

Bas B Oude Munnink

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

5,259
citations

279701

23
h-index

182361

51
g-index

64
all docs

64
docs citations

64
times ranked

10669
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 infection in cats and dogs in infected mink farms. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3001-3007.	1.3	81
2	Clinical and In Vitro Evidence Favoring Immunoglobulin Treatment of a Chronic Norovirus Infection in a Patient With Common Variable Immunodeficiency. <i>Journal of Infectious Diseases</i> , 2022, 226, 1781-1789.	1.9	12
3	An early warning system for emerging SARS-CoV-2 variants. <i>Nature Medicine</i> , 2022, 28, 1110-1115.	15.2	47
4	Antigenic cartography of SARS-CoV-2 reveals that Omicron BA.1 and BA.2 are antigenically distinct. <i>Science Immunology</i> , 2022, 7, .	5.6	89
5	Reinfection of Severe Acute Respiratory Syndrome Coronavirus 2 in an Immunocompromised Patient: A Case Report. <i>Clinical Infectious Diseases</i> , 2021, 73, e2841-e2842.	2.9	77
6	Unraveling the Modes of Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) During a Nursing Home Outbreak: Looking Beyond the Church Superspreading Event. <i>Clinical Infectious Diseases</i> , 2021, 73, S163-S169.	2.9	18
7	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
8	Economic evaluation of whole genome sequencing for pathogen identification and surveillance – results of case studies in Europe and the Americas 2016 to 2019. <i>Eurosurveillance</i> , 2021, 26, .	3.9	25
9	viromeBrowser: A Shiny App for Browsing Virome Sequencing Analysis Results. <i>Viruses</i> , 2021, 13, 437.	1.5	1
10	Are presymptomatic SARS-CoV-2 infections in nursing home residents unrecognised symptomatic infections? Sequence and metadata from weekly testing in an extensive nursing home outbreak. <i>Age and Ageing</i> , 2021, 50, 1454-1463.	0.7	18
11	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
12	SARS-CoV-2 variants of concern partially escape humoral but not T cell responses in COVID-19 convalescent donors and vaccine recipients. <i>Science Immunology</i> , 2021, 6, .	5.6	455
13	COVID-19: first long-term care facility outbreak in the Netherlands following cross-border introduction from Germany, March 2020. <i>BMC Infectious Diseases</i> , 2021, 21, 418.	1.3	14
14	Recommendations for the introduction of metagenomic next-generation sequencing in clinical virology, part II: bioinformatic analysis and reporting. <i>Journal of Clinical Virology</i> , 2021, 138, 104812.	1.6	39
15	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021, 6, 821-823.	5.9	221
16	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717.	18.7	133
17	Pathology and Pathogenesis of Eurasian Blackbirds (<i>Turdus merula</i>) Naturally Infected with Usutu Virus. <i>Viruses</i> , 2021, 13, 1481.	1.5	15
18	Occupational and environmental exposure to SARS-CoV-2 in and around infected mink farms. <i>Occupational and Environmental Medicine</i> , 2021, 78, 893-899.	1.3	18

