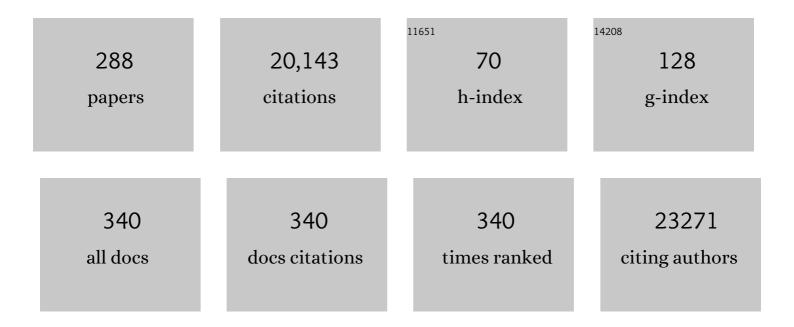
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Receptor and viral determinants of SARS-coronavirus adaptation to human ACE2. EMBO Journal, 2005, 24, 1634-1643.	7.8	892
2	Animal models for COVID-19. Nature, 2020, 586, 509-515.	27.8	705
3	Virus taxonomy in the age of metagenomics. Nature Reviews Microbiology, 2017, 15, 161-168.	28.6	590
4	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. Nature Biotechnology, 2019, 37, 632-639.	17.5	569
5	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). Archives of Virology, 2018, 163, 2601-2631.	2.1	567
6	Distinct Patterns of IFITM-Mediated Restriction of Filoviruses, SARS Coronavirus, and Influenza A Virus. PLoS Pathogens, 2011, 7, e1001258.	4.7	518
7	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). Archives of Virology, 2017, 162, 2505-2538.	2.1	506
8	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	17.5	414
9	Proposal for a revised taxonomy of the family Filoviridae: classification, names of taxa and viruses, and virus abbreviations. Archives of Virology, 2010, 155, 2083-2103.	2.1	407
10	Taxonomy of the order Mononegavirales: update 2016. Archives of Virology, 2016, 161, 2351-2360.	2.1	407
11	Origins and Evolution of the Global RNA Virome. MBio, 2018, 9, .	4.1	383
12	Molecular Evidence of Sexual Transmission of Ebola Virus. New England Journal of Medicine, 2015, 373, 2448-2454.	27.0	380
13	Global Organization and Proposed Megataxonomy of the Virus World. Microbiology and Molecular Biology Reviews, 2020, 84, .	6.6	378
14	Transferrin receptor 1 is a cellular receptor for New World haemorrhagic fever arenaviruses. Nature, 2007, 446, 92-96.	27.8	374
15	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	27.8	346
16	Antiviral Potential of ERK/MAPK and PI3K/AKT/mTOR Signaling Modulation for Middle East Respiratory Syndrome Coronavirus Infection as Identified by Temporal Kinome Analysis. Antimicrobial Agents and Chemotherapy, 2015, 59, 1088-1099.	3.2	344
17	Ebola virus disease. Nature Reviews Disease Primers, 2020, 6, 13.	30.5	340
18	Taxonomy of the order Bunyavirales: update 2019. Archives of Virology, 2019, 164, 1949-1965.	2.1	285

#	Article	IF	CITATIONS
19	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. Cell, 2015, 161, 1516-1526.	28.9	275
20	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Archives of Virology, 2016, 161, 2921-2949.	2.1	263
21	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). Archives of Virology, 2019, 164, 2417-2429.	2.1	257
22	Reorganization and expansion of the nidoviral family Arteriviridae. Archives of Virology, 2016, 161, 755-768.	2.1	254
23	Animal Origins of the Severe Acute Respiratory Syndrome Coronavirus: Insight from ACE2-S-Protein Interactions. Journal of Virology, 2006, 80, 4211-4219.	3.4	247
24	Retroviruses Pseudotyped with the Severe Acute Respiratory Syndrome Coronavirus Spike Protein Efficiently Infect Cells Expressing Angiotensin-Converting Enzyme 2. Journal of Virology, 2004, 78, 10628-10635.	3.4	240
25	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980.	2.1	224
26	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. Nature Microbiology, 2021, 6, 821-823.	13.3	221
27	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Archives of Virology, 2021, 166, 2633-2648.	2.1	219
28	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). Archives of Virology, 2020, 165, 2737-2748.	2.1	202
29	The new scope of virus taxonomy: partitioning the virosphere into 15 hierarchical ranks. Nature Microbiology, 2020, 5, 668-674.	13.3	198
30	What's new in the renin-angiotensin system?. Cellular and Molecular Life Sciences, 2004, 61, 2738-2743.	5.4	197
