Piet Maes

List of Publications by Year
in descending order

164 papers	11,833 citations	47006 47 h-index	34986 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. Nature, 2022, 602, 671-675.	27.8	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. Journal of Virology, 2008, 82, 3204-3219.	3.4	791
3	In vitro inhibition of severe acute respiratory syndrome coronavirus by chloroquine. Biochemical and Biophysical Research Communications, 2004, 323, 264-268.	2.1	530
4	Experimental Treatment with Favipiravir for Ebola Virus Disease (the JIKI Trial): A Historically Controlled, Single-Arm Proof-of-Concept Trial in Guinea. PLoS Medicine, 2016, 13, e1001967.	8.4	382
5	RotaC: A web-based tool for the complete genome classification of group A rotaviruses. BMC Microbiology, 2009, 9, 238.	3.3	365
6	Remdesivir, Molnupiravir and Nirmatrelvir remain active against SARS-CoV-2 Omicron and other variants of concern. Antiviral Research, 2022, 198, 105252.	4.1	302
7	The Papillomavirus Episteme: a major update to the papillomavirus sequence database. Nucleic Acids Research, 2017, 45, D499-D506.	14.5	298
8	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965.	2.1	285
9	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. Scientific Reports, 2015, 5, 16532.	3.3	277
10	Temporal and spatial analysis of the 2014â€“2015 Ebola virus outbreak in West Africa. Nature, 2015, 524, 97-101.	27.8	272
11	Antiviral Activity of Chloroquine against Human Coronavirus OC43 Infection in Newborn Mice. Antimicrobial Agents and Chemotherapy, 2009, 53, 3416-3421.	3.2	245
12	Serum neutralization of SARS-CoV-2 Omicron sublineages BA.1 and BA.2 in patients receiving monoclonal antibodies. Nature Medicine, 2022, 28, 1297-1302.	30.7	235
13	STAT2 signaling restricts viral dissemination but drives severe pneumonia in SARS-CoV-2 infected hamsters. Nature Communications, 2020, 11, 5838.	12.8	225
14	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980.	2.1	224
15	Symptomatic Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Reinfection by a Phylogenetically Distinct Strain. Clinical Infectious Diseases, 2021, 73, 354-356.	5.8	218
16	Evolutionary History of the Closely Related Group 2 Coronaviruses: Porcine Hemagglutinating Encephalomyelitis Virus, Bovine Coronavirus, and Human Coronavirus OC43. Journal of Virology, 2006, 80, 7270-7274.	3.4	212
17	Relating increasing hantavirus incidences to the changing climate: the mast connection. International Journal of Health Geographics, 2009, 8, 1.	2.5	198
18	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	2.1	184

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19	Genome-wide CRISPR screening identifies TMEM106B as a proviral host factor for SARS-CoV-2. Nature Genetics, 2021, 53, 435-444.	21.4	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. Journal of Clinical Microbiology, 2020, 58, .	3.9	160
21	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	2.1	157
22	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	2.1	153
23	Hantaviruses: Immunology, Treatment, and Prevention. Viral Immunology, 2004, 17, 481-497.	1.3	148
24	High-Throughput Analysis of Human Cytomegalovirus Genome Diversity Highlights the Widespread Occurrence of Gene-Disrupting Mutations and Pervasive Recombination. Journal of Virology, 2015, 89, 7673-7695.	3.4	148
25	A novel pancoronavirus RT-PCR assay: frequent detection of human coronavirus NL63 in children hospitalized with respiratory tract infections in Belgium. BMC Infectious Diseases, 2005, 5, 6.	2.9	143
26	Inhibition of SARS-coronavirus infection in vitro by S-nitroso-N-acetylpenicillamine, a nitric oxide donor compound. International Journal of Infectious Diseases, 2004, 8, 223-226.	3.3	142
27	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	2.1	115
28	Development of One-Step, Real-Time, Quantitative Reverse Transcriptase PCR Assays for Absolute Quantitation of Human Coronaviruses OC43 and 229E. Journal of Clinical Microbiology, 2005, 43, 5452-5456.	3.9	111
29	Classify viruses â€" the gain is worth the pain. Nature, 2019, 566, 318-320.	27.8	104
30	The omicron (B.1.1.529) SARS-CoV-2 variant of concern does not readily infect Syrian hamsters. Antiviral Research, 2022, 198, 105253.	4.1	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?. Blood, 2004, 103, 3122-3130.	1.4	102
32	Comparing infectivity and virulence of emerging SARS-CoV-2 variants in Syrian hamsters. EBioMedicine, 2021, 68, 103403.	6.1	102
33	Complex evolution and epidemiology of Dobrava-Belgrade hantavirus: definition of genotypes and their characteristics. Archives of Virology, 2013, 158, 521-529.	2.1	98
34	Hantaviridae: Current Classification and Future Perspectives. Viruses, 2019, 11, 788.	3.3	94
35	The SARS-CoV-2 and other human coronavirus spike proteins are fine-tuned towards temperature and proteases of the human airways. PLoS Pathogens, 2021, 17, e1009500.	4.7	91
36	Hemorrhagic Fever with Renal Syndrome in the New, and Hantavirus Pulmonary Syndrome in the old world: Paradi(se)gm lost or regained?. Virus Research, 2014, 187, 55-58.	2.2	90

