Andrew Rambaut

List of Publications by Year
in descending order

255 papers	109,097 citations	1027 117 h-index	748 256 g-index
294 all docs	294 docs citations	294 times ranked	86067 citing authors

#	Article	IF	Citations
1	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. Cell, 2022, 185, 467-484.e15.	13.5	788
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	13.7	1,210
3	Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences. BMC Genomics, 2022, 23, 121.	1.2	60
4	Tracking SARS-CoV-2 Mutations & Variants Through the COG-UK-Mutation Explorer. Virus Evolution, 2022, 8, veac023.	2.2	19
5	Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination. PLoS Pathogens, 2022, 18, e1010023.	2.1	17
6	An early warning system for emerging SARS-CoV-2 variants. Nature Medicine, 2022, 28, 1110-1115.	15.2	47
7	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. Nature Medicine, 2022, 28, 1785-1790.	15.2	456
8	Massive Parallelization Boosts Big Bayesian Multidimensional Scaling. Journal of Computational and Graphical Statistics, 2021, 30, 11-24.	0.9	15
9	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 2021, 184, 64-75.e11.	13.5	843
10	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. Nature Microbiology, 2021, 6, 112-122.	5.9	88
11	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nature Microbiology, 2021, 6, 415-415.	5.9	65
12	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. Science, 2021, 371, 708-712.	6.0	335
13	Relax, Keep Walking â€" A Practical Guide to Continuous Phylogeographic Inference with BEAST. Molecular Biology and Evolution, 2021, 38, 3486-3493.	3.5	31
14	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. Nature, 2021, 593, 266-269.	13.7	1,001
15	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	13.5	541
16	Ebola Virus Transmission Initiated by Relapse of Systemic Ebola Virus Disease. New England Journal of Medicine, 2021, 384, 1240-1247.	13.9	57
17	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. Science, 2021, 372, 815-821.	6.0	1,125
18	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. Wellcome Open Research, 2021, 6, 121.	0.9	115

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19	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. Nature Microbiology, 2021, 6, 821-823.	5.9	221
20	SARS-CoV-2 variants, spike mutations and immune escape. Nature Reviews Microbiology, 2021, 19, 409-424.	13.6	2,650
21	Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda. Nature Microbiology, 2021, 6, 1094-1101.	5.9	82
22	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	2.9	375
23	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. Science, 2021, 373, 889-895.	6.0	142
24	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. Genome Biology, 2021, 22, 196.	3.8	53
25	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. Virus Evolution, 2021, 7, veab064.	2.2	774
26	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. Wellcome Open Research, 2021, 6, 121.	0.9	129
27	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. Cell, 2021, 184, 5179-5188.e8.	13.5	182
28	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. Nature Communications, 2021, 12, 5705.	5.8	24
29	The origins of SARS-CoV-2: A critical review. Cell, 2021, 184, 4848-4856.	13.5	330
30	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. Nature, 2021, 597, 539-543.	13.7	113
31	Monitoring key epidemiological parameters of SARS-CoV-2 transmission. Nature Medicine, 2021, 27, 1854-1855.	15.2	28
32	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	6.0	111
33	Temporal signal and the phylodynamic threshold of SARS-CoV-2. Virus Evolution, 2020, 6, veaa061.	2.2	317
34	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nature Microbiology, 2020, 5, 1403-1407.	5.9	2,291
35	Rapid SARS-CoV-2 whole-genome sequencing and analysis for informed public health decision-making in the Netherlands. Nature Medicine, 2020, 26, 1405-1410.	15.2	273
36	Evolution and epidemic spread of SARS-CoV-2 in Brazil. Science, 2020, 369, 1255-1260.	6.0	454