31	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
32	Taxonomy of the order Mononegavirales: update 2017. Archives of Virology, 2017, 162, 2493-2504.	2.1	173
33	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. Archives of Virology, 2018, 163, 1125-1129.	2.1	172
34	Past, present, and future of arenavirus taxonomy. Archives of Virology, 2015, 160, 1851-1874.	2.1	158
35	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	2.1	157
36	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	2.1	153

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37	The S proteins of human coronavirus NL63 and severe acute respiratory syndrome coronavirus bind overlapping regions of ACE2. Virology, 2007, 367, 367-374.	2.4	145
38	Filoviruses. A compendium of 40 years of epidemiological, clinical, and laboratory studies. Archives of Virology Supplementum, 2008, 20, 13-360.	3.0	141
39	The Primed Ebolavirus Glycoprotein (19-Kilodalton GP _{1,2}): Sequence and Residues Critical for Host Cell Binding. Journal of Virology, 2009, 83, 2883-2891.	3.4	140
40	Infectious Lassa Virus, but Not Filoviruses, Is Restricted by BST-2/Tetherin. Journal of Virology, 2010, 84, 10569-10580.	3.4	125
41	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. Science, 2022, 376, 156-162.	12.6	124
42	<i>Cressdnaviricota</i> : a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. Journal of Virology, 2020, 94, .	3.4	118
43	Conserved Receptor-binding Domains of Lake Victoria Marburgvirus and Zaire Ebolavirus Bind a Common Receptor. Journal of Biological Chemistry, 2006, 281, 15951-15958.	3.4	115
44	Taxonomy of the order Bunyavirales: second update 2018. Archives of Virology, 2019, 164, 927-941.	2.1	115
45	Receptor determinants of zoonotic transmission of New World hemorrhagic fever arenaviruses. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2664-2669.	7.1	112
46	Filovirus receptor NPC1 contributes to species-specific patterns of ebolavirus susceptibility in bats. ELife, 2015, 4, .	6.0	110
47	IFITM-2 and IFITM-3 but Not IFITM-1 Restrict Rift Valley Fever Virus. Journal of Virology, 2013, 87, 8451-8464.	3.4	109
48	Neglected filoviruses. FEMS Microbiology Reviews, 2016, 40, 494-519.	8.6	106
49	Identification and pathological characterization of persistent asymptomatic Ebola virus infection in rhesus monkeys. Nature Microbiology, 2017, 2, 17113.	13.3	104
50	Classify viruses — the gain is worth the pain. Nature, 2019, 566, 318-320.	27.8	104
51	Minigenomes, transcription and replication competent virus-like particles and beyond: Reverse genetics systems for filoviruses and other negative stranded hemorrhagic fever viruses. Antiviral Research, 2011, 91, 195-208.	4.1	103
52	Human polyclonal immunoglobulin G from transchromosomic bovines inhibits MERS-CoV in vivo. Science Translational Medicine, 2016, 8, 326ra21.	12.4	102
53	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). Archives of Virology, 2019, 164, 943-946.	2.1	102
54	Virus nomenclature below the species level: a standardized nomenclature for natural variants of viruses assigned to the family Filoviridae. Archives of Virology, 2013, 158, 301-311.	2.1	99

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55	Taxonomic reorganization of the family Bornaviridae. Archives of Virology, 2015, 160, 621-632.	2.1	97
56	Hantaviridae: Current Classification and Future Perspectives. Viruses, 2019, 11, 788.	3.3	94
57	Crimean-Congo hemorrhagic fever: Current and future prospects of vaccines and therapies. Antiviral Research, 2011, 90, 85-92.	4.1	91
58	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. MBio, 2014, 5, e01360-14.	4.1	89
