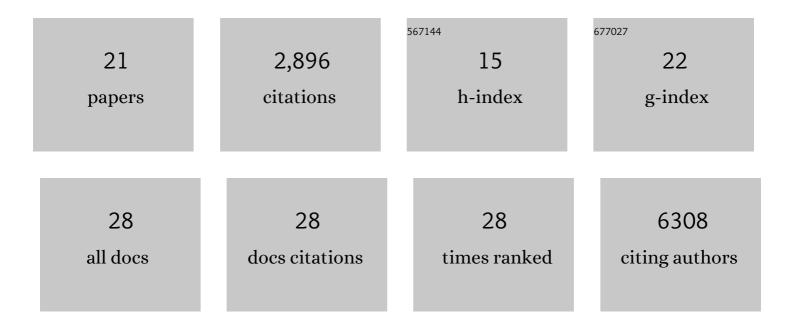
## David F Nieuwenhuijse

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7808245/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. Science, 2021, 371, 172-177.	6.0	878
2	viromeBrowser: A Shiny App for Browsing Virome Sequencing Analysis Results. Viruses, 2021, 13, 437.	1.5	1
3	Monitoring SARS-CoV-2 Circulation and Diversity through Community Wastewater Sequencing, the Netherlands and Belgium. Emerging Infectious Diseases, 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. International Journal of Infectious Diseases, 2021, 109, 24-32.	1.5	5
5	The next phase of SARS-CoV-2 surveillance: real-time molecular epidemiology. Nature Medicine, 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. Nature Communications, 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. Nature Medicine, 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. Antimicrobial Resistance and Infection Control, 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. Lancet Infectious Diseases, The, 2020, 20, 1273-1280.	4.6	220
10	Setting a baseline for global urban virome surveillance in sewage. Scientific Reports, 2020, 10, 13748.	1.6	39
11	The International Virus Bioinformatics Meeting 2020. Viruses, 2020, 12, 1398.	1.5	3
12	Genomic monitoring to understand the emergence and spread of Usutu virus in the Netherlands, 2016–2018. Scientific Reports, 2020, 10, 2798.	1.6	43
13	Virus Metagenomics in Farm Animals: A Systematic Review. Viruses, 2020, 12, 107.	1.5	47
14	Validating Whole Genome Nanopore Sequencing, using Usutu Virus as an Example. Journal of Visualized Experiments, 2020, , .	0.2	15
15	Metavirome Sequencing to Evaluate Norovirus Diversity in Sewage and Related Bioaccumulated Oysters. Frontiers in Microbiology, 2019, 10, 2394.	1.5	26
16	A64â $\in$ fViral sequence classification using deep learning algorithms. Virus Evolution, 2019, 5, .	2.2	0
17	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 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. Journal of Infectious Diseases, 2018, 218, 614-623.	1.9	25
20	Studies into the mechanism of measles-associated immune suppression during a measles outbreak in the Netherlands. Nature Communications, 2018, 9, 4944.	5.8	83
21	Metagenomic Sequencing for Surveillance of Food- and Waterborne Viral Diseases. Frontiers in Microbiology, 2017, 8, 230.	1.5	57