

John T Mccrone

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

8,612
citations

361413

20
h-index

642732

23
g-index

33
all docs

33
docs citations

33
times ranked

13510
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Epidemiology of Early SARS-CoV-2 Transmission Dynamics, Gujarat, India. <i>Emerging Infectious Diseases</i> , 2022, 28, 751-758.	4.3	4
2	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
3	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
4	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
5	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
6	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	27.8	1,001
7	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
8	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021, 7, veab051.	4.9	14
9	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
10	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	4.9	774
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	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
13	Influenza B Viruses Exhibit Lower Within-Host Diversity than Influenza A Viruses in Human Hosts. <i>Journal of Virology</i> , 2020, 94, .	3.4	46
14	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
15	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
16	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	28.9	236
17	Genetic bottlenecks in intraspecies virus transmission. <i>Current Opinion in Virology</i> , 2018, 28, 20-25.	5.4	118
18	A speedâ€“fidelity trade-off determines the mutation rate and virulence of an RNA virus. <i>PLoS Biology</i> , 2018, 16, e2006459.	5.6	88

#	ARTICLE	IF	CITATIONS
19	Stochastic processes constrain the within and between host evolution of influenza virus. <i>ELife</i> , 2018, 7, .	6.0	179
20	Vaccination has minimal impact on the intrahost diversity of H3N2 influenza viruses. <i>PLoS Pathogens</i> , 2017, 13, e1006194.	4.7	90
21	Next-Generation Sequencing of Influenza Viruses in a Household Cohort Accurately Identifies Transmission Pairs and Reveals a Bottleneck Size of Close to One. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	0
22	The Mutational Robustness of Influenza A Virus. <i>PLoS Pathogens</i> , 2016, 12, e1005856.	4.7	82
23	Measurements of Intrahost Viral Diversity Are Extremely Sensitive to Systematic Errors in Variant Calling. <i>Journal of Virology</i> , 2016, 90, 6884-6895.	3.4	109