

# Oliver G. Pybus

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/6605307/oliver-g-pybus-publications-by-citations.pdf>

**Version:** 2023-03-30

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Bayesian coalescent inference of past population dynamics from molecular sequences. <i>Molecular Biology and Evolution</i> , <b>2005</b> , 22, 1185-92	8	2255
409	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , <b>2009</b> , 459, 1122-5	47.5	1534
408	Pandemic potential of a strain of influenza A (H1N1): early findings. <i>Science</i> , <b>2009</b> , 324, 1557-61	32.2	1395
407	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , <b>2020</b> , 368, 493-497	32.2	1329
406	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1403-1407	25.8	1194
405	Global distribution and prevalence of hepatitis C virus genotypes. <i>Hepatology</i> , <b>2015</b> , 61, 77-87	10.9	1046
404	An investigation of transmission control measures during the first 50 days of the COVID-19 epidemic in China. <i>Science</i> , <b>2020</b> , 368, 638-642	32.2	986
403	Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , <b>2016</b> , 2, vew007	3.6	937
402	Unifying the epidemiological and evolutionary dynamics of pathogens. <i>Science</i> , <b>2004</b> , 303, 327-32	32.2	917
401	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , <b>2016</b> , 352, 345-349	32.2	700
400	The genomic and epidemiological dynamics of human influenza A virus. <i>Nature</i> , <b>2008</b> , 453, 615-9	47.5	687
399	Testing macro-evolutionary models using incomplete molecular phylogenies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2000</b> , 267, 2267-72	4.3	610
398	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , <b>2021</b> , 372, 815-821	32.2	566
397	Rates of molecular evolution in RNA viruses: a quantitative phylogenetic analysis. <i>Journal of Molecular Evolution</i> , <b>2002</b> , 54, 156-65	3	524
396	Rise and fall of the Beringian steppe bison. <i>Science</i> , <b>2004</b> , 306, 1561-5	32.2	517
395	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , <b>2017</b> , 12, 1261-1276	18.1	514
394	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , <b>2021</b> , 184, 64-75.e11	54.5	500

393	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet, The</i> , <b>2021</b> , 397, 452-455	36.2	463
392	Evolutionary analysis of the dynamics of viral infectious disease. <i>Nature Reviews Genetics</i> , <b>2009</b> , 10, 540-50	1	401
391	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , <b>2014</b> , 346, 56-61	32.2	370
390	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , <b>2017</b> , 546, 406-410	19.5	363
389	Adaptation of HIV-1 to human leukocyte antigen class I. <i>Nature</i> , <b>2009</b> , 458, 641-5	47.5	359
388	The epidemic behavior of the hepatitis C virus. <i>Science</i> , <b>2001</b> , 292, 2323-5	32.2	350
387	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , <b>2013</b> , 502, 241-4	47.5	338
386	Correlating viral phenotypes with phylogeny: accounting for phylogenetic uncertainty. <i>Infection, Genetics and Evolution</i> , <b>2008</b> , 8, 239-46	4.4	322
385	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> , <b>2007</b> , 21, 983-91	3.4	324
384	Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , <b>2003</b> , 18, 481-488	10.6	299
383	Past and future spread of the arbovirus vectors <i>Aedes aegypti</i> and <i>Aedes albopictus</i> . <i>Nature Microbiology</i> , <b>2019</b> , 4, 854-863	25.8	295
382	An integrated framework for the inference of viral population history from reconstructed genealogies. <i>Genetics</i> , <b>2000</b> , 155, 1429-37	3.9	275
381	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , <b>2020</b> , 369, 1255-1260	32.2	270
380	Emergence and potential for spread of Chikungunya virus in Brazil. <i>BMC Medicine</i> , <b>2015</b> , 13, 102	11.1	267
379	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , <b>2021</b> , 371, 288-292	32.2	257
378	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> , <b>2003</b> , 100, 6588-92	11.1	254
377	Evidence of a large, international network of HCV transmission in HIV-positive men who have sex with men. <i>Gastroenterology</i> , <b>2009</b> , 136, 1609-17	7.8	247
376	Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , <b>2016</b> , 354, 213-217	32.2	243

375	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , <b>2017</b> , 544, 309-315	47.5	238
374	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , <b>2017</b> , 546, 401-405	47.5	233
373	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1003932	7.4	227
372	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> , <b>2005</b> , 102, 4425-9	11.1	204
371	The epidemiology and iatrogenic transmission of hepatitis C virus in Egypt: a Bayesian coalescent approach. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 381-7	8	200
370	Exploring the demographic history of DNA sequences using the generalized skyline plot. <i>Molecular Biology and Evolution</i> , <b>2001</b> , 18, 2298-305	8	192
369	Epidemiological data from the COVID-19 outbreak, real-time case information. <i>Scientific Data</i> , <b>2020</b> , 7, 106	8	190
368	Evolutionary genetics of human enterovirus 71: origin, population dynamics, natural selection, and seasonal periodicity of the VP1 gene. <i>Journal of Virology</i> , <b>2010</b> , 84, 3339-50	6.3	182
367	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , <b>2018</b> , 361, 894-899	32.2	180
366	Long-term evolution and transmission dynamics of swine influenza A virus. <i>Nature</i> , <b>2011</b> , 473, 519-22	47.5	179
365	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , <b>2019</b> , 4, 10-19	25.8	175
364	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , <b>2020</b> , 181, 997-1003.e9	54.5	173
363	Host switch leads to emergence of Plasmodium vivax malaria in humans. <i>Molecular Biology and Evolution</i> , <b>2005</b> , 22, 1686-93	8	173
362	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , <b>2020</b> , 11, 2688	16.9	166
361	Discovery and analysis of the first endogenous lentivirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 6261-5	11.1	170
360	Dominant influence of an HLA-B27 restricted CD8+ T cell response in mediating HCV clearance and evolution. <i>Hepatology</i> , <b>2006</b> , 43, 563-72	10.9	171
359	Genetic history of hepatitis C virus in East Asia. <i>Journal of Virology</i> , <b>2009</b> , 83, 1071-82	6.3	168
358	Measurably evolving pathogens in the genomic era. <i>Trends in Ecology and Evolution</i> , <b>2015</b> , 30, 306-13	10.6	167

