS-CoV-2 whole-genome sequencing and analysis for informed public health decision-making in the Netherlands. <i>Nature Medicine</i> , 2020, 26, 1405-1410.	30.7	273
77	Temporal and spatial analysis of the 2014â€“2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101.	27.8	272
78	The evolution of Ebola virus: Insights from the 2013â€“2016 epidemic. <i>Nature</i> , 2016, 538, 193-200.	27.8	264
79	Ancient Hybridization and an Irish Origin for the Modern Polar Bear Matriline. <i>Current Biology</i> , 2011, 21, 1251-1258.	3.9	257
80	Determinants of rate variation in mammalian DNA sequence evolution. <i>Journal of Molecular Evolution</i> , 1996, 43, 610-621.	1.8	254
81	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016, 5, .	6.0	237
82	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	28.9	236
83	Spread, Circulation, and Evolution of the Middle East Respiratory Syndrome Coronavirus. <i>MBio</i> , 2014, 5, .	4.1	235
84	Estimating Divergence Dates and Substitution Rates in the <i>Drosophila</i> Phylogeny. <i>Molecular Biology and Evolution</i> , 2012, 29, 3459-3473.	8.9	230
85	Widespread intra-serotype recombination in natural populations of dengue virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 7352-7357.	7.1	226
86	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
87	The Epidemiology and Iatrogenic Transmission of Hepatitis C Virus in Egypt: A Bayesian Coalescent Approach. <i>Molecular Biology and Evolution</i> , 2003, 20, 381-387.	8.9	225
88	Inferring the Rate and Time-Scale of Dengue Virus Evolution. <i>Molecular Biology and Evolution</i> , 2003, 20, 122-129.	8.9	222
89	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021, 6, 821-823.	13.3	221
90	COVID-19 in health-care workers in three hospitals in the south of the Netherlands: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1273-1280.	9.1	220

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91	A synchronized global sweep of the internal genes of modern avian influenza virus. <i>Nature</i> , 2014, 508, 254-257.	27.8	206
92	Resurgence of Ebola Virus Disease in Guinea Linked to a Survivor With Virus Persistence in Seminal Fluid for More Than 500 Days. <i>Clinical Infectious Diseases</i> , 2016, 63, 1353-1356.	5.8	201
93	Genesis and pathogenesis of the 1918 pandemic H1N1 influenza A virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8107-8112.	7.1	197
94	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182
95	Livestock Origin for a Human Pandemic Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2013, 4, .	4.1	177
96	HIV evolutionary dynamics within and among hosts. <i>AIDS Reviews</i> , 2006, 8, 125-40.	1.0	176
97	Evolutionary Genomics of <i>Staphylococcus aureus</i> Reveals Insights into the Origin and Molecular Basis of Ruminant Host Adaptation. <i>Genome Biology and Evolution</i> , 2010, 2, 454-466.	2.5	174
98	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9107-9112.	7.1	174
99	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6.	28.9	173
100	MERS-CoV spillover at the camel-human interface. <i>ELife</i> , 2018, 7, .	6.0	172
101	Genetic analysis of West Nile New York 1999 encephalitis virus. <i>Lancet, The</i> , 1999, 354, 1971-1972.	13.7	168
102	Viral evolution and the emergence of SARS coronavirus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004, 359, 1059-1065.	4.0	165
103	Inference of Viral Evolutionary Rates from Molecular Sequences. <i>Advances in Parasitology</i> , 2003, 54, 331-358.	3.2	161
104	Molecular Phylodynamics of the Heterosexual HIV Epidemic in the United Kingdom. <i>PLoS Pathogens</i> , 2009, 5, e1000590.	4.7	155
105	An Observational, Laboratory-Based Study of Outbreaks of Middle East Respiratory Syndrome Coronavirus in Jeddah and Riyadh, Kingdom of Saudi Arabia, 2014. <i>Clinical Infectious Diseases</i> , 2015, 60, 369-377.	5.8	154
106	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
107	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19359-19364.	7.1	146
108	Phylogeny and the origin of HIV-1. <i>Nature</i> , 2001, 410, 1047-1048.	27.8	143

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109	Flight of the Dodo. <i>Science</i> , 2002, 295, 1683-1683.	12.6	143
110	The effect of genetic structure on molecular dating and tests for temporal signal. <i>Methods in Ecology and Evolution</i> , 2016, 7, 80-89.	5.2	143
111	MERS coronaviruses from camels in Africa exhibit region-dependent genetic diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3144-3149.	7.1	142
112	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
113	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
114	The evolution of genome compression and genomic novelty in RNA viruses. <i>Genome Research</i> , 2007, 17, 1496-1504.	5.5	139
115	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
116	Pacing a small cage: mutation and RNA viruses. <i>Trends in Ecology and Evolution</i> , 2008, 23, 188-193.	8.7	136
117	Phylogenetic Evidence for Deleterious Mutation Load in RNA Viruses and Its Contribution to Viral Evolution. <i>Molecular Biology and Evolution</i> , 2007, 24, 845-852.	8.9	133
118	Full-Genome Deep Sequencing and Phylogenetic Analysis of Novel Human Betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013, 19, 736-42B.	4.3	131
119	Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020, 94, .	3.4	129
120	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	129
121	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015, 6, 6696.	12.8	128
122	The Power of Relative Rates Tests Depends on the Data. <i>Journal of Molecular Evolution</i> , 2000, 50, 296-301.	1.8	124
123	Phylodynamic Reconstruction Reveals Norovirus GII.4 Epidemic Expansions and their Molecular Determinants. <i>PLoS Pathogens</i> , 2010, 6, e1000884.	4.7	124
124	Phylodynamics and Human-Mediated Dispersal of a Zoonotic Virus. <i>PLoS Pathogens</i> , 2010, 6, e1001166.	4.7	124
125	Real-time digital pathogen surveillance “the time is now”. <i>Genome Biology</i> , 2015, 16, 155.	8.8	123
126	Comparative analyses for adaptive radiations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2000, 355, 1599-1605.	4.0	120



