

Oliver G. Pybus

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.

410
papers

39,515
citations

95
h-index

191
g-index

474
ext. papers

50,161
ext. citations

12.2
avg, IF

7.69
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 410 | Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , 2022 , 13, 1012 | 16.9 | 0 |
| 409 | The relationship between rising temperatures and malaria incidence in Hainan, China, from 1984 to 2010: a longitudinal cohort study.. <i>Lancet Planetary Health</i> , 2022 , 6, e350-e358 | 9 | 0 |
| 408 | Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza.. <i>Molecular Biology and Evolution</i> , 2022 , | 8 | 4 |
| 407 | Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant.. <i>Nature Communications</i> , 2022 , 13, 460 | 16.9 | 76 |
| 406 | Mapping environmental suitability of <i>Haemagogus</i> and <i>Sabethes</i> spp. mosquitoes to understand sylvatic transmission risk of yellow fever virus in Brazil.. <i>PLoS Neglected Tropical Diseases</i> , 2022 , 16, e0010019 | 4.6 | 0 |
| 405 | Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , 2022 , | 47.5 | 130 |
| 404 | Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences.. <i>BMC Genomics</i> , 2022 , 23, 121 | 4.3 | 5 |
| 403 | A computationally tractable birth-death model that combines phylogenetic and epidemiological data.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009805 | 4.8 | 0 |
| 402 | Malaria elimination on Hainan Island despite climate change. <i>Communications Medicine</i> , 2022 , 2, | | 1 |
| 401 | Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.. <i>Nature Communications</i> , 2022 , 13, 751 | 16.9 | 4 |
| 400 | Phylogenetic analysis of migration, differentiation, and class switching in B cells.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009885 | 4.8 | 0 |
| 399 | Understanding Sabiá virus infections (Brazilian mammarenavirus).. <i>Travel Medicine and Infectious Disease</i> , 2022 , 48, 102351 | 8.2 | |
| 398 | Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017-2019.. <i>PLoS Neglected Tropical Diseases</i> , 2022 , 16, e0010255 | 4.6 | 0 |
| 397 | Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , 2021 , 73, e2436-e2443 | 41.3 | 8 |
| 396 | Serial interval distribution of SARS-CoV-2 infection in Brazil. <i>Journal of Travel Medicine</i> , 2021 , 28, | 12.5 | 15 |
| 395 | Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing. <i>Journal of Infection</i> , 2021 , 82, e44-e48 | 18.5 | 4 |
| 394 | Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021 , 184, 64-75.e11 | 54.5 | 500 |

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|-----|---|------|-----|
| 393 | Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , 2021 , 371, 288-292 | 32.2 | 257 |
| 392 | Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021 , 6, 415 | 25.8 | 33 |
| 391 | Phylodynamics for cell biologists. <i>Science</i> , 2021 , 371, | 32.2 | 7 |
| 390 | SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021 , 6, 821-823 | 25.8 | 85 |
| 389 | Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021 , 7, veab051.6 | 3.6 | 2 |
| 388 | 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 | 10.3 | 154 |
| 387 | Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895 | 32.2 | 36 |
| 386 | Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021 , 7, veab064 | 3.6 | 139 |
| 385 | Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study. <i>Lancet Infectious Diseases</i> , 2021 , | 24.7 | 159 |
| 384 | Global disparities in SARS-CoV-2 genomic surveillance 2021 , | | 22 |
| 383 | Vaccine nationalism and the dynamics and control of SARS-CoV-2. <i>Science</i> , 2021 , 373, eabj7364 | 32.2 | 16 |
| 382 | 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 | 4.7 | 49 |
| 381 | Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021 , 184, 5179-5188.e8 | 54.5 | 39 |
| 380 | A mechanistic evolutionary model explains the time-dependent pattern of substitution rates in viruses. <i>Current Biology</i> , 2021 , 31, 4689-4696.e5 | 6.1 | 5 |
| 379 | Assessing the impact of COVID-19 border restrictions on dengue transmission in Yunnan Province, China: an observational epidemiological and phylogenetic analysis. <i>The Lancet Regional Health - Western Pacific</i> , 2021 , 14, 100259 | 4.9 | 2 |
| 378 | Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021 , 7, veab036 | 3.6 | 1 |
| 377 | Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712 | 32.2 | 153 |
| 376 | Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes 2021 , | | 6 |

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| 375 | Relax, Keep Walking - A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3486-3493 | 8 | 2 |
| 374 | A review of models applied to the geographic spread of Zika virus. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2021 , 115, 956-964 | 2 | |
| 373 | Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet, The</i> , 2021 , 397, 452-455 | 36.2 | 463 |
| 372 | Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil 2021 , | | 48 |
| 371 | Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. <i>Emerging Infectious Diseases</i> , 2021 , 27, 970-972 | 9.9 | 39 |
| 370 | Partial immunity and SARS-CoV-2 mutations-Response. <i>Science</i> , 2021 , 372, 354-355 | 32.2 | 2 |
| 369 | "Kankasha" in Kassala: A prospective observational cohort study of the clinical characteristics, epidemiology, genetic origin, and chronic impact of the 2018 epidemic of Chikungunya virus infection in Kassala, Sudan. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009387 | 4.6 | 4 |
| 368 | Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes. <i>Science</i> , 2021 , 372, 363-370 | 32.2 | 81 |
| 367 | Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021 , 372, 815-821 | 32.2 | 566 |
| 366 | Are skyline plot-based demographic estimates overly dependent on smoothing prior assumptions?. <i>Systematic Biology</i> , 2021 , | 8.2 | 4 |
| 365 | Identification of site-specific evolutionary trajectories shared across human betacoronaviruses 2021 , | | 2 |
| 364 | 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 | 4.7 | 48 |
| 363 | Global prevalence and phylogeny of hepatitis B virus (HBV) drug and vaccine resistance mutations. <i>Journal of Viral Hepatitis</i> , 2021 , 28, 1110-1120 | 3.3 | 0 |
| 362 | Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 , | | 2 |
| 361 | Monitoring key epidemiological parameters of SARS-CoV-2 transmission. <i>Nature Medicine</i> , 2021 , 27, 1854-1854 | 18.5 | 4 |
| 360 | Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021 , 374, eabl9551 | 32.2 | 28 |
| 359 | Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. <i>ELife</i> , 2021 , 10, | 8.6 | 2 |
| 358 | Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 , | | 2 |