357	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, The</i> , <b>2021</b> ,	24.7	159
356	HIV evolutionary dynamics within and among hosts. <i>AIDS Reviews</i> , <b>2006</b> , 8, 125-40	1.4	160
355	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> , <b>2012</b> , 109, 15066-71	11.1	159
354	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , <b>2020</b> , 369, 582-587	32.2	155
353	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> , <b>2008</b> , 105, 20362-7	11.1	159
352	Open access epidemiological data from the COVID-19 outbreak. <i>Lancet Infectious Diseases, The</i> , <b>2020</b> , 20, 534	24.7	163
351	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> , <b>2021</b> , 35, 109292	10.3	154
350	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , <b>2021</b> , 371, 708-712	32.2	153
349	The global spread of hepatitis C virus 1a and 1b: a phylodynamic and phylogeographic analysis. <i>PLoS Medicine</i> , <b>2009</b> , 6, e1000198	11.3	151
348	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , <b>2021</b> , 7, veab064	3.6	139
347	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , <b>2020</b> , 4, 856-865	12.5	144
346	Spread of yellow fever virus outbreak in Angola and the Democratic Republic of the Congo 2015-16: a modelling study. <i>Lancet Infectious Diseases, The</i> , <b>2017</b> , 17, 330-338	24.7	139
345	The rapidly expanding CRF01_AE epidemic in China is driven by multiple lineages of HIV-1 viruses introduced in the 1990s. <i>Aids</i> , <b>2013</b> , 27, 1793-802	3.4	138
344	Synonymous substitution rates predict HIV disease progression as a result of underlying replication dynamics. <i>PLoS Computational Biology</i> , <b>2007</b> , 3, e29	4.8	137
343	The hepatitis C virus epidemic among injecting drug users. <i>Infection, Genetics and Evolution</i> , <b>2005</b> , 5, 131-44	11.4	130
342	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , <b>2016</b> , 8, 97	14	129
341	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , <b>2010</b> , 7, 111	3.4	134
340	Macroevolution of complex retroviruses. <i>Science</i> , <b>2009</b> , 325, 1512	32.2	130

339	A standardized framework for accurate, high-throughput genotyping of recombinant and non-recombinant viral sequences. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W634-42	19.4	127
338	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , <b>2022</b> ,	47.5	130
337	Inference of viral evolutionary rates from molecular sequences. <i>Advances in Parasitology</i> , <b>2003</b> , 54, 331-58	12.5	125
336	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , <b>2020</b> , 1, e99-e100	21.6	122
335	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> , <b>2008</b> , 82, 9206-15	6.3	121
334	GENIE: estimating demographic history from molecular phylogenies. <i>Bioinformatics</i> , <b>2002</b> , 18, 1404-5	6.8	119
333	Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant		120
332	Human immunodeficiency virus. Phylogeny and the origin of HIV-1. <i>Nature</i> , <b>2001</b> , 410, 1047-8	47.5	121
331	Full-genome deep sequencing and phylogenetic analysis of novel human betacoronavirus. <i>Emerging Infectious Diseases</i> , <b>2013</b> , 19, 736-42B	9.9	116
330	Phylogenetic evidence for deleterious mutation load in RNA viruses and its contribution to viral evolution. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 845-52	8	117
329	The genomic rate of molecular adaptation of the human influenza A virus. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 2443-51	8	115
328	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 19860-5	11.1	109
327	Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , <b>2015</b> , 89, 9920-31	6.3	109
326	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> , <b>2007</b> , 16, 401-13	5.5	107
325	The evolution of genome compression and genomic novelty in RNA viruses. <i>Genome Research</i> , <b>2007</b> , 17, 1496-504	9.4	109
324	The mode and tempo of hepatitis C virus evolution within and among hosts. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 131	2.9	105
323	Pacing a small cage: mutation and RNA viruses. <i>Trends in Ecology and Evolution</i> , <b>2008</b> , 23, 188-93	10.6	106
322	Invasion and maintenance of dengue virus type 2 and type 4 in the Americas. <i>Journal of Virology</i> , <b>2005</b> , 79, 14680-7	6.3	105

321	U.S. Human immunodeficiency virus type 1 epidemic: date of origin, population history, and characterization of early strains. <i>Journal of Virology</i> , <b>2003</b> , 77, 6359-66	6.3	102
320	Molecular epidemiology: HIV-1 and HCV sequences from Libyan outbreak. <i>Nature</i> , <b>2006</b> , 444, 836-7	47.5	105
319	A Bayesian phylogenetic method to estimate unknown sequence ages. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 879-87	8	97
318	Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR. <i>EBioMedicine</i> , <b>2020</b> , 59, 102960	8.6	98
317	Crowding and the shape of COVID-19 epidemics. <i>Nature Medicine</i> , <b>2020</b> , 26, 1829-1834	49.3	94
316	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. <i>Retrovirology</i> , <b>2009</b> , 6, 49	3.4	97
315	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> , <b>2004</b> , 13, 537-49	5.5	93
314	Ancient urbanization predicts genetic resistance to tuberculosis. <i>Evolution; International Journal of Organic Evolution</i> , <b>2011</b> , 65, 842-8	3.7	91
313	JC virus evolution and its association with human populations. <i>Journal of Virology</i> , <b>2006</b> , 80, 9928-33	6.3	89
312	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , <b>2016</b> , 2, vew016	3.6	87
311	The molecular population genetics of HIV-1 group O. <i>Genetics</i> , <b>2004</b> , 167, 1059-68	3.9	89
310	Phylogenetic analysis of hepatitis C virus isolates indicates a unique pattern of endemic infection in Cameroon. <i>Journal of General Virology</i> , <b>2003</b> , 84, 2333-2341	4.7	88
309	Defining HIV-1 transmission clusters based on sequence data. <i>Aids</i> , <b>2017</b> , 31, 1211-1222	3.4	87
308	Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.3	83
307	Evolutionary dynamics of local pandemic H1N1/2009 influenza virus lineages revealed by whole-genome analysis. <i>Journal of Virology</i> , <b>2012</b> , 86, 11-8	6.3	84
306	Epidemic dynamics revealed in dengue evolution. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 811-8	8	85
305	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , <b>2021</b> , 6, 821-823	25.8	85
304	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> , <b>2004</b> , 101, 9704-9	11.1	84

