

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	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
2	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
3	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
4	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	4.9	774
5	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	28.9	541
6	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
7	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
8	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
9	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
10	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
11	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	28.9	182
12	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
13	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
14	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
15	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
16	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	6.5	110
17	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	13.3	88
18	Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda. <i>Nature Microbiology</i> , 2021, 6, 1094-1101.	13.3	82

#	ARTICLE	IF	CITATIONS
19	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021, 6, 415-415.	13.3	65
20	Pango lineage designation and assignment using SARS-CoV-2 spike gene nucleotide sequences. <i>BMC Genomics</i> , 2022, 23, 121.	2.8	60
21	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	8.8	53
22	Faster Evolving Primate Genes Are More Likely to Duplicate. <i>Molecular Biology and Evolution</i> , 2018, 35, 107-118.	8.9	38
23	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
24	Genetic diversity and cross-species transmission of kobuviruses in Vietnam. <i>Virus Evolution</i> , 2018, 4, vey002.	4.9	18
25	Making genomic surveillance deliver: A lineage classification and nomenclature system to inform rabies elimination. <i>PLoS Pathogens</i> , 2022, 18, e1010023.	4.7	17