

John T Mccrone

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7107636/publications.pdf>

Version: 2024-02-01

23
papers

8,612
citations

411340

20
h-index

721071

23
g-index

33
all docs

33
docs citations

33
times ranked

14385
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. | 2.0 | 4 |
| 2 | 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 |
| 3 | Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122. | 5.9 | 88 |
| 4 | 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 |
| 5 | Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712. | 6.0 | 335 |
| 6 | Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269. | 13.7 | 1,001 |
| 7 | 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 |
| 8 | Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021, 7, veab051. | 2.2 | 14 |
| 9 | Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895. | 6.0 | 142 |
| 10 | Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064. | 2.2 | 774 |
| 11 | Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8. | 13.5 | 182 |
| 12 | Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543. | 13.7 | 113 |
| 13 | Influenza B Viruses Exhibit Lower Within-Host Diversity than Influenza A Viruses in Human Hosts. <i>Journal of Virology</i> , 2020, 94, . | 1.5 | 46 |
| 14 | 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 |
| 15 | Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110. | 5.8 | 118 |
| 16 | Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9. | 13.5 | 236 |
| 17 | Genetic bottlenecks in intraspecies virus transmission. <i>Current Opinion in Virology</i> , 2018, 28, 20-25. | 2.6 | 118 |
| 18 | A speedâ€“fidelity trade-off determines the mutation rate and virulence of an RNA virus. <i>PLoS Biology</i> , 2018, 16, e2006459. | 2.6 | 88 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Stochastic processes constrain the within and between host evolution of influenza virus. <i>ELife</i> , 2018, 7, . | 2.8 | 179 |
| 20 | Vaccination has minimal impact on the intrahost diversity of H3N2 influenza viruses. <i>PLoS Pathogens</i> , 2017, 13, e1006194. | 2.1 | 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, . | 0.4 | 0 |
| 22 | The Mutational Robustness of Influenza A Virus. <i>PLoS Pathogens</i> , 2016, 12, e1005856. | 2.1 | 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. | 1.5 | 109 |