

Piet Maes

List of Publications by Year in descending order

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Version: 2024-02-01

164
papers

11,833
citations

46984

47
h-index

34964

98
g-index

196
all docs

196
docs citations

196
times ranked

16515
citing authors

#	ARTICLE	IF	CITATIONS
1	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. <i>Nature</i> , 2022, 602, 671-675.	13.7	1,202
2	Full Genome-Based Classification of Rotaviruses Reveals a Common Origin between Human Wa-Like and Porcine Rotavirus Strains and Human DS-1-Like and Bovine Rotavirus Strains. <i>Journal of Virology</i> , 2008, 82, 3204-3219.	1.5	791
3	In vitro inhibition of severe acute respiratory syndrome coronavirus by chloroquine. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 264-268.	1.0	530
4	Experimental Treatment with Favipiravir for Ebola Virus Disease (the JIKI Trial): A Historically Controlled, Single-Arm Proof-of-Concept Trial in Guinea. <i>PLoS Medicine</i> , 2016, 13, e1001967.	3.9	382
5	RotaC: A web-based tool for the complete genome classification of group A rotaviruses. <i>BMC Microbiology</i> , 2009, 9, 238.	1.3	365
6	Remdesivir, Molnupiravir and Nirmatrelvir remain active against SARS-CoV-2 Omicron and other variants of concern. <i>Antiviral Research</i> , 2022, 198, 105252.	1.9	302
7	The Papillomavirus Episteme: a major update to the papillomavirus sequence database. <i>Nucleic Acids Research</i> , 2017, 45, D499-D506.	6.5	298
8	Taxonomy of the order Bunyvirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1949-1965.	0.9	285
9	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , 2015, 5, 16532.	1.6	277
10	Temporal and spatial analysis of the 2014–2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101.	13.7	272
11	Antiviral Activity of Chloroquine against Human Coronavirus OC43 Infection in Newborn Mice. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3416-3421.	1.4	245
12	Serum neutralization of SARS-CoV-2 Omicron sublineages BA.1 and BA.2 in patients receiving monoclonal antibodies. <i>Nature Medicine</i> , 2022, 28, 1297-1302.	15.2	235
13	STAT2 signaling restricts viral dissemination but drives severe pneumonia in SARS-CoV-2 infected hamsters. <i>Nature Communications</i> , 2020, 11, 5838.	5.8	225
14	Taxonomy of the order Mononegavirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1967-1980.	0.9	224
15	Symptomatic Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Reinfection by a Phylogenetically Distinct Strain. <i>Clinical Infectious Diseases</i> , 2021, 73, 354-356.	2.9	218
16	Evolutionary History of the Closely Related Group 2 Coronaviruses: Porcine Hemagglutinating Encephalomyelitis Virus, Bovine Coronavirus, and Human Coronavirus OC43. <i>Journal of Virology</i> , 2006, 80, 7270-7274.	1.5	212
17	Relating increasing hantavirus incidences to the changing climate: the mast connection. <i>International Journal of Health Geographics</i> , 2009, 8, 1.	1.2	198
18	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyvirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	0.9	184