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|-----|---|------|------|
| 357 | Track Omicron [®] spread with molecular data. <i>Science</i> , 2021 , 374, eabn4543 | 32.2 | 41 |
| 356 | Neutralisation of SARS-CoV-2 lineage P.1 by antibodies elicited through natural SARS-CoV-2 infection or vaccination with an inactivated SARS-CoV-2 vaccine: an immunological study. <i>Lancet Microbe, The</i> , 2021 , 2, e527-e535 | 21.6 | 34 |
| 355 | Progress and challenges in virus genomic epidemiology. <i>Trends in Parasitology</i> , 2021 , 37, 1038-1049 | 6.2 | 3 |
| 354 | Evolutionary Analyses of Base-Pairing Interactions in DNA and RNA Secondary Structures. <i>Molecular Biology and Evolution</i> , 2020 , 37, 576-592 | 8 | 4 |
| 353 | Crowding and the shape of COVID-19 epidemics. <i>Nature Medicine</i> , 2020 , 26, 1829-1834 | 49.3 | 94 |
| 352 | A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020 , 5, 1403-1407 | 25.8 | 1194 |
| 351 | Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020 , 11, 5620 | 16.9 | 6 |
| 350 | Genomic Surveillance of Yellow Fever Virus Epizootic in S ^o Paulo, Brazil, 2016 - 2018. <i>PLoS Pathogens</i> , 2020 , 16, e1008699 | 7.4 | 15 |
| 349 | Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260 | 32.2 | 270 |
| 348 | Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020 , 4, 856-865 | 12.5 | 144 |
| 347 | Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR. <i>EBioMedicine</i> , 2020 , 59, 102960 | 8.6 | 98 |
| 346 | Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , 2020 , 11, 5511 | 16.9 | 8 |
| 345 | Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020 , 181, 997-1003.e9 | 54.5 | 173 |
| 344 | Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020 , 11, 2688 | 16.9 | 166 |
| 343 | An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe, The</i> , 2020 , 1, e99-e100 | 21.6 | 122 |
| 342 | Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020 , 369, 582-587 | 32.2 | 155 |
| 341 | Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , 2020 , 27, | 12.5 | 79 |
| 340 | Epidemiological data from the COVID-19 outbreak, real-time case information. <i>Scientific Data</i> , 2020 , 7, 106 | 8 | 190 |

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| 339 | The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020 , 368, 493-497 | 32.2 | 1329 |
| 338 | An investigation of transmission control measures during the first 50 days of the COVID-19 epidemic in China. <i>Science</i> , 2020 , 368, 638-642 | 32.2 | 986 |
| 337 | Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 5949-5954 | 11.1 | 15 |
| 336 | Transmission of hepatitis C virus in HIV-positive and PrEP-using MSM in England. <i>Journal of Viral Hepatitis</i> , 2020 , 27, 721-730 | 3.3 | 6 |
| 335 | Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020 , 94, | 6.3 | 83 |
| 334 | Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2414-2429 | 8 | 10 |
| 333 | Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0007897 | 4.6 | 2 |
| 332 | Open access epidemiological data from the COVID-19 outbreak. <i>Lancet Infectious Diseases</i> , 2020 , 20, 534 | 24.7 | 163 |
| 331 | Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7 | 10.3 | 24 |
| 330 | Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020 , 5, 443-454 | 25.8 | 56 |
| 329 | Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020 , 94, | 6.3 | 5 |
| 328 | Dynamics of conflict during the Ebola outbreak in the Democratic Republic of the Congo 2018-2019. <i>BMC Medicine</i> , 2020 , 18, 113 | 11.1 | 6 |
| 327 | Phylodynamics Helps to Evaluate the Impact of an HIV Prevention Intervention. <i>Viruses</i> , 2020 , 12, | 6 | 7 |
| 326 | Genomic detection of a virus lineage replacement event of dengue virus serotype 2 in Brazil, 2019. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020 , 115, e190423 | 2.5 | 10 |
| 325 | 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 | 2.1 | 49 |
| 324 | Towards an understanding of the avian virome. <i>Journal of General Virology</i> , 2020 , 101, 785-790 | 4.7 | 8 |
| 323 | The effect of human mobility and control measures on the COVID-19 epidemic in China 2020 , | | 24 |
| 322 | A Genomic Survey of SARS-CoV-2 Reveals Multiple Introductions into Northern California without a Predominant Lineage 2020 , | | 20 |

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| 321 | Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing 2020 , 14, e0007897 | | |
| 320 | Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing 2020 , 14, e0007897 | | |
| 319 | Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing 2020 , 14, e0007897 | | |
| 318 | The multifurcating skyline plot. <i>Virus Evolution</i> , 2019 , 5, vez031 | 3.6 | 7 |
| 317 | Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , 2019 , 19, 1138-1147 | 24.7 | 40 |
| 316 | Parallel molecular evolution and adaptation in viruses. <i>Current Opinion in Virology</i> , 2019 , 34, 90-96 | 7.1 | 18 |
| 315 | Comparative micro-epidemiology of pathogenic avian influenza virus outbreaks in a wild bird population. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019 , 374, 20180259 | 5.7 | 13 |
| 314 | A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007231 | 4.6 | 19 |
| 313 | Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 784-787 | 9.9 | 16 |
| 312 | Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007065 | 4.6 | 36 |
| 311 | Past and future spread of the arbovirus vectors <i>Aedes aegypti</i> and <i>Aedes albopictus</i> . <i>Nature Microbiology</i> , 2019 , 4, 854-863 | 25.8 | 295 |
| 310 | 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, | 9.4 | 7 |
| 309 | A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019 , 5, | 3.6 | 78 |
| 308 | A38 Genomic epidemiology quantifies gaps in <i>Aedes</i> -borne virus transmission in the Americas. <i>Virus Evolution</i> , 2019 , 5, | 3.6 | 78 |
| 307 | A60 Revealing the evolution of virulence in RNA viruses. <i>Virus Evolution</i> , 2019 , 5, | 3.6 | 78 |
| 306 | Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , 2019 , 9, 5151 | 4.7 | 55 |
| 305 | Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , 2019 , 93, | 6.3 | 6 |
| 304 | Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019 , 25, 206-211 | 49.3 | 52 |

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|-----|---|------|-----|
| 303 | Robust Design for Coalescent Model Inference. <i>Systematic Biology</i> , 2019 , 68, 730-743 | 8.2 | 14 |
| 302 | Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019 , 220, 233-243 | 6.8 | 11 |
| 301 | Reverse immunodynamics: a new method for identifying targets of protective immunity. <i>Scientific Reports</i> , 2019 , 9, 2164 | 4.7 | 2 |
| 300 | A structural basis for antibody-mediated neutralization of Nipah virus reveals a site of vulnerability at the fusion glycoprotein apex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 25057-25067 | 11.1 | 25 |
| 299 | Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 22664-22672 | 11.1 | 26 |
| 298 | Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019 , 15, e1007976 | 7.4 | 25 |
| 297 | High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. <i>Journal of Infectious Diseases</i> , 2019 , 219, 1722-1729 | 6.8 | 8 |
| 296 | The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , 2019 , 35, 155-163 | 1.5 | 0 |
| 295 | Highly Diverse Hepatitis C Strains Detected in Sub-Saharan Africa Have Unknown Susceptibility to Direct-Acting Antiviral Treatments. <i>Hepatology</i> , 2019 , 69, 1426-1441 | 10.9 | 26 |
| 294 | Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019 , 4, 10-19 | 25.8 | 175 |
| 293 | Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018 , 172, 1160-1162 | 54.5 | 38 |
| 292 | Exact Bayesian inference for phylogenetic birth-death models. <i>Bioinformatics</i> , 2018 , 34, 3638-3645 | 6.8 | 9 |
| 291 | Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018 , 2, 659-668 | 12.1 | 65 |
| 290 | Molecular epidemiology reveals the role of war in the spread of HIV in Ukraine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1051-1056 | 11.1 | 30 |
| 289 | The Effect of RNA Substitution Models on Viroid and RNA Virus Phylogenies. <i>Genome Biology and Evolution</i> , 2018 , 10, 657-666 | 3.7 | 5 |
| 288 | Taming the BEAST-A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018 , 67, 170-174 | 8.2 | 42 |
| 287 | Genomic surveillance of avian-origin influenza A viruses causing human disease. <i>Genome Medicine</i> , 2018 , 10, 50 | 14 | 5 |
| 286 | Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , 2018 , 15, 7 | 3.4 | 11 |

