

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	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
3	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
4	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
5	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
6	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
7	Isolation of infectious Lloviu virus from Schreiberâ€™s bats in Hungary. <i>Nature Communications</i> , 2022, 13, 1706.	5.8	31
8	Identification of novel Ebola virus inhibitors using biologically contained virus. <i>Antiviral Research</i> , 2022, 200, 105294.	1.9	5
9	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
10	SARS-CoV-2 Permissive glioblastoma cell line for high throughput antiviral screening. <i>Antiviral Research</i> , 2022, 203, 105342.	1.9	9
11	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
12	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
13	Anatomy of Omicron BA.1 and BA.2 neutralizing antibodies in COVID-19 mRNA vaccinees. <i>Nature Communications</i> , 2022, 13, .	5.8	20
14	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
15	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
16	The characterization of multiple novel paramyxoviruses highlights the diverse nature of the subfamily Orthoparamyxovirinae. <i>Virus Evolution</i> , 2022, 8, .	2.2	20
17	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
18	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

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19	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
20	Advancing Marburg virus antiviral screening: Optimization of a novel T7 polymerase-independent minigenome system. <i>Antiviral Research</i> , 2021, 185, 104977.	1.9	6
21	Chloroquine, an Anti-Malaria Drug as Effective Prevention for Hantavirus Infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 580532.	1.8	5
22	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
23	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
24	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
25	A confirmed case of COVID-19 reinfection with a genetically distinct strain: a case report from Belgium. <i>Acta Clinica Belgica</i> , 2021, , 1-2.	0.5	0
26	Comparing infectivity and virulence of emerging SARS-CoV-2 variants in Syrian hamsters. <i>EBioMedicine</i> , 2021, 68, 103403.	2.7	102
27	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
28	Exploration of the <i>Ixodes ricinus</i> virosphere unveils an extensive virus diversity including novel coltivirus and other reoviruses. <i>Virus Evolution</i> , 2021, 7, veab066.	2.2	8
29	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
30	Phylogenomic Characterization of Lopma Virus and Praja Virus, Two Novel Rodent-Borne Arteriviruses. <i>Viruses</i> , 2021, 13, 1842.	1.5	4
31	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
32	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
33	Organ-specific genome diversity of replication-competent SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 6612.	5.8	49
34	Novel Filoviruses, Hantavirus, and Rhabdovirus in Freshwater Fish, Switzerland, 2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 3082-3091.	2.0	16
35	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
36	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

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37	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	0.9	184
38	Common occurrence of Belerina virus, a novel paramyxovirus found in Belgian hedgehogs. Scientific Reports, 2020, 10, 19341.	1.6	17
39	Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. PLoS Neglected Tropical Diseases, 2020, 14, e0008117.	1.3	8
40	Novel hepatitis B virus subgenotype A8 and quasi-subgenotype D12 in African"Belgian chronic carriers. International Journal of Infectious Diseases, 2020, 93, 98-101.	1.5	11
41	Meeting report: Eleventh International Conference on Hantaviruses. Antiviral Research, 2020, 176, 104733.	1.9	8
42	First genomic characterization of a Belgian Enterovirus C104 using sequence-independent Nanopore sequencing. Infection, Genetics and Evolution, 2020, 81, 104267.	1.0	7
43	Honey-bee"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.	3.3	36
44	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. Virus Evolution, 2019, 5, vez009.	2.2	16
45	Hantaviridae: Current Classification and Future Perspectives. Viruses, 2019, 11, 788.	1.5	94
46	Classify viruses " the gain is worth the pain. Nature, 2019, 566, 318-320.	13.7	104
47	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-1244.	0.9	70
48	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	0.9	115
49	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. MSphere, 2019, 4, .	1.3	57
50	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, .	0.3	11
51	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965.	0.9	285
52	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980.	0.9	224
53	Human cytomegalovirus genomics and transcriptomics through the lens of next-generation sequencing: revision and future challenges. Virus Genes, 2019, 55, 138-164.	0.7	39
54	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.	2.7	11

