

Andrew Rambaut

List of Publications by Citations

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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.

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|--------------------|--------------------------|-----------------|-----------------|
| 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 | BEAST: Bayesian evolutionary analysis by sampling trees. <i>BMC Evolutionary Biology</i> , 2007 , 7, 214 | 3 | 9349 |
| 281 | Bayesian phylogenetics with BEAUti and the BEAST 1.7. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1969-73 | 8.3 | 7409 |
| 280 | Relaxed phylogenetics and dating with confidence. <i>PLoS Biology</i> , 2006 , 4, e88 | 9.7 | 4483 |
| 279 | BEAST 2: a software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2014 , 10, e1003537 | 5 | 3659 |
| 278 | Posterior Summarization in Bayesian Phylogenetics Using Tracer 1.7. <i>Systematic Biology</i> , 2018 , 67, 901-904 | 9.4 | 3267 |
| 277 | The proximal origin of SARS-CoV-2. <i>Nature Medicine</i> , 2020 , 26, 450-452 | 50.5 | 2687 |
| 276 | Bayesian coalescent inference of past population dynamics from molecular sequences. <i>Molecular Biology and Evolution</i> , 2005 , 22, 1185-92 | 8.3 | 2280 |
| 275 | Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009 , 459, 1122-5 | 50.4 | 1535 |
| 274 | Pandemic potential of a strain of influenza A (H1N1): early findings. <i>Science</i> , 2009 , 324, 1557-61 | 33.3 | 1403 |
| 273 | A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020 , 5, 1403-1407 | 26.6 | 1250 |
| 272 | Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. <i>Virus Evolution</i> , 2018 , 4, vey016 | 3.7 | 1199 |
| 271 | Bayesian phylogeography finds its roots. <i>PLoS Computational Biology</i> , 2009 , 5, e1000520 | 5 | 1101 |
| 270 | BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019 , 15, e1006650 | 5 | 1014 |
| 269 | Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , 2016 , 2, vew007 | 3.7 | 961 |
| 268 | SARS-CoV-2 variants, spike mutations and immune escape. <i>Nature Reviews Microbiology</i> , 2021 , 19, 409-424 | 42.2 | 873 |
| 267 | Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014 , 345, 1369-72 | 33.3 | 847 |
| 266 | Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016 , 530, 228-232 | 50.4 | 845 |

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| 265 | 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 |
| 264 | The genomic and epidemiological dynamics of human influenza A virus. <i>Nature</i> , 2008 , 453, 615-9 | 50.4 | 685 |
| 263 | Seq-Gen: an application for the Monte Carlo simulation of DNA sequence evolution along phylogenetic trees. <i>Bioinformatics</i> , 1997 , 13, 235-8 | 7.2 | 631 |
| 262 | Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021 , 372, 815-821 | 33.3 | 603 |
| 261 | Choosing appropriate substitution models for the phylogenetic analysis of protein-coding sequences. <i>Molecular Biology and Evolution</i> , 2006 , 23, 7-9 | 8.3 | 562 |
| 260 | Rates of molecular evolution in RNA viruses: a quantitative phylogenetic analysis. <i>Journal of Molecular Evolution</i> , 2002 , 54, 156-65 | 3.1 | 519 |
| 259 | Rise and fall of the Beringian steppe bison. <i>Science</i> , 2004 , 306, 1561-5 | 33.3 | 518 |
| 258 | 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 |
| 257 | Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021 , 593, 266-269 | 50.4 | 452 |
| 256 | Phylogeography takes a relaxed random walk in continuous space and time. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1877-85 | 8.3 | 450 |
| 255 | 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 |
| 254 | Persistent HIV-1 replication maintains the tissue reservoir during therapy. <i>Nature</i> , 2016 , 530, 51-56 | 50.4 | 419 |
| 253 | Evolutionary analysis of the dynamics of viral infectious disease. <i>Nature Reviews Genetics</i> , 2009 , 10, 540-50.1 | 50.1 | 402 |
| 252 | BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. <i>Systematic Biology</i> , 2012 , 61, 170-3 | 8.4 | 374 |
| 251 | The causes and consequences of HIV evolution. <i>Nature Reviews Genetics</i> , 2004 , 5, 52-61 | 30.1 | 372 |
| 250 | HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61 | 33.3 | 370 |
| 249 | SPREAD: spatial phylogenetic reconstruction of evolutionary dynamics. <i>Bioinformatics</i> , 2011 , 27, 2910-2 | 7.2 | 369 |
| 248 | Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017 , 546, 406-410.4 | 50.4 | 366 |