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37	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. Nature Microbiology, 2020, 5, 1408-1417.	5.9	772
38	COVID-19 in health-care workers in three hospitals in the south of the Netherlands: a cross-sectional study. Lancet Infectious Diseases, The, 2020, 20, 1273-1280.	4.6	220
39	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. Nature Communications, 2020, 11, 5110.	5.8	118
40	The emergence of SARS-CoV-2 in Europe and North America. Science, 2020, 370, 564-570.	6.0	331
41	Determinants of dengue virus dispersal in the Americas. Virus Evolution, 2020, 6, veaa074.	2.2	5
42	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. Cell, 2020, 181, 997-1003.e9.	13.5	236
43	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. Journal of Infectious Diseases, 2020, 222, 1670-1680.	1.9	12
44	Gradients Do Grow on Trees: A Linear-Time $O(N)$-Dimensional Gradient for Statistical Phylogenetics. Molecular Biology and Evolution, 2020, 37, 3047-3060.	3.5	22
45	The proximal origin of SARS-CoV-2. Nature Medicine, 2020, 26, 450-452.	15.2	3,871
46	Rapid and Sensitive Direct Detection and Identification of Poliovirus from Stool and Environmental Surveillance Samples by Use of Nanopore Sequencing. Journal of Clinical Microbiology, 2020, 58, .	1.8	33
47	Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2. Journal of Virology, 2020, 94, .	1.5	129
48	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. Molecular Biology and Evolution, 2020, 37, 1832-1842.	3.5	25
49	Importation and early local transmission of COVID-19 in Brazil, 2020. Revista Do Instituto De Medicina Tropical De Sao Paulo, 2020, 62, e30.	0.5	80
50	Early Insights from Statistical and Mathematical Modeling of Key Epidemiologic Parameters of COVID-19. Emerging Infectious Diseases, 2020, 26, e1-e14.	2.0	50
51	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. Journal of Clinical Microbiology, 2019, 57, .	1.8	17
52	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. Methods in Molecular Biology, 2019, 1910, 691-722.	0.4	11
53	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. Molecular Biology and Evolution, 2019, 36, 1793-1803.	3.5	39
54	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. Virus Evolution, 2019, 5, vez003.	2.2	26

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55	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. Systematic Biology, 2019, 68, 1052-1061.	2.7	139
56	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. PLoS Computational Biology, 2019, 15, e1006650.	1.5	2,484
57	PANGEA-HIV 2. Current Opinion in HIV and AIDS, 2019, 14, 173-180.	1.5	28
58	Fogarty International Center collaborative networks in infectious disease modeling: Lessons learnt in research and capacity building. Epidemics, 2019, 26, 116-127.	1.5	16
59	Tracking virus outbreaks in the twenty-first century. Nature Microbiology, 2019, 4, 10-19.	5.9	305
60	MERS coronaviruses from camels in Africa exhibit region-dependent genetic diversity. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3144-3149.	3.3	142
61	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. Cell Reports, 2018, 22, 1159-1168.	2.9	37
62	Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. Systematic Biology, 2018, 67, 901-904.	2.7	6,726
63	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. Statistics in Medicine, 2018, 37, 195-206.	0.8	4
64	MERS-CoV spillover at the camel-human interface. ELife, 2018, 7, .	2.8	172
65	Pandemics: spend on surveillance, not prediction. Nature, 2018, 558, 180-182.	13.7	120
66	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. Virus Evolution, 2018, 4, vey016.	2.2	2,401
67	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. Nature Communications, 2018, 9, 2222.	5.8	59
68	Emerging Concepts of Data Integration in Pathogen Phylodynamics. Systematic Biology, 2017, 66, syw054.	2.7	87
69	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	13.7	346
70	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature, 2017, 546, 401-405.	13.7	298
71	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. Nature, 2017, 546, 406-410.	13.7	515
72	Zika virus evolution and spread in the Americas. Nature, 2017, 546, 411-415.	13.7	323