303	Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes. <i>Science</i> , <b>2021</b> , 372, 363-370	32.2	81
302	Eight challenges in phylodynamic inference. <i>Epidemics</i> , <b>2015</b> , 10, 88-92	5	83
301	Impact of HIV on host-virus interactions during early hepatitis C virus infection. <i>Journal of Infectious Diseases</i> , <b>2008</b> , 197, 1558-66	6.8	83
300	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> , <b>2014</b> , 9, e115815	3.6	80
299	Phylogeography and population dynamics of dengue viruses in the Americas. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 1533-43	8	81
298	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , <b>2019</b> , 5,	3.6	78
297	A38 Genomic epidemiology quantifies gaps in Aedes-borne virus transmission in the Americas. <i>Virus Evolution</i> , <b>2019</b> , 5,	3.6	78
296	A60 Revealing the evolution of virulence in RNA viruses. <i>Virus Evolution</i> , <b>2019</b> , 5,	3.6	78
295	Virus evolution and transmission in an ever more connected world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 282, 20142878	4.3	78
294	HLA Footprints on Human Immunodeficiency Virus Type 1 Are Associated with Interclade Polymorphisms and Intraclade Phylogenetic Clustering. <i>Journal of Virology</i> , <b>2011</b> , 85, 4635-4635	6.3	78
293	Analysis of the Evolutionary Forces in an Immunodominant CD8 Epitope in Hepatitis C Virus at a Population Level. <i>Journal of Virology</i> , <b>2011</b> , 85, 4634-4634	6.3	78
292	Full-Length Characterization of Hepatitis C Virus Subtype 3a Reveals Novel Hypervariable Regions under Positive Selection during Acute Infection. <i>Journal of Virology</i> , <b>2010</b> , 84, 1664-1664	6.3	78
291	Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , <b>2020</b> , 27,	12.5	79
290	Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant.. <i>Nature Communications</i> , <b>2022</b> , 13, 460	16.9	76
289	Phylogeography and molecular epidemiology of hepatitis C virus genotype 2 in Africa. <i>Journal of General Virology</i> , <b>2009</b> , 90, 2086-96	4.7	75
288	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> , <b>2007</b> , 104, 7711-6	11.1	76
287	Phylogenetic surveillance of viral genetic diversity and the evolving molecular epidemiology of human immunodeficiency virus type 1. <i>Journal of Virology</i> , <b>2007</b> , 81, 13050-6	6.3	72
286	The evolutionary dynamics of endogenous retroviruses. <i>Trends in Microbiology</i> , <b>2005</b> , 13, 463-8	12	72



285	New inferences from tree shape: numbers of missing taxa and population growth rates. <i>Systematic Biology</i> , <b>2002</b> , 51, 881-8	8.2	71
284	Investigating the origin and spread of hepatitis C virus genotype 5a. <i>Journal of Virology</i> , <b>2006</b> , 80, 4220-6.3	6.3	71
283	High-resolution phylogenetic analysis of hepatitis C virus adaptation and its relationship to disease progression. <i>Journal of Virology</i> , <b>2004</b> , 78, 3447-54	6.3	71
282	Viral gene sequences reveal the variable history of hepatitis C virus infection among countries. <i>Journal of Infectious Diseases</i> , <b>2004</b> , 190, 1098-108	6.8	69
281	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , <b>2016</b> , 32, 3204-3206	6.8	68
280	Widespread infection with homologues of human parvoviruses B19, PARV4, and human bocavirus of chimpanzees and gorillas in the wild. <i>Journal of Virology</i> , <b>2010</b> , 84, 10289-96	6.3	65
279	Comparative population dynamics of HIV-1 subtypes B and C: subtype-specific differences in patterns of epidemic growth. <i>Infection, Genetics and Evolution</i> , <b>2005</b> , 5, 199-208	4.4	64
278	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 659-668	12.1	65
277	Phylogenetic analysis of the dissemination of HIV-1 CRF01_AE in Vietnam. <i>Virology</i> , <b>2009</b> , 391, 51-6	3.5	64
276	Evolutionary and molecular analysis of the emergent severe fever with thrombocytopenia syndrome virus. <i>Epidemics</i> , <b>2013</b> , 5, 1-10	5	61
275	Explaining the geographic spread of emerging epidemics: a framework for comparing viral phylogenies and environmental landscape data. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 82	3.4	59
274	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , <b>2018</b> , 23, 855-864.e7	22.8	61
273	Phylogeny, niches, and relative abundance in natural communities. <i>Ecology</i> , <b>2008</b> , 89, 962-70	4.5	58
272	Evolution of the human immunodeficiency virus envelope gene is dominated by purifying selection. <i>Genetics</i> , <b>2006</b> , 174, 1441-53	3.9	58
271	Increasing prevalence of HIV-1 subtype A in Greece: estimating epidemic history and origin. <i>Journal of Infectious Diseases</i> , <b>2007</b> , 196, 1167-76	6.8	61
270	Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005694	4.6	57
269	A reversal of fortunes: climate change winners and losers on Antarctic Peninsula penguins. <i>Scientific Reports</i> , <b>2014</b> , 4, 5024	4.7	56
268	Phylogeography and epidemic history of hepatitis C virus genotype 4 in Africa. <i>Virology</i> , <b>2014</b> , 464-465, 233-243	3.5	55