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|-----|--|------|-----|
| 285 | Westward Spread of Highly Pathogenic Avian Influenza A(H7N9) Virus among Humans, China. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1095-1098 | 9.9 | 8 |
| 284 | Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899 | 32.2 | 180 |
| 283 | Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018 , 9, 2222 | 16.9 | 38 |
| 282 | Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , 2018 , 147, e34 | 4.2 | 22 |
| 281 | The generation of a simian adenoviral vectored HCV vaccine encoding genetically conserved gene segments to target multiple HCV genotypes. <i>Vaccine</i> , 2018 , 36, 313-321 | 3.9 | 24 |
| 280 | Conserved secondary structures predicted within the 5' packaging signal region of influenza A virus PB2 segment. <i>Meta Gene</i> , 2018 , 15, 75-79 | 0.7 | 5 |
| 279 | A Protective Monoclonal Antibody Targets a Site of Vulnerability on the Surface of Rift Valley Fever Virus. <i>Cell Reports</i> , 2018 , 25, 3750-3758.e4 | 10.3 | 27 |
| 278 | Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018 , 14, e1007392 | 7.4 | 17 |
| 277 | A naturally protective epitope of limited variability as an influenza vaccine target. <i>Nature Communications</i> , 2018 , 9, 3859 | 16.9 | 23 |
| 276 | Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of LBeck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018 , 285, | 4.3 | 14 |
| 275 | Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1795-1805 | 9.9 | 22 |
| 274 | Where do all the subtypes go? Temporal dynamics of H8-H12 influenza A viruses in waterfowl. <i>Virus Evolution</i> , 2018 , 4, vey025 | 3.6 | 11 |
| 273 | Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018 , 23, 855-864.e7 | 22.8 | 61 |
| 272 | Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , 2018 , 10, | | 30 |
| 271 | Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017 , 13, e1006749 | 7.4 | 54 |
| 270 | Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017 , 7, 15216 | 4.7 | 33 |
| 269 | Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2563-2571 | 8 | 38 |
| 268 | Cross-border spread, lineage displacement and evolutionary rate estimation of rabies virus in Yunnan Province, China. <i>Virology Journal</i> , 2017 , 14, 102 | 5.9 | 12 |

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|-----|---|------|-----|
| 267 | Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1742-1744 | 9.9 | 50 |
| 266 | Characterization of Hepatitis C Virus (HCV) Envelope Diversification from Acute to Chronic Infection within a Sexually Transmitted HCV Cluster by Using Single-Molecule, Real-Time Sequencing. <i>Journal of Virology</i> , 2017 , 91, | 6.3 | 12 |
| 265 | Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315 | 47.5 | 238 |
| 264 | Defining HIV-1 transmission clusters based on sequence data. <i>Aids</i> , 2017 , 31, 1211-1222 | 3.4 | 87 |
| 263 | Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405 | 47.5 | 233 |
| 262 | Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017 , 546, 406-410 | 47.5 | 363 |
| 261 | Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017 , 12, 1261-1276 | 18.1 | 514 |
| 260 | First Complete Genome Sequences of Zika Virus Isolated from Febrile Patient Sera in Ecuador. <i>Genome Announcements</i> , 2017 , 5, | | 4 |
| 259 | Short-Sighted Virus Evolution and a Germline Hypothesis for Chronic Viral Infections. <i>Trends in Microbiology</i> , 2017 , 25, 336-348 | 12 | 31 |
| 258 | Optimal point process filtering and estimation of the coalescent process. <i>Journal of Theoretical Biology</i> , 2017 , 421, 153-167 | 2.3 | 9 |
| 257 | A Phylogenetic Codon Substitution Model for Antibody Lineages. <i>Genetics</i> , 2017 , 206, 417-427 | 3.9 | 36 |
| 256 | Spread of yellow fever virus outbreak in Angola and the Democratic Republic of the Congo 2015-16: a modelling study. <i>Lancet Infectious Diseases</i> , 2017 , 17, 330-338 | 24.7 | 139 |
| 255 | Role of HIV-specific CD8 T cells in pediatric HIV cure strategies after widespread early viral escape. <i>Journal of Experimental Medicine</i> , 2017 , 214, 3239-3261 | 16.2 | 14 |
| 254 | Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005694 | 4.6 | 57 |
| 253 | Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017 , 6, | 8.6 | 53 |
| 252 | Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016 , 2, vew016 | 3.6 | 87 |
| 251 | Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , 2016 , 354, 213-217 | 32.2 | 243 |
| 250 | Reducing HIV infection in people who inject drugs is impossible without targeting recently-infected subjects. <i>Aids</i> , 2016 , 30, 2885-2890 | 3.4 | 13 |

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|-----|--|------|-----|
| 249 | Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , 2016 , 2, vew007 | 3.6 | 937 |
| 248 | The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , 2016 , 214, 556-64 | 6.8 | 50 |
| 247 | Explaining the geographic spread of emerging epidemics: a framework for comparing viral phylogenies and environmental landscape data. <i>BMC Bioinformatics</i> , 2016 , 17, 82 | 3.4 | 59 |
| 246 | SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016 , 32, 3204-3206 | 6.8 | 68 |
| 245 | The Diversity and Molecular Evolution of B-Cell Receptors during Infection. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1147-57 | 8 | 46 |
| 244 | Hepacivirus cross-species transmission and the origins of the hepatitis C virus. <i>Current Opinion in Virology</i> , 2016 , 16, 1-7 | 7.1 | 49 |
| 243 | Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016 , 352, 345-349 | 32.2 | 700 |
| 242 | Epidemic History and Iatrogenic Transmission of Blood-borne Viruses in Mid-20th Century Kinshasa. <i>Journal of Infectious Diseases</i> , 2016 , 214, 353-60 | 6.8 | 16 |
| 241 | Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intra-host HIV Infection. <i>Genetics</i> , 2016 , 202, 1449-72 | 3.9 | 8 |
| 240 | Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1788-92 | 9.9 | 35 |
| 239 | Evolution and Transmission of Respiratory Syncytial Group A (RSV-A) Viruses in Guangdong, China 2008-2015. <i>Frontiers in Microbiology</i> , 2016 , 7, 1263 | 5.5 | 13 |
| 238 | Virus genomics and evolution: the transformative effect of new technologies and multidisciplinary collaboration on virus research and outbreak management. <i>Genome Biology</i> , 2016 , 17, 159 | 17.7 | 1 |
| 237 | Faster Adaptation in Smaller Populations: Counterintuitive Evolution of HIV during Childhood Infection. <i>PLoS Computational Biology</i> , 2016 , 12, e1004694 | 4.8 | 6 |
| 236 | Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , 2016 , 22, 2104-2112 | 9.9 | 22 |
| 235 | Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016 , 22, 671-8 | 9.9 | 34 |
| 234 | Computational and molecular analysis of conserved influenza A virus RNA secondary structures involved in infectious virion production. <i>RNA Biology</i> , 2016 , 13, 883-94 | 4.7 | 29 |
| 233 | Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016 , 8, 97 | 14 | 129 |
| 232 | Antibody responses to avian influenza viruses in wild birds broaden with age. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016 , 283, | 4.3 | 18 |