59	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. Systematic Biology, 2020, 69, 110-123.	5.6	89
60	Evolution and Spread of Ebola Virus in Liberia, 2014–2015. Cell Host and Microbe, 2015, 18, 659-669.	11.0	87
61	Discussions and decisions of the 2012–2014 International Committee on Taxonomy of Viruses (ICTV) Filoviridae Study Group, January 2012–June 2013. Archives of Virology, 2014, 159, 821-830.	2.1	85
62	A classification system for virophages and satellite viruses. Archives of Virology, 2016, 161, 233-247.	2.1	85
63	New filovirus disease classification and nomenclature. Nature Reviews Microbiology, 2019, 17, 261-263.	28.6	84
64	Sulfated Tyrosines Contribute to the Formation of the C5a Docking Site of the Human C5a Anaphylatoxin Receptor. Journal of Experimental Medicine, 2001, 193, 1059-1066.	8.5	83
65	Nomenclature- and Database-Compatible Names for the Two Ebola Virus Variants that Emerged in Guinea and the Democratic Republic of the Congo in 2014. Viruses, 2014, 6, 4760-4799.	3.3	83
66	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. Archives of Virology, 2016, 161, 1095-1099.	2.1	83
67	- Hemorrhagic Fever with Renal Syndrome. , 2016, , 436-455.		81
68	Local, national, and regional viral haemorrhagic fever pandemic potential in Africa: a multistage analysis. Lancet, The, 2017, 390, 2662-2672.	13.7	80
69	Molecular detection of SARS-CoV-2 in formalin-fixed, paraffin-embedded specimens. JCI Insight, 2020, 5, .	5.0	80
70	Ebola Virion Attachment and Entry into Human Macrophages Profoundly Effects Early Cellular Gene Expression. PLoS Neglected Tropical Diseases, 2011, 5, e1359.	3.0	79
71	Monitoring of Ebola Virus Makona Evolution through Establishment of Advanced Genomic Capability in Liberia. Emerging Infectious Diseases, 2015, 21, 1135-1143.	4.3	79
72	Ortervirales: New Virus Order Unifying Five Families of Reverse-Transcribing Viruses. Journal of Virology, 2018, 92, .	3.4	79

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73	ICTV Virus Taxonomy Profile: Filoviridae. Journal of General Virology, 2019, 100, 911-912.	2.9	78
74	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. Archives of Virology, 2017, 162, 1441-1446.	2.1	72
75	Genetic variability of Crimean-Congo haemorrhagic fever virus in Russia and Central Asia. Journal of General Virology, 2003, 84, 1199-1206.	2.9	70
76	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-1244.	2.1	70
77	Stabilization of Human Immunodeficiency Virus Type 1 Envelope Glycoprotein Trimers by Disulfide Bonds Introduced into the gp41 Glycoprotein Ectodomain. Journal of Virology, 1998, 72, 7620-7625.	3.4	70
78	Evaluation of Perceived Threat Differences Posed by Filovirus Variants. Biosecurity and Bioterrorism, 2011, 9, 361-371.	1.2	68
79	Emergence of Ebola Virus Escape Variants in Infected Nonhuman Primates Treated with the MB-003 Antibody Cocktail. Cell Reports, 2015, 12, 2111-2120.	6.4	68
80	ICTV Virus Taxonomy Profile: Arenaviridae. Journal of General Virology, 2019, 100, 1200-1201.	2.9	66
81	Marburg virus disease. Postgraduate Medical Journal, 1973, 49, 542-546.	1.8	62
82	Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics. MBio, 2015, 6, .	4.1	62
83	Reduced evolutionary rate in reemerged Ebola virus transmission chains. Science Advances, 2016, 2, e1600378.	10.3	62
84	Medical countermeasures during the 2018 Ebola virus disease outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo: a rapid genomic assessment. Lancet Infectious Diseases, The, 2019, 19, 648-657.	9.1	62
85	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
86	Exceptional Simian Hemorrhagic Fever Virus Diversity in a Wild African Primate Community. Journal of Virology, 2013, 87, 688-691.	3.4	61