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55	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	0.9	157
56	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	0.9	153
57	Antibiotic Resistance Plasmids Cointegrated into a Megaplasmid Harboring the <i>bla</i> _{OXA-427} Carbapenemase Gene. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	20
58	A Novel Hantavirus of the European Mole, Bruges Virus, Is Involved in Frequent Nova Virus Coinfections. Genome Biology and Evolution, 2018, 10, 45-55.	1.1	23
59	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. Gut, 2018, 67, 1558-1559.	6.1	46
60	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.	1.3	5
61	Host switching pathogens, infectious outbreaks and zoonosis: A Marie Skłodowska-Curie innovative training network (HONOURs). Virus Research, 2018, 257, 120-124.	1.1	2
62	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. BMC Genomics, 2018, 19, 617.	1.2	35
63	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.	1.6	59
64	Expanding the Arterivirus Host Spectrum: Olivier's Shrew Virus 1, A Novel Arterivirus Discovered in African Giant Shrews. Scientific Reports, 2018, 8, 11171.	1.6	6
65	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evolution, 2018, 4, vey008.	2.2	90
66	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.	1.3	5
67	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
68	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. Emerging Microbes and Infections, 2017, 6, 1-7.	3.0	44
69	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. BMC Genomics, 2017, 18, 249.	1.2	42
70	Identification of a novel species of papillomavirus in giraffe lesions using nanopore sequencing. Veterinary Microbiology, 2017, 201, 26-31.	0.8	13
71	The Papillomavirus Episteme: a major update to the papillomavirus sequence database. Nucleic Acids Research, 2017, 45, D499-D506.	6.5	298
72	Grotenhout Virus, a Novel Nairovirus Found in Ixodes ricinus in Belgium. Genome Announcements, 2017, 5, .	0.8	19

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73	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
74	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
75	A lethal disease model for New World hantaviruses using immunosuppressed Syrian hamsters. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006042.	1.3	13
76	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
77	Comment on "A Cluster of Three Cases of Hantavirus Pulmonary Syndrome among Canadian Military Personnel": <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016, 2016, 1-3.	0.7	3
78	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
79	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
80	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
81	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209.	1.6	44
82	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
83	Letter to the editor: The first tick-borne encephalitis case in the Netherlands: reflections and a note of caution. <i>Eurosurveillance</i> , 2016, 21, .	3.9	1
84	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
85	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
86	Temporal and spatial analysis of the 2014-2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101.	13.7	272
87	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
88	Complete Genome Sequence of Nova Virus, a Hantavirus Circulating in the European Mole in Belgium. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
89	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
90	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

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91	A decade of norovirus genetic diversity in Belgium. <i>Infection, Genetics and Evolution</i> , 2015, 30, 37-44.	1.0	7
92	Genomic Diversity of Hepatitis B Virus Infection Associated With Fulminant Hepatitis B Development. <i>Hepatitis Monthly</i> , 2015, 15, e29477.	0.1	26
93	Genomic and Functional Characteristics of Human Cytomegalovirus Revealed by Next-Generation Sequencing. <i>Viruses</i> , 2014, 6, 1049-1072.	1.5	53
94	Complete Genome Sequence of Equid Herpesvirus 3. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
95	Modelling seasonal and multi-annual variation in bank vole populations and nephropathia epidemica. <i>Biosystems Engineering</i> , 2014, 121, 25-37.	1.9	8
96	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
97	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
98	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
99	A Method Enabling High-Throughput Sequencing of Human Cytomegalovirus Complete Genomes from Clinical Isolates. <i>PLoS ONE</i> , 2014, 9, e95501.	1.1	23
100	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
101	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
102	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
103	Another case of α -European hantavirus pulmonary syndrome α -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
104	Complete Genome Sequence of a Papillomavirus Isolated from the European Mole. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
105	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
106	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
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	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

