

Oliver G. Pybus

List of Publications by Year in descending order

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Version: 2024-02-01

374
papers

58,727
citations

1877

105
h-index

1834

216
g-index

475
all docs

475
docs citations

475
times ranked

60226
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	4.6	612
2	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, 39, .	3.5	42
3	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.	5.8	304
4	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.	1.3	19
5	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	13.7	1,210
6	Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences. <i>BMC Genomics</i> , 2022, 23, 121.	1.2	60
7	A computationally tractable birth-death model that combines phylogenetic and epidemiological data. <i>PLoS Computational Biology</i> , 2022, 18, e1009805.	1.5	7
8	Malaria elimination on Hainan Island despite climate change. <i>Communications Medicine</i> , 2022, 2, .	1.9	5
9	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	5.8	27
10	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	5.8	10
11	The relationship between rising temperatures and malaria incidence in Hainan, China, from 1984 to 2010: a longitudinal cohort study. <i>Lancet Planetary Health</i> , The, 2022, 6, e350-e358.	5.1	15
12	Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India. <i>Emerging Infectious Diseases</i> , 2022, 28, 751-758.	2.0	4
13	Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. <i>Nature Reviews Genetics</i> , 2022, 23, 547-562.	7.7	70
14	Phylogenetic analysis of migration, differentiation, and class switching in B cells. <i>PLoS Computational Biology</i> , 2022, 18, e1009885.	1.5	40
15	Understanding Sabiã virus infections (Brazilian mammarenavirus). <i>Travel Medicine and Infectious Disease</i> , 2022, 48, 102351.	1.5	7
16	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.	1.3	9
17	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. <i>Nature Medicine</i> , 2022, 28, 1785-1790.	15.2	456
18	SARS-CoV-2 Omicron is an immune escape variant with an altered cell entry pathway. <i>Nature Microbiology</i> , 2022, 7, 1161-1179.	5.9	352

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19	Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , 2021, 73, e2436-e2443.	2.9	40
20	Serial interval distribution of SARS-CoV-2 infection in Brazil. <i>Journal of Travel Medicine</i> , 2021, 28, .	1.4	32
21	Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing. <i>Journal of Infection</i> , 2021, 82, e44-e48.	1.7	7
22	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	13.5	843
23	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , 2021, 371, 288-292.	6.0	412
24	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021, 6, 415-415.	5.9	65
25	Phylodynamics for cell biologists. <i>Science</i> , 2021, 371, .	6.0	51
26	Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. <i>Virus Evolution</i> , 2021, 7, veab036.	2.2	11
27	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	6.0	335
28	Relax, Keep Walking â€” A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493.	3.5	31
29	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.	0.7	4
30	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet, The</i> , 2021, 397, 452-455.	6.3	720
31	Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 970-972.	2.0	54
32	Partial immunity and SARS-CoV-2 mutationsâ€™Response. <i>Science</i> , 2021, 372, 354-355.	6.0	2
33	â€œKankashaâ€ 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.	1.3	13
34	Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes. <i>Science</i> , 2021, 372, 363-370.	6.0	185
35	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	6.0	1,125
36	Are Skyline Plot-Based Demographic Estimates Overly Dependent on Smoothing Prior Assumptions?. <i>Systematic Biology</i> , 2021, 71, 121-138.	2.7	10

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37	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. Wellcome Open Research, 2021, 6, 121.	0.9	115
38	Global prevalence and phylogeny of hepatitis B virus (HBV) drug and vaccine resistance mutations. Journal of Viral Hepatitis, 2021, 28, 1110-1120.	1.0	12
39	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. Nature Microbiology, 2021, 6, 821-823.	5.9	221
40	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. Virus Evolution, 2021, 7, veab051.	2.2	14
41	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	2.9	375
42	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. Science, 2021, 373, 889-895.	6.0	142
43	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. Virus Evolution, 2021, 7, veab064.	2.2	774
44	Vaccine nationalism and the dynamics and control of SARS-CoV-2. Science, 2021, 373, eabj7364.	6.0	80
45	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. Wellcome Open Research, 2021, 6, 121.	0.9	129
46	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. Cell, 2021, 184, 5179-5188.e8.	13.5	182
47	A mechanistic evolutionary model explains the time-dependent pattern of substitution rates in viruses. Current Biology, 2021, 31, 4689-4696.e5.	1.8	30
48	Assessing the impact of COVID-19 border restrictions on dengue transmission in Yunnan Province, China: an observational epidemiological and phylogenetic analysis. The Lancet Regional Health - Western Pacific, 2021, 14, 100259.	1.3	11
49	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. Lancet Microbe, The, 2021, 2, e527-e535.	3.4	92
50	Progress and challenges in virus genomic epidemiology. Trends in Parasitology, 2021, 37, 1038-1049.	1.5	45
51	Monitoring key epidemiological parameters of SARS-CoV-2 transmission. Nature Medicine, 2021, 27, 1854-1855.	15.2	28
52	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	6.0	111
53	Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. ELife, 2021, 10, .	2.8	28
54	Track Omicron™s spread with molecular data. Science, 2021, 374, 1454-1455.	6.0	103