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73	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. Bioinformatics, 2017, 33, 1798-1805.	1.8	35
74	Lorenzo-Redondo et al. reply. Nature, 2017, 551, E10-E10.	13.7	5
75	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. PLoS Pathogens, 2017, 13, e1006749.	2.1	78
76	The effects of sampling strategy on the quality of reconstruction of viral population dynamics using Bayesian skyline family coalescent methods: A simulation study. Virus Evolution, 2016, 2, vew003.	2.2	69
77	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014â€"2015. Emerging Infectious Diseases, 2016, 22, 2149-2152.	2.0	21
78	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. PLoS Pathogens, 2016, 12, e1005525.	2.1	65
79	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. ELife, 2016, 5, .	2.8	237
80	Reduced evolutionary rate in reemerged Ebola virus transmission chains. Science Advances, 2016, 2, e1600378.	4.7	62
81	SpreaD3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. Molecular Biology and Evolution, 2016, 33, 2167-2169.	3.5	413
82	Resurgence of Ebola Virus Disease in Guinea Linked to a Survivor With Virus Persistence in Seminal Fluid for More Than 500 Days. Clinical Infectious Diseases, 2016, 63, 1353-1356.	2.9	201
83	The evolution of Ebola virus: Insights from the 2013â€"2016 epidemic. Nature, 2016, 538, 193-200.	13.7	264
84	Comment on â€œMutation rate and genotype variation of Ebola virus from Mali case sequencesâ€. Science, 2016, 353, 658-658.	6.0	6
85	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. Virus Evolution, 2016, 2, vew016.	2.2	105
86	Role for migratory wild birds in the global spread of avian influenza H5N8. Science, 2016, 354, 213-217.	6.0	362
87	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. Epidemics, 2016, 17, 27-34.	1.5	13
88	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013â€"2016 Epidemic. Cell, 2016, 167, 1088-1098.e6.	13.5	173
89	The effect of genetic structure on molecular dating and tests for temporal signal. Methods in Ecology and Evolution, 2016, 7, 80-89.	2.2	143
90	Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). Virus Evolution, 2016, 2, vew007.	2.2	1,638

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91	Persistent HIV-1 replication maintains the tissue reservoir during therapy. Nature, 2016, 530, 51-56.	13.7	550
92	Epidemic History and Iatrogenic Transmission of Blood-borne Viruses in Mid-20th Century Kinshasa. Journal of Infectious Diseases, 2016, 214, 353-360.	1.9	19
93	MERS-CoV recombination: implications about the reservoir and potential for adaptation. Virus Evolution, 2016, 2, vev023.	2.2	60
94	Real-time, portable genome sequencing for Ebola surveillance. Nature, 2016, 530, 228-232.	13.7	1,179
95	Notes from The Field: Ebola Virus Disease Cluster â€" Northern Sierra Leone, January 2016. Morbidity and Mortality Weekly Report, 2016, 65, 681-682.	9.0	16
96	Simultaneously estimating evolutionary history and repeated traits phylogenetic signal: applications to viral and host phenotypic evolution. Methods in Ecology and Evolution, 2015, 6, 67-82.	2.2	22
97	Relationship between haemagglutination inhibition titre and immunity to influenza in ferrets. Vaccine, 2015, 33, 5380-5385.	1.7	7
98	Real-time digital pathogen surveillance â€" the time is now. Genome Biology, 2015, 16, 155.	3.8	123
99	Reassortment between Influenza B Lineages and the Emergence of a Coadapted PB1â€"PB2â€"HA Gene Complex. Molecular Biology and Evolution, 2015, 32, 162-172.	3.5	63
100	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. Nature, 2015, 523, 217-220.	13.7	445
101	Evolution and Spread of Ebola Virus in Liberia, 2014â€"2015. Cell Host and Microbe, 2015, 18, 659-669.	5.1	87
102	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. Cell, 2015, 161, 1516-1526.	13.5	275
103	Temporal and spatial analysis of the 2014â€"2015 Ebola virus outbreak in West Africa. Nature, 2015, 524, 97-101.	13.7	272
104	Global migration of influenza A viruses in swine. Nature Communications, 2015, 6, 6696.	5.8	128
105	Lessons from Ebola: Improving infectious disease surveillance to inform outbreak management. Science Translational Medicine, 2015, 7, 307rv5.	5.8	82
106	The Vietnam Initiative on Zoonotic Infections (VIZIONS): A Strategic Approach to Studying Emerging Zoonotic Infectious Diseases. EcoHealth, 2015, 12, 726-735.	0.9	47
107	An Observational, Laboratory-Based Study of Outbreaks of Middle East Respiratory Syndrome Coronavirus in Jeddah and Riyadh, Kingdom of Saudi Arabia, 2014. Clinical Infectious Diseases, 2015, 60, 369-377.	2.9	154
108	Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set. PLoS Computational Biology, 2015, 11, e1004613.	1.5	89