267	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> , <b>2011</b> , 18, 42-52	3.3	56
266	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , <b>2020</b> , 5, 443-454	25.8	56
265	Evaluating the effects of SARS-CoV-2 Spike mutation D614G on transmissibility and pathogenicity		52
264	B-cell depletion reveals a role for antibodies in the control of chronic HIV-1 infection. <i>Nature Communications</i> , <b>2010</b> , 1, 102	16.9	56
263	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , <b>2017</b> , 6,	8.6	53
262	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> , <b>2015</b> , 34, 267-77	4.4	54
261	The impact of transmission control measures during the first 50 days of the COVID-19 epidemic in China		54
260	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> , <b>2001</b> , 356, 855-66	5.7	55
259	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006749	7.4	54
258	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , <b>2019</b> , 9, 5151	4.7	55
257	Analysis of the evolutionary forces in an immunodominant CD8 epitope in hepatitis C virus at a population level. <i>Journal of Virology</i> , <b>2008</b> , 82, 3438-51	6.3	55
256	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> , <b>2009</b> , 106, 21242-6	11.1	53
255	Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , <b>2019</b> , 25, 206-211	49.3	52
254	Risk factors for hepatitis C virus transmission in colonial Cameroon. <i>Clinical Infectious Diseases</i> , <b>2010</b> , 51, 768-76	11.3	54
253	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil <b>2021</b> ,		48
252	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> , <b>2011</b> , 28, 1593-603	8	51
251	Evolutionary and transmission dynamics of reassortant H5N1 influenza virus in Indonesia. <i>PLoS Pathogens</i> , <b>2008</b> , 4, e1000130	7.4	50
250	The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , <b>2016</b> , 214, 556-64	6.8	50

249	Investigating the endemic transmission of the hepatitis C virus. <i>International Journal for Parasitology</i> , <b>2007</b> , 37, 839-49	4.1	51
248	Hepacivirus cross-species transmission and the origins of the hepatitis C virus. <i>Current Opinion in Virology</i> , <b>2016</b> , 16, 1-7	7.1	49
247	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23, 1742-1744	9.9	50
246	Changing epidemiology of human parvovirus 4 infection in sub-Saharan Africa. <i>Emerging Infectious Diseases</i> , <b>2010</b> , 16, 1605-7	9.9	49
245	Importation and early local transmission of COVID-19 in Brazil, 2020. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , <b>2020</b> , 62, e30	2.1	49
244	Questioning the evidence for genetic recombination in the 1918 "Spanish flu" virus. <i>Science</i> , <b>2002</b> , 296, 211 discussion 211	32.2	49
243	Evolutionary and Phylogenetic Analysis of the Hepaciviruses and Pegiviruses. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 2996-3008	3.7	47
242	Integrating phylodynamics and epidemiology to estimate transmission diversity in viral epidemics. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002876	4.8	47
241	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> , <b>2021</b> , 6, 121	4.7	49
240	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , <b>2016</b> , 8,		47
239	The Diversity and Molecular Evolution of B-Cell Receptors during Infection. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 1147-57	8	46
238	Phylogenetic clustering of hepatitis C virus among people who inject drugs in Vancouver, Canada. <i>Hepatology</i> , <b>2014</b> , 60, 1571-1580	10.9	46
237	Origin and evolution of the unique hepatitis C virus circulating recombinant form 2k/1b. <i>Journal of Virology</i> , <b>2012</b> , 86, 2212-20	6.3	46
236	Yellow fever virus maintenance in Trinidad and its dispersal throughout the Americas. <i>Journal of Virology</i> , <b>2010</b> , 84, 9967-77	6.3	44
235	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , <b>2021</b> , 6, 121	4.7	48
234	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> , <b>2004</b> , 21, 603-11	8	48
233	Genetic diversity and models of viral evolution for the hepatitis C virus. <i>FEMS Microbiology Letters</i> , <b>2002</b> , 214, 143-52	2.8	44
232	Taming the BEAST-A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , <b>2018</b> , 67, 170-174	8.2	42

231	Different epidemic potentials of the HIV-1B and C subtypes. <i>Journal of Molecular Evolution</i> , <b>2005</b> , 60, 598-605	3	43
230	Colonial history and contemporary transmission shape the genetic diversity of hepatitis C virus genotype 2 in Amsterdam. <i>Journal of Virology</i> , <b>2012</b> , 86, 7677-87	6.3	41
229	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> , <b>2010</b> , 28 Suppl 2, B39-44	3.9	40
228	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , <b>2021</b> , 184, 5179-5188.e8	54.5	39
227	Population genetic history of hepatitis C virus 1b infection in China. <i>Journal of General Virology</i> , <b>2006</b> , 87, 73-82	4.7	41
226	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , <b>2019</b> , 19, 1138-1147	24.7	40
225	A phylogenetic method for detecting positive epistasis in gene sequences and its application to RNA virus evolution. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 1724-30	8	40
224	Track Omicron <sup>®</sup> spread with molecular data. <i>Science</i> , <b>2021</b> , 374, eabn4543	32.2	41
223	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , <b>2018</b> , 172, 1160-1162	54.5	38
222	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , <b>2018</b> , 9, 2222	16.9	38
221	Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2563-2571	8	38
220	Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 970-972	9.9	39
219	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007065	4.6	36
218	A Molecular-Level Account of the Antigenic Hantaviral Surface. <i>Cell Reports</i> , <b>2016</b> , 15, 959-967	10.3	36
217	Estimating reassortment rates in co-circulating Eurasian swine influenza viruses. <i>Journal of General Virology</i> , <b>2012</b> , 93, 2326-2336	4.7	36
216	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , <b>2021</b> , 373, 889-895	32.2	36
215	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 1788-92	9.9	35
214	The evolutionary dynamics of influenza A virus adaptation to mammalian hosts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 368, 20120382	5.7	35