| | | | |
|-----|--|------|------|
| 231 | A Molecular-Level Account of the Antigenic Hantaviral Surface. <i>Cell Reports</i> , 2016 , 15, 959-967 | 10.3 | 36 |
| 230 | Transmission of hepatitis C virus infection among younger and older people who inject drugs in Vancouver, Canada. <i>Journal of Hepatology</i> , 2016 , 64, 1247-55 | 3.1 | 18 |
| 229 | Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016 , 41, 142-145 | 4.5 | 19 |
| 228 | Genome Sequence of a Candidate World Health Organization Reference Strain of Zika Virus for Nucleic Acid Testing. <i>Genome Announcements</i> , 2016 , 4, | | 18 |
| 227 | Sequencing Methods Developed for Hepatitis C Identifies a New Virus, Human Hepegivirus 1, in Patients with Advanced Cirrhosis. <i>Journal of Hepatology</i> , 2016 , 64, S414-S415 | 3.1 | |
| 226 | HIV Maintains an Evolving and Dispersed Population in Multiple Tissues during Suppressive Combined Antiretroviral Therapy in Individuals with Cancer. <i>Journal of Virology</i> , 2016 , 90, 8984-93 | 6.3 | 30 |
| 225 | Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016 , 8, | | 47 |
| 224 | Venue-Based Networks May Underpin HCV Transmissions amongst HIV-Infected Gay and Bisexual Men. <i>PLoS ONE</i> , 2016 , 11, e0162002 | 3.6 | 6 |
| 223 | Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , 2016 , 12, e1005894 | 7.4 | 25 |
| 222 | Genetic diversity and phenotypic associations of feline caliciviruses from cats in Switzerland. <i>Journal of General Virology</i> , 2016 , 97, 3253-3266 | 4.7 | 7 |
| 221 | Population Genetic Modeling of Viruses 2016 , 293-328 | | |
| 220 | Measurably evolving pathogens in the genomic era. <i>Trends in Ecology and Evolution</i> , 2015 , 30, 306-13 | 10.6 | 167 |
| 219 | Emergence and potential for spread of Chikungunya virus in Brazil. <i>BMC Medicine</i> , 2015 , 13, 102 | 11.1 | 267 |
| 218 | Evolution and Diversity of the Human Leukocyte Antigen(HLA). <i>Evolution, Medicine and Public Health</i> , 2015 , 2015, 1 | 2.9 | 7 |
| 217 | Global distribution and prevalence of hepatitis C virus genotypes. <i>Hepatology</i> , 2015 , 61, 77-87 | 10.9 | 1046 |
| 216 | Hepatitis C virus genotype 4 in England: diversity and demographic associations. <i>Journal of Medical Virology</i> , 2015 , 87, 417-23 | 19.3 | 3 |
| 215 | Evolutionary and Phylogenetic Analysis of the Hepaciviruses and Pegiviruses. <i>Genome Biology and Evolution</i> , 2015 , 7, 2996-3008 | 3.7 | 47 |
| 214 | Virus evolution and transmission in an ever more connected world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015 , 282, 20142878 | 4.3 | 78 |

| | | | |
|-----|--|------|-----|
| 213 | An expanded taxonomy of hepatitis C virus genotype 6: Characterization of 22 new full-length viral genomes. <i>Virology</i> , 2015 , 476, 355-363 | 3.5 | 19 |
| 212 | Wild waterfowl migration and domestic duck density shape the epidemiology of highly pathogenic H5N8 influenza in the Republic of Korea. <i>Infection, Genetics and Evolution</i> , 2015 , 34, 267-77 | 4.4 | 54 |
| 211 | Discovery of a polyomavirus in European badgers (<i>Meles meles</i>) and the evolution of host range in the family Polyomaviridae. <i>Journal of General Virology</i> , 2015 , 96, 1411-1422 | 4.7 | 12 |
| 210 | Characterization of Hepatitis C Virus Recombination in Cameroon by Use of Nonspecific Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 3155-64 | 9.4 | 26 |
| 209 | Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , 2015 , 89, 9920-31 | 6.3 | 109 |
| 208 | Eight challenges in phylodynamic inference. <i>Epidemics</i> , 2015 , 10, 88-92 | 5 | 83 |
| 207 | Effects of neutralizing antibodies on escape from CD8+ T-cell responses in HIV-1 infection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, | 5.7 | 4 |
| 206 | Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, | 5.7 | 22 |
| 205 | A reversal of fortunes: climate change winners and losers on Antarctic Peninsula penguins. <i>Scientific Reports</i> , 2014 , 4, 5024 | 4.7 | 56 |
| 204 | Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , 2014 , 10, e1003932 | 7.4 | 227 |
| 203 | Contact between bird species of different lifespans can promote the emergence of highly pathogenic avian influenza strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10767-72 | 11.1 | 10 |
| 202 | P1191 HETEROGENEOUS EVOLUTIONARY DYNAMICS OF CHRONIC HEPATITIS-C INFECTION PREDICT LONG-TERM PERSISTENCE OF VIRUS THROUGH TREATMENT. <i>Journal of Hepatology</i> , 2014 , 60, S483 | 3.1 | |
| 201 | Occurrence and reassortment of avian influenza A (H7N9) viruses derived from coinfecting birds in China. <i>Journal of Virology</i> , 2014 , 88, 13344-51 | 6.3 | 13 |
| 200 | Phylogeography and epidemic history of hepatitis C virus genotype 4 in Africa. <i>Virology</i> , 2014 , 464-465, 233-243 | 3.5 | 55 |
| 199 | HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61 | 32.2 | 370 |
| 198 | HIV-1 epidemic in Russia: an evolutionary epidemiology analysis. <i>Lancet, The</i> , 2014 , 383, S71 | 36.2 | 3 |
| 197 | European surveillance network for influenza in pigs: surveillance programs, diagnostic tools and Swine influenza virus subtypes identified in 14 European countries from 2010 to 2013. <i>PLoS ONE</i> , 2014 , 9, e115815 | 3.6 | 80 |
| 196 | Phylogenetic clustering of hepatitis C virus among people who inject drugs in Vancouver, Canada. <i>Hepatology</i> , 2014 , 60, 1571-1580 | 10.9 | 46 |

| | | | |
|-----|---|------|-----|
| 195 | Intercontinental dispersal of HIV-1 subtype B associated with transmission among men who have sex with men in Japan. <i>Journal of Virology</i> , 2014 , 88, 9864-76 | 6.3 | 18 |
| 194 | Viral evolution explains the associations among hepatitis C virus genotype, clinical outcomes, and human genetic variation. <i>Infection, Genetics and Evolution</i> , 2013 , 20, 418-21 | 4.4 | 10 |
| 193 | Viral phylogeny in court: the unusual case of the Valencian anesthetist. <i>BMC Biology</i> , 2013 , 11, 83 | 7 | 13 |
| 192 | Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19860-5 | 11.1 | 109 |
| 191 | Hepatitis C virus infections in the Democratic Republic of Congo exhibit a cohort effect. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 386-94 | 4.4 | 30 |
| 190 | The evolutionary dynamics of influenza A virus adaptation to mammalian hosts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120382 | 5.7 | 35 |
| 189 | Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. <i>Infection, Genetics and Evolution</i> , 2013 , 18, 367-78 | 4.4 | 19 |
| 188 | Evolutionary and molecular analysis of the emergent severe fever with thrombocytopenia syndrome virus. <i>Epidemics</i> , 2013 , 5, 1-10 | 5 | 61 |
| 187 | Characterization of full-length hepatitis C virus sequences for subtypes 1e, 1h and 1l, and a novel variant revealed Cameroon as an area in origin for genotype 1. <i>Journal of General Virology</i> , 2013 , 94, 1780-1790 | 4.7 | 16 |
| 186 | Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013 , 19, 736-42B | 9.9 | 116 |
| 185 | The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013 , 502, 241-4 | 47.5 | 338 |
| 184 | Integrating phylodynamics and epidemiology to estimate transmission diversity in viral epidemics. <i>PLoS Computational Biology</i> , 2013 , 9, e1002876 | 4.8 | 47 |
| 183 | Evolutionary epidemiology: preparing for an age of genomic plenty. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120193 | 5.7 | 27 |
| 182 | Evolutionary analysis of hepatitis C virus gene sequences from 1953. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20130168 | 5.7 | 15 |
| 181 | Eight novel hepatitis C virus genomes reveal the changing taxonomic structure of genotype 6. <i>Journal of General Virology</i> , 2013 , 94, 76-80 | 4.7 | 15 |
| 180 | The rapidly expanding CRF01_AE epidemic in China is driven by multiple lineages of HIV-1 viruses introduced in the 1990s. <i>Aids</i> , 2013 , 27, 1793-802 | 3.4 | 138 |
| 179 | Infection frequency of hepatitis C virus and IL28B haplotypes in Papua New Guinea, Fiji, and Kiribati. <i>PLoS ONE</i> , 2013 , 8, e66749 | 3.6 | 7 |
| 178 | Phylogeography and population dynamics of dengue viruses in the Americas. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1533-43 | 8 | 81 |