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109	Integrating influenza antigenic dynamics with molecular evolution. ELife, 2014, 3, e01914.	2.8	299
110	Improving pandemic influenza risk assessment. ELife, 2014, 3, e03883.	2.8	53
111	The Genealogical Population Dynamics of HIV-1 in a Large Transmission Chain: Bridging within and among Host Evolutionary Rates. PLoS Computational Biology, 2014, 10, e1003505.	1.5	79
112	BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. PLoS Computational Biology, 2014, 10, e1003537.	1.5	5,301
113	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. PLoS Pathogens, 2014, 10, e1003932.	2.1	330
114	Genesis and pathogenesis of the 1918 pandemic H1N1 influenza A virus. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8107-8112.	3.3	197
115	Spread, Circulation, and Evolution of the Middle East Respiratory Syndrome Coronavirus. MBio, 2014, 5, .	1.8	235
116	A synchronized global sweep of the internal genes of modern avian influenza virus. Nature, 2014, 508, 254-257.	13.7	206
117	Multiple introductions of salmonid alphavirus from a wild reservoir have caused independent and self-sustainable epizootics in aquaculture. Journal of General Virology, 2014, 95, 52-59.	1.3	29
118	OutbreakTools: A new platform for disease outbreak analysis using the R software. Epidemics, 2014, 7, 28-34.	1.5	37
119	Inferring Heterogeneous Evolutionary Processes Through Time: from Sequence Substitution to Phylogeography. Systematic Biology, 2014, 63, 493-504.	2.7	75
120	Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. Lancet Infectious Diseases, The, 2014, 14, 50-56.	4.6	298
121	Possible Footprints of APOBEC3F and/or Other APOBEC3 Deaminases, but Not APOBEC3G, on HIV-1 from Patients with Acute/Early and Chronic Infections. Journal of Virology, 2014, 88, 12882-12894.	1.5	21
122	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. Science, 2014, 345, 1369-1372.	6.0	1,083
123	The early spread and epidemic ignition of HIV-1 in human populations. Science, 2014, 346, 56-61.	6.0	515
124	π€BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. BMC Bioinformatics, 2014, 15, 133.	1.2	22
125	Phylogenetic Analysis of Guinea 2014 EBOV Ebolavirus Outbreak. PLOS Currents, 2014, 6, .	1.4	62
126	The genesis and source of the H7N9 influenza viruses causing human infections in China. Nature, 2013, 502, 241-244.	13.7	429