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37	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evolution, 2018, 4, vey008.	4.9	90
38	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. Nature, 0, , .	27.8	88
39	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. Molecular Biology and Evolution, 2021, 38, 1608-1613.	8.9	79
40	Investigating the Origin and Spread of Hepatitis C Virus Genotype 5a. Journal of Virology, 2006, 80, 4220-4226.	3.4	77
41	A proposal for new criteria for the classification of hantaviruses, based on S and M segment protein sequences. Infection, Genetics and Evolution, 2009, 9, 813-820.	2.3	71
42	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-1244.	2.1	70
43	A unifying hypothesis and a single name for a complex globally emerging infection: hantavirus disease. European Journal of Clinical Microbiology and Infectious Diseases, 2012, 31, 1-5.	2.9	67
44	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2021, 166, 3513-3566.	2.1	62
45	Recent approaches in hantavirus vaccine development. Expert Review of Vaccines, 2009, 8, 67-76.	4.4	59
46	Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. Scientific Reports, 2018, 8, 9830.	3.3	59
47	Are hepatitis B virus â€œsubgenotypesâ€•defined accurately?. Journal of Clinical Virology, 2010, 47, 356-360.	3.1	57
48	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. MSphere, 2019, 4, .	2.9	57
49	Genomic and Functional Characteristics of Human Cytomegalovirus Revealed by Next-Generation Sequencing. Viruses, 2014, 6, 1049-1072.	3.3	53
50	Organ-specific genome diversity of replication-competent SARS-CoV-2. Nature Communications, 2021, 12, 6612.	12.8	49
51	Beechnuts and outbreaks of nephropathia epidemica (NE): of mast, mice and men. Nephrology Dialysis Transplantation, 2010, 25, 1740-1746.	0.7	47
52	Novel hepatitis B virus subgenotype A6 in African-Belgian patients. Journal of Clinical Virology, 2010, 47, 93-96.	3.1	46
53	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. Gut, 2018, 67, 1558-1559.	12.1	46
54	Another case of â€œEuropean hantavirus pulmonary syndromeâ€•with severe lung, prior to kidney, involvement, and diagnosed by viral inclusions in lung macrophages. European Journal of Clinical Microbiology and Infectious Diseases, 2013, 32, 1341-1345.	2.9	44