213	A Phylogenetic Codon Substitution Model for Antibody Lineages. <i>Genetics</i> , <b>2017</b> , 206, 417-427	3.9	36
212	HLA footprints on human immunodeficiency virus type 1 are associated with interclade polymorphisms and intraclade phylogenetic clustering. <i>Journal of Virology</i> , <b>2009</b> , 83, 4605-15	6.3	36
211	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> , <b>2021</b> , 2, e527-e535	21.6	34
210	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 671-8	9.9	34
209	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> , <b>2010</b> , 54, 129-36	3.1	34
208	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , <b>2017</b> , 7, 15216	4.7	33
207	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> , <b>2012</b> , 109, 14562-7	11.1	33
206	Explosive HIV-1 subtype B epidemics in Asia driven by geographic and risk group founder events. <i>Virology</i> , <b>2010</b> , 402, 223-7	3.5	32
205	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , <b>2021</b> , 6, 415	25.8	33
204	Evolution and dispersal of St. Louis encephalitis virus in the Americas. <i>Infection, Genetics and Evolution</i> , <b>2009</b> , 9, 709-15	4.4	32
203	Hepatitis C virus infections in the Democratic Republic of Congo exhibit a cohort effect. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 19, 386-94	4.4	30
202	Short-Sighted Virus Evolution and a Germline Hypothesis for Chronic Viral Infections. <i>Trends in Microbiology</i> , <b>2017</b> , 25, 336-348	12	31
201	Epidemiology: Sexual transmission of HIV in Africa. <i>Nature</i> , <b>2003</b> , 422, 679	47.5	32
200	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> , <b>2018</b> , 115, 1051-1056	11.1	30
199	HIV Maintains an Evolving and Dispersed Population in Multiple Tissues during Suppressive Combined Antiretroviral Therapy in Individuals with Cancer. <i>Journal of Virology</i> , <b>2016</b> , 90, 8984-93	6.3	30
198	A new evolutionary model for hepatitis C virus chronic infection. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002656	7.4	29
197	Large-scale spatial and temporal genetic diversity of feline calicivirus. <i>Journal of Virology</i> , <b>2012</b> , 86, 11356-67	6.5	31
196	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> , <b>2007</b> , 88, 1505-1518	4.7	28

195	A Bayesian statistical analysis of human T-cell lymphotropic virus evolutionary rates. <i>Infection, Genetics and Evolution</i> , <b>2005</b> , 5, 291-8	4.4	30
194	Computational and molecular analysis of conserved influenza A virus RNA secondary structures involved in infectious virion production. <i>RNA Biology</i> , <b>2016</b> , 13, 883-94	4.7	29
193	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , <b>2018</b> , 10,		30
192	Phylogenetics of H5N1 avian influenza virus in Indonesia. <i>Molecular Ecology</i> , <b>2012</b> , 21, 3062-77	5.5	27
191	A Protective Monoclonal Antibody Targets a Site of Vulnerability on the Surface of Rift Valley Fever Virus. <i>Cell Reports</i> , <b>2018</b> , 25, 3750-3758.e4	10.3	27
190	High prevalence of hepatitis C virus infection and predominance of genotype 4 in rural Gabon. <i>Journal of Medical Virology</i> , <b>2008</b> , 80, 1581-7	19.3	25
189	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , <b>2021</b> , 374, eabl9551	32.2	28
188	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> , <b>2019</b> , 116, 22664-22672	11.1	26
187	Highly Diverse Hepatitis C Strains Detected in Sub-Saharan Africa Have Unknown Susceptibility to Direct-Acting Antiviral Treatments. <i>Hepatology</i> , <b>2019</b> , 69, 1426-1441	10.9	26
186	Evolutionary epidemiology: preparing for an age of genomic plenty. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 368, 20120193	5.7	27
185	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> , <b>2007</b> , 88, 1519-1525	4.7	26
184	Characterization of Hepatitis C Virus Recombination in Cameroon by Use of Nonspecific Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 3155-64	9.4	26
183	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> , <b>2019</b> , 116, 25057-25067	11.1	25
182	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007976	7.4	25
181	Variable epidemic histories of hepatitis C virus genotype 2 infection in West Africa and Cameroon. <i>Infection, Genetics and Evolution</i> , <b>2008</b> , 8, 676-81	4.4	24
180	Exceptional Heterogeneity in Viral Evolutionary Dynamics Characterises Chronic Hepatitis C Virus Infection. <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1005894	7.4	25
179	Increased positive selection pressure in persistent (SSPE) versus acute measles virus infections. <i>Journal of General Virology</i> , <b>2002</b> , 83, 1419-1430	4.7	25
178	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , <b>2020</b> , 30, 2275-2283.e7	10.3	24

177	Crowding and the epidemic intensity of COVID-19 transmission		23
176	The generation of a simian adenoviral vectored HCV vaccine encoding genetically conserved gene segments to target multiple HCV genotypes. <i>Vaccine</i> , <b>2018</b> , 36, 313-321	3.9	24
175	A naturally protective epitope of limited variability as an influenza vaccine target. <i>Nature Communications</i> , <b>2018</b> , 9, 3859	16.9	23
174	Global disparities in SARS-CoV-2 genomic surveillance <b>2021</b> ,		22
173	Full-length characterization of hepatitis C virus subtype 3a reveals novel hypervariable regions under positive selection during acute infection. <i>Journal of Virology</i> , <b>2009</b> , 83, 11456-66	6.3	23
172	The effect of human mobility and control measures on the COVID-19 epidemic in China <b>2020</b> ,		24
171	Model selection and the molecular clock. <i>PLoS Biology</i> , <b>2006</b> , 4, e151	9.4	23
170	The mid-depth method and HIV-1: a practical approach for testing hypotheses of viral epidemic history. <i>Molecular Biology and Evolution</i> , <b>1999</b> , 16, 953-9	8	23
169	Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , <b>2018</b> , 147, e34	4.2	22
168	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 2104-2112	9.9	22
167	Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24, 1795-1805	9.9	22
166	Dynamics of immunoglobulin sequence diversity in HIV-1 infected individuals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370,	5.7	22
165	Complete genome sequencing and phylogenetic analysis of HCV isolates from China reveals a new subtype, designated 6u. <i>Journal of Medical Virology</i> , <b>2008</b> , 80, 1740-6	19.3	23
164	Estimating the date of origin of an HIV-1 circulating recombinant form. <i>Virology</i> , <b>2009</b> , 387, 229-34	3.5	22
163	Tracing the origin of Brazilian HTLV-1 as determined by analysis of host and viral genes. <i>Aids</i> , <b>2006</b> , 20, 780-2	3.4	22
162	Comparative population dynamics of mosquito-borne flaviviruses. <i>Infection, Genetics and Evolution</i> , <b>2003</b> , 3, 87-95	4.4	22
161	The recombinant origin of emerging human norovirus GII.4/2008: intra-genotypic exchange of the capsid P2 domain. <i>Journal of General Virology</i> , <b>2012</b> , 93, 817-822	4.7	21
160	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> , <b>2012</b> , 32, 675-88	7.6	21

