

Oliver G. Pybus

List of Publications by Year in descending order

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377
papers

58,727
citations

1614

105
h-index

1599

216
g-index

475
all docs

475
docs citations

475
times ranked

55518
citing authors

#	ARTICLE	IF	CITATIONS
1	Bayesian Coalescent Inference of Past Population Dynamics from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2005, 22, 1185-1192.	8.9	2,782
2	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020, 5, 1403-1407.	13.3	2,291
3	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020, 368, 493-497.	12.6	2,168
4	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	27.8	1,870
5	Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. <i>Science</i> , 2009, 324, 1557-1561.	12.6	1,665
6	Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). <i>Virus Evolution</i> , 2016, 2, vew007.	4.9	1,638
7	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.	12.6	1,554
8	Global distribution and prevalence of hepatitis C virus genotypes. <i>Hepatology</i> , 2015, 61, 77-87.	7.3	1,293
9	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	27.8	1,210
10	Unifying the Epidemiological and Evolutionary Dynamics of Pathogens. <i>Science</i> , 2004, 303, 327-332.	12.6	1,159
11	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	12.6	1,125
12	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.	12.0	898
13	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016, 352, 345-349.	12.6	877
14	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
15	The genomic and epidemiological dynamics of human influenza A virus. <i>Nature</i> , 2008, 453, 615-619.	27.8	824
16	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	4.9	774
17	Testing macroevolutionary models using incomplete molecular phylogenies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 2267-2272.	2.6	723
18	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet</i> , The, 2021, 397, 452-455.	13.7	720

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19	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.	13.3	699
20	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> , The, 2022, 22, 35-42.	9.1	612
21	Rise and Fall of the Beringian Steppe Bison. <i>Science</i> , 2004, 306, 1561-1565.	12.6	601
22	Rates of Molecular Evolution in RNA Viruses: A Quantitative Phylogenetic Analysis. <i>Journal of Molecular Evolution</i> , 2002, 54, 156-165.	1.8	596
23	Evolutionary analysis of the dynamics of viral infectious disease. <i>Nature Reviews Genetics</i> , 2009, 10, 540-550.	16.3	526
24	The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014, 346, 56-61.	12.6	515
25	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	27.8	515
26	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. <i>Nature Medicine</i> , 2022, 28, 1785-1790.	30.7	456
27	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
28	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013, 502, 241-244.	27.8	429
29	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , 2021, 371, 288-292.	12.6	412
30	Correlating viral phenotypes with phylogeny: Accounting for phylogenetic uncertainty. <i>Infection, Genetics and Evolution</i> , 2008, 8, 239-246.	2.3	408
31	Adaptation of HIV-1 to human leukocyte antigen class I. <i>Nature</i> , 2009, 458, 641-645.	27.8	408
32	The Epidemic Behavior of the Hepatitis C Virus. <i>Science</i> , 2001, 292, 2323-2325.	12.6	405
33	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.	6.4	375
34	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, 983-991.	2.2	374
35	Measurably evolving populations. <i>Trends in Ecology and Evolution</i> , 2003, 18, 481-488.	8.7	371
36	Emergence and potential for spread of Chikungunya virus in Brazil. <i>BMC Medicine</i> , 2015, 13, 102.	5.5	369

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37	Role for migratory wild birds in the global spread of avian influenza H5N8. <i>Science</i> , 2016, 354, 213-217.	12.6	362
38	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	13.3	352
39	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
40	An Integrated Framework for the Inference of Viral Population History From Reconstructed Genealogies. <i>Genetics</i> , 2000, 155, 1429-1437.	2.9	346
41	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
42	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. <i>PLoS Pathogens</i> , 2014, 10, e1003932.	4.7	330
43	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, 6588-6592.	7.1	315
44	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	13.3	305
45	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020, 11, 2688.	12.8	304
46	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.	12.8	304
47	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
48	Evidence of a Large, International Network of HCV Transmission in HIV-Positive Men Who Have Sex With Men. <i>Gastroenterology</i> , 2009, 136, 1609-1617.	1.3	285
49	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020, 4, 856-865.	12.0	281
50	Epidemiological data from the COVID-19 outbreak, real-time case information. <i>Scientific Data</i> , 2020, 7, 106.	5.3	280
51	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	12.6	279
52	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	12.6	253
53	Exploring the Demographic History of DNA Sequences Using the Generalized Skyline Plot. <i>Molecular Biology and Evolution</i> , 2001, 18, 2298-2305.	8.9	244
54	Editorial: A home for virology, ecology, epidemiology, and evolutionary biology. <i>Virus Evolution</i> , 2015, 1, 1-3.	4.9	242