| | | | |
|-----|---|------|-----|
| 177 | 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 | 11.1 | 159 |
| 176 | Human parvovirus 4 infection, Cameroon. <i>Emerging Infectious Diseases</i> , 2012 , 18, 680-3 | 9.9 | 18 |
| 175 | Unexpected maintenance of hepatitis C viral diversity following liver transplantation. <i>Journal of Virology</i> , 2012 , 86, 8432-9 | 6.3 | 18 |
| 174 | Phylodynamics of H5N1 avian influenza virus in Indonesia. <i>Molecular Ecology</i> , 2012 , 21, 3062-77 | 5.5 | 27 |
| 173 | A new evolutionary model for hepatitis C virus chronic infection. <i>PLoS Pathogens</i> , 2012 , 8, e1002656 | 7.4 | 29 |
| 172 | Colonial history and contemporary transmission shape the genetic diversity of hepatitis C virus genotype 2 in Amsterdam. <i>Journal of Virology</i> , 2012 , 86, 7677-87 | 6.3 | 41 |
| 171 | Evolutionary dynamics of local pandemic H1N1/2009 influenza virus lineages revealed by whole-genome analysis. <i>Journal of Virology</i> , 2012 , 86, 11-8 | 6.3 | 84 |
| 170 | The recombinant origin of emerging human norovirus GII.4/2008: intra-genotypic exchange of the capsid P2 domain. <i>Journal of General Virology</i> , 2012 , 93, 817-822 | 4.7 | 21 |
| 169 | Origin and evolution of the unique hepatitis C virus circulating recombinant form 2k/1b. <i>Journal of Virology</i> , 2012 , 86, 2212-20 | 6.3 | 46 |
| 168 | Profibrogenic chemokines and viral evolution predict rapid progression of hepatitis C to cirrhosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 14562-7 | 11.1 | 33 |
| 167 | Large-scale spatial and temporal genetic diversity of feline calicivirus. <i>Journal of Virology</i> , 2012 , 86, 11356-67 | 6.7 | 31 |
| 166 | The ecology and age structure of a highly pathogenic avian influenza virus outbreak in wild mute swans. <i>Parasitology</i> , 2012 , 139, 1914-23 | 2.6 | 15 |
| 165 | New findings regarding the epidemic history and population dynamics of Japan-indigenous genotype 3 hepatitis E virus inferred by molecular evolution. <i>Liver International</i> , 2012 , 32, 675-88 | 7.6 | 21 |
| 164 | Estimating reassortment rates in co-circulating Eurasian swine influenza viruses. <i>Journal of General Virology</i> , 2012 , 93, 2326-2336 | 4.7 | 36 |
| 163 | New trends of HCV infection in China revealed by genetic analysis of viral sequences determined from first-time volunteer blood donors. <i>Journal of Viral Hepatitis</i> , 2011 , 18, 42-52 | 3.3 | 56 |
| 162 | Ancient urbanization predicts genetic resistance to tuberculosis. <i>Evolution; International Journal of Organic Evolution</i> , 2011 , 65, 842-8 | 3.7 | 91 |
| 161 | Long-term evolution and transmission dynamics of swine influenza A virus. <i>Nature</i> , 2011 , 473, 519-22 | 47.5 | 179 |
| 160 | The genomic rate of molecular adaptation of the human influenza A virus. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2443-51 | 8 | 115 |

| | | | |
|-----|---|------|-----|
| 159 | The mode and tempo of hepatitis C virus evolution within and among hosts. <i>BMC Evolutionary Biology</i> , 2011 , 11, 131 | 2.9 | 105 |
| 158 | HLA Footprints on Human Immunodeficiency Virus Type 1 Are Associated with Interclade Polymorphisms and Intraclade Phylogenetic Clustering. <i>Journal of Virology</i> , 2011 , 85, 4635-4635 | 6.3 | 78 |
| 157 | Analysis of the Evolutionary Forces in an Immunodominant CD8 Epitope in Hepatitis C Virus at a Population Level. <i>Journal of Virology</i> , 2011 , 85, 4634-4634 | 6.3 | 78 |
| 156 | Testing spatiotemporal hypothesis of bacterial evolution using methicillin-resistant <i>Staphylococcus aureus</i> ST239 genome-wide data within a bayesian framework. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1593-603 | 8 | 51 |
| 155 | A Bayesian phylogenetic method to estimate unknown sequence ages. <i>Molecular Biology and Evolution</i> , 2011 , 28, 879-87 | 8 | 97 |
| 154 | Viral mutation and substitution: units and levels. <i>Current Opinion in Virology</i> , 2011 , 1, 430-5 | 7.1 | 19 |
| 153 | Measuring the Temporal Structure in Serially-Sampled Phylogenies. <i>Methods in Ecology and Evolution</i> , 2011 , 2, 437-445 | 7.5 | 17 |
| 152 | Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010 , 7, 111 | 3.4 | 134 |
| 151 | Reconstructing the epidemic history of HIV-1 circulating recombinant forms CRF07_BC and CRF08_BC in East Asia: the relevance of genetic diversity and phylodynamics for vaccine strategies. <i>Vaccine</i> , 2010 , 28 Suppl 2, B39-44 | 3.9 | 40 |
| 150 | Epidemic dynamics revealed in dengue evolution. <i>Molecular Biology and Evolution</i> , 2010 , 27, 811-8 | 8 | 85 |
| 149 | Risk factors for hepatitis C virus transmission in colonial Cameroon. <i>Clinical Infectious Diseases</i> , 2010 , 51, 768-76 | 11.3 | 54 |
| 148 | B-cell depletion reveals a role for antibodies in the control of chronic HIV-1 infection. <i>Nature Communications</i> , 2010 , 1, 102 | 16.9 | 56 |
| 147 | Explosive HIV-1 subtype B epidemics in Asia driven by geographic and risk group founder events. <i>Virology</i> , 2010 , 402, 223-7 | 3.5 | 32 |
| 146 | Detecting natural selection in RNA virus populations using sequence summary statistics. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 421-30 | 4.4 | 20 |
| 145 | Possible sources and spreading routes of highly pathogenic avian influenza virus subtype H5N1 infections in poultry and wild birds in Central Europe in 2007 inferred through likelihood analyses. <i>Infection, Genetics and Evolution</i> , 2010 , 10, 1075-84 | 4.4 | 14 |
| 144 | The seroprevalence of hepatitis C virus (HCV) among 559,890 first-time volunteer blood donors in China reflects regional heterogeneity in HCV prevalence and changes in blood donor recruitment models. <i>Transfusion</i> , 2010 , 50, 1505-11 | 2.8 | 17 |
| 143 | Identification of a novel second-generation circulating recombinant form (CRF48_01B) in Malaysia: a descendant of the previously identified CRF33_01B. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2010 , 54, 129-36 | 3.1 | 34 |
| 142 | Evolutionary genetics of human enterovirus 71: origin, population dynamics, natural selection, and seasonal periodicity of the VP1 gene. <i>Journal of Virology</i> , 2010 , 84, 3339-50 | 6.3 | 182 |

