

Rene Niehus

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5626690/publications.pdf>

Version: 2024-02-01

13
papers

2,657
citations

706676

14
h-index

1113639

15
g-index

21
all docs

21
docs citations

21
times ranked

5650
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimating internationally imported cases during the early COVID-19 pandemic. <i>Nature Communications</i> , 2021, 12, 311.	5.8	35
2	How to detect and reduce potential sources of biases in studies of SARS-CoV-2 and COVID-19. <i>European Journal of Epidemiology</i> , 2021, 36, 179-196.	2.5	93
3	The evolution of strategy in bacterial warfare via the regulation of bacteriocins and antibiotics. <i>ELife</i> , 2021, 10, .	2.8	40
4	The gut microbiota is associated with immune cell dynamics in humans. <i>Nature</i> , 2020, 588, 303-307.	13.7	273
5	Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. <i>Nature Medicine</i> , 2020, 26, 506-510.	15.2	1,067
6	Identifying Locations with Possible Undetected Imported Severe Acute Respiratory Syndrome Coronavirus 2 Cases by Using Importation Predictions. <i>Emerging Infectious Diseases</i> , 2020, 26, 1465-1469.	2.0	32
7	Using observational data to quantify bias of traveller-derived COVID-19 prevalence estimates in Wuhan, China. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 803-808.	4.6	58
8	Practical considerations for measuring the effective reproductive number, Rt. <i>PLoS Computational Biology</i> , 2020, 16, e1008409.	1.5	343
9	Quantifying antibiotic impact on within-patient dynamics of extended-spectrum beta-lactamase resistance. <i>ELife</i> , 2020, 9, .	2.8	21
10	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. <i>Environmental Microbiomes</i> , 2019, 14, 7.	2.2	69
11	The evolution of siderophore production as a competitive trait. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1443-1455.	1.1	119
12	Migration and horizontal gene transfer divide microbial genomes into multiple niches. <i>Nature Communications</i> , 2015, 6, 8924.	5.8	112
13	Evolutionary limits to cooperation in microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17941-17946.	3.3	178