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55	Measurably evolving pathogens in the genomic era. <i>Trends in Ecology and Evolution</i> , 2015, 30, 306-313.	8.7	241
56	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	28.9	236
57	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	7.3	232
58	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, 15066-15071.	7.1	226
59	The Epidemiology and Iatrogenic Transmission of Hepatitis C Virus in Egypt: A Bayesian Coalescent Approach. <i>Molecular Biology and Evolution</i> , 2003, 20, 381-387.	8.9	225
60	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, 4425-4429.	7.1	225
61	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021, 6, 821-823.	13.3	221
62	Long-term evolution and transmission dynamics of swine influenza A virus. <i>Nature</i> , 2011, 473, 519-522.	27.8	219
63	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, 3339-3350.	3.4	211
64	Open access epidemiological data from the COVID-19 outbreak. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 534.	9.1	205
65	Crowding and the shape of COVID-19 epidemics. <i>Nature Medicine</i> , 2020, 26, 1829-1834.	30.7	204
66	Host Switch Leads to Emergence of Plasmodium vivax Malaria in Humans. <i>Molecular Biology and Evolution</i> , 2005, 22, 1686-1693.	8.9	199
67	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, 6261-6265.	7.1	193
68	Dominant influence of an HLA-B27 restricted CD8+ T cell response in mediating HCV clearance and evolution. <i>Hepatology</i> , 2006, 43, 563-572.	7.3	191
69	Genetic History of Hepatitis C Virus in East Asia. <i>Journal of Virology</i> , 2009, 83, 1071-1082.	3.4	190
70	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> , The, 2017, 17, 330-338.	9.1	185
71	Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes. <i>Science</i> , 2021, 372, 363-370.	12.6	185
72	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, 20362-20367.	7.1	183

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73	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016, 8, 97.	8.2	182
74	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182
75	The Global Spread of Hepatitis C Virus 1a and 1b: A Phylodynamic and Phylogeographic Analysis. <i>PLoS Medicine</i> , 2009, 6, e1000198.	8.4	177
76	HIV evolutionary dynamics within and among hosts. <i>AIDS Reviews</i> , 2006, 8, 125-40.	1.0	176
77	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, 1793-1802.	2.2	171
78	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, 19860-19865.	7.1	170
79	Inference of Viral Evolutionary Rates from Molecular Sequences. <i>Advances in Parasitology</i> , 2003, 54, 331-358.	3.2	161
80	Synonymous Substitution Rates Predict HIV Disease Progression as a Result of Underlying Replication Dynamics. <i>PLoS Computational Biology</i> , 2007, 3, e29.	3.2	152
81	The Genomic Rate of Molecular Adaptation of the Human Influenza A Virus. <i>Molecular Biology and Evolution</i> , 2011, 28, 2443-2451.	8.9	150
82	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.	6.1	149
83	Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013. <i>Journal of Virology</i> , 2015, 89, 9920-9931.	3.4	148
84	Macroevolution of Complex Retroviruses. <i>Science</i> , 2009, 325, 1512-1512.	12.6	146
85	Phylogeny and the origin of HIV-1. <i>Nature</i> , 2001, 410, 1047-1048.	27.8	143
86	The hepatitis C virus epidemic among injecting drug users. <i>Infection, Genetics and Evolution</i> , 2005, 5, 131-139.	2.3	143
87	A standardized framework for accurate, high-throughput genotyping of recombinant and non-recombinant viral sequences. <i>Nucleic Acids Research</i> , 2009, 37, W634-W642.	14.5	142
88	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
89	Disease-associated XMRV sequences are consistent with laboratory contamination. <i>Retrovirology</i> , 2010, 7, 111.	2.0	141
90	The evolution of genome compression and genomic novelty in RNA viruses. <i>Genome Research</i> , 2007, 17, 1496-1504.	5.5	139