159	A Genomic Survey of SARS-CoV-2 Reveals Multiple Introductions into Northern California without a Predominant Lineage <b>2020</b> ,		20
158	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 41, 142-145		19
157	Viral mutation and substitution: units and levels. <i>Current Opinion in Virology</i> , <b>2011</b> , 1, 430-5	7.1	19
156	Detecting natural selection in RNA virus populations using sequence summary statistics. <i>Infection, Genetics and Evolution</i> , <b>2010</b> , 10, 421-30	4.4	20
155	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> ,	47.5	21
154	An expanded taxonomy of hepatitis C virus genotype 6: Characterization of 22 new full-length viral genomes. <i>Virology</i> , <b>2015</b> , 476, 355-363	3.5	19
153	Antibody responses to avian influenza viruses in wild birds broaden with age. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2016</b> , 283,	4.3	18
152	Transmission of hepatitis C virus infection among younger and older people who inject drugs in Vancouver, Canada. <i>Journal of Hepatology</i> , <b>2016</b> , 64, 1247-55	3.1	18
151	Genome Sequence of a Candidate World Health Organization Reference Strain of Zika Virus for Nucleic Acid Testing. <i>Genome Announcements</i> , <b>2016</b> , 4,		18
150	Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 18, 367-78	4.4	19
149	Unexpected maintenance of hepatitis C viral diversity following liver transplantation. <i>Journal of Virology</i> , <b>2012</b> , 86, 8432-9	6.3	18
148	Intercontinental dispersal of HIV-1 subtype B associated with transmission among men who have sex with men in Japan. <i>Journal of Virology</i> , <b>2014</b> , 88, 9864-76	6.3	18
147	Parallel molecular evolution and adaptation in viruses. <i>Current Opinion in Virology</i> , <b>2019</b> , 34, 90-96	7.1	18
146	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007231	4.6	19
145	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , <b>2018</b> , 14, e1007392	7.4	17
144	Human parvovirus 4 infection, Cameroon. <i>Emerging Infectious Diseases</i> , <b>2012</b> , 18, 680-3	9.9	18
143	Measuring the Temporal Structure in Serially-Sampled Phylogenies. <i>Methods in Ecology and Evolution</i> , <b>2011</b> , 2, 437-445	7.5	17
142	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> , <b>2010</b> , 50, 1505-11	2.8	17



141	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> , <b>2006</b> , 13, 121-30	3.3	18
140	Epidemic History and Iatrogenic Transmission of Blood-borne Viruses in Mid-20th Century Kinshasa. <i>Journal of Infectious Diseases</i> , <b>2016</b> , 214, 353-60	6.8	16
139	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , <b>2019</b> , 25, 784-787	9.9	16
138	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> , <b>2013</b> , 94, 1780-1790	4.7	16
137	Eight novel hepatitis C virus genomes reveal the changing taxonomic structure of genotype 6. <i>Journal of General Virology</i> , <b>2013</b> , 94, 76-80	4.7	15
136	The ecology and age structure of a highly pathogenic avian influenza virus outbreak in wild mute swans. <i>Parasitology</i> , <b>2012</b> , 139, 1914-23	2.6	15
135	Genomic Surveillance of Yellow Fever Virus Epizootic in Sã Paulo, Brazil, 2016 - 2018. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008699	7.4	15
134	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> , <b>2020</b> , 117, 5949-5954	11.1	15
133	Role of HIV-specific CD8 T cells in pediatric HIV cure strategies after widespread early viral escape. <i>Journal of Experimental Medicine</i> , <b>2017</b> , 214, 3239-3261	16.2	14
132	Serial interval distribution of SARS-CoV-2 infection in Brazil. <i>Journal of Travel Medicine</i> , <b>2021</b> , 28,	12.5	15
131	Vaccine nationalism and the dynamics and control of SARS-CoV-2. <i>Science</i> , <b>2021</b> , 373, eabj7364	32.2	16
130	COVID-19 herd immunity in the Brazilian Amazon		15
129	Robust Design for Coalescent Model Inference. <i>Systematic Biology</i> , <b>2019</b> , 68, 730-743	8.2	14
128	Evolutionary analysis of hepatitis C virus gene sequences from 1953. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 368, 20130168	5.7	15
127	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> , <b>2010</b> , 10, 1075-84	4.4	14
126	Reducing HIV infection in people who inject drugs is impossible without targeting recently-infected subjects. <i>Aids</i> , <b>2016</b> , 30, 2885-2890	3.4	13
125	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> , <b>2019</b> , 374, 20180259	5.7	13
124	Evolution and Transmission of Respiratory Syncytial Group A (RSV-A) Viruses in Guangdong, China 2008-2015. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1263	5.5	13