| | | | |
|-----|---|------|------|
| 141 | Yellow fever virus maintenance in Trinidad and its dispersal throughout the Americas. <i>Journal of Virology</i> , 2010 , 84, 9967-77 | 6.3 | 44 |
| 140 | Widespread infection with homologues of human parvoviruses B19, PARV4, and human bocavirus of chimpanzees and gorillas in the wild. <i>Journal of Virology</i> , 2010 , 84, 10289-96 | 6.3 | 65 |
| 139 | Full-Length Characterization of Hepatitis C Virus Subtype 3a Reveals Novel Hypervariable Regions under Positive Selection during Acute Infection. <i>Journal of Virology</i> , 2010 , 84, 1664-1664 | 6.3 | 78 |
| 138 | Generation of neutralizing antibodies and divergence of SIVmac239 in cynomolgus macaques following short-term early antiretroviral therapy. <i>PLoS Pathogens</i> , 2010 , 6, e1001084 | 7.4 | 8 |
| 137 | Elevated caspase-3 expression and T-cell activation in elite suppressors. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2010 , 54, 110-1 | 3.1 | 4 |
| 136 | Changing epidemiology of human parvovirus 4 infection in sub-Saharan Africa. <i>Emerging Infectious Diseases</i> , 2010 , 16, 1605-7 | 9.9 | 49 |
| 135 | Re-emergent hepatitis C viremia after apparent clearance in HIV-positive men who have sex with men: reinfection or late recurrence?. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2010 , 53, 547-50 | 3.1 | 11 |
| 134 | Macroevolution of complex retroviruses. <i>Science</i> , 2009 , 325, 1512 | 32.2 | 130 |
| 133 | Epistatic interactions between genetic disorders of hemoglobin can explain why the sickle-cell gene is uncommon in the Mediterranean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 21242-6 | 11.1 | 53 |
| 132 | Pandemic potential of a strain of influenza A (H1N1): early findings. <i>Science</i> , 2009 , 324, 1557-61 | 32.2 | 1395 |
| 131 | The global spread of hepatitis C virus 1a and 1b: a phylodynamic and phylogeographic analysis. <i>PLoS Medicine</i> , 2009 , 6, e1000198 | 11.3 | 151 |
| 130 | HLA footprints on human immunodeficiency virus type 1 are associated with interclade polymorphisms and intraclade phylogenetic clustering. <i>Journal of Virology</i> , 2009 , 83, 4605-15 | 6.3 | 36 |
| 129 | Full-length characterization of hepatitis C virus subtype 3a reveals novel hypervariable regions under positive selection during acute infection. <i>Journal of Virology</i> , 2009 , 83, 11456-66 | 6.3 | 23 |
| 128 | Phylogeography and molecular epidemiology of hepatitis C virus genotype 2 in Africa. <i>Journal of General Virology</i> , 2009 , 90, 2086-96 | 4.7 | 75 |
| 127 | Estimating the date of origin of an HIV-1 circulating recombinant form. <i>Virology</i> , 2009 , 387, 229-34 | 3.5 | 22 |
| 126 | Phylodynamic analysis of the dissemination of HIV-1 CRF01_AE in Vietnam. <i>Virology</i> , 2009 , 391, 51-6 | 3.5 | 64 |
| 125 | Adaptation of HIV-1 to human leukocyte antigen class I. <i>Nature</i> , 2009 , 458, 641-5 | 47.5 | 359 |
| 124 | Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009 , 459, 1122-5 | 47.5 | 1534 |

| | | | |
|-----|--|------|-----|
| 123 | Evolutionary analysis of the dynamics of viral infectious disease. <i>Nature Reviews Genetics</i> , 2009 , 10, 540-50.1 | 4.0 | 101 |
| 122 | Evolution and dispersal of St. Louis encephalitis virus in the Americas. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 709-15 | 4.4 | 32 |
| 121 | Evidence of a large, international network of HCV transmission in HIV-positive men who have sex with men. <i>Gastroenterology</i> , 2009 , 136, 1609-17 | 7.8 | 247 |
| 120 | Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. <i>Retrovirology</i> , 2009 , 6, 49 | 3.4 | 97 |
| 119 | Genetic history of hepatitis C virus in East Asia. <i>Journal of Virology</i> , 2009 , 83, 1071-82 | 6.3 | 168 |
| 118 | Paleovirology reveals the macroevolution of complex retroviruses. <i>Retrovirology</i> , 2009 , 6, | 3.4 | 1 |
| 117 | A standardized framework for accurate, high-throughput genotyping of recombinant and non-recombinant viral sequences. <i>Nucleic Acids Research</i> , 2009 , 37, W634-42 | 19.4 | 127 |
| 116 | High prevalence of hepatitis C virus infection and predominance of genotype 4 in rural Gabon. <i>Journal of Medical Virology</i> , 2008 , 80, 1581-7 | 19.3 | 25 |
| 115 | Complete genome sequencing and phylogenetic analysis of HCV isolates from China reveals a new subtype, designated 6u. <i>Journal of Medical Virology</i> , 2008 , 80, 1740-6 | 19.3 | 23 |
| 114 | Correlating viral phenotypes with phylogeny: accounting for phylogenetic uncertainty. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 239-46 | 4.4 | 322 |
| 113 | Variable epidemic histories of hepatitis C virus genotype 2 infection in West Africa and Cameroon. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 676-81 | 4.4 | 24 |
| 112 | The genomic and epidemiological dynamics of human influenza A virus. <i>Nature</i> , 2008 , 453, 615-9 | 47.5 | 687 |
| 111 | Phylogeny, niches, and relative abundance in natural communities. <i>Ecology</i> , 2008 , 89, 962-70 | 4.5 | 58 |
| 110 | Pacing a small cage: mutation and RNA viruses. <i>Trends in Ecology and Evolution</i> , 2008 , 23, 188-93 | 10.6 | 106 |
| 109 | Molecular Epidemiology of H5N1 Avian Influenza Virus: Correlations between Antigenic Drift, Geographical Migration and Expansion of Viral Diversity. <i>International Journal of Infectious Diseases</i> , 2008 , 12, e58-e59 | 5.2 | |
| 108 | Analysis of the evolutionary forces in an immunodominant CD8 epitope in hepatitis C virus at a population level. <i>Journal of Virology</i> , 2008 , 82, 3438-51 | 6.3 | 55 |
| 107 | Impact of HIV on host-virus interactions during early hepatitis C virus infection. <i>Journal of Infectious Diseases</i> , 2008 , 197, 1558-66 | 6.8 | 83 |
| 106 | A transitional endogenous lentivirus from the genome of a basal primate and implications for lentivirus evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 20362-7 | 11.1 | 159 |

