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List of Articles by Year in descending order

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41 peer-reviewed articles	4,504 peer-reviewed citations	375634 24 peer-reviewed h-index	47384 7.23 score
48 documents	6156 doc citations	369479 26 h-index	19501 citing authors

#	Article	IF	Citations
1	The global H5N1 influenza panzootic in mammals. Nature, 2024, 637, 304-313.	30.6	451
2	On the importance of assessing topological convergence in Bayesian phylogenetic inference. Virus Evolution, 2024, 10, .	2.2	7
3	Fitting stochastic epidemic models to gene genealogies using linear noise approximation. Annals of Applied Statistics, 2023, 17, .	0.8	2
4	Phylogeographic analysis of dengue virus serotype 1 and cosmopolitan serotype 2 in Africa. International Journal of Infectious Diseases, 2023, 133, 46-52.	1.4	11
5	Accumulated metagenomic studies reveal recent migration, whole genome evolution, and undiscovered diversity of orthomyxoviruses. Journal of Virology, 2023, 97, .	2.4	8
6	Antibody escape and global spread of SARS-CoV-2 lineage A.27. Nature Communications, 2022, 13, .	10.8	32
7	Lower respiratory tract infections in children requiring mechanical ventilation: a multicentre prospective surveillance study incorporating airway metagenomics. Lancet Microbe, The, 2022, 3, e284-e293.	8.0	61
8	Predicting the evolution of the Lassa virus endemic area and population at risk over the next decades. Nature Communications, 2022, 13, .	10.8	93
9	Global disparities in SARS-CoV-2 genomic surveillance. Nature Communications, 2022, 13, .	10.8	279
10	Polymorphism of genetic ambigrams. Virus Evolution, 2021, 7, .	2.2	9
11	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. Viruses, 2021, 13, 1359.	2.2	7
12	Global genome analysis reveals a vast and dynamic anellovirus landscape within the human virome. Cell Host and Microbe, 2021, 29, 1305-1315.e6.	12.2	107
13	Emergence of an early SARS-CoV-2 epidemic in the United States. Cell, 2021, 184, 4939-4952.e15.	23.4	53
14	Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies. Nature Communications, 2021, 12, .	10.8	85
15	Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions. Nature Communications, 2021, 12, .	10.8	71
16	Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17104-17111.	5.2	63
17	Estimating effective population size changes from preferentially sampled genetic sequences. PLoS Computational Biology, 2020, 16, e1007774.	1.9	24
18	Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations. Virus Evolution, 2019, 5, .	2.2	38

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19	The ability of single genes vs full genomes to resolve time and space in outbreak analysis. BMC Evolutionary Biology, 2019, 19, .	3.1	55
20	MERS coronaviruses from camels in Africa exhibit region-dependent genetic diversity. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3144-3149.	5.2	184
21	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. Nature Communications, 2018, 9, .	10.8	71
22	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	30.6	429
23	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature, 2017, 546, 401-405.	30.6	345
24	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. PLoS Pathogens, 2017, 13, e1006749.	2.9	109
25	The evolution of Ebola virus: Insights from the 2013–2016 epidemic. Nature, 2016, 538, 193-200.	30.6	313
26	Preliminary Evaluation of the Effect of Investigational Ebola Virus Disease Treatments on Viral Genome Sequences. Journal of Infectious Diseases, 2016, 214, S333-S341.	2.2	12
27	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. Virus Evolution, 2016, 2, vew016.	2.2	124
28	MERS-CoV recombination: implications about the reservoir and potential for adaptation. Virus Evolution, 2016, 2, vev023.	2.2	71
29	Real-time, portable genome sequencing for Ebola surveillance. Nature, 2016, 530, 228-232.	30.6	1,472
30	Reassortment between Influenza B Lineages and the Emergence of a Coadapted PB1–PB2–HA Gene Complex. Molecular Biology and Evolution, 2015, 32, 162-172.	3.1	82
31	Evolution and Spread of Ebola Virus in Liberia, 2014–2015. Cell Host and Microbe, 2015, 18, 659-669.	12.2	89
32	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. Cell, 2015, 161, 1516-1526.	23.4	305
33	Temporal and spatial analysis of the 2014–2015 Ebola virus outbreak in West Africa. Nature, 2015, 524, 97-101.	30.6	304
34	The genetics of host–virus coevolution in invertebrates. Current Opinion in Virology, 2014, 8, 73-78.	3.2	42
35	Integrating influenza antigenic dynamics with molecular evolution. ELife, 0, 3, .	1.0	424
36	Are arthropods at the heart of virus evolution?. ELife, 0, 4, .	1.0	34

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37	MERS-CoV spillover at the camel-human interface. ELife, 0, 7, .	1.0	229
38	Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay. ELife, 0, 10, .	1.0	131
39	Phylogenetic Analysis of Guinea 2014 EBOV Ebolavirus Outbreak. PLOS Currents, 0, , .	1.6	65
40	The global antigenic diversity of swine influenza A viruses. ELife, 0, 5, .	1.0	198
41	HIPSTR: highest independent posterior subtree reconstruction in TreeAnnotator X. Bioinformatics, 0, 41, .	3.2	20