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91	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, 9206-9215.	3.4	138
92	Pacing a small cage: mutation and RNA viruses. <i>Trends in Ecology and Evolution</i> , 2008, 23, 188-193.	8.7	136
93	Phylogenetic Evidence for Deleterious Mutation Load in RNA Viruses and Its Contribution to Viral Evolution. <i>Molecular Biology and Evolution</i> , 2007, 24, 845-852.	8.9	133
94	Full-Genome Deep Sequencing and Phylogenetic Analysis of Novel Human Betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013, 19, 736-42B.	4.3	131
95	Eight challenges in phylodynamic inference. <i>Epidemics</i> , 2015, 10, 88-92.	3.0	131
96	Defining HIV-1 transmission clusters based on sequence data. <i>Aids</i> , 2017, 31, 1211-1222.	2.2	131
97	Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020, 94, .	3.4	129
98	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.	1.8	129
99	GENIE: estimating demographic history from molecular phylogenies. <i>Bioinformatics</i> , 2002, 18, 1404-1405.	4.1	126
100	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016, 32, 3204-3206.	4.1	124
101	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
102	The mode and tempo of hepatitis C virus evolution within and among hosts. <i>BMC Evolutionary Biology</i> , 2011, 11, 131.	3.2	122
103	A Bayesian Phylogenetic Method to Estimate Unknown Sequence Ages. <i>Molecular Biology and Evolution</i> , 2011, 28, 879-887.	8.9	119
104	Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	119
105	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> , 2006, 16, 401-413.	3.9	118
106	Invasion and Maintenance of Dengue Virus Type 2 and Type 4 in the Americas. <i>Journal of Virology</i> , 2005, 79, 14680-14687.	3.4	116
107	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.	1.8	115
108	HIV-1 and HCV sequences from Libyan outbreak. <i>Nature</i> , 2006, 444, 836-837.	27.8	114

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109	Tracing the HIV-1 subtype B mobility in Europe: a phylogeographic approach. <i>Retrovirology</i> , 2009, 6, 49.	2.0	114
110	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	13.3	114
111	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, 6359-6366.	3.4	112
112	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
113	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, 537-549.	3.9	109
114	ANCIENT URBANIZATION PREDICTS GENETIC RESISTANCE TO TUBERCULOSIS. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 842-848.	2.3	108
115	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.	2.5	107
116	The Molecular Population Genetics of HIV-1 Group O. <i>Genetics</i> , 2004, 167, 1059-1068.	2.9	105
117	JC Virus Evolution and Its Association with Human Populations. <i>Journal of Virology</i> , 2006, 80, 9928-9933.	3.4	105
118	Phylogeography and Population Dynamics of Dengue Viruses in the Americas. <i>Molecular Biology and Evolution</i> , 2012, 29, 1533-1543.	8.9	105
119	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	4.9	105
120	Track Omicron™s spread with molecular data. <i>Science</i> , 2021, 374, 1454-1455.	12.6	103
121	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.	2.9	102
122	Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. <i>Journal of Virology</i> , 2012, 86, 11-18.	3.4	101
123	Impact of HIV on Host-Virus Interactions during Early Hepatitis C Virus Infection. <i>Journal of Infectious Diseases</i> , 2008, 197, 1558-1566.	4.0	98
124	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, 7711-7716.	7.1	96
125	Virus evolution and transmission in an ever more connected world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142878.	2.6	96
126	Explaining the geographic spread of emerging epidemics: a framework for comparing viral phylogenies and environmental landscape data. <i>BMC Bioinformatics</i> , 2016, 17, 82.	2.6	94