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19	Genome-wide CRISPR screening identifies TMEM106B as a proviral host factor for SARS-CoV-2. <i>Nature Genetics</i> , 2021, 53, 435-444.	9.4	162
20	A Recurrent Mutation at Position 26340 of SARS-CoV-2 Is Associated with Failure of the E Gene Quantitative Reverse Transcription-PCR Utilized in a Commercial Dual-Target Diagnostic Assay. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	160
21	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2295-2310.	0.9	157
22	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	0.9	153
23	Hantaviruses: Immunology, Treatment, and Prevention. <i>Viral Immunology</i> , 2004, 17, 481-497.	0.6	148
24	High-Throughput Analysis of Human Cytomegalovirus Genome Diversity Highlights the Widespread Occurrence of Gene-Disrupting Mutations and Pervasive Recombination. <i>Journal of Virology</i> , 2015, 89, 7673-7695.	1.5	148
25	A novel pancoronavirus RT-PCR assay: frequent detection of human coronavirus NL63 in children hospitalized with respiratory tract infections in Belgium. <i>BMC Infectious Diseases</i> , 2005, 5, 6.	1.3	143
26	Inhibition of SARS-coronavirus infection in vitro by S-nitroso-N-acetylpenicillamine, a nitric oxide donor compound. <i>International Journal of Infectious Diseases</i> , 2004, 8, 223-226.	1.5	142
27	Taxonomy of the order Bunyavirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 927-941.	0.9	115
28	Development of One-Step, Real-Time, Quantitative Reverse Transcriptase PCR Assays for Absolute Quantitation of Human Coronaviruses OC43 and 229E. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5452-5456.	1.8	111
29	Classify viruses "the gain is worth the pain. <i>Nature</i> , 2019, 566, 318-320.	13.7	104
30	The omicron (B.1.1.529) SARS-CoV-2 variant of concern does not readily infect Syrian hamsters. <i>Antiviral Research</i> , 2022, 198, 105253.	1.9	104
31	Down-regulation of HLA-A and HLA-Bw6, but not HLA-Bw4, allospecificities in leukemic cells: an escape mechanism from CTL and NK attack?. <i>Blood</i> , 2004, 103, 3122-3130.	0.6	102
32	Comparing infectivity and virulence of emerging SARS-CoV-2 variants in Syrian hamsters. <i>EBioMedicine</i> , 2021, 68, 103403.	2.7	102
33	Complex evolution and epidemiology of Dobrava-Belgrade hantavirus: definition of genotypes and their characteristics. <i>Archives of Virology</i> , 2013, 158, 521-529.	0.9	98
34	Hantaviridae: Current Classification and Future Perspectives. <i>Viruses</i> , 2019, 11, 788.	1.5	94
35	The SARS-CoV-2 and other human coronavirus spike proteins are fine-tuned towards temperature and proteases of the human airways. <i>PLoS Pathogens</i> , 2021, 17, e1009500.	2.1	91
36	Hemorrhagic Fever with Renal Syndrome in the New, and Hantavirus Pulmonary Syndrome in the old world: Paradi(se)gm lost or regained?. <i>Virus Research</i> , 2014, 187, 55-58.	1.1	90

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37	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. <i>Virus Evolution</i> , 2018, 4, vey008.	2.2	90
38	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. <i>Nature</i> , 0, , .	13.7	88
39	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 1608-1613.	3.5	79
40	Investigating the Origin and Spread of Hepatitis C Virus Genotype 5a. <i>Journal of Virology</i> , 2006, 80, 4220-4226.	1.5	77
41	A proposal for new criteria for the classification of hantaviruses, based on S and M segment protein sequences. <i>Infection, Genetics and Evolution</i> , 2009, 9, 813-820.	1.0	71
42	Taxonomy of the order Mononegavirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 1233-1244.	0.9	70
43	A unifying hypothesis and a single name for a complex globally emerging infection: hantavirus disease. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2012, 31, 1-5.	1.3	67
44	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	0.9	62
45	Recent approaches in hantavirus vaccine development. <i>Expert Review of Vaccines</i> , 2009, 8, 67-76.	2.0	59
46	Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. <i>Scientific Reports</i> , 2018, 8, 9830.	1.6	59
47	Are hepatitis B virus "subgenotypes" defined accurately?. <i>Journal of Clinical Virology</i> , 2010, 47, 356-360.	1.6	57
48	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	1.3	57
49	Genomic and Functional Characteristics of Human Cytomegalovirus Revealed by Next-Generation Sequencing. <i>Viruses</i> , 2014, 6, 1049-1072.	1.5	53
50	Organ-specific genome diversity of replication-competent SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 6612.	5.8	49
51	Beechnuts and outbreaks of nephropathia epidemica (NE): of mast, mice and men. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 1740-1746.	0.4	47
52	Novel hepatitis B virus subgenotype A6 in African-Belgian patients. <i>Journal of Clinical Virology</i> , 2010, 47, 93-96.	1.6	46
53	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018, 67, 1558-1559.	6.1	46
54	Another case of "European hantavirus pulmonary syndrome" with severe lung, prior to kidney, involvement, and diagnosed by viral inclusions in lung macrophages. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2013, 32, 1341-1345.	1.3	44

