

David F Nieuwenhuijse

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

2,896
citations

567144

15
h-index

677027

22
g-index

28
all docs

28
docs citations

28
times ranked

6308
citing authors

#	ARTICLE	IF	CITATIONS
1	Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. <i>Science</i> , 2021, 371, 172-177.	6.0	878
2	viromeBrowser: A Shiny App for Browsing Virome Sequencing Analysis Results. <i>Viruses</i> , 2021, 13, 437.	1.5	1
3	Monitoring SARS-CoV-2 Circulation and Diversity through Community Wastewater Sequencing, the Netherlands and Belgium. <i>Emerging Infectious Diseases</i> , 2021, 27, 1405-1415.	2.0	168
4	A mixed-methods approach to elucidate SARS-CoV-2 transmission routes and clustering in outbreaks in native workers and labour migrants in the fruit and vegetable packaging industry in South Holland, the Netherlands, May to July 2020. <i>International Journal of Infectious Diseases</i> , 2021, 109, 24-32.	1.5	5
5	The next phase of SARS-CoV-2 surveillance: real-time molecular epidemiology. <i>Nature Medicine</i> , 2021, 27, 1518-1524.	15.2	178
6	Adaptation, spread and transmission of SARS-CoV-2 in farmed minks and associated humans in the Netherlands. <i>Nature Communications</i> , 2021, 12, 6802.	5.8	81
7	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.	15.2	273
8	Why psychiatry is different - challenges and difficulties in managing a nosocomial outbreak of coronavirus disease (COVID-19) in hospital care. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 190.	1.5	19
9	COVID-19 in health-care workers in three hospitals in the south of the Netherlands: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1273-1280.	4.6	220
10	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020, 10, 13748.	1.6	39
11	The International Virus Bioinformatics Meeting 2020. <i>Viruses</i> , 2020, 12, 1398.	1.5	3
12	Genomic monitoring to understand the emergence and spread of Usutu virus in the Netherlands, 2016–2018. <i>Scientific Reports</i> , 2020, 10, 2798.	1.6	43
13	Virus Metagenomics in Farm Animals: A Systematic Review. <i>Viruses</i> , 2020, 12, 107.	1.5	47
14	Validating Whole Genome Nanopore Sequencing, using Usutu Virus as an Example. <i>Journal of Visualized Experiments</i> , 2020, , .	0.2	15
15	Metavirome Sequencing to Evaluate Norovirus Diversity in Sewage and Related Bioaccumulated Oysters. <i>Frontiers in Microbiology</i> , 2019, 10, 2394.	1.5	26
16	A64–fViral sequence classification using deep learning algorithms. <i>Virus Evolution</i> , 2019, 5, .	2.2	0
17	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	5.8	612
18	The COMPARE Data Hubs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	28

#	ARTICLE	IF	CITATIONS
19	Induction of Cross-Clade Antibody and T-Cell Responses by a Modified Vaccinia Virus Ankara-Based Influenza A(H5N1) Vaccine in a Randomized Phase 1/2a Clinical Trial. <i>Journal of Infectious Diseases</i> , 2018, 218, 614-623.	1.9	25
20	Studies into the mechanism of measles-associated immune suppression during a measles outbreak in the Netherlands. <i>Nature Communications</i> , 2018, 9, 4944.	5.8	83
21	Metagenomic Sequencing for Surveillance of Food- and Waterborne Viral Diseases. <i>Frontiers in Microbiology</i> , 2017, 8, 230.	1.5	57