87	Dichorhavirus: a proposed new genus for Brevipalpus mite-transmitted, nuclear, bacilliform, bipartite, negative-strand RNA plant viruses. Archives of Virology, 2014, 159, 607-619.	2.1	61
88	Inhibition of Ebola Virus Entry by a C-peptide Targeted to Endosomes. Journal of Biological Chemistry, 2011, 286, 15854-15861.	3.4	59
89	Virus nomenclature below the species level: a standardized nomenclature for filovirus strains and variants rescued from cDNA. Archives of Virology, 2014, 159, 1229-37.	2.1	59
90	Relatives of rubella virus in diverse mammals. Nature, 2020, 586, 424-428.	27.8	58

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91	Genomic Characterization of the Genus Nairovirus (Family Bunyaviridae). Viruses, 2016, 8, 164.	3.3	57
92	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. Archives of Virology, 2017, 162, 1153-1157.	2.1	57
93	ICTV Virus Taxonomy Profile: Nairoviridae. Journal of General Virology, 2020, 101, 798-799.	2.9	56
94	Cell entry by a novel European filovirus requires host endosomal cysteine proteases and Niemann–Pick C1. Virology, 2014, 468-470, 637-646.	2.4	55
95	Persistent Marburg Virus Infection in the Testes of Nonhuman Primate Survivors. Cell Host and Microbe, 2018, 24, 405-416.e3.	11.0	55
96	Virus nomenclature below the species level: a standardized nomenclature for laboratory animal-adapted strains and variants of viruses assigned to the family Filoviridae. Archives of Virology, 2013, 158, 1425-1432.	2.1	54
97	Crimean–Congo hemorrhagic fever virus utilizes a clathrin- and early endosome-dependent entry pathway. Virology, 2013, 444, 45-54.	2.4	54
98	Viruses Defined by the Position of the Virosphere within the Replicator Space. Microbiology and Molecular Biology Reviews, 2021, 85, e0019320.	6.6	53
99	"Super-Spreaders―and Person-to-Person Transmission of Andes Virus in Argentina. New England Journal of Medicine, 2020, 383, 2230-2241.	27.0	52
100	Binomial nomenclature for virus species: a consultation. Archives of Virology, 2020, 165, 519-525.	2.1	51
101	Ebola virus disease candidate vaccines under evaluation in clinical trials. Expert Review of Vaccines, 2016, 15, 1101-1112.	4.4	50
102	Spumaretroviruses: Updated taxonomy and nomenclature. Virology, 2018, 516, 158-164.	2.4	50
103	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. Viruses, 2014, 6, 3663-3682.	3.3	49
104	Zoonotic Potential of Simian Arteriviruses. Journal of Virology, 2016, 90, 630-635.	3.4	48
105	Ebola Virus Genome Plasticity as a Marker of Its Passaging History: A Comparison of In Vitro Passaging to Non-Human Primate Infection. PLoS ONE, 2012, 7, e50316.	2.5	44
106	Recent successes in therapeutics for Ebola virus disease: no time for complacency. Lancet Infectious Diseases, The, 2020, 20, e231-e237.	9.1	42
107	Ebolavirus Δ-Peptide Immunoadhesins Inhibit Marburgvirus and Ebolavirus Cell Entry. Journal of Virology, 2011, 85, 8502-8513.	3.4	41
108	Diversity and ecological footprint of Global Ocean RNA viruses. Science, 2022, 376, 1202-1208.	12.6	41

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109	Ebola Virus VP40 Modulates Cell Cycle and Biogenesis of Extracellular Vesicles. Journal of Infectious Diseases, 2018, 218, S365-S387.	4.0	40
110	Simian Hemorrhagic Fever Virus Cell Entry Is Dependent on CD163 and Uses a Clathrin-Mediated Endocytosis-Like Pathway. Journal of Virology, 2015, 89, 844-856.	3.4	38
111	Clarification and guidance on the proper usage of virus and virus species names. Archives of Virology, 2010, 155, 445-453.	2.1	36
112	High Genetic Diversity and Adaptive Potential of Two Simian Hemorrhagic Fever Viruses in a Wild Primate Population. PLoS ONE, 2014, 9, e90714.	2.5	36