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55	Evolutionary Analyses of Base-Pairing Interactions in DNA and RNA Secondary Structures. <i>Molecular Biology and Evolution</i> , 2020, 37, 576-592.	3.5	6
56	Crowding and the shape of COVID-19 epidemics. <i>Nature Medicine</i> , 2020, 26, 1829-1834.	15.2	204
57	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020, 5, 1403-1407.	5.9	2,291
58	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	5.8	35
59	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	2.1	39
60	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	6.0	454
61	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020, 4, 856-865.	6.2	281
62	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.	2.7	149
63	Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , 2020, 11, 5511.	5.8	23
64	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	13.5	236
65	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020, 11, 2688.	5.8	304
66	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	3.4	232
67	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
68	Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , 2020, 27, .	1.4	119
69	Epidemiological data from the COVID-19 outbreak, real-time case information. <i>Scientific Data</i> , 2020, 7, 106.	2.4	280
70	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020, 368, 493-497.	6.0	2,168
71	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.	6.0	1,554
72	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.	3.3	43

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73	Transmission of hepatitis C virus in HIV-positive and PrEP-using MSM in England. <i>Journal of Viral Hepatitis</i> , 2020, 27, 721-730.	1.0	16
74	Identification of Common Deletions in the Spike Protein of Severe Acute Respiratory Syndrome Coronavirus 2. <i>Journal of Virology</i> , 2020, 94, .	1.5	129
75	Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences. <i>Molecular Biology and Evolution</i> , 2020, 37, 2414-2429.	3.5	30
76	Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007897.	1.3	10
77	Open access epidemiological data from the COVID-19 outbreak. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 534.	4.6	205
78	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	2.9	37
79	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	5.9	114
80	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020, 94, .	1.5	17
81	Dynamics of conflict during the Ebola outbreak in the Democratic Republic of the Congo 2018-2019. <i>BMC Medicine</i> , 2020, 18, 113.	2.3	23
82	Phylodynamics Helps to Evaluate the Impact of an HIV Prevention Intervention. <i>Viruses</i> , 2020, 12, 469.	1.5	17
83	Towards an understanding of the avian virome. <i>Journal of General Virology</i> , 2020, 101, 785-790.	1.3	18
84	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.	0.8	30
85	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.	0.5	80
86	Title is missing!. , 2020, 14, e0007897.		0
87	Title is missing!. , 2020, 14, e0007897.		0
88	Title is missing!. , 2020, 14, e0007897.		0
89	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, .	1.8	17
90	A32-Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019, 5, .	2.2	0

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91	A38â€fGenomic epidemiology quantifies gaps in Aedes-borne virus transmission in the Americas. <i>Virus Evolution</i> , 2019, 5, .	2.2	0
92	A60â€fRevealing the evolution of virulence in RNA viruses. <i>Virus Evolution</i> , 2019, 5, .	2.2	0
93	The multifurcating skyline plot. <i>Virus Evolution</i> , 2019, 5, vez031.	2.2	8
94	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1138-1147.	4.6	63
95	Parallel molecular evolution and adaptation in viruses. <i>Current Opinion in Virology</i> , 2019, 34, 90-96.	2.6	35
96	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.	1.8	23
97	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007231.	1.3	44
98	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 784-787.	2.0	36
99	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	1.3	75
100	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.	5.9	699
101	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , 2019, 9, 5151.	1.6	89
102	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , 2019, 93, .	1.5	13
103	Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019, 25, 206-211.	15.2	94
104	Robust Design for Coalescent Model Inference. <i>Systematic Biology</i> , 2019, 68, 730-743.	2.7	27
105	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.	1.9	23
106	Reverse immunodynamics: a new method for identifying targets of protective immunity. <i>Scientific Reports</i> , 2019, 9, 2164.	1.6	3
107	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.	3.3	53
108	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.	3.3	71