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| 247 | The epidemic behavior of the hepatitis C virus. <i>Science</i> , 2001 , 292, 2323-5 | 33.3 | 350 |
| 246 | The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013 , 502, 241-4 | 50.4 | 337 |
| 245 | Inferring confidence sets of possibly misspecified gene trees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002 , 269, 137-42 | 4.4 | 335 |
| 244 | Complete mitochondrial genome sequences of two extinct moas clarify ratite evolution. <i>Nature</i> , 2001 , 409, 704-7 | 50.4 | 332 |
| 243 | 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 |
| 242 | Correlating viral phenotypes with phylogeny: accounting for phylogenetic uncertainty. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 239-46 | 4.5 | 325 |
| 241 | 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 |
| 240 | Phylogenetic evidence for recombination in dengue virus. <i>Molecular Biology and Evolution</i> , 1999 , 16, 405-9 | 8.3 | 310 |
| 239 | Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015 , 523, 217-20 | 50.4 | 302 |
| 238 | Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , 2003 , 18, 481-488 | 10.9 | 300 |
| 237 | Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data | | 299 |
| 236 | 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, 19545-50 | 11.5 | 294 |
| 235 | Comparative analysis by independent contrasts (CAIC): an Apple Macintosh application for analysing comparative data. <i>Bioinformatics</i> , 1995 , 11, 247-51 | 7.2 | 293 |
| 234 | Many-core algorithms for statistical phylogenetics. <i>Bioinformatics</i> , 2009 , 25, 1370-6 | 7.2 | 291 |
| 233 | Clinical features and virological analysis of a case of Middle East respiratory syndrome coronavirus infection. <i>Lancet Infectious Diseases</i> , 2013 , 13, 745-51 | 25.5 | 288 |
| 232 | Episodic sexual transmission of HIV revealed by molecular phylodynamics. <i>PLoS Medicine</i> , 2008 , 5, e50 | 11.6 | 288 |
| 231 | An integrated framework for the inference of viral population history from reconstructed genealogies. <i>Genetics</i> , 2000 , 155, 1429-37 | 4 | 277 |
| 230 | Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260 | 33.3 | 277 |

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| 229 | Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017 , 546, 411-415 | 50.4 | 253 |
| 228 | Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , 2016 , 354, 213-217 | 33.3 | 252 |
| 227 | Spread3: Interactive Visualization of Spatiotemporal History and Trait Evolutionary Processes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2167-9 | 8.3 | 241 |
| 226 | Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315 | 50.4 | 238 |
| 225 | Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405 | 50.4 | 235 |
| 224 | 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 |
| 223 | Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility. <i>Lancet Infectious Diseases, The</i> , 2014 , 14, 50-56 | 25.5 | 231 |
| 222 | 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 |
| 221 | Temporal and spatial analysis of the 2014-2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015 , 524, 97-101 | 50.4 | 229 |
| 220 | Estimating divergence dates from molecular sequences. <i>Molecular Biology and Evolution</i> , 1998 , 15, 442-88,3 | 8.3 | 229 |
| 219 | 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, 18566-70 | 11.5 | 219 |
| 218 | Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014 , 3, e01914 | 8.9 | 213 |
| 217 | Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015 , 161, 1516-26 | 56.2 | 210 |
| 216 | Determinants of rate variation in mammalian DNA sequence evolution. <i>Journal of Molecular Evolution</i> , 1996 , 43, 610-21 | 3.1 | 209 |
| 215 | Spread, circulation, and evolution of the Middle East respiratory syndrome coronavirus. <i>MBio</i> , 2014 , 5, | 7.8 | 207 |
| 214 | Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , 2022 , | 50.4 | 205 |
| 213 | Ancient hybridization and an Irish origin for the modern polar bear matriline. <i>Current Biology</i> , 2011 , 21, 1251-8 | 6.3 | 203 |
| 212 | The epidemiology and iatrogenic transmission of hepatitis C virus in Egypt: a Bayesian coalescent approach. <i>Molecular Biology and Evolution</i> , 2003 , 20, 381-7 | 8.3 | 202 |

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| 211 | 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, 7352-7 | 11.5 | 190 |
| 210 | The evolution of Ebola virus: Insights from the 2013-2016 epidemic. <i>Nature</i> , 2016 , 538, 193-200 | 50.4 | 185 |
| 209 | The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020 , 370, 564-570 | 33.3 | 183 |
| 208 | Inferring the rate and time-scale of dengue virus evolution. <i>Molecular Biology and Evolution</i> , 2003 , 20, 122-9 | 8.3 | 181 |
| 207 | Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019 , 4, 10-19 | 26.6 | 179 |
| 206 | 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 |
| 205 | Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021 , 7, veab064 | 3.7 | 176 |
| 204 | Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020 , 181, 997-1003.e9 | 56.2 | 175 |
| 203 | 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 |
| 202 | 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 |
| 201 | HIV evolutionary dynamics within and among hosts. <i>AIDS Reviews</i> , 2006 , 8, 125-40 | 1.5 | 160 |
| 200 | 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 |
| 199 | Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712 | 33.3 | 159 |
| 198 | A synchronized global sweep of the internal genes of modern avian influenza virus. <i>Nature</i> , 2014 , 508, 254-7 | 50.4 | 158 |
| 197 | Estimating divergence dates and substitution rates in the Drosophila phylogeny. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3459-73 | 8.3 | 158 |
| 196 | SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses.. <i>Cell</i> , 2022 , | 56.2 | 154 |
| 195 | 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 |
| 194 | Genetic analysis of West Nile New York 1999 encephalitis virus. <i>Lancet, The</i> , 1999 , 354, 1971-2 | 40 | 149 |