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55	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. Scientific Reports, 2016, 6, 34209.	3.3	44
56	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. Emerging Microbes and Infections, 2017, 6, 1-7.	6.5	44
57	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. BMC Genomics, 2017, 18, 249.	2.8	42
58	An affinity-enhanced, broadly neutralizing heavy chainâ€"only antibody protects against SARS-CoV-2 infection in animal models. Science Translational Medicine, 2021, 13, eabi7826.	12.4	41
59	Human cytomegalovirus genomics and transcriptomics through the lens of next-generation sequencing: revision and future challenges. Virus Genes, 2019, 55, 138-164.	1.6	39
60	First evidence of fatal hantavirus nephropathy in India, mimicking leptospirosis. Nephrology Dialysis Transplantation, 2006, 21, 826-827.	0.7	36
61	Honey-beeâ€"associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10511-10519.	7.1	36
62	Molecular evolutionary analysis and mutational pattern of fullâ€length genomes of hepatitis B virus isolated from Belgian patients with different clinical manifestations. Journal of Medical Virology, 2010, 82, 379-389.	5.0	35
63	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. BMC Genomics, 2018, 19, 617.	2.8	35
64	Tumor Necrosis Factor-Î± Genetic Predisposing Factors Can Influence Clinical Severity in Nephropathia Epidemica. Viral Immunology, 2006, 19, 558-564.	1.3	33
65	Phylogenetic analysis of hepatitis B virus full-length genomes reveals evidence for a large nosocomial outbreak in Belgium. Journal of Clinical Virology, 2009, 46, 61-68.	3.1	33
66	Growth kinetics of SARS-coronavirus in Vero E6 cells. Biochemical and Biophysical Research Communications, 2005, 329, 1147-1151.	2.1	32
67	Analysis of Diagnostic Findings From the European Mobile Laboratory in GuÃ©ckÃ©dou, Guinea, March 2014 Through March 2015. Journal of Infectious Diseases, 2016, 214, S250-S257.	4.0	32
68	Concomitant leptospirosis-hantavirus co-infection in acute patients hospitalized in Sri Lanka: implications for a potentially worldwide underestimated problem. Epidemiology and Infection, 2015, 143, 2081-2093.	2.1	31
69	Isolation of infectious Lloviu virus from Schreiberâ€™s bats in Hungary. Nature Communications, 2022, 13, 1706.	12.8	31
70	The virota and its transkingdom interactions in the healthy infant gut. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114619119.	7.1	30
71	Using the Gravity Model to Estimate the Spatial Spread of Vector-Borne Diseases. International Journal of Environmental Research and Public Health, 2012, 9, 4346-4364.	2.6	29
72	Evolutionary analysis of HBV â€œSâ€•antigen genetic diversity in Iranian blood donors: A nationwide study. Journal of Medical Virology, 2014, 86, 144-155.	5.0	28

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73	Spatioâ€temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. Molecular Ecology, 2016, 25, 5994-6008.	3.9	28
74	ACUTE KIDNEY INJURY IN EMERGING, NON-TROPICAL INFECTIONS. Acta Clinica Belgica, 2007, 62, 387-395.	1.2	27
75	Exhaled breath condensate sampling is not a new method for detection of respiratory viruses. Virology Journal, 2011, 8, 98.	3.4	26
76	Genomic Diversity of Hepatitis B Virus Infection Associated With Fulminant Hepatitis B Development. Hepatitis Monthly, 2015, 15, e29477.	0.2	26
77	Plasma Exchange--Associated Immunoglobulin M--Negative Hantavirus Disease after a Camping Holiday in Southern France. Clinical Infectious Diseases, 2004, 38, 1350-1356.	5.8	24
78	Viral load quantitation of SARS-coronavirus RNA using a one-step real-time RT-PCR. International Journal of Infectious Diseases, 2006, 10, 32-37.	3.3	24
79	Modelâ€based Prediction of Nephropathia Epidemica Outbreaks Based on Climatological and Vegetation Data and Bank Vole Population Dynamics. Zoonoses and Public Health, 2013, 60, 461-477.	2.2	24
80	Chromatography Paper Strip Method for Collection, Transportation, and Storage of Rotavirus RNA in Stool Samples. Journal of Clinical Microbiology, 2004, 42, 1605-1608.	3.9	23
81	HBV subgenotype misclassification expands quasi-subgenotype A3. Clinical Microbiology and Infection, 2011, 17, 947-949.	6.0	23
82	Molecular characterization of hepatitis B virus strains circulating in Belgian patients coâ€infected with HIV and HBV: Overt and occult infection. Journal of Medical Virology, 2011, 83, 1876-1884.	5.0	23
83	A Novel Hantavirus of the European Mole, Bruges Virus, Is Involved in Frequent Nova Virus Coinfections. Genome Biology and Evolution, 2018, 10, 45-55.	2.5	23
84	A Method Enabling High-Throughput Sequencing of Human Cytomegalovirus Complete Genomes from Clinical Isolates. PLoS ONE, 2014, 9, e95501.	2.5	23
85	Chromatography paper strip sampling of enteric adenoviruses type 40 and 41 positive stool specimens. Virology Journal, 2005, 2, 6.	3.4	22
86	Glycoprotein-Specific Antibodies Produced by DNA Vaccination Protect Guinea Pigs from Lethal Argentine and Venezuelan Hemorrhagic Fever. Journal of Virology, 2016, 90, 3515-3529.	3.4	21
87	Truncated Recombinant Dobrava Hantavirus Nucleocapsid Proteins Induce Strong, Long-Lasting Immune Responses in Mice. Intervirology, 2006, 49, 253-260.	2.8	20
88	Antibiotic Resistance Plasmids Cointegrated into a Megaplasmid Harboring the bla _{OXA-427} Carbapenemase Gene. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	20
89	Anatomy of Omicron BA.1 and BA.2 neutralizing antibodies in COVID-19 mRNA vaccinees. Nature Communications, 2022, 13, .	12.8	20
90	The characterization of multiple novel paramyxoviruses highlights the diverse nature of the subfamilyOrthoparamyxovirinae. Virus Evolution, 2022, 8, .	4.9	20