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55	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209.	1.6	44
56	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7.	3.0	44
57	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , 2017, 18, 249.	1.2	42
58	An affinity-enhanced, broadly neutralizing heavy chain-only antibody protects against SARS-CoV-2 infection in animal models. <i>Science Translational Medicine</i> , 2021, 13, eabi7826.	5.8	41
59	Human cytomegalovirus genomics and transcriptomics through the lens of next-generation sequencing: revision and future challenges. <i>Virus Genes</i> , 2019, 55, 138-164.	0.7	39
60	First evidence of fatal hantavirus nephropathy in India, mimicking leptospirosis. <i>Nephrology Dialysis Transplantation</i> , 2006, 21, 826-827.	0.4	36
61	Honey-bee-associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10511-10519.	3.3	36
62	Molecular evolutionary analysis and mutational pattern of full-length genomes of hepatitis B virus isolated from Belgian patients with different clinical manifestations. <i>Journal of Medical Virology</i> , 2010, 82, 379-389.	2.5	35
63	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. <i>BMC Genomics</i> , 2018, 19, 617.	1.2	35
64	Tumor Necrosis Factor- γ Genetic Predisposing Factors Can Influence Clinical Severity in Nephropathia Epidemica. <i>Viral Immunology</i> , 2006, 19, 558-564.	0.6	33
65	Phylogenetic analysis of hepatitis B virus full-length genomes reveals evidence for a large nosocomial outbreak in Belgium. <i>Journal of Clinical Virology</i> , 2009, 46, 61-68.	1.6	33
66	Growth kinetics of SARS-coronavirus in Vero E6 cells. <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 1147-1151.	1.0	32
67	Analysis of Diagnostic Findings From the European Mobile Laboratory in GuÃ©ckÃ©dou, Guinea, March 2014 Through March 2015. <i>Journal of Infectious Diseases</i> , 2016, 214, S250-S257.	1.9	32
68	Concomitant leptospirosis-hantavirus co-infection in acute patients hospitalized in Sri Lanka: implications for a potentially worldwide underestimated problem. <i>Epidemiology and Infection</i> , 2015, 143, 2081-2093.	1.0	31
69	Isolation of infectious Lloviu virus from Schreiber's bats in Hungary. <i>Nature Communications</i> , 2022, 13, 1706.	5.8	31
70	The virota and its transkingdom interactions in the healthy infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114619119.	3.3	30
71	Using the Gravity Model to Estimate the Spatial Spread of Vector-Borne Diseases. <i>International Journal of Environmental Research and Public Health</i> , 2012, 9, 4346-4364.	1.2	29
72	Evolutionary analysis of HBV α -antigen genetic diversity in Iranian blood donors: A nationwide study. <i>Journal of Medical Virology</i> , 2014, 86, 144-155.	2.5	28

