

Áine N O'toole

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

9,087
citations

304743

22
h-index

526287

27
g-index

42
all docs

42
docs citations

42
times ranked

13195
citing authors

#	ARTICLE	IF	CITATIONS
1	Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences. BMC Genomics, 2022, 23, 121.	2.8	60
2	Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination. PLoS Pathogens, 2022, 18, e1010023.	4.7	17
3	Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. Nature Medicine, 2022, 28, 1785-1790.	30.7	456
4	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	6.5	110
5	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 2021, 184, 64-75.e11.	28.9	843
6	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. Nature Microbiology, 2021, 6, 112-122.	13.3	88
7	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nature Microbiology, 2021, 6, 415-415.	13.3	65
8	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. Science, 2021, 371, 708-712.	12.6	335
9	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. Nature, 2021, 593, 266-269.	27.8	1,001
10	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. Cell, 2021, 184, 1171-1187.e20.	28.9	541
11	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.	1.8	115
12	Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda. Nature Microbiology, 2021, 6, 1094-1101.	13.3	82
13	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.	6.4	375
14	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. Science, 2021, 373, 889-895.	12.6	142
15	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. Genome Biology, 2021, 22, 196.	8.8	53
16	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. Virus Evolution, 2021, 7, veab064.	4.9	774
17	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.	1.8	129
18	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. Cell, 2021, 184, 5179-5188.e8.	28.9	182

#	ARTICLE	IF	CITATIONS
19	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. <i>Nature Communications</i> , 2021, 12, 5705.	12.8	24
20	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
21	Rapid SARS-CoV-2 whole-genome sequencing and analysis for informed public health decision-making in the Netherlands. <i>Nature Medicine</i> , 2020, 26, 1405-1410.	30.7	273
22	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110.	12.8	118
23	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. <i>Eurosurveillance</i> , 2020, 25, .	7.0	186
24	Genetic diversity and cross-species transmission of kobuviruses in Vietnam. <i>Virus Evolution</i> , 2018, 4, vey002.	4.9	18
25	Faster Evolving Primate Genes Are More Likely to Duplicate. <i>Molecular Biology and Evolution</i> , 2018, 35, 107-118.	8.9	38