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| 193 | 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 |
| 192 | Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020 , 6, veaa061 | 3.7 | 147 |
| 191 | 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 |
| 190 | Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016 , 5, | 8.9 | 142 |
| 189 | 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 |
| 188 | Synonymous substitution rates predict HIV disease progression as a result of underlying replication dynamics. <i>PLoS Computational Biology</i> , 2007 , 3, e29 | 5 | 138 |
| 187 | Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016 , 167, 1088-1098.e6 | 56.2 | 135 |
| 186 | Molecular phylodynamics of the heterosexual HIV epidemic in the United Kingdom. <i>PLoS Pathogens</i> , 2009 , 5, e1000590 | 7.6 | 134 |
| 185 | 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 |
| 184 | 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 |
| 183 | Livestock origin for a human pandemic clone of community-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2013 , 4, | 7.8 | 132 |
| 182 | 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 |
| 181 | Inference of viral evolutionary rates from molecular sequences. <i>Advances in Parasitology</i> , 2003 , 54, 331-582 | 5.2 | 127 |
| 180 | Flight of the dodo. <i>Science</i> , 2002 , 295, 1683 | 33.3 | 122 |
| 179 | Viral evolution and the emergence of SARS coronavirus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004 , 359, 1059-65 | 5.8 | 121 |
| 178 | Phylogenetic evidence for deleterious mutation load in RNA viruses and its contribution to viral evolution. <i>Molecular Biology and Evolution</i> , 2007 , 24, 845-52 | 8.3 | 119 |
| 177 | Human immunodeficiency virus. Phylogeny and the origin of HIV-1. <i>Nature</i> , 2001 , 410, 1047-8 | 50.4 | 119 |
| 176 | A dynamic nomenclature proposal for SARS-CoV-2 to assist genomic epidemiology | | 118 |

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|-----|--|------|-----|
| 175 | Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013 , 19, 736-42B | 10.2 | 117 |
| 174 | Phyldynamic reconstruction reveals norovirus GII.4 epidemic expansions and their molecular determinants. <i>PLoS Pathogens</i> , 2010 , 6, e1000884 | 7.6 | 114 |
| 173 | The evolution of genome compression and genomic novelty in RNA viruses. <i>Genome Research</i> , 2007 , 17, 1496-504 | 9.7 | 109 |
| 172 | MERS-CoV spillover at the camel-human interface. <i>ELife</i> , 2018 , 7, | 8.9 | 109 |
| 171 | Pacing a small cage: mutation and RNA viruses. <i>Trends in Ecology and Evolution</i> , 2008 , 23, 188-93 | 10.9 | 106 |
| 170 | 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 |
| 169 | Comparative analyses for adaptive radiations. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2000 , 355, 1599-605 | 5.8 | 103 |
| 168 | The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021 , 184, 4848-4856 | 56.2 | 103 |
| 167 | Phylogenetics and human-mediated dispersal of a zoonotic virus. <i>PLoS Pathogens</i> , 2010 , 6, e1001166 | 7.6 | 102 |
| 166 | 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 |
| 165 | Spatial dynamics of human-origin H1 influenza A virus in North American swine. <i>PLoS Pathogens</i> , 2011 , 7, e1002077 | 7.6 | 101 |
| 164 | The power of relative rates tests depends on the data. <i>Journal of Molecular Evolution</i> , 2000 , 50, 296-301 | 3.1 | 101 |
| 163 | Molecular epidemiology: HIV-1 and HCV sequences from Libyan outbreak. <i>Nature</i> , 2006 , 444, 836-7 | 50.4 | 99 |
| 162 | A Bayesian phylogenetic method to estimate unknown sequence ages. <i>Molecular Biology and Evolution</i> , 2011 , 28, 879-87 | 8.3 | 98 |
| 161 | Recombination between sequences of hepatitis B virus from different genotypes. <i>Journal of Molecular Evolution</i> , 1996 , 42, 97-102 | 3.1 | 97 |
| 160 | Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015 , 6, 6696 | 17.4 | 91 |
| 159 | Real-time digital pathogen surveillance - the time is now. <i>Genome Biology</i> , 2015 , 16, 155 | 18.3 | 91 |
| 158 | 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, 8503-9 | 6.6 | 91 |