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109	In Vivo Evaluation of Antiviral Compounds on Respiratory Syncytial Virus Using a Juvenile Vervet Monkey (<i>Chlorocebus pygerythrus</i>) Infection Model. <i>Methods in Molecular Biology</i> , 2013, 1030, 373-382.	0.4	0
110	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
111	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
112	Susceptibility of the PER.C6 cell line for infection with clinical human respiratory syncytial virus isolates. <i>Journal of Virological Methods</i> , 2012, 181, 37-42.	1.0	4
113	Providing strong evidence of nosocomial outbreak of hepatitis B virus infection. <i>Journal of Hospital Infection</i> , 2012, 80, 269-270.	1.4	6
114	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
115	Smoking and other risk factors for hantavirus infections: the whole story. <i>Epidemiology and Infection</i> , 2011, 139, 1284-1286.	1.0	5
116	HBV subgenotype misclassification expands quasi-subgenotype A3. <i>Clinical Microbiology and Infection</i> , 2011, 17, 947-949.	2.8	23
117	Exhaled breath condensate sampling is not a new method for detection of respiratory viruses. <i>Virology Journal</i> , 2011, 8, 98.	1.4	26
118	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
119	A dynamic data-based model describing nephropathia epidemica in Belgium. <i>Biosystems Engineering</i> , 2011, 109, 77-89.	1.9	16
120	Severe crescentic glomerulonephritis linked to an acute Hantaan virus infection?. <i>Nephrology Dialysis Transplantation</i> , 2011, 26, 1448-1449.	0.4	2
121	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
122	Puumala virus reference strain for hantavirus serodiagnosis in France. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2010, 29, 1-2.	1.3	4
123	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
124	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
125	Beechnuts and outbreaks of nephropathia epidemica (NE): of mast, mice and men. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 1740-1746.	0.4	47
126	Novel hepatitis B virus subgenotype A6 in African-Belgian patients. <i>Journal of Clinical Virology</i> , 2010, 47, 93-96.	1.6	46

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127	Are hepatitis B virus "subgenotypes" defined accurately?. <i>Journal of Clinical Virology</i> , 2010, 47, 356-360.	1.6	57
128	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
129	RotaC: A web-based tool for the complete genome classification of group A rotaviruses. <i>BMC Microbiology</i> , 2009, 9, 238.	1.3	365
130	Relating increasing hantavirus incidences to the changing climate: the mast connection. <i>International Journal of Health Geographics</i> , 2009, 8, 1.	1.2	198
131	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
132	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
133	Recent approaches in hantavirus vaccine development. <i>Expert Review of Vaccines</i> , 2009, 8, 67-76.	2.0	59
134	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
135	Truncated Recombinant Puumala Virus Nucleocapsid Proteins Protect Mice Against Challenge in Vivo. <i>Viral Immunology</i> , 2008, 21, 49-60.	0.6	18
136	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
137	Hantaviruses: Underestimated Respiratory Viruses?. <i>Clinical Infectious Diseases</i> , 2008, 46, 477-479.	2.9	7
138	<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
139	ACUTE KIDNEY INJURY IN EMERGING, NON-TROPICAL INFECTIONS. <i>Acta Clinica Belgica</i> , 2007, 62, 387-395.	0.5	27
140	Symptomatic Human Hantavirus in the Americas. <i>Emerging Infectious Diseases</i> , 2007, 13, 345-346.	2.0	7
141	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
142	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
143	First evidence of fatal hantavirus nephropathy in India, mimicking leptospirosis. <i>Nephrology Dialysis Transplantation</i> , 2006, 21, 826-827.	0.4	36
144	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

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145	Investigating the Origin and Spread of Hepatitis C Virus Genotype 5a. <i>Journal of Virology</i> , 2006, 80, 4220-4226.	1.5	77
146	Truncated Recombinant Dobrava Hantavirus Nucleocapsid Proteins Induce Strong, Long-Lasting Immune Responses in Mice. <i>Intervirology</i> , 2006, 49, 253-260.	1.2	20
147	Tumor Necrosis Factor- α Genetic Predisposing Factors Can Influence Clinical Severity in Nephropathia Epidemica. <i>Viral Immunology</i> , 2006, 19, 558-564.	0.6	33
148	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
149	Frequency of the CCR5- Δ 32 Mutant Allele Is Not Increased in Belgian Hepatitis C Virus-Infected Patients. <i>Viral Immunology</i> , 2005, 18, 232-235.	0.6	9
150	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
151	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
152	Growth kinetics of SARS-coronavirus in Vero E6 cells. <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 1147-1151.	1.0	32
153	Chromatography paper strip sampling of enteric adenoviruses type 40 and 41 positive stool specimens. <i>Virology Journal</i> , 2005, 2, 6.	1.4	22
154	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
155	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
156	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
157	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
158	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
159	Hantaviruses: Immunology, Treatment, and Prevention. <i>Viral Immunology</i> , 2004, 17, 481-497.	0.6	148
160	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
161	Poliovirus sampling by using sodium dodecyl sulfate/EDTA-pretreated chromatography paper strips. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 711-715.	1.0	2
162	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

#	ARTICLE	IF	CITATIONS
163	Hantavirus infections in Europe. Lancet Infectious Diseases, The, 2003, 3, 752-753.	4.6	12
164	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. Nature, 0, , .	13.7	88