

Andrew Rambaut

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

282 papers	75,056 citations	109 h-index	273 g-index
294 ext. papers	95,813 ext. citations	16.5 avg, IF	8.54 L-index

#	Paper	IF	Citations
282	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses.. <i>Cell</i> , 2022 ,	56.2	154
281	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , 2022 ,	50.4	205
280	Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences.. <i>BMC Genomics</i> , 2022 , 23, 121	4.5	9
279	Tracking SARS-CoV-2 mutations and variants through the COG-UK-Mutation Explorer.. <i>Virus Evolution</i> , 2022 , 8, veac023	3.7	1
278	Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination.. <i>PLoS Pathogens</i> , 2022 , 18, e1010023	7.6	2
277	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		3
276	Monitoring key epidemiological parameters of SARS-CoV-2 transmission. <i>Nature Medicine</i> , 2021 , 27, 1854-1855	30.3	33
275	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021 , 374, eabl9551	33.3	31
274	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil 2021 ,		53
273	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021 , 593, 266-269	50.4	452
272	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021 , 184, 1171-1187.e20	56.2	331
271	Ebola Virus Transmission Initiated by Relapse of Systemic Ebola Virus Disease. <i>New England Journal of Medicine</i> , 2021 , 384, 1240-1247	59.2	16
270	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021 , 372, 815-821	33.3	603
269	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	4.8	46
268	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021 , 6, 821-823	26.6	91
267	SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021 , 19, 409-424	24.2	873
266	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	26.6	39

265	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	10.6	172
264	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895	33.3	41
263	Massive parallelization boosts big Bayesian multidimensional scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021 , 30, 11-24	1.4	7
262	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021 , 184, 64-75.e11	56.2	518
261	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021 , 6, 112-122	26.6	39
260	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021 , 6, 415	26.6	35
259	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712	33.3	159
258	Relax, Keep Walking - A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3486-3493	8.3	4
257	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021 , 7, veab064	3.7	176
256	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	4.8	50
255	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021 , 184, 5179-5188.e8	56.2	48
254	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. <i>Nature Communications</i> , 2021 , 12, 5705	17.4	2
253	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021 , 184, 4848-4856	56.2	103
252	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021 , 597, 539-543	50.4	19
251	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		2
250	Determinants of dengue virus dispersal in the Americas. <i>Virus Evolution</i> , 2020 , 6, veaa074	3.7	1
249	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020 , 181, 997-1003.e9	56.2	175
248	Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial. <i>Journal of Infectious Diseases</i> , 2020 , 222, 1670-1680	7	3

247	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	8.3	5
246	The proximal origin of SARS-CoV-2. <i>Nature Medicine</i> , 2020 , 26, 450-452	50.5	2687
245	Rapid and Sensitive Direct Detection and Identification of Poliovirus from Stool and Environmental Surveillance Samples by Use of Nanopore Sequencing. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	12
244	Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020 , 94,	6.6	89
243	Online Bayesian Phylodynamic Inference in BEAST with Application to Epidemic Reconstruction. <i>Molecular Biology and Evolution</i> , 2020 , 37, 1832-1842	8.3	9
242	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	2.2	50
241	Early Insights from Statistical and Mathematical Modeling of Key Epidemiologic Parameters of COVID-19. <i>Emerging Infectious Diseases</i> , 2020 , 26, e1-e14	10.2	29
240	The emergence of SARS-CoV-2 in Europe and the US 2020 ,		35
239	Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study 2020 ,		5
238	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020 , 6, veaa061	3.7	147
237	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020 , 5, 1403-1407	26.6	1250
236	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	50.5	167
235	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260	33.3	277
234	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020 , 5, 1408-1417	26.6	447
233	COVID-19 in health-care workers in three hospitals in the south of the Netherlands: a cross-sectional study. <i>Lancet Infectious Diseases</i> , 2020 , 20, 1273-1280	25.5	144
232	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020 , 11, 5110	17.4	49
231	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020 , 370, 564-570	33.3	183
230	Bayesian Inference of Evolutionary Histories under Time-Dependent Substitution Rates. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1793-1803	8.3	24