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91	Grotenhout Virus, a Novel Nairovirus Found in Ixodes ricinus in Belgium. Genome Announcements, 2017, 5, .	0.8	19
92	Characterization of a Novel Polyomavirus Isolated from a Fibroma on the Trunk of an African Elephant (Loxodonta africana). PLoS ONE, 2013, 8, e77884.	2.5	19
93	<i>In vitro</i> antiviral activity of some novel isatin derivatives against HCV and SARS-CoV viruses. Indian Journal of Pharmaceutical Sciences, 2008, 70, 91.	1.0	19
94	Truncated Recombinant Puumala Virus Nucleocapsid Proteins Protect Mice Against Challengein Vivo. Viral Immunology, 2008, 21, 49-60.	1.3	18
95	Satellite Derived Forest Phenology and Its Relation with Nephropathia Epidemica in Belgium. International Journal of Environmental Research and Public Health, 2010, 7, 2486-2500.	2.6	18
96	Challenges in preparing and implementing a clinical trial at field level in an Ebola emergency: A case study in Guinea, West Africa. PLoS Neglected Tropical Diseases, 2017, 11, e0005545.	3.0	17
97	Common occurrence of Belerina virus, a novel paramyxovirus found in Belgian hedgehogs. Scientific Reports, 2020, 10, 19341.	3.3	17
98	A dynamic data-based model describing nephropathia epidemica in Belgium. Biosystems Engineering, 2011, 109, 77-89.	4.3	16
99	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. Virus Evolution, 2019, 5, vez009.	4.9	16
100	Novel Filoviruses, Hantavirus, and Rhabdovirus in Freshwater Fish, Switzerland, 2017. Emerging Infectious Diseases, 2021, 27, 3082-3091.	4.3	16
101	Evaluation of a norovirus sampling method using sodium dodecyl sulfate/EDTA-pretreated chromatography paper strips. Journal of Virological Methods, 2004, 122, 45-48.	2.1	15
102	Relating land cover and spatial distribution of nephropathia epidemica and Lyme borreliosis in Belgium. International Journal of Environmental Health Research, 2013, 23, 132-154.	2.7	15
103	Hepatitis C Virus NS5B Sequence-Based Genotyping Analysis of Patients From the Sharkia Governorate, Egypt. Hepatitis Monthly, 2013, 13, e12706.	0.2	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. Journal of Medical Virology, 2014, 86, 745-757.	5.0	15
105	Evaluation of the efficacy of disinfectants against Puumala hantavirus by real-time RT-PCR. Journal of Virological Methods, 2007, 141, 111-115.	2.1	14
106	Remotely sensed vegetation moisture as explanatory variable of Lyme borreliosis incidence. International Journal of Applied Earth Observation and Geoinformation, 2012, 18, 1-12.	2.8	13
107	Ecological Niche Modelling of Bank Voles in Western Europe. International Journal of Environmental Research and Public Health, 2013, 10, 499-514.	2.6	13
108	Identification of a novel species of papillomavirus in giraffe lesions using nanopore sequencing. Veterinary Microbiology, 2017, 201, 26-31.	1.9	13