113	Genetic and Phylogenetic Characterization of Tataguine and Witwatersrand Viruses and Other Orthobunyaviruses of the Anopheles A, Capim, GuamÃ _i , Koongol, Mapputta, Tete, and Turlock Serogroups. Viruses, 2015, 7, 5987-6008.	3.3	36
114	Use of Unamplified RNA/cDNA–Hybrid Nanopore Sequencing for Rapid Detection and Characterization of RNA Viruses. Emerging Infectious Diseases, 2016, 22, 1448-1451.	4.3	36
115	A novel negative-stranded RNA virus mediates sex ratio in its parasitoid host. PLoS Pathogens, 2017, 13, e1006201.	4.7	35
116	Recombinant Lassa Virus Expressing Green Fluorescent Protein as a Tool for High-Throughput Drug Screens and Neutralizing Antibody Assays. Viruses, 2018, 10, 655.	3.3	35
117	Machupo Virus Glycoprotein Determinants for Human Transferrin Receptor 1 Binding and Cell Entry. PLoS ONE, 2011, 6, e21398.	2.5	34
118	A Lassa Fever Live-Attenuated Vaccine Based on Codon Deoptimization of the Viral Glycoprotein Gene. MBio, 2020, 11, .	4.1	34
119	Epidemiology of Crimean-Congo Hemorrhagic Fever (CCHF) in Africa—Underestimated for Decades. American Journal of Tropical Medicine and Hygiene, 2021, 104, 1978-1990.	1.4	34
120	Interactome analysis of the lymphocytic choriomeningitis virus nucleoprotein in infected cells reveals ATPase Na+/K+ transporting subunit Alpha 1 and prohibitin as host-cell factors involved in the life cycle of mammarenaviruses. PLoS Pathogens, 2018, 14, e1006892.	4.7	34
121	CD26/DPP4 Cell-Surface Expression in Bat Cells Correlates with Bat Cell Susceptibility to Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Infection and Evolution of Persistent Infection. PLoS ONE, 2014, 9, e112060.	2.5	33
122	Differentiating between viruses and virus species by writing their names correctly. Archives of Virology, 2022, 167, 1231-1234.	2.1	33
123	Kanyawara Virus: A Novel Rhabdovirus Infecting Newly Discovered Nycteribiid Bat Flies Infesting Previously Unknown Pteropodid Bats in Uganda. Scientific Reports, 2017, 7, 5287.	3.3	32
124	A Forgotten Episode of Marburg Virus Disease: Belgrade, Yugoslavia, 1967. Microbiology and Molecular Biology Reviews, 2020, 84, .	6.6	32
125	Perspective on taxonomic classification of uncultivated viruses. Current Opinion in Virology, 2021, 51, 207-215.	5.4	31
126	siRNA Screen Identifies Trafficking Host Factors that Modulate Alphavirus Infection. PLoS Pathogens, 2016, 12, e1005466.	4.7	30

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127	The ReFRAME library as a comprehensive drug repurposing library to identify mammarenavirus inhibitors. Antiviral Research, 2019, 169, 104558.	4.1	30
128	Viral genomics in Ebola virus research. Nature Reviews Microbiology, 2020, 18, 365-378.	28.6	30
129	A proposal to change existing virus species names to non-Latinized binomials. Archives of Virology, 2010, 155, 1909-1919.	2.1	29
130	Nyamiviridae: Proposal for a new family in the order Mononegavirales. Archives of Virology, 2013, 158, 2209-2226.	2.1	29
131	Guide to the Correct Use of Filoviral Nomenclature. Current Topics in Microbiology and Immunology, 2017, 411, 447-460.	1.1	29
132	EPS8 Facilitates Uncoating of Influenza A Virus. Cell Reports, 2019, 29, 2175-2183.e4.	6.4	29
133	Two Novel Simian Arteriviruses in Captive and Wild Baboons (Papio spp.). Journal of Virology, 2014, 88, 13231-13239.	3.4	28
134	Influenza A Virus Polymerase Is a Site for Adaptive Changes during Experimental Evolution in Bat Cells. Journal of Virology, 2014, 88, 12572-12585.	3.4	28
135	Middle East respiratory syndrome: obstacles and prospects for vaccine development. Expert Review of Vaccines, 2015, 14, 949-962.	4.4	27