229	SANTA-SIM: simulating viral sequence evolution dynamics under selection and recombination. <i>Virus Evolution</i> , 2019 , 5, vez003	3.7	15
228	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019 , 68, 1052-1061	8.4	71
227	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019 , 15, e1006650	5	1014
226	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	7
225	High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE. <i>Methods in Molecular Biology</i> , 2019 , 1910, 691-722	1.4	3
224	PANGAEA-HIV 2: Phylogenetics And Networks for Generalised Epidemics in Africa. <i>Current Opinion in HIV and AIDS</i> , 2019 , 14, 173-180	4.2	14
223	Fogarty International Center collaborative networks in infectious disease modeling: Lessons learnt in research and capacity building. <i>Epidemics</i> , 2019 , 26, 116-127	5.1	10
222	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019 , 4, 10-19	26.6	179
221	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	11.5	105
220	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018 , 22, 1159-1168	10.6	27
219	Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. <i>Systematic Biology</i> , 2018 , 67, 901-904	36.4	3267
218	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. <i>Statistics in Medicine</i> , 2018 , 37, 195-206	2.3	2
217	Pandemics: spend on surveillance, not prediction. <i>Nature</i> , 2018 , 558, 180-182	50.4	77
216	Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018 , 4, vey016	3.7	1199
215	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018 , 9, 2222	17.4	39
214	MERS-CoV spillover at the camel-human interface. <i>ELife</i> , 2018 , 7,	8.9	109
213	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
212	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235

211	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017 , 546, 406-410.4	50.4	366
210	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017 , 546, 411-415	50.4	253
209	Adaptive MCMC in Bayesian phylogenetics: an application to analyzing partitioned data in BEAST. <i>Bioinformatics</i> , 2017 , 33, 1798-1805	7.2	21
208	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017 , 13, e1006749	7.6	55
207	Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017 , 66, e47-e65.4	65.4	55
206	Lorenzo-Redondo et al. reply. <i>Nature</i> , 2017 , 551, E10	50.4	5
205	Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences". <i>Science</i> , 2016 , 353, 658	33.3	5
204	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016 , 2, vew016	3.7	89
203	Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , 2016 , 354, 213-217	33.3	252
202	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. <i>Epidemics</i> , 2016 , 17, 27-34	5.1	9
201	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016 , 167, 1088-1098.e6	56.2	135
200	The effect of genetic structure on molecular dating and tests for temporal signal. <i>Methods in Ecology and Evolution</i> , 2016 , 7, 80-89	7.7	90
199	Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , 2016 , 2, vew007	3.7	961
198	Persistent HIV-1 replication maintains the tissue reservoir during therapy. <i>Nature</i> , 2016 , 530, 51-56	50.4	419
197	Epidemic History and Iatrogenic Transmission of Blood-borne Viruses in Mid-20th Century Kinshasa. <i>Journal of Infectious Diseases</i> , 2016 , 214, 353-60	7	16
196	MERS-CoV recombination: implications about the reservoir and potential for adaptation. <i>Virus Evolution</i> , 2016 , 2, vew023	3.7	45
195	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016 , 530, 228-232	50.4	845
194	Notes from The Field: Ebola Virus Disease Cluster - Northern Sierra Leone, January 2016. <i>Morbidity and Mortality Weekly Report</i> , 2016 , 65, 681-2	31.7	14

193	Author response: Origins of the 2009 H1N1 influenza pandemic in swine in Mexico 2016 ,		2
192	The effects of sampling strategy on the quality of reconstruction of viral population dynamics using Bayesian skyline family coalescent methods: A simulation study. <i>Virus Evolution</i> , 2016 , 2, vew003	3.7	39
191	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014-2015. <i>Emerging Infectious Diseases</i> , 2016 , 22, 2149-2152	10.2	17
190	Revealing the Micro-scale Signature of Endemic Zoonotic Disease Transmission in an African Urban Setting. <i>PLoS Pathogens</i> , 2016 , 12, e1005525	7.6	45
189	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016 , 5,	8.9	142
188	Reduced evolutionary rate in reemerged Ebola virus transmission chains. <i>Science Advances</i> , 2016 , 2, e1600378	10.3	53
187	Spread3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2167-9	8.3	241
186	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	11.6	134
185	The evolution of Ebola virus: Insights from the 2013-2016 epidemic. <i>Nature</i> , 2016 , 538, 193-200	50.4	185
184	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015 , 161, 1516-26	56.2	210
183	Temporal and spatial analysis of the 2014-2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015 , 524, 97-101	50.4	229
182	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015 , 6, 6696	17.4	91
181	Lessons from Ebola: Improving infectious disease surveillance to inform outbreak management. <i>Science Translational Medicine</i> , 2015 , 7, 307rv5	17.5	67
180	The Vietnam Initiative on Zoonotic Infections (VIZIONS): A Strategic Approach to Studying Emerging Zoonotic Infectious Diseases. <i>EcoHealth</i> , 2015 , 12, 726-35	3.1	37
179	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, 369-77	11.6	133
178	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	7.7	15
177	Relationship between haemagglutination inhibition titre and immunity to influenza in ferrets. <i>Vaccine</i> , 2015 , 33, 5380-5385	4.1	7
176	Real-time digital pathogen surveillance - the time is now. <i>Genome Biology</i> , 2015 , 16, 155	18.3	91