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109	A lethal disease model for New World hantaviruses using immunosuppressed Syrian hamsters. PLoS Neglected Tropical Diseases, 2017, 11, e0006042.	3.0	13
110	Nationwide Harmonization Effort for Semi-Quantitative Reporting of SARS-CoV-2 PCR Test Results in Belgium. Viruses, 2022, 14, 1294.	3.3	13
111	Hantavirus infections in Europe. Lancet Infectious Diseases, The, 2003, 3, 752-753.	9.1	12
112	Complete Genome Sequence of Equid Herpesvirus 3. Genome Announcements, 2014, 2, .	0.8	12
113	Identification of the First SARS-CoV-2 Lineage B.1.1.529 Virus Detected in Europe. Microbiology Resource Announcements, 2022, 11, e0116121.	0.6	12
114	Phylogenetic analysis of Puumala virus strains from Central Europe highlights the need for a full-genome perspective on hantavirus evolution. Virus Genes, 2017, 53, 913-917.	1.6	11
115	Complete Genome Sequence of a New Ebola Virus Strain Isolated during the 2017 Likati Outbreak in the Democratic Republic of the Congo. Microbiology Resource Announcements, 2019, 8, .	0.6	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. Systematic Biology, 2019, 68, 828-839.	5.6	11
117	Novel hepatitis B virus subgenotype A8 and quasi-subgenotype D12 in Africanâ€"Belgian chronic carriers. International Journal of Infectious Diseases, 2020, 93, 98-101.	3.3	11
118	Genome Sequence of Ruloma Virus, a Novel Paramyxovirus Clustering Basally to Members of the Genus Jeilongvirus. Microbiology Resource Announcements, 2021, 10, .	0.6	11
119	Genomic evidence of co-identification with Omicron and Delta SARS-CoV-2 variants: a report of two cases. International Journal of Infectious Diseases, 2022, 122, 212-214.	3.3	11
120	Detection of Puumala Hantavirus Antibody with ELISA Using a Recombinant Truncated Nucleocapsid Protein Expressed inEscherichia coli. Viral Immunology, 2004, 17, 315-321.	1.3	10
121	Replication reduction neutralization test, a quantitative RT-PCR-based technique for the detection of neutralizing hantavirus antibodies. Journal of Virological Methods, 2009, 159, 295-299.	2.1	10
122	Hantavirus nephropathy as a pseudo-import pathology from Ecuador. European Journal of Clinical Microbiology and Infectious Diseases, 2010, 29, 59-62.	2.9	10
123	Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. Scientific Reports, 2021, 11, 18580.	3.3	10
124	Frequency of the CCR5-Î"32 Mutant Allele Is Not Increased in Belgian Hepatitis C Virus-Infected Patients. Viral Immunology, 2005, 18, 232-235.	1.3	9
125	SARS-CoV-2 Permissive glioblastoma cell line for high throughput antiviral screening. Antiviral Research, 2022, 203, 105342.	4.1	9
126	Modelling seasonal and multi-annual variation in bank vole populations and nephropathia epidemica. Biosystems Engineering, 2014, 121, 25-37.	4.3	8

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127	A single bat species in Cameroon harbors multiple highly divergent papillomaviruses in stool identified by metagenomics analysis. Virology Reports, 2016, 6, 74-80.	0.4	8
128	Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. PLoS Neglected Tropical Diseases, 2020, 14, e0008117.	3.0	8
129	Meeting report: Eleventh International Conference on Hantaviruses. Antiviral Research, 2020, 176, 104733.	4.1	8
130	Exploration of the Ixodes ricinus virosphere unveils an extensive virus diversity including novel coltiviruses and other reoviruses. Virus Evolution, 2021, 7, veab066.	4.9	8
131	Intracellular flow cytometry complements RT-qPCR detection of circulating SARS-CoV-2 variants of concern. BioTechniques, 2022, 72, 245-254.	1.8	8
132	Potent neutralizing anti-SARS-CoV-2 human antibodies cure infection with SARS-CoV-2 variants in hamster model. IScience, 2022, 25, 104705.	4.1	8
133	Use of a Commercially Available Line Probe Assay for Genotyping of Hepatitis C Virus 5a Strains. Journal of Clinical Microbiology, 2005, 43, 6117-6119.	3.9	7
134	Symptomatic Human Hantavirus in the Americas. Emerging Infectious Diseases, 2007, 13, 345-346.	4.3	7
135	Hantaviruses: Underestimated Respiratory Viruses?. Clinical Infectious Diseases, 2008, 46, 477-479.	5.8	7
136	Seasonal vegetation variables and their impact on the spatio-temporal patterns of nephropathia epidemica and Lyme borreliosis in Belgium. Applied Geography, 2013, 45, 230-240.	3.7	7
137	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. Journal of Clinical Virology, 2015, 63, 38-41.	3.1	7
138	A decade of norovirus genetic diversity in Belgium. Infection, Genetics and Evolution, 2015, 30, 37-44.	2.3	7
139	First genomic characterization of a Belgian Enterovirus C104 using sequence-independent Nanopore sequencing. Infection, Genetics and Evolution, 2020, 81, 104267.	2.3	7
140	The role of airborne transmission in a large single source outbreak of SARS-CoV-2 in a Belgian nursing home in 2020. Epidemics, 2022, 40, 100589.	3.0	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. Viruses, 2022, 14, 1257.	3.3	7
142	Providing strong evidence of nosocomial outbreak of hepatitis B virus infection. Journal of Hospital Infection, 2012, 80, 269-270.	2.9	6
143	Expanding the Arterivirus Host Spectrum: Olivierâ€™s Shrew Virus 1, A Novel Arterivirus Discovered in African Giant Shrews. Scientific Reports, 2018, 8, 11171.	3.3	6
144	Advancing Marburg virus antiviral screening: Optimization of a novel T7 polymerase-independent minigenome system. Antiviral Research, 2021, 185, 104977.	4.1	6