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| 157 | 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 |
| 156 | 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 |
| 155 | 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 |
| 154 | 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 |
| 153 | The molecular population genetics of HIV-1 group O. <i>Genetics</i> , 2004 , 167, 1059-68 | 4 | 89 |
| 152 | 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 |
| 151 | JC virus evolution and its association with human populations. <i>Journal of Virology</i> , 2006 , 80, 9928-33 | 6.6 | 83 |
| 150 | Phylogeography and population dynamics of dengue viruses in the Americas. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1533-43 | 8.3 | 81 |
| 149 | Pandemics: spend on surveillance, not prediction. <i>Nature</i> , 2018 , 558, 180-182 | 50.4 | 77 |
| 148 | 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 |
| 147 | Heterotachy and tree building: a case study with plastids and eubacteria. <i>Molecular Biology and Evolution</i> , 2006 , 23, 40-5 | 8.3 | 77 |
| 146 | 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, 8543-51 | 6.6 | 75 |
| 145 | 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 |
| 144 | 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 | | 74 |
| 143 | Phylogenetic surveillance of viral genetic diversity and the evolving molecular epidemiology of human immunodeficiency virus type 1. <i>Journal of Virology</i> , 2007 , 81, 13050-6 | 6.6 | 72 |
| 142 | The evolutionary dynamics of endogenous retroviruses. <i>Trends in Microbiology</i> , 2005 , 13, 463-8 | 12.4 | 72 |
| 141 | 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 |
| 140 | The early molecular epidemiology of the swine-origin A/H1N1 human influenza pandemic. <i>PLOS Currents</i> , 2009 , 1, RRN1003 | | 71 |

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|-----|---|------|----|
| 139 | Lessons from Ebola: Improving infectious disease surveillance to inform outbreak management. <i>Science Translational Medicine</i> , 2015 , 7, 307rv5 | 17.5 | 67 |
| 138 | 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, 8743-61 | 6.6 | 67 |
| 137 | Evolutionary genomics of host adaptation in vesicular stomatitis virus. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1138-47 | 8.3 | 67 |
| 136 | Evolution and Spread of Ebola Virus in Liberia, 2014-2015. <i>Cell Host and Microbe</i> , 2015 , 18, 659-69 | 23.4 | 66 |
| 135 | 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 |
| 134 | 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 |
| 133 | Comparative population dynamics of HIV-1 subtypes B and C: subtype-specific differences in patterns of epidemic growth. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 199-208 | 4.5 | 64 |
| 132 | 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 |
| 131 | Canalization of the evolutionary trajectory of the human influenza virus. <i>BMC Biology</i> , 2012 , 10, 38 | 7.3 | 61 |
| 130 | Molecular footprint of drug-selective pressure in a human immunodeficiency virus transmission chain. <i>Journal of Virology</i> , 2005 , 79, 11981-9 | 6.6 | 61 |
| 129 | Evaluating the effects of SARS-CoV-2 Spike mutation D614G on transmissibility and pathogenicity | | 58 |
| 128 | Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , 2011 , 1, 423-97.5 | | 56 |
| 127 | Origin of AIDS: contaminated polio vaccine theory refuted. <i>Nature</i> , 2004 , 428, 820 | 50.4 | 56 |
| 126 | Epidemic Reconstruction in a Phylogenetics Framework: Transmission Trees as Partitions of the Node Set. <i>PLoS Computational Biology</i> , 2015 , 11, e1004613 | 5 | 56 |
| 125 | Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017 , 13, e1006749 | 7.6 | 55 |
| 124 | Emerging Concepts of Data Integration in Pathogen Phylodynamics. <i>Systematic Biology</i> , 2017 , 66, e47-e654 | 65.4 | 55 |
| 123 | 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 |
| 122 | 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 |

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| 121 | Inferring heterogeneous evolutionary processes through time: from sequence substitution to phylogeography. <i>Systematic Biology</i> , 2014 , 63, 493-504 | 8.4 | 54 |
| 120 | Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic | | 54 |
| 119 | The circulating SARS-CoV-2 spike variant N439K maintains fitness while evading antibody-mediated immunity | | 53 |
| 118 | Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil 2021 , | | 53 |
| 117 | Reduced evolutionary rate in reemerged Ebola virus transmission chains. <i>Science Advances</i> , 2016 , 2, e1600378 | 10.3 | 53 |
| 116 | Human origins and ancient human DNA. <i>Science</i> , 2001 , 292, 1655-6 | 33.3 | 52 |
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