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109	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019, 15, e1007976.	2.1	37
110	High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. <i>Journal of Infectious Diseases</i> , 2019, 219, 1722-1729.	1.9	11
111	Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , 2019, 147, e34.	1.0	29
112	The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 155-163.	0.5	7
113	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.	3.6	36
114	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	5.9	305
115	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162.	13.5	56
116	Exact Bayesian inference for phylogenetic birth-death models. <i>Bioinformatics</i> , 2018, 34, 3638-3645.	1.8	12
117	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	3.4	124
118	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.	3.3	65
119	The Effect of RNA Substitution Models on Viroid and RNA Virus Phylogenies. <i>Genome Biology and Evolution</i> , 2018, 10, 657-666.	1.1	8
120	Taming the BEAST – A Community Teaching Material Resource for BEAST 2. <i>Systematic Biology</i> , 2018, 67, 170-174.	2.7	79
121	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.	1.7	32
122	Conserved secondary structures predicted within the 5' packaging signal region of influenza A virus PB2 segment. <i>Meta Gene</i> , 2018, 15, 75-79.	0.3	6
123	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.	2.9	41
124	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018, 14, e1007392.	2.1	35
125	A naturally protective epitope of limited variability as an influenza vaccine target. <i>Nature Communications</i> , 2018, 9, 3859.	5.8	32
126	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of Lübeck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180991.	1.2	21

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127	Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. <i>Emerging Infectious Diseases</i> , 2018, 24, 1795-1805.	2.0	26
128	Where do all the subtypes go? Temporal dynamics of H8â€“H12 influenza A viruses in waterfowl. <i>Virus Evolution</i> , 2018, 4, vey025.	2.2	23
129	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.	5.1	82
130	Genomic surveillance of avian-origin influenza A viruses causing human disease. <i>Genome Medicine</i> , 2018, 10, 50.	3.6	7
131	Rapid HIV disease progression following superinfection in an HLA-B*27:05/B*57:01-positive transmission recipient. <i>Retrovirology</i> , 2018, 15, 7.	0.9	13
132	Westward Spread of Highly Pathogenic Avian Influenza A(H7N9) Virus among Humans, China. <i>Emerging Infectious Diseases</i> , 2018, 24, 1095-1098.	2.0	12
133	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	6.0	279
134	Phyldynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	5.8	59
135	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , 2018, 10, .	1.4	43
136	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, .	1.5	17
137	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
138	Defining HIV-1 transmission clusters based on sequence data. <i>Aids</i> , 2017, 31, 1211-1222.	1.0	131
139	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
140	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	13.7	515
141	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.	5.5	898
142	First Complete Genome Sequences of Zika Virus Isolated from Febrile Patient Sera in Ecuador. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
143	Short-Sighted Virus Evolution and a Germline Hypothesis for Chronic Viral Infections. <i>Trends in Microbiology</i> , 2017, 25, 336-348.	3.5	50
144	Optimal point process filtering and estimation of the coalescent process. <i>Journal of Theoretical Biology</i> , 2017, 421, 153-167.	0.8	13

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145	A Phylogenetic Codon Substitution Model for Antibody Lineages. <i>Genetics</i> , 2017, 206, 417-427.	1.2	56
146	Spread of yellow fever virus outbreak in Angola and the Democratic Republic of the Congo 2015â€“16: a modelling study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 330-338.	4.6	185
147	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.	4.2	31
148	O14.3â€“...How war and risky sexual behaviours shape the ukrainian hiv epidemic: a phylogeographic analysis. , 2017, , .		0
149	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017, 7, 15216.	1.6	40
150	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.	3.5	64
151	Cross-border spread, lineage displacement and evolutionary rate estimation of rabies virus in Yunnan Province, China. <i>Virology Journal</i> , 2017, 14, 102.	1.4	24
152	A10â€“fThe evolution and molecular epidemiology of epidemic GII.17 noroviruses. <i>Virus Evolution</i> , 2017, 3, .	2.2	0
153	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017, 23, 1742-1744.	2.0	69
154	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , 2017, 13, e1006749.	2.1	78
155	Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005694.	1.3	86
156	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017, 6, .	2.8	80
157	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016, 22, 1788-1792.	2.0	45
158	Evolution and Transmission of Respiratory Syncytial Group A (RSV-A) Viruses in Guangdong, China 2008â€“2015. <i>Frontiers in Microbiology</i> , 2016, 07, 1263.	1.5	19
159	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.	3.8	1
160	Faster Adaptation in Smaller Populations: Counterintuitive Evolution of HIV during Childhood Infection. <i>PLoS Computational Biology</i> , 2016, 12, e1004694.	1.5	8
161	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , 2016, 22, 2104-2112.	2.0	33
162	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016, 22, 671-678.	2.0	46

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163	Computational and molecular analysis of conserved influenza A virus RNA secondary structures involved in infectious virion production. <i>RNA Biology</i> , 2016, 13, 883-894.	1.5	36
164	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016, 8, 97.	3.6	182
165	Antibody responses to avian influenza viruses in wild birds broaden with age. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20162159.	1.2	34
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