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127	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. Lancet, The, 2013, 382, 1993-2002.	6.3	282
128	Relaxed Phylogenetics and the Palaeoptera Problem: Resolving Deep Ancestral Splits in the Insect Phylogeny. Systematic Biology, 2013, 62, 285-297.	2.7	53
129	Improving Bayesian Population Dynamics Inference: A Coalescent-Based Model for Multiple Loci. Molecular Biology and Evolution, 2013, 30, 713-724.	3.5	449
130	Clinical features and virological analysis of a case of Middle East respiratory syndrome coronavirus infection. Lancet Infectious Diseases, The, 2013, 13, 745-751.	4.6	343
131	Livestock Origin for a Human Pandemic Clone of Community-Associated Methicillin-Resistant Staphylococcus aureus. MBio, 2013, 4, .	1.8	177
132	Reconstructing Geographical Movements and Host Species Transitions of Foot-and-Mouth Disease Virus Serotype SAT 2. MBio, 2013, 4, e00591-13.	1.8	50
133	Full-Genome Deep Sequencing and Phylogenetic Analysis of Novel Human Betacoronavirus. Emerging Infectious Diseases, 2013, 19, 736-42B.	2.0	131
134	Estimating the Rate of Intersubtype Recombination in Early HIV-1 Group M Strains. Journal of Virology, 2013, 87, 1967-1973.	1.5	24
135	Simultaneously reconstructing viral cross-species transmission history and identifying the underlying constraints. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120196.	1.8	141
136	APOBEC3G-Induced Hypermutation of Human Immunodeficiency Virus Type-1 Is Typically a Discrete â€œAll or Nothingâ€•Phenomenon. PLoS Genetics, 2012, 8, e1002550.	1.5	65
137	Estimating Divergence Dates and Substitution Rates in the Drosophila Phylogeny. Molecular Biology and Evolution, 2012, 29, 3459-3473.	3.5	230
138	Molecular dating of human-to-bovid host jumps by <i>Staphylococcus aureus</i> reveals an association with the spread of domestication. Biology Letters, 2012, 8, 829-832.	1.0	77
139	Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. Journal of Virology, 2012, 86, 11-18.	1.5	101
140	Origin and Evolution of the Unique Hepatitis C Virus Circulating Recombinant Form 2k/1b. Journal of Virology, 2012, 86, 2212-2220.	1.5	56
141	BEAGLE: An Application Programming Interface and High-Performance Computing Library for Statistical Phylogenetics. Systematic Biology, 2012, 61, 170-173.	2.7	555
142	Bayesian Phylogenetics with BEAUti and the BEAST 1.7. Molecular Biology and Evolution, 2012, 29, 1969-1973.	3.5	9,040
143	Analysis of high-depth sequence data for studying viral diversity: a comparison of next generation sequencing platforms using Segminator II. BMC Bioinformatics, 2012, 13, 47.	1.2	58
144	Canalization of the evolutionary trajectory of the human influenza virus. BMC Biology, 2012, 10, 38.	1.7	84

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145	Phylogeography and Population Dynamics of Dengue Viruses in the Americas. Molecular Biology and Evolution, 2012, 29, 1533-1543.	3.5	105
146	Unifying the spatial epidemiology and molecular evolution of emerging epidemics. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15066-15071.	3.3	226
147	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant <i>Staphylococcus aureus</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9107-9112.	3.3	174
148	Improving the Accuracy of Demographic and Molecular Clock Model Comparison While Accommodating Phylogenetic Uncertainty. Molecular Biology and Evolution, 2012, 29, 2157-2167.	3.5	1,053
149	Origin and fate of A/H1N1 influenza in Scotland during 2009. Journal of General Virology, 2012, 93, 1253-1260.	1.3	14
150	A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. Molecular Biology and Evolution, 2011, 28, 879-887.	3.5	119
151	Toward a quantitative understanding of viral phylogeography. Current Opinion in Virology, 2011, 1, 423-429.	2.6	74
152	Ancient Hybridization and an Irish Origin for the Modern Polar Bear Matriline. Current Biology, 2011, 21, 1251-1258.	1.8	257
153	SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. Bioinformatics, 2011, 27, 2910-2912.	1.8	451
154	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19359-19364.	3.3	146
155	Spatial Dynamics of Human-Origin H1 Influenza A Virus in North American Swine. PLoS Pathogens, 2011, 7, e1002077.	2.1	116
156	Genomic Analysis of Hepatitis B Virus Reveals Antigen State and Genotype as Sources of Evolutionary Rate Variation. Viruses, 2011, 3, 83-101.	1.5	49
157	Endemic Dengue Associated with the Co-Circulation of Multiple Viral Lineages and Localized Density-Dependent Transmission. PLoS Pathogens, 2011, 7, e1002064.	2.1	86
158	Using Time-Structured Data to Estimate Evolutionary Rates of Double-Stranded DNA Viruses. Molecular Biology and Evolution, 2010, 27, 2038-2051.	3.5	279
159	Phylodynamic Reconstruction Reveals Norovirus GII.4 Epidemic Expansions and their Molecular Determinants. PLoS Pathogens, 2010, 6, e1000884.	2.1	124
160	Phylodynamics and Human-Mediated Dispersal of a Zoonotic Virus. PLoS Pathogens, 2010, 6, e1001166.	2.1	124
161	The Evolutionary Analysis of Emerging Low Frequency HIV-1 CXCR4 Using Variants through Timeâ€"An Ultra-Deep Approach. PLoS Computational Biology, 2010, 6, e1001022.	1.5	72
162	Evolutionary Genomics of Staphylococcus aureus Reveals Insights into the Origin and Molecular Basis of Ruminant Host Adaptation. Genome Biology and Evolution, 2010, 2, 454-466.	1.1	174