136	2018 Ebola virus disease outbreak in Équateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. Lancet Infectious Diseases, The, 2019, 19, 641-647.	9.1	27
137	Arteriviruses, Pegiviruses, and Lentiviruses Are Common among Wild African Monkeys. Journal of Virology, 2016, 90, 6724-6737.	3.4	26
138	Comparison of N - and O -linked glycosylation patterns of ebolavirus glycoproteins. Virology, 2017, 502, 39-47.	2.4	26
139	Asymmetric and non-stoichiometric glycoprotein recognition by two distinct antibodies results in broad protection against ebolaviruses. Cell, 2022, 185, 995-1007.e18.	28.9	26
140	ICTV Virus Taxonomy Profile: Bornaviridae. Journal of General Virology, 2021, 102, .	2.9	24
141	Histology, immunohistochemistry, and in situ hybridization reveal overlooked Ebola virus target tissues in the Ebola virus disease guinea pig model. Scientific Reports, 2018, 8, 1250.	3.3	23
142	Comparison of Multiplexed Immunofluorescence Imaging to Chromogenic Immunohistochemistry of Skin Biomarkers in Response to Monkeypox Virus Infection. Viruses, 2020, 12, 787.	3.3	23
143	Reidentification of Ebola Virus E718 and ME as Ebola Virus/H.sapiens-tc/COD/1976/Yambuku-Ecran. Genome Announcements, 2014, 2, .	0.8	22
144	Implementation of Objective PASC-Derived Taxon Demarcation Criteria for Official Classification of Filoviruses. Viruses, 2017, 9, 106.	3.3	22

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145	<i>Adnaviria</i> : a New Realm for Archaeal Filamentous Viruses with Linear A-Form Double-Stranded DNA Genomes. Journal of Virology, 2021, 95, e0067321.	3.4	22
146	An Emerging Biothreat: Crimean-Congo Hemorrhagic Fever Virus in Southern and Western Asia. American Journal of Tropical Medicine and Hygiene, 2019, 100, 16-23.	1.4	22
147	Ebola virus persistence and disease recrudescence in the brains of antibody-treated nonhuman primate survivors. Science Translational Medicine, 2022, 14, eabi5229.	12.4	22
148	Historical Outbreaks of Simian Hemorrhagic Fever in Captive Macaques Were Caused by Distinct Arteriviruses. Journal of Virology, 2015, 89, 8082-8087.	3.4	21
149	Diversity, Transmission, and Cophylogeny of Ledanteviruses (Rhabdoviridae: Ledantevirus) and Nycteribiid Bat Flies Parasitizing Angolan Soft-Furred Fruit Bats in Bundibugyo District, Uganda. Microorganisms, 2020, 8, 750.	3.6	21
150	Nipah virus persists in the brains of nonhuman primate survivors. JCI Insight, 2019, 4, .	5.0	21
151	Error baseline rates of five sample preparation methods used to characterize RNA virus populations. PLoS ONE, 2017, 12, e0171333.	2.5	21
152	Drug discovery technologies and strategies for Machupo virus and other New World arenaviruses. Expert Opinion on Drug Discovery, 2012, 7, 613-632.	5.0	20
153	Comparison of SYBR green I real-time RT-PCR with conventional agarose gel-based RT-PCR for the diagnosis of infectious bronchitis virus infection in chickens in Morocco. BMC Research Notes, 2016, 9, 231.	1.4	20
154	Genetic analysis of the M RNA segment of Crimean-Congo hemorrhagic fever virus strains involved in the recent outbreaks in Russia. Archives of Virology, 2004, 149, 2199-2213.	2.1	19
155	Induction of ebolavirus cross-species immunity using retrovirus-like particles bearing the Ebola virus glycoprotein lacking the mucin-like domain. Virology Journal, 2012, 9, 32.	3.4	19
156	The NIAID Integrated Research Facility at Frederick, Maryland: a unique international resource to facilitate medical countermeasure development for BSL-4 pathogens. Pathogens and Disease, 2014, 71, 213-218.	2.0	19
157	Ebola virus persistence as a new focus in clinical research. Current Opinion in Virology, 2017, 23, 43-48.	5.4	18
158	Reply to Holmes and Duchêne, "Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?â€: Deep