175	Reassortment between influenza B lineages and the emergence of a coadapted PB1-PB2-HA gene complex. <i>Molecular Biology and Evolution</i> , 2015 , 32, 162-72	8.3	48
174	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015 , 523, 217-20	5.0	302
173	Evolution and Spread of Ebola Virus in Liberia, 2014-2015. <i>Cell Host and Microbe</i> , 2015 , 18, 659-69	23.4	66
172	Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set. <i>PLoS Computational Biology</i> , 2015 , 11, e1004613	5	56
171	A synchronized global sweep of the internal genes of modern avian influenza virus. <i>Nature</i> , 2014 , 508, 254-7	50.4	158
170	Multiple introductions of salmonid alphavirus from a wild reservoir have caused independent and self-sustainable epizootics in aquaculture. <i>Journal of General Virology</i> , 2014 , 95, 52-59	4.9	23
169	OutbreakTools: a new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014 , 7, 28-34	5.1	32
168	Inferring heterogeneous evolutionary processes through time: from sequence substitution to phylogeography. <i>Systematic Biology</i> , 2014 , 63, 493-504	8.4	54
167	Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. <i>Lancet Infectious Diseases</i> , 2014 , 14, 50-56	25.5	231
166	Possible footprints of APOBEC3F and/or other APOBEC3 deaminases, but not APOBEC3G, on HIV-1 from patients with acute/early and chronic infections. <i>Journal of Virology</i> , 2014 , 88, 12882-94	6.6	14
165	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014 , 345, 1369-72	33.3	847
164	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61	33.3	370
163	BUSS: a parallel BEAST/BEAGLE utility for sequence simulation under complex evolutionary scenarios. <i>BMC Bioinformatics</i> , 2014 , 15, 133	3.6	18
162	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014 , 3, e01914	8.9	213
161	Improving pandemic influenza risk assessment. <i>ELife</i> , 2014 , 3, e03883	8.9	45
160	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	5	66
159	BEAST 2: a software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2014 , 10, e1003537	5	3659
158	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , 2014 , 10, e1003932	7.6	230

157	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, 8107-12	11.5	150
156	Spread, circulation, and evolution of the Middle East respiratory syndrome coronavirus. <i>MBio</i> , 2014 , 5,	7.8	207
155	Phylogenetic Analysis of Guinea 2014 EBOV Ebolavirus Outbreak. <i>PLOS Currents</i> , 2014 , 6,		51
154	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013 , 502, 241-4	50.4	337
153	Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. <i>Lancet, The</i> , 2013 , 382, 1993-2002	40	234
152	Relaxed phylogenetics and the palaeoptera problem: resolving deep ancestral splits in the insect phylogeny. <i>Systematic Biology</i> , 2013 , 62, 285-97	8.4	45
151	Improving Bayesian population dynamics inference: a coalescent-based model for multiple loci. <i>Molecular Biology and Evolution</i> , 2013 , 30, 713-24	8.3	312
150	Clinical features and virological analysis of a case of Middle East respiratory syndrome coronavirus infection. <i>Lancet Infectious Diseases, The</i> , 2013 , 13, 745-51	25.5	288
149	Livestock origin for a human pandemic clone of community-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2013 , 4,	7.8	132
148	Reconstructing geographical movements and host species transitions of foot-and-mouth disease virus serotype SAT 2. <i>MBio</i> , 2013 , 4, e00591-13	7.8	43
147	Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013 , 19, 736-42B	10.2	117
146	Estimating the rate of intersubtype recombination in early HIV-1 group M strains. <i>Journal of Virology</i> , 2013 , 87, 1967-73	6.6	19
145	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	5.8	101
144	BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. <i>Systematic Biology</i> , 2012 , 61, 170-3	8.4	374
143	Bayesian phylogenetics with BEAUti and the BEAST 1.7. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1969-83	83	7409
142	Analysis of high-depth sequence data for studying viral diversity: a comparison of next generation sequencing platforms using Segminator II. <i>BMC Bioinformatics</i> , 2012 , 13, 47	3.6	55
141	Canalization of the evolutionary trajectory of the human influenza virus. <i>BMC Biology</i> , 2012 , 10, 38	7.3	61
140	Phylogeography and population dynamics of dengue viruses in the Americas. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1533-43	8.3	81