123	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of LBeck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2018</b> , 285,	4.3	14
122	Occurrence and reassortment of avian influenza A (H7N9) viruses derived from coinfecting birds in China. <i>Journal of Virology</i> , <b>2014</b> , 88, 13344-51	6.3	13
121	Chronology of the HIV-1 CRF07_BC expansion in East Asia. <i>Aids</i> , <b>2008</b> , 22, 156-8	3.4	14
120	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> , <b>2015</b> , 96, 1411-1422	4.7	12
119	Cross-border spread, lineage displacement and evolutionary rate estimation of rabies virus in Yunnan Province, China. <i>Virology Journal</i> , <b>2017</b> , 14, 102	5.9	12
118	Viral phylogeny in court: the unusual case of the Valencian anesthetist. <i>BMC Biology</i> , <b>2013</b> , 11, 83	7	13
117	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> , <b>2017</b> , 91,	6.3	12
116	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa		12
115	Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , <b>2018</b> , 15, 7	3.4	11
114	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 220, 233-243	6.8	11
113	Where do all the subtypes go? Temporal dynamics of H8-H12 influenza A viruses in waterfowl. <i>Virus Evolution</i> , <b>2018</b> , 4, vey025	3.6	11
112	Viral evolution explains the associations among hepatitis C virus genotype, clinical outcomes, and human genetic variation. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 20, 418-21	4.4	10
111	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> , <b>2010</b> , 53, 547-50	3.1	11
110	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> , <b>2014</b> , 111, 10767-72	11.1	10
109	Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 2414-2429	8	10
108	Genomic detection of a virus lineage replacement event of dengue virus serotype 2 in Brazil, 2019. <i>Memorias Do Instituto Oswaldo Cruz</i> , <b>2020</b> , 115, e190423	2.5	10
107	Exact Bayesian inference for phylogenetic birth-death models. <i>Bioinformatics</i> , <b>2018</b> , 34, 3638-3645	6.8	9
106	Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, e2436-e2443	11.3	8

105	Optimal point process filtering and estimation of the coalescent process. <i>Journal of Theoretical Biology</i> , <b>2017</b> , 421, 153-167	2.3	9
104	Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK		10
103	Coalescent Inference Using Serially Sampled, High-Throughput Sequencing Data from Intra-host HIV Infection. <i>Genetics</i> , <b>2016</b> , 202, 1449-72	3.9	8
102	Westward Spread of Highly Pathogenic Avian Influenza A(H7N9) Virus among Humans, China. <i>Emerging Infectious Diseases</i> , <b>2018</b> , 24, 1095-1098	9.9	8
101	Evolution and Diversity of the Human Leukocyte Antigen(HLA). <i>Evolution, Medicine and Public Health</i> , <b>2015</b> , 2015, 1	2.9	7
100	High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 219, 1722-1729	6.8	8
99	Generation of neutralizing antibodies and divergence of SIVmac239 in cynomolgus macaques following short-term early antiretroviral therapy. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1001084	7.4	8
98	Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , <b>2020</b> , 11, 5511	16.9	8
97	Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes <b>2021</b> ,		6
96	Phylogenetic analysis of migration, differentiation, and class switching in B cells		8
95	The multifurcating skyline plot. <i>Virus Evolution</i> , <b>2019</b> , 5, vez031	3.6	7
94	Metagenomic Next-Generation Sequencing of the 2014 Ebola Virus Disease Outbreak in the Democratic Republic of the Congo. <i>Journal of Clinical Microbiology</i> , <b>2019</b> , 57,	9.4	7
93	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , <b>2020</b> , 11, 5620	16.9	6
92	Transmission of hepatitis C virus in HIV-positive and PrEP-using MSM in England. <i>Journal of Viral Hepatitis</i> , <b>2020</b> , 27, 721-730	3.3	6
91	Infection frequency of hepatitis C virus and IL28B haplotypes in Papua New Guinea, Fiji, and Kiribati. <i>PLoS ONE</i> , <b>2013</b> , 8, e66749	3.6	7
90	Genetic diversity and phenotypic associations of feline caliciviruses from cats in Switzerland. <i>Journal of General Virology</i> , <b>2016</b> , 97, 3253-3266	4.7	7
89	Towards an understanding of the avian virome. <i>Journal of General Virology</i> , <b>2020</b> , 101, 785-790	4.7	8
88	Host specificity and species jumps in fish-parasite systems		5

87	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.3	6
86	Faster Adaptation in Smaller Populations: Counterintuitive Evolution of HIV during Childhood Infection. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004694	4.8	6
85	Dynamics of conflict during the Ebola outbreak in the Democratic Republic of the Congo 2018-2019. <i>BMC Medicine</i> , <b>2020</b> , 18, 113	11.1	6
84	Phylodynamics for cell biologists. <i>Science</i> , <b>2021</b> , 371,	32.2	7
83	Venue-Based Networks May Underpin HCV Transmissions amongst HIV-Infected Gay and Bisexual Men. <i>PLoS ONE</i> , <b>2016</b> , 11, e0162002	3.6	6
82	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples		6
81	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
80	Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China		6
79	The Effect of RNA Substitution Models on Viroid and RNA Virus Phylogenies. <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 657-666	3.7	5
78	Conserved secondary structures predicted within the 5' packaging signal region of influenza A virus PB2 segment. <i>Meta Gene</i> , <b>2018</b> , 15, 75-79	0.7	5
77	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.3	5
76	Phylodynamics Helps to Evaluate the Impact of an HIV Prevention Intervention. <i>Viruses</i> , <b>2020</b> , 12,	6	7
75	Natural selection and adaptation of molecular sequences407-418		4
74	Routes for COVID-19 importation in Brazil		5
73	Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR		4
72	Population Genetics of HIV: Parameter Estimation Using Genealogy-based Methods <b>2002</b> , 217-252		5
71	Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences.. <i>BMC Genomics</i> , <b>2022</b> , 23, 121	4.3	5
70	Genomic surveillance of avian-origin influenza A viruses causing human disease. <i>Genome Medicine</i> , <b>2018</b> , 10, 50	14	5