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127	Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019, 25, 206-211.	30.7	94
128	Epidemic Dynamics Revealed in Dengue Evolution. <i>Molecular Biology and Evolution</i> , 2010, 27, 811-818.	8.9	92
129	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</i> , The, 2021, 2, e527-e535.	7.3	92
130	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, 9704-9709.	7.1	90
131	Phylogeography and molecular epidemiology of hepatitis C virus genotype 2 in Africa. <i>Journal of General Virology</i> , 2009, 90, 2086-2096.	2.9	89
132	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , 2019, 9, 5151.	3.3	89
133	Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005694.	3.0	86
134	The evolutionary dynamics of endogenous retroviruses. <i>Trends in Microbiology</i> , 2005, 13, 463-468.	7.7	84
135	Evolutionary and molecular analysis of the emergent severe fever with thrombocytopenia syndrome virus. <i>Epidemics</i> , 2013, 5, 1-10.	3.0	84
136	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, 855-866.	4.0	82
137	A reversal of fortunes: climate change "winners" and "losers" in Antarctic Peninsula penguins. <i>Scientific Reports</i> , 2014, 4, 5024.	3.3	82
138	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.	11.0	82
139	High-Resolution Phylogenetic Analysis of Hepatitis C Virus Adaptation and Its Relationship to Disease Progression. <i>Journal of Virology</i> , 2004, 78, 3447-3454.	3.4	81
140	Phylogenetic Surveillance of Viral Genetic Diversity and the Evolving Molecular Epidemiology of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2007, 81, 13050-13056.	3.4	81
141	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, 1593-1603.	8.9	81
142	Vaccine nationalism and the dynamics and control of SARS-CoV-2. <i>Science</i> , 2021, 373, eabj7364.	12.6	80
143	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.	1.1	80
144	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017, 6, .	6.0	80

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145	Taming the BEAST—A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	5.6	79
146	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017, 13, e1006749.	4.7	78
147	Investigating the Origin and Spread of Hepatitis C Virus Genotype 5a. <i>Journal of Virology</i> , 2006, 80, 4220-4226.	3.4	77
148	New Inferences from Tree Shape: Numbers of Missing Taxa and Population Growth Rates. <i>Systematic Biology</i> , 2002, 51, 881-888.	5.6	76
149	Viral Gene Sequences Reveal the Variable History of Hepatitis C Virus Infection among Countries. <i>Journal of Infectious Diseases</i> , 2004, 190, 1098-1108.	4.0	76
150	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, 267-277.	2.3	76
151	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	3.0	75
152	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, 10289-10296.	3.4	73
153	The Diversity and Molecular Evolution of B-Cell Receptors during Infection. <i>Molecular Biology and Evolution</i> , 2016, 33, 1147-1157.	8.9	72
154	Phylogenetic analysis of the dissemination of HIV-1 CRF01_AE in Vietnam. <i>Virology</i> , 2009, 391, 51-56.	2.4	71
155	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.	7.1	71
156	PHYLOGENY, NICHES, AND RELATIVE ABUNDANCE IN NATURAL COMMUNITIES. <i>Ecology</i> , 2008, 89, 962-970.	3.2	70
157	Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. <i>Nature Reviews Genetics</i> , 2022, 23, 547-562.	16.3	70
158	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017, 23, 1742-1744.	4.3	69
159	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.	2.3	68
160	Increasing Prevalence of HIV-1 Subtype A in Greece: Estimating Epidemic History and Origin. <i>Journal of Infectious Diseases</i> , 2007, 196, 1167-1176.	4.0	68
161	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.	2.0	68
162	Investigating the endemic transmission of the hepatitis C virus. <i>International Journal for Parasitology</i> , 2007, 37, 839-849.	3.1	66

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