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19	Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples. <i>Journal of Clinical Virology</i> , 2021, 141, 104908.	1.6	28
20	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
21	The next phase of SARS-CoV-2 surveillance: real-time molecular epidemiology. <i>Nature Medicine</i> , 2021, 27, 1518-1524.	15.2	178
22	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
23	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
24	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
25	Case report of a neonate with high viral SARSCoV-2 loads and long-term virus shedding. <i>Journal of Infection and Public Health</i> , 2020, 13, 1878-1884.	1.9	12
26	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , 2020, 10, 13748.	1.6	39
27	First molecular analysis of rabies virus in Qatar and clinical cases imported into Qatar, a case report. <i>International Journal of Infectious Diseases</i> , 2020, 96, 323-326.	1.5	8
28	Tracking echovirus eleven outbreaks in Guangdong, China: a metatranscriptomic, phylogenetic, and epidemiological study. <i>Virus Evolution</i> , 2020, 6, veaa029.	2.2	14
29	Novel opportunities for NGS-based one health surveillance of foodborne viruses. <i>One Health Outlook</i> , 2020, 2, 14.	1.4	22
30	Validating Whole Genome Nanopore Sequencing, using Usutu Virus as an Example. <i>Journal of Visualized Experiments</i> , 2020, , .	0.2	15
31	Comparative pathogenesis of COVID-19, MERS, and SARS in a nonhuman primate model. <i>Science</i> , 2020, 368, 1012-1015.	6.0	802
32	SARS-CoV-2 infection in farmed minks, the Netherlands, April and May 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	573
33	Detection of West Nile virus in a common whitethroat (<i>Curruca communis</i>) and <i>Culex</i> mosquitoes in the Netherlands, 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	40
34	Exploring utility of genomic epidemiology to trace origins of highly pathogenic influenza A/H7N9 in Guangdong. <i>Virus Evolution</i> , 2020, 6, veaa097.	2.2	6
35	Metavirome Sequencing to Evaluate Norovirus Diversity in Sewage and Related Bioaccumulated Oysters. <i>Frontiers in Microbiology</i> , 2019, 10, 2394.	1.5	26
36	A6â€fViral sequence classification using deep learning algorithms. <i>Virus Evolution</i> , 2019, 5, .	2.2	0

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37	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	34
38	Co-circulation of genetically distinct highly pathogenic avian influenza A clade 2.3.4.4 (H5N6) viruses in wild waterfowl and poultry in Europe and East Asia, 2017–18. <i>Virus Evolution</i> , 2019, 5, vez004.	2.2	63
39	MERS-CoV in Camels but Not Camel Handlers, Sudan, 2015 and 2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 2333-2335.	2.0	21
40	Virus discovery reveals frequent infection by diverse novel members of the Flaviviridae in wild lemurs. <i>Archives of Virology</i> , 2019, 164, 509-522.	0.9	11
41	Antigenic Variation of Avian Influenza A(H5N6) Viruses, Guangdong Province, China, 2014–2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 1932-1945.	2.0	11
42	Characterization of Posa and Posa-like virus genomes in fecal samples from humans, pigs, rats, and bats collected from a single location in Vietnam. <i>Virus Evolution</i> , 2017, 3, vex022.	2.2	25
43	Widespread activity of multiple lineages of Usutu virus, western Europe, 2016. <i>Eurosurveillance</i> , 2017, 22, .	3.9	115
44	Reduced maternal levels of common viruses during pregnancy predict offspring psychosis: Potential role of enhanced maternal immune activity?. <i>Schizophrenia Research</i> , 2015, 166, 248-254.	1.1	13
45	Identification of a Novel Human Rhinovirus C Type by Antibody Capture VIDISCA-454. <i>Viruses</i> , 2015, 7, 239-251.	1.5	2
46	A novel genus in the order Picornavirales detected in human stool. <i>Journal of General Virology</i> , 2015, 96, 3440-3443.	1.3	23
47	Persistent viremia by a novel parvovirus in a slow loris (<i>Nycticebus coucang</i>) with diffuse histiocytic sarcoma. <i>Frontiers in Microbiology</i> , 2014, 5, 655.	1.5	14
48	Full Genome Virus Detection in Fecal Samples Using Sensitive Nucleic Acid Preparation, Deep Sequencing, and a Novel Iterative Sequence Classification Algorithm. <i>PLoS ONE</i> , 2014, 9, e93269.	1.1	71
49	Autologous Antibody Capture to Enrich Immunogenic Viruses for Viral Discovery. <i>PLoS ONE</i> , 2013, 8, e78454.	1.1	16
50	Performance of VIDISCA-454 in Feces-Suspensions and Serum. <i>Viruses</i> , 2012, 4, 1328-1334.	1.5	37