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73	Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016, 25, 5994-6008.	2.0	28
74	ACUTE KIDNEY INJURY IN EMERGING, NON-TROPICAL INFECTIONS. <i>Acta Clinica Belgica</i> , 2007, 62, 387-395.	0.5	27
75	Exhaled breath condensate sampling is not a new method for detection of respiratory viruses. <i>Virology Journal</i> , 2011, 8, 98.	1.4	26
76	Genomic Diversity of Hepatitis B Virus Infection Associated With Fulminant Hepatitis B Development. <i>Hepatitis Monthly</i> , 2015, 15, e29477.	0.1	26
77	Plasma Exchange-Associated Immunoglobulin M-Negative Hantavirus Disease after a Camping Holiday in Southern France. <i>Clinical Infectious Diseases</i> , 2004, 38, 1350-1356.	2.9	24
78	Viral load quantitation of SARS-coronavirus RNA using a one-step real-time RT-PCR. <i>International Journal of Infectious Diseases</i> , 2006, 10, 32-37.	1.5	24
79	Model-Based Prediction of Nephropathia Epidemica Outbreaks Based on Climatological and Vegetation Data and Bank Vole Population Dynamics. <i>Zoonoses and Public Health</i> , 2013, 60, 461-477.	0.9	24
80	Chromatography Paper Strip Method for Collection, Transportation, and Storage of Rotavirus RNA in Stool Samples. <i>Journal of Clinical Microbiology</i> , 2004, 42, 1605-1608.	1.8	23
81	HBV subgenotype misclassification expands quasi-subgenotype A3. <i>Clinical Microbiology and Infection</i> , 2011, 17, 947-949.	2.8	23
82	Molecular characterization of hepatitis B virus strains circulating in Belgian patients co-infected with HIV and HBV: Overt and occult infection. <i>Journal of Medical Virology</i> , 2011, 83, 1876-1884.	2.5	23
83	A Novel Hantavirus of the European Mole, Bruges Virus, Is Involved in Frequent Nova Virus Coinfections. <i>Genome Biology and Evolution</i> , 2018, 10, 45-55.	1.1	23
84	A Method Enabling High-Throughput Sequencing of Human Cytomegalovirus Complete Genomes from Clinical Isolates. <i>PLoS ONE</i> , 2014, 9, e95501.	1.1	23
85	Chromatography paper strip sampling of enteric adenoviruses type 40 and 41 positive stool specimens. <i>Virology Journal</i> , 2005, 2, 6.	1.4	22
86	Glycoprotein-Specific Antibodies Produced by DNA Vaccination Protect Guinea Pigs from Lethal Argentine and Venezuelan Hemorrhagic Fever. <i>Journal of Virology</i> , 2016, 90, 3515-3529.	1.5	21
87	Truncated Recombinant Dobrava Hantavirus Nucleocapsid Proteins Induce Strong, Long-Lasting Immune Responses in Mice. <i>Intervirology</i> , 2006, 49, 253-260.	1.2	20
88	Antibiotic Resistance Plasmids Cointegrated into a Megaplasmid Harboring the <i>bla</i> _{OXA-427} Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	20
89	Anatomy of Omicron BA.1 and BA.2 neutralizing antibodies in COVID-19 mRNA vaccinees. <i>Nature Communications</i> , 2022, 13, .	5.8	20
90	The characterization of multiple novel paramyxoviruses highlights the diverse nature of the subfamily <i>Orthoparamyxovirinae</i> . <i>Virus Evolution</i> , 2022, 8, .	2.2	20

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91	Grotenhout Virus, a Novel Nairovirus Found in Ixodes ricinus in Belgium. <i>Genome Announcements</i> , 2017, 5, .	0.8	19
92	Characterization of a Novel Polyomavirus Isolated from a Fibroma on the Trunk of an African Elephant (<i>Loxodonta africana</i>). <i>PLoS ONE</i> , 2013, 8, e77884.	1.1	19
93	<i>In vitro&/i> antiviral activity of some novel isatin derivatives against HCV and SARS-CoV viruses. <i>Indian Journal of Pharmaceutical Sciences</i> , 2008, 70, 91.	1.0	19
94	Truncated Recombinant Puumala Virus Nucleocapsid Proteins Protect Mice Against Challenge in Vivo. <i>Viral Immunology</i> , 2008, 21, 49-60.	0.6	18
95	Satellite Derived Forest Phenology and Its Relation with Nephropathia Epidemica in Belgium. <i>International Journal of Environmental Research and Public Health</i> , 2010, 7, 2486-2500.	1.2	18
96	Challenges in preparing and implementing a clinical trial at field level in an Ebola emergency: A case study in Guinea, West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005545.	1.3	17
97	Common occurrence of Belerina virus, a novel paramyxovirus found in Belgian hedgehogs. <i>Scientific Reports</i> , 2020, 10, 19341.	1.6	17
98	A dynamic data-based model describing nephropathia epidemica in Belgium. <i>Biosystems Engineering</i> , 2011, 109, 77-89.	1.9	16
99	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019, 5, vez009.	2.2	16
100	Novel Filoviruses, Hantavirus, and Rhabdovirus in Freshwater Fish, Switzerland, 2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 3082-3091.	2.0	16
101	Evaluation of a norovirus sampling method using sodium dodecyl sulfate/EDTA-pretreated chromatography paper strips. <i>Journal of Virological Methods</i> , 2004, 122, 45-48.	1.0	15
102	Relating land cover and spatial distribution of nephropathia epidemica and Lyme borreliosis in Belgium. <i>International Journal of Environmental Health Research</i> , 2013, 23, 132-154.	1.3	15
103	Hepatitis C Virus NS5B Sequence-Based Genotyping Analysis of Patients From the Sharkia Governorate, Egypt. <i>Hepatitis Monthly</i> , 2013, 13, e12706.	0.1	15
104	Molecular characterization of hepatitis B virus (HBV) strains circulating in the northern coast of the Persian Gulf and its comparison with worldwide distribution of HBV subgenotype D1. <i>Journal of Medical Virology</i> , 2014, 86, 745-757.	2.5	15
105	Evaluation of the efficacy of disinfectants against Puumala hantavirus by real-time RT-PCR. <i>Journal of Virological Methods</i> , 2007, 141, 111-115.	1.0	14
106	Remotely sensed vegetation moisture as explanatory variable of Lyme borreliosis incidence. <i>International Journal of Applied Earth Observation and Geoinformation</i> , 2012, 18, 1-12.	1.4	13
107	Ecological Niche Modelling of Bank Voles in Western Europe. <i>International Journal of Environmental Research and Public Health</i> , 2013, 10, 499-514.	1.2	13
108	Identification of a novel species of papillomavirus in giraffe lesions using nanopore sequencing. <i>Veterinary Microbiology</i> , 2017, 201, 26-31.	0.8	13