| | | | |
|-----|--|------|-----|
| 105 | Evolutionary and transmission dynamics of reassortant H5N1 influenza virus in Indonesia. <i>PLoS Pathogens</i> , 2008 , 4, e1000130 | 7.4 | 50 |
| 104 | Temporal and spatial dynamics of human immunodeficiency virus type 1 circulating recombinant forms 08_BC and 07_BC in Asia. <i>Journal of Virology</i> , 2008 , 82, 9206-15 | 6.3 | 121 |
| 103 | Chronology of the HIV-1 CRF07_BC expansion in East Asia. <i>Aids</i> , 2008 , 22, 156-8 | 3.4 | 14 |
| 102 | Mitogenetic structure of brown bears (<i>Ursus arctos</i> L.) in northeastern Europe and a new time frame for the formation of European brown bear lineages. <i>Molecular Ecology</i> , 2007 , 16, 401-13 | 5.5 | 107 |
| 101 | The generation of influenza outbreaks by a network of host immune responses against a limited set of antigenic types. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7711-6 | 11.1 | 76 |
| 100 | Complete genomes for hepatitis C virus subtypes 6f, 6i, 6j and 6m: viral genetic diversity among Thai blood donors and infected spouses. <i>Journal of General Virology</i> , 2007 , 88, 1505-1518 | 4.7 | 28 |
| 99 | Increasing prevalence of HIV-1 subtype A in Greece: estimating epidemic history and origin. <i>Journal of Infectious Diseases</i> , 2007 , 196, 1167-76 | 6.8 | 61 |
| 98 | Synonymous substitution rates predict HIV disease progression as a result of underlying replication dynamics. <i>PLoS Computational Biology</i> , 2007 , 3, e29 | 4.8 | 137 |
| 97 | Recent epidemic of acute hepatitis C virus in HIV-positive men who have sex with men linked to high-risk sexual behaviours. <i>Aids</i> , 2007 , 21, 983-91 | 3.4 | 324 |
| 96 | Complete genomes of hepatitis C virus (HCV) subtypes 6c, 6l, 6o, 6p and 6q: completion of a full panel of genomes for HCV genotype 6. <i>Journal of General Virology</i> , 2007 , 88, 1519-1525 | 4.7 | 26 |
| 95 | 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 | 117 |
| 94 | 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 | 6.3 | 72 |
| 93 | Discovery and analysis of the first endogenous lentivirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 6261-5 | 11.1 | 170 |
| 92 | The evolution of genome compression and genomic novelty in RNA viruses. <i>Genome Research</i> , 2007 , 17, 1496-504 | 9.4 | 109 |
| 91 | Investigating the endemic transmission of the hepatitis C virus. <i>International Journal for Parasitology</i> , 2007 , 37, 839-49 | 4.1 | 51 |
| 90 | Molecular epidemiology: HIV-1 and HCV sequences from Libyan outbreak. <i>Nature</i> , 2006 , 444, 836-7 | 47.5 | 105 |
| 89 | Do antiviral CD8+ T cells select hepatitis C virus escape mutants? Analysis in diverse epitopes targeted by human intrahepatic CD8+ T lymphocytes. <i>Journal of Viral Hepatitis</i> , 2006 , 13, 121-30 | 3.3 | 18 |
| 88 | Dominant influence of an HLA-B27 restricted CD8+ T cell response in mediating HCV clearance and evolution. <i>Hepatology</i> , 2006 , 43, 563-72 | 10.9 | 171 |

| | | | |
|----|---|------|------|
| 87 | Evolution of the human immunodeficiency virus envelope gene is dominated by purifying selection. <i>Genetics</i> , 2006 , 174, 1441-53 | 3.9 | 58 |
| 86 | JC virus evolution and its association with human populations. <i>Journal of Virology</i> , 2006 , 80, 9928-33 | 6.3 | 89 |
| 85 | Investigating the origin and spread of hepatitis C virus genotype 5a. <i>Journal of Virology</i> , 2006 , 80, 4220-6.3 | 6.3 | 71 |
| 84 | Population genetic history of hepatitis C virus 1b infection in China. <i>Journal of General Virology</i> , 2006 , 87, 73-82 | 4.7 | 41 |
| 83 | A phylogenetic method for detecting positive epistasis in gene sequences and its application to RNA virus evolution. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1724-30 | 8 | 40 |
| 82 | Model selection and the molecular clock. <i>PLoS Biology</i> , 2006 , 4, e151 | 9.4 | 23 |
| 81 | Tracing the origin of Brazilian HTLV-1 as determined by analysis of host and viral genes. <i>Aids</i> , 2006 , 20, 780-2 | 3.4 | 22 |
| 80 | HIV evolutionary dynamics within and among hosts. <i>AIDS Reviews</i> , 2006 , 8, 125-40 | 1.4 | 160 |
| 79 | Host switch leads to emergence of Plasmodium vivax malaria in humans. <i>Molecular Biology and Evolution</i> , 2005 , 22, 1686-93 | 8 | 173 |
| 78 | Invasion and maintenance of dengue virus type 2 and type 4 in the Americas. <i>Journal of Virology</i> , 2005 , 79, 14680-7 | 6.3 | 105 |
| 77 | Genetic analysis reveals the complex structure of HIV-1 transmission within defined risk groups. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 4425-9 | 11.1 | 204 |
| 76 | Bayesian coalescent inference of past population dynamics from molecular sequences. <i>Molecular Biology and Evolution</i> , 2005 , 22, 1185-92 | 8 | 2255 |
| 75 | The evolutionary dynamics of endogenous retroviruses. <i>Trends in Microbiology</i> , 2005 , 13, 463-8 | 12 | 72 |
| 74 | A Bayesian statistical analysis of human T-cell lymphotropic virus evolutionary rates. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 291-8 | 4.4 | 30 |
| 73 | 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 | 4.4 | 64 |
| 72 | The hepatitis C virus epidemic among injecting drug users. <i>Infection, Genetics and Evolution</i> , 2005 , 5, 131-4 | 4.4 | 130 |
| 71 | Different epidemic potentials of the HIV-1B and C subtypes. <i>Journal of Molecular Evolution</i> , 2005 , 60, 598-605 | 3 | 43 |
| 70 | Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. <i>PLoS Computational Biology</i> , 2005 , preprint, e29 | 4.8 | |

