

Christopher Ruis

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17
papers

1,754
citations

9
h-index

18
g-index

18
ext. papers

2,924
ext. citations

17.9
avg, IF

5.55
L-index

#	Paper	IF	Citations
17	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020 , 5, 1403-1407	26.6	1250
16	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712	33.3	159
15	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020 , 21, 180	18.3	108
14	The emerging GII.P16-GII.4 Sydney 2012 norovirus lineage is circulating worldwide, arose by late-2014 and contains polymerase changes that may increase virus transmission. <i>PLoS ONE</i> , 2017 , 12, e0179572	3.7	52
13	Norovirus Whole-Genome Sequencing by SureSelect Target Enrichment: a Robust and Sensitive Method. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 2530-7	9.7	50
12	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895	33.3	41
11	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021 , 6, 415	26.6	35
10	Stepwise pathogenic evolution of. <i>Science</i> , 2021 , 372,	33.3	23
9	A comprehensive characterization of chronic norovirus infection in immunodeficient hosts. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 144, 1450-1453	11.5	10
8	Preadaptation of pandemic GII.4 noroviruses in unsampled virus reservoirs years before emergence. <i>Virus Evolution</i> , 2020 , 6, veaa067	3.7	9
7	Progress and challenges in virus genomic epidemiology. <i>Trends in Parasitology</i> , 2021 , 37, 1038-1049	6.4	4
6	Dissemination of Mycobacterium abscessus via global transmission networks. <i>Nature Microbiology</i> , 2021 , 6, 1279-1288	26.6	4
5	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		3
4	Global phylogeny of Treponema pallidum lineages reveals recent expansion and spread of contemporary syphilis. <i>Nature Microbiology</i> , 2021 , 6, 1549-1560	26.6	2
3	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		2
2	Novel Insights Into the Spread of Enteric Pathogens Using Genomics. <i>Journal of Infectious Diseases</i> , 2020 , 221, S319-S330	7	1
1	Contemporary syphilis is characterised by rapid global spread of pandemic Treponema pallidum lineages		1