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109	A lethal disease model for New World hantaviruses using immunosuppressed Syrian hamsters. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006042.	1.3	13
110	Nationwide Harmonization Effort for Semi-Quantitative Reporting of SARS-CoV-2 PCR Test Results in Belgium. <i>Viruses</i> , 2022, 14, 1294.	1.5	13
111	Hantavirus infections in Europe. <i>Lancet Infectious Diseases</i> , The, 2003, 3, 752-753.	4.6	12
112	Complete Genome Sequence of Equid Herpesvirus 3. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
113	Identification of the First SARS-CoV-2 Lineage B.1.1.529 Virus Detected in Europe. <i>Microbiology Resource Announcements</i> , 2022, 11, e0116121.	0.3	12
114	Phylogenetic analysis of Puumala virus strains from Central Europe highlights the need for a full-genome perspective on hantavirus evolution. <i>Virus Genes</i> , 2017, 53, 913-917.	0.7	11
115	Complete Genome Sequence of a New Ebola Virus Strain Isolated during the 2017 Likati Outbreak in the Democratic Republic of the Congo. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	11
116	Strengthening the Interaction of the Virology Community with the International Committee on Taxonomy of Viruses (ICTV) by Linking Virus Names and Their Abbreviations to Virus Species. <i>Systematic Biology</i> , 2019, 68, 828-839.	2.7	11
117	Novel hepatitis B virus subgenotype A8 and quasi-subgenotype D12 in African Belgian chronic carriers. <i>International Journal of Infectious Diseases</i> , 2020, 93, 98-101.	1.5	11
118	Genome Sequence of Ruloma Virus, a Novel Paramyxovirus Clustering Basally to Members of the Genus <i>Jeilongvirus</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	11
119	Genomic evidence of co-identification with Omicron and Delta SARS-CoV-2 variants: a report of two cases. <i>International Journal of Infectious Diseases</i> , 2022, 122, 212-214.	1.5	11
120	Detection of Puumala Hantavirus Antibody with ELISA Using a Recombinant Truncated Nucleocapsid Protein Expressed in <i>Escherichia coli</i> . <i>Viral Immunology</i> , 2004, 17, 315-321.	0.6	10
121	Replication reduction neutralization test, a quantitative RT-PCR-based technique for the detection of neutralizing hantavirus antibodies. <i>Journal of Virological Methods</i> , 2009, 159, 295-299.	1.0	10
122	Hantavirus nephropathy as a pseudo-import pathology from Ecuador. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2010, 29, 59-62.	1.3	10
123	Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. <i>Scientific Reports</i> , 2021, 11, 18580.	1.6	10
124	Frequency of the CCR5-Δ32 Mutant Allele Is Not Increased in Belgian Hepatitis C Virus-Infected Patients. <i>Viral Immunology</i> , 2005, 18, 232-235.	0.6	9
125	SARS-CoV-2 Permissive glioblastoma cell line for high throughput antiviral screening. <i>Antiviral Research</i> , 2022, 203, 105342.	1.9	9
126	Modelling seasonal and multi-annual variation in bank vole populations and nephropathia epidemica. <i>Biosystems Engineering</i> , 2014, 121, 25-37.	1.9	8