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127	Pandemics: spend on surveillance, not prediction. <i>Nature</i> , 2018, 558, 180-182.	27.8	120
128	A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. <i>Molecular Biology and Evolution</i> , 2011, 28, 879-887.	8.9	119
129	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
130	Spatial Dynamics of Human-Origin H1 Influenza A Virus in North American Swine. <i>PLoS Pathogens</i> , 2011, 7, e1002077.	4.7	116
131	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	115
132	HIV-1 and HCV sequences from Libyan outbreak. <i>Nature</i> , 2006, 444, 836-837.	27.8	114
133	Heterotachy and Tree Building: A Case Study with Plastids and Eubacteria. <i>Molecular Biology and Evolution</i> , 2006, 23, 40-45.	8.9	114
134	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
135	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
136	The Molecular Population Genetics of HIV-1 Group O. <i>Genetics</i> , 2004, 167, 1059-1068.	2.9	105
137	JC Virus Evolution and Its Association with Human Populations. <i>Journal of Virology</i> , 2006, 80, 9928-9933.	3.4	105
138	Phylogeography and Population Dynamics of Dengue Viruses in the Americas. <i>Molecular Biology and Evolution</i> , 2012, 29, 1533-1543.	8.9	105
139	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	4.9	105
140	Recombination between sequences of hepatitis B virus from different genotypes. <i>Journal of Molecular Evolution</i> , 1996, 42, 97-102.	1.8	101
141	Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. <i>Journal of Virology</i> , 2012, 86, 11-18.	3.4	101
142	Phylogenetic Analysis Reveals a Correlation between the Expansion of Very Virulent Infectious Bursal Disease Virus and Reassortment of Its Genome Segment B. <i>Journal of Virology</i> , 2006, 80, 8503-8509.	3.4	100
143	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
144	Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set. <i>PLoS Computational Biology</i> , 2015, 11, e1004613.	3.2	89

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145	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	13.3	88
146	Evolution and Spread of Ebola Virus in Liberia, 2014–2015. <i>Cell Host and Microbe</i> , 2015, 18, 659-669.	11.0	87
147	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017, 66, syw054.	5.6	87
148	Accommodating the Effect of Ancient DNA Damage on Inferences of Demographic Histories. <i>Molecular Biology and Evolution</i> , 2009, 26, 245-248.	8.9	86
149	Endemic Dengue Associated with the Co-Circulation of Multiple Viral Lineages and Localized Density-Dependent Transmission. <i>PLoS Pathogens</i> , 2011, 7, e1002064.	4.7	86
150	The evolutionary dynamics of endogenous retroviruses. <i>Trends in Microbiology</i> , 2005, 13, 463-468.	7.7	84
151	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
152	Canalization of the evolutionary trajectory of the human influenza virus. <i>BMC Biology</i> , 2012, 10, 38.	3.8	84
153	The early molecular epidemiology of the swine-origin A/H1N1 human influenza pandemic. <i>PLOS Currents</i> , 2009, 1, RRN1003.	1.4	83
154	Evolutionary Genomics of Host Adaptation in Vesicular Stomatitis Virus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1138-1147.	8.9	82
155	Lessons from Ebola: Improving infectious disease surveillance to inform outbreak management. <i>Science Translational Medicine</i> , 2015, 7, 307rv5.	12.4	82
156	Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda. <i>Nature Microbiology</i> , 2021, 6, 1094-1101.	13.3	82
157	Phylogenetic Surveillance of Viral Genetic Diversity and the Evolving Molecular Epidemiology of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2007, 81, 13050-13056.	3.4	81
158	Importation and early local transmission of COVID-19 in Brazil, 2020. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2020, 62, e30.	1.1	80
159	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
160	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017, 13, e1006749.	4.7	78
161	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
162	Conserved Footprints of APOBEC3G on Hypermutated Human Immunodeficiency Virus Type 1 and Human Endogenous Retrovirus HERV-K(HML2) Sequences. <i>Journal of Virology</i> , 2008, 82, 8743-8761.	3.4	75

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163	Inferring Heterogeneous Evolutionary Processes Through Time: from Sequence Substitution to Phylogeography. <i>Systematic Biology</i> , 2014, 63, 493-504.	5.6	75
164	Contaminated polio vaccine theory refuted. <i>Nature</i> , 2004, 428, 820-820.	27.8	74
165	Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , 2011, 1, 423-429.	5.4	74
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