69	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> , <b>2015</b> , 370,	5.7	4
68	Elevated caspase-3 expression and T-cell activation in elite suppressors. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , <b>2010</b> , 54, 110-1	3.1	4
67	Evolutionary Analyses of Base-Pairing Interactions in DNA and RNA Secondary Structures. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 576-592	8	4
66	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0007897	4.6	2
65	First Complete Genome Sequences of Zika Virus Isolated from Febrile Patient Sera in Ecuador. <i>Genome Announcements</i> , <b>2017</b> , 5,		4
64	Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing. <i>Journal of Infection</i> , <b>2021</b> , 82, e44-e48	18.5	4
63	A mechanistic evolutionary model explains the time-dependent pattern of substitution rates in viruses. <i>Current Biology</i> , <b>2021</b> , 31, 4689-4696.e5	6.1	5
62	Are skyline plot-based demographic estimates overly dependent on smoothing prior assumptions?. <i>Systematic Biology</i> , <b>2021</b> ,	8.2	4
61	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016–2018		4
60	Monitoring key epidemiological parameters of SARS-CoV-2 transmission. <i>Nature Medicine</i> , <b>2021</b> , 27, 1854-1855	4.9	4
59	Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza.. <i>Molecular Biology and Evolution</i> , <b>2022</b> ,	8	4
58	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.. <i>Nature Communications</i> , <b>2022</b> , 13, 751	16.9	4
57	Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages		5
56	Hepatitis C virus genotype 4 in England: diversity and demographic associations. <i>Journal of Medical Virology</i> , <b>2015</b> , 87, 417-23	19.3	3
55	HIV-1 epidemic in Russia: an evolutionary epidemiology analysis. <i>Lancet, The</i> , <b>2014</b> , 383, S71	36.2	3
54	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission		3
53	Vaccine nationalism and the dynamics and control of SARS-CoV-2		3
52	Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant		3

51	Emergence and widespread circulation of a recombinant SARS-CoV-2 lineage in North America		3
50	Progress and challenges in virus genomic epidemiology. <i>Trends in Parasitology</i> , <b>2021</b> , 37, 1038-1049	6.2	3
49	Reverse immunodynamics: a new method for identifying targets of protective immunity. <i>Scientific Reports</i> , <b>2019</b> , 9, 2164	4.7	2
48	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , <b>2021</b> , 7, veab051.6	3.6	2
47	Genomic epidemiology of early SARS-CoV-2 transmission dynamics in Gujarat, India		2
46	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> , <b>2021</b> , 14, 100259	4.9	2
45	Relax, Keep Walking - A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 3486-3493	8	2
44	Partial immunity and SARS-CoV-2 mutations-Response. <i>Science</i> , <b>2021</b> , 372, 354-355	32.2	2
43	"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> , <b>2021</b> , 15, e0009387	4.6	4
42	Identification of site-specific evolutionary trajectories shared across human betacoronaviruses <b>2021</b> ,		2
41	Parallel Evolution in the Emergence of Highly Pathogenic Avian Influenza A Viruses		2
40	The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK		1
39	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. <b>2021</b> ,		2
38	Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. <i>ELife</i> , <b>2021</b> , 10,	8.6	2
37	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. <b>2021</b> ,		2
36	Are skyline plot-based demographic estimates overly dependent on smoothing prior assumptions?		2
35	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination		2
34	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2

33	Virus genomics and evolution: the transformative effect of new technologies and multidisciplinary collaboration on virus research and outbreak management. <i>Genome Biology</i> , <b>2016</b> , 17, 159	17.7	1
32	Human B cell lineages engaged by germinal centers following influenza vaccination are measurably evolving		1
31	Purifying selection determines the short-term time dependency of evolutionary rates in SARS-CoV-2 and pH1N1 influenza		1
30	Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences		1
29	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , <b>2021</b> , 7, veab036	3.6	1
28	Prisoner of War dynamics explains the time-dependent pattern of substitution rates in viruses		2
27	Paleovirology reveals the macroevolution of complex retroviruses. <i>Retrovirology</i> , <b>2009</b> , 6,	3.4	1
26	Emergence of the Zika virus Asian lineage in Angola		1
25	The evolutionary dynamics of Oropouche Virus (OROV) in South America		1
24	Oropouche virus cases identified in Ecuador using an optimised rRT-PCR informed by metagenomic sequencing		1
23	Malaria elimination on Hainan Island despite climate change. <i>Communications Medicine</i> , <b>2022</b> , 2,		1
22	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak		1
21	Jointly inferring the dynamics of population size and sampling intensity from molecular sequences		1
20	Coalescent inference using serially sampled, high-throughput sequencing data from intra-host HIV infection		1
19	The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , <b>2019</b> , 35, 155-163	1.5	0
18	Global prevalence and phylogeny of hepatitis B virus (HBV) drug and vaccine resistance mutations. <i>Journal of Viral Hepatitis</i> , <b>2021</b> , 28, 1110-1120	3.3	0
17	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , <b>2022</b> , 13, 1012	16.9	0
16	The relationship between rising temperatures and malaria incidence in Hainan, China, from 1984 to 2010: a longitudinal cohort study.. <i>Lancet Planetary Health</i> , <b>2022</b> , 6, e350-e358	9	0

15	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> , <b>2022</b> , 16, e0010019	4.6	○
14	A computationally tractable birth-death model that combines phylogenetic and epidemiological data.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009805	4.8	○
13	Phylogenetic analysis of migration, differentiation, and class switching in B cells.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009885	4.8	○
12	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017-2019.. <i>PLoS Neglected Tropical Diseases</i> , <b>2022</b> , 16, e0010255	4.6	○
11	The evolutionary epidemiology of the hepatitis C virus	4.50-4.72	
10	Sequencing Methods Developed for Hepatitis C Identifies a New Virus, Human Heppegivirus 1, in Patients with Advanced Cirrhosis. <i>Journal of Hepatology</i> , <b>2016</b> , 64, S414-S415	3.1	
9	P1191 HETEROGENEOUS EVOLUTIONARY DYNAMICS OF CHRONIC HEPATITIS-C INFECTION PREDICT LONG-TERM PERSISTENCE OF VIRUS THROUGH TREATMENT. <i>Journal of Hepatology</i> , <b>2014</b> , 60, S483	3.1	
8	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> , <b>2008</b> , 12, e58-e59	5.2	
7	A review of models applied to the geographic spread of Zika virus. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , <b>2021</b> , 115, 956-964	2	
6	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. <i>PLoS Computational Biology</i> , <b>2005</b> , preprint, e29	4.8	
5	Population Genetic Modeling of Viruses	2016, 293-328	
4	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing	2020, 14, e0007897	
3	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing	2020, 14, e0007897	
2	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing	2020, 14, e0007897	
1	Understanding Sabiá virus infections (Brazilian mammarenavirus).. <i>Travel Medicine and Infectious Disease</i> , <b>2022</b> , 48, 102351	8.2	