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163	Phylogeography Takes a Relaxed Random Walk in Continuous Space and Time. Molecular Biology and Evolution, 2010, 27, 1877-1885.	3.5	580
164	Bayesian evolutionary analysis by sampling trees. , 2009, , 564-591.		20
165	Many-core algorithms for statistical phylogenetics. Bioinformatics, 2009, 25, 1370-1376.	1.8	380
166	Accommodating the Effect of Ancient DNA Damage on Inferences of Demographic Histories. Molecular Biology and Evolution, 2009, 26, 245-248.	3.5	86
167	Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. Science, 2009, 324, 1557-1561.	6.0	1,665
168	Response—Influenza. Science, 2009, 325, 1072-1073.	6.0	2
169	Bayesian Phylogeography Finds Its Roots. PLoS Computational Biology, 2009, 5, e1000520.	1.5	1,519
170	Molecular Phylodynamics of the Heterosexual HIV Epidemic in the United Kingdom. PLoS Pathogens, 2009, 5, e1000590.	2.1	155
171	The RNA Virus Database. Nucleic Acids Research, 2009, 37, D431-D435.	6.5	14
172	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. Nature, 2009, 459, 1122-1125.	13.7	1,870
173	Evolutionary analysis of the dynamics of viral infectious disease. Nature Reviews Genetics, 2009, 10, 540-550.	7.7	526
174	Recent human-to-poultry host jump, adaptation, and pandemic spread of <i>Staphylococcus aureus</i>. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19545-19550.	3.3	363
175	The early molecular epidemiology of the swine-origin A/H1N1 human influenza pandemic. PLOS Currents, 2009, 1, RRN1003.	1.4	83
176	Reconstructing the initial global spread of a human influenza pandemicA Bayesian spatial-temporal model for the global spread of H1N1pdm. PLOS Currents, 2009, 1, RRN1031.	1.4	97
177	Correlating viral phenotypes with phylogeny: Accounting for phylogenetic uncertainty. Infection, Genetics and Evolution, 2008, 8, 239-246.	1.0	408
178	The genomic and epidemiological dynamics of human influenza A virus. Nature, 2008, 453, 615-619.	13.7	824
179	Breeding racehorses: what price good genes?. Biology Letters, 2008, 4, 173-175.	1.0	9
180	Reply to Pape et al.: The phylogeography of HIV-1 group M subtype B. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, E16-E16.	3.3	9

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181	Pacing a small cage: mutation and RNA viruses. Trends in Ecology and Evolution, 2008, 23, 188-193.	4.2	136
182	Conserved Footprints of APOBEC3G on Hypermutated Human Immunodeficiency Virus Type 1 and Human Endogenous Retrovirus HERV-K(HML2) Sequences. Journal of Virology, 2008, 82, 8743-8761.	1.5	75
183	Episodic Sexual Transmission of HIV Revealed by Molecular Phylodynamics. PLoS Medicine, 2008, 5, e50.	3.9	326
184	Evolutionary Genomics of Host Adaptation in Vesicular Stomatitis Virus. Molecular Biology and Evolution, 2008, 25, 1138-1147.	3.5	82
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