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145	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. Viruses, 2021, 13, 1359.	3.3	6
146	Smoking and other risk factors for hantavirus infections: the whole story. Epidemiology and Infection, 2011, 139, 1284-1286.	2.1	5
147	A rare case of HBV genotype fluctuation (shifting and reversion) after liver transplantation. Journal of Clinical Virology, 2015, 71, 93-97.	3.1	5
148	Acute hantavirus infection presenting as haemolytic-uraemic syndrome (HUS): the importance of early clinical diagnosis. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 135-140.	2.9	5
149	Chloroquine, an Anti-Malaria Drug as Effective Prevention for Hantavirus Infections. Frontiers in Cellular and Infection Microbiology, 2021, 11, 580532.	3.9	5
150	Genomic characterization of Erethizon dorsatum papillomavirus 2, a new papillomavirus species marked by its exceptional genome size. Journal of General Virology, 2018, 99, 1699-1704.	2.9	5
151	Identification of novel Ebola virus inhibitors using biologically contained virus. Antiviral Research, 2022, 200, 105294.	4.1	5
152	Puumala virus reference strain for hantavirus serodiagnosis in France. European Journal of Clinical Microbiology and Infectious Diseases, 2010, 29, 1-2.	2.9	4
153	Susceptibility of the PER.C6 cell line for infection with clinical human respiratory syncytial virus isolates. Journal of Virological Methods, 2012, 181, 37-42.	2.1	4
154	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. Viruses, 2021, 13, 1842.	3.3	4
155	Complete Genome Sequence of Nova Virus, a Hantavirus Circulating in the European Mole in Belgium. Genome Announcements, 2015, 3, .	0.8	3
156	Comment on â€œA Cluster of Three Cases of Hantavirus Pulmonary Syndrome among Canadian Military Personnelâ€• Canadian Journal of Infectious Diseases and Medical Microbiology, 2016, 2016, 1-3.	1.9	3
157	Virus Hunting: Discovery of New Episomal Circular Viruses by Rolling Circle Techniques. Current Protocols in Microbiology, 2017, 44, 1E.12.1-1E.12.18.	6.5	3
158	Poliovirus sampling by using sodium dodecyl sulfate/EDTA-pretreated chromatography paper strips. Biochemical and Biophysical Research Communications, 2004, 325, 711-715.	2.1	2
159	Severe crescentic glomerulonephritis linked to an acute Hantaan virus infection?. Nephrology Dialysis Transplantation, 2011, 26, 1448-1449.	0.7	2
160	Host switching pathogens, infectious outbreaks and zoonosis: A Marie SkÅ‚odowska-Curie innovative training network (HONOURs). Virus Research, 2018, 257, 120-124.	2.2	2
161	Complete Genome Sequence of a Papillomavirus Isolated from the European Mole. Genome Announcements, 2013, 1, .	0.8	1
162	Letter to the editor: The first tick-borne encephalitis case in the Netherlands: reflections and a note of caution. Eurosurveillance, 2016, 21, .	7.0	1

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163	A confirmed case of COVID-19 reinfection with a genetically distinct strain: a case report from Belgium. Acta Clinica Belgica, 2021, , 1-2.	1.2	0
164	In Vivo Evaluation of Antiviral Compounds on Respiratory Syncytial Virus Using a Juvenile Vervet Monkey (Chlorocebus pygerythrus) Infection Model. Methods in Molecular Biology, 2013, 1030, 373-382.	0.9	0