| | | | |
|----|--|------|-----|
| 69 | The low evolutionary rate of human T-cell lymphotropic virus type-1 confirmed by analysis of vertical transmission chains. <i>Molecular Biology and Evolution</i> , 2004 , 21, 603-11 | 8 | 48 |
| 68 | High-resolution phylogenetic analysis of hepatitis C virus adaptation and its relationship to disease progression. <i>Journal of Virology</i> , 2004 , 78, 3447-54 | 6.3 | 71 |
| 67 | Viral gene sequences reveal the variable history of hepatitis C virus infection among countries. <i>Journal of Infectious Diseases</i> , 2004 , 190, 1098-108 | 6.8 | 69 |
| 66 | Historical demography of Mullerian mimicry in the neotropical <i>Heliconius</i> butterflies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 9704-9 | 11.1 | 84 |
| 65 | The molecular population genetics of HIV-1 group O. <i>Genetics</i> , 2004 , 167, 1059-68 | 3.9 | 89 |
| 64 | Unifying the epidemiological and evolutionary dynamics of pathogens. <i>Science</i> , 2004 , 303, 327-32 | 32.2 | 917 |
| 63 | Genetic structure of the deep-sea coral <i>Lophelia pertusa</i> in the northeast Atlantic revealed by microsatellites and internal transcribed spacer sequences. <i>Molecular Ecology</i> , 2004 , 13, 537-49 | 5.5 | 93 |
| 62 | Rise and fall of the Beringian steppe bison. <i>Science</i> , 2004 , 306, 1561-5 | 32.2 | 517 |
| 61 | Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , 2003 , 18, 481-488 | 10.6 | 299 |
| 60 | Inference of viral evolutionary rates from molecular sequences. <i>Advances in Parasitology</i> , 2003 , 54, 331-58 | 5.8 | 125 |
| 59 | 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 | 200 |
| 58 | U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains. <i>Journal of Virology</i> , 2003 , 77, 6359-66 | 6.3 | 102 |
| 57 | Phylogenetic analysis of hepatitis C virus isolates indicates a unique pattern of endemic infection in Cameroon. <i>Journal of General Virology</i> , 2003 , 84, 2333-2341 | 4.7 | 88 |
| 56 | Epidemiology: Sexual transmission of HIV in Africa. <i>Nature</i> , 2003 , 422, 679 | 47.5 | 32 |
| 55 | Comparative population dynamics of mosquito-borne flaviviruses. <i>Infection, Genetics and Evolution</i> , 2003 , 3, 87-95 | 4.4 | 22 |
| 54 | Tracing the origin and history of the HIV-2 epidemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 6588-92 | 11.1 | 254 |
| 53 | Increased positive selection pressure in persistent (SSPE) versus acute measles virus infections. <i>Journal of General Virology</i> , 2002 , 83, 1419-1430 | 4.7 | 25 |
| 52 | Population Genetics of HIV: Parameter Estimation Using Genealogy-based Methods 2002 , 217-252 | | 5 |

| | | | |
|----|--|------|-----|
| 51 | Rates of molecular evolution in RNA viruses: a quantitative phylogenetic analysis. <i>Journal of Molecular Evolution</i> , 2002 , 54, 156-65 | 3 | 524 |
| 50 | Genetic diversity and models of viral evolution for the hepatitis C virus. <i>FEMS Microbiology Letters</i> , 2002 , 214, 143-52 | 2.8 | 44 |
| 49 | GENIE: estimating demographic history from molecular phylogenies. <i>Bioinformatics</i> , 2002 , 18, 1404-5 | 6.8 | 119 |
| 48 | New inferences from tree shape: numbers of missing taxa and population growth rates. <i>Systematic Biology</i> , 2002 , 51, 881-8 | 8.2 | 71 |
| 47 | Questioning the evidence for genetic recombination in the 1918 "Spanish flu" virus. <i>Science</i> , 2002 , 296, 211 discussion 211 | 32.2 | 49 |
| 46 | The epidemic behavior of the hepatitis C virus. <i>Science</i> , 2001 , 292, 2323-5 | 32.2 | 350 |
| 45 | Exploring the demographic history of DNA sequences using the generalized skyline plot. <i>Molecular Biology and Evolution</i> , 2001 , 18, 2298-305 | 8 | 192 |
| 44 | Human immunodeficiency virus. Phylogeny and the origin of HIV-1. <i>Nature</i> , 2001 , 410, 1047-8 | 47.5 | 121 |
| 43 | Using human immunodeficiency virus type 1 sequences to infer historical features of the acquired immune deficiency syndrome epidemic and human immunodeficiency virus evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2001 , 356, 855-66 | 5.7 | 55 |
| 42 | An integrated framework for the inference of viral population history from reconstructed genealogies. <i>Genetics</i> , 2000 , 155, 1429-37 | 3.9 | 275 |
| 41 | Testing macro-evolutionary models using incomplete molecular phylogenies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000 , 267, 2267-72 | 4.3 | 610 |
| 40 | The mid-depth method and HIV-1: a practical approach for testing hypotheses of viral epidemic history. <i>Molecular Biology and Evolution</i> , 1999 , 16, 953-9 | 8 | 23 |
| 39 | The evolutionary epidemiology of the hepatitis C virus 450-472 | | |
| 38 | Host specificity and species jumps in fish-parasite systems 401-419 | | 5 |
| 37 | Human B cell lineages engaged by germinal centers following influenza vaccination are measurably evolving | | 1 |
| 36 | Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission | | 3 |
| 35 | Vaccine nationalism and the dynamics and control of SARS-CoV-2 | | 3 |
| 34 | Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza | | 1 |

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| 33 | Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant | 120 |
| 32 | Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant | 3 |
| 31 | Genomic epidemiology of early SARS-CoV-2 transmission dynamics in Gujarat, India | 2 |
| 30 | Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences | 1 |
| 29 | Prisoner of War dynamics explains the time-dependent pattern of substitution rates in viruses | 2 |
| 28 | Natural selection and adaptation of molecular sequences 407-418 | 4 |
| 27 | Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples | 6 |
| 26 | The impact of transmission control measures during the first 50 days of the COVID-19 epidemic in China | 54 |
| 25 | Routes for COVID-19 importation in Brazil | 5 |
| 24 | Crowding and the epidemic intensity of COVID-19 transmission | 23 |
| 23 | Phylogenetic analysis of migration, differentiation, and class switching in B cells | 8 |
| 22 | Evolution and epidemic spread of SARS-CoV-2 in Brazil | 6 |
| 21 | Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR | 4 |
| 20 | Evaluating the effects of SARS-CoV-2 Spike mutation D614G on transmissibility and pathogenicity | 52 |
| 19 | COVID-19 herd immunity in the Brazilian Amazon | 15 |
| 18 | Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK | 10 |
| 17 | Parallel Evolution in the Emergence of Highly Pathogenic Avian Influenza A Viruses | 2 |
| 16 | Emergence of the Zika virus Asian lineage in Angola | 1 |

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| 15 | Genomic Surveillance of Yellow Fever Virus Epizootic in S̃ Paulo, Brazil, 2016–2018 | 4 |
| 14 | The evolutionary dynamics of Oropouche Virus (OROV) in South America | 1 |
| 13 | Oropouche virus cases identified in Ecuador using an optimised rRT-PCR informed by metagenomic sequencing | |
| 12 | The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK | 1 |
| 11 | Emergence and widespread circulation of a recombinant SARS-CoV-2 lineage in North America | 3 |
| 10 | Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , | 47.5 21 |
| 9 | Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa | 12 |
| 8 | Are skyline plot-based demographic estimates overly dependent on smoothing prior assumptions? | 2 |
| 7 | Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China | 6 |
| 6 | Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak | 1 |
| 5 | Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination | 2 |
| 4 | Jointly inferring the dynamics of population size and sampling intensity from molecular sequences | 1 |
| 3 | Coalescent inference using serially sampled, high-throughput sequencing data from intra-host HIV infection | 1 |
| 2 | Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic | 2 |
| 1 | Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages | 5 |