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127	A single bat species in Cameroon harbors multiple highly divergent papillomaviruses in stool identified by metagenomics analysis. <i>Virology Reports</i> , 2016, 6, 74-80.	0.4	8
128	Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008117.	1.3	8
129	Meeting report: Eleventh International Conference on Hantaviruses. <i>Antiviral Research</i> , 2020, 176, 104733.	1.9	8
130	Exploration of the <i>Ixodes ricinus</i> virosphere unveils an extensive virus diversity including novel coltiviruses and other reoviruses. <i>Virus Evolution</i> , 2021, 7, veab066.	2.2	8
131	Intracellular flow cytometry complements RT-qPCR detection of circulating SARS-CoV-2 variants of concern. <i>BioTechniques</i> , 2022, 72, 245-254.	0.8	8
132	Potent neutralizing anti-SARS-CoV-2 human antibodies cure infection with SARS-CoV-2 variants in hamster model. <i>IScience</i> , 2022, 25, 104705.	1.9	8
133	Use of a Commercially Available Line Probe Assay for Genotyping of Hepatitis C Virus 5a Strains. <i>Journal of Clinical Microbiology</i> , 2005, 43, 6117-6119.	1.8	7
134	Symptomatic Human Hantavirus in the Americas. <i>Emerging Infectious Diseases</i> , 2007, 13, 345-346.	2.0	7
135	Hantaviruses: Underestimated Respiratory Viruses?. <i>Clinical Infectious Diseases</i> , 2008, 46, 477-479.	2.9	7
136	Seasonal vegetation variables and their impact on the spatio-temporal patterns of nephropathia epidemica and Lyme borreliosis in Belgium. <i>Applied Geography</i> , 2013, 45, 230-240.	1.7	7
137	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015, 63, 38-41.	1.6	7
138	A decade of norovirus genetic diversity in Belgium. <i>Infection, Genetics and Evolution</i> , 2015, 30, 37-44.	1.0	7
139	First genomic characterization of a Belgian Enterovirus C104 using sequence-independent Nanopore sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104267.	1.0	7
140	The role of airborne transmission in a large single source outbreak of SARS-CoV-2 in a Belgian nursing home in 2020. <i>Epidemics</i> , 2022, 40, 100589.	1.5	7
141	High Incidence of SARS-CoV-2 Variant of Concern Breakthrough Infections Despite Residual Humoral and Cellular Immunity Induced by BNT162b2 Vaccination in Healthcare Workers: A Long-Term Follow-Up Study in Belgium. <i>Viruses</i> , 2022, 14, 1257.	1.5	7
142	Providing strong evidence of nosocomial outbreak of hepatitis B virus infection. <i>Journal of Hospital Infection</i> , 2012, 80, 269-270.	1.4	6
143	Expanding the Arterivirus Host Spectrum: Olivier's Shrew Virus 1, A Novel Arterivirus Discovered in African Giant Shrews. <i>Scientific Reports</i> , 2018, 8, 11171.	1.6	6
144	Advancing Marburg virus antiviral screening: Optimization of a novel T7 polymerase-independent minigenome system. <i>Antiviral Research</i> , 2021, 185, 104977.	1.9	6

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145	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. <i>Viruses</i> , 2021, 13, 1359.	1.5	6
146	Smoking and other risk factors for hantavirus infections: the whole story. <i>Epidemiology and Infection</i> , 2011, 139, 1284-1286.	1.0	5
147	A rare case of HBV genotype fluctuation (shifting and reversion) after liver transplantation. <i>Journal of Clinical Virology</i> , 2015, 71, 93-97.	1.6	5
148	Acute hantavirus infection presenting as haemolytic-uraemic syndrome (HUS): the importance of early clinical diagnosis. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2018, 37, 135-140.	1.3	5
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