139	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, 15066-71	11.5	159
138	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, 9107-12	11.5	138
137	Improving the accuracy of demographic and molecular clock model comparison while accommodating phylogenetic uncertainty. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2157-67	8.3	779
136	APOBEC3G-induced hypermutation of human immunodeficiency virus type-1 is typically a discrete "all or nothing" phenomenon. <i>PLoS Genetics</i> , 2012 , 8, e1002550	6	55
135	Estimating divergence dates and substitution rates in the <i>Drosophila</i> phylogeny. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3459-73	8.3	158
134	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, 829-32	3.6	63
133	Evolutionary dynamics of local pandemic H1N1/2009 influenza virus lineages revealed by whole-genome analysis. <i>Journal of Virology</i> , 2012 , 86, 11-8	6.6	87
132	Origin and evolution of the unique hepatitis C virus circulating recombinant form 2k/1b. <i>Journal of Virology</i> , 2012 , 86, 2212-20	6.6	46
131	Origin and fate of A/H1N1 influenza in Scotland during 2009. <i>Journal of General Virology</i> , 2012 , 93, 1253-1260	13.60	13
130	A Bayesian phylogenetic method to estimate unknown sequence ages. <i>Molecular Biology and Evolution</i> , 2011 , 28, 879-87	8.3	98
129	Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , 2011 , 1, 423-9	7.5	56
128	Ancient hybridization and an Irish origin for the modern polar bear matriline. <i>Current Biology</i> , 2011 , 21, 1251-8	6.3	203
127	SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. <i>Bioinformatics</i> , 2011 , 27, 2910-2	7.2	369
126	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, 19359-64	11.5	130
125	Spatial dynamics of human-origin H1 influenza A virus in North American swine. <i>PLoS Pathogens</i> , 2011 , 7, e1002077	7.6	101
124	Genomic analysis of hepatitis B virus reveals antigen state and genotype as sources of evolutionary rate variation. <i>Viruses</i> , 2011 , 3, 83-101	6.2	42
123	Endemic dengue associated with the co-circulation of multiple viral lineages and localized density-dependent transmission. <i>PLoS Pathogens</i> , 2011 , 7, e1002064	7.6	74
122	Using time-structured data to estimate evolutionary rates of double-stranded DNA viruses. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2038-51	8.3	178

121	Phyldynamic reconstruction reveals norovirus GII.4 epidemic expansions and their molecular determinants. <i>PLoS Pathogens</i> , 2010 , 6, e1000884	7.6	114
120	Phylogenetics and human-mediated dispersal of a zoonotic virus. <i>PLoS Pathogens</i> , 2010 , 6, e1001166	7.6	102
119	The evolutionary analysis of emerging low frequency HIV-1 CXCR4 using variants through time--an ultra-deep approach. <i>PLoS Computational Biology</i> , 2010 , 6, e1001022	5	64
118	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, 454-66	3.9	147
117	Phylogeography takes a relaxed random walk in continuous space and time. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1877-85	8.3	450
116	Many-core algorithms for statistical phylogenetics. <i>Bioinformatics</i> , 2009 , 25, 1370-6	7.2	291
115	Accommodating the effect of ancient DNA damage on inferences of demographic histories. <i>Molecular Biology and Evolution</i> , 2009 , 26, 245-8	8.3	77
114	Pandemic potential of a strain of influenza A (H1N1): early findings. <i>Science</i> , 2009 , 324, 1557-61	33.3	1403
113	Response--Influenza. <i>Science</i> , 2009 , 325, 1072-1073	33.3	1
112	Bayesian phylogeography finds its roots. <i>PLoS Computational Biology</i> , 2009 , 5, e1000520	5	1101
111	Molecular phylogenetics of the heterosexual HIV epidemic in the United Kingdom. <i>PLoS Pathogens</i> , 2009 , 5, e1000590	7.6	134
110	The RNA virus database. <i>Nucleic Acids Research</i> , 2009 , 37, D431-5	20.1	13
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22	Identification of a common deletion in the spike protein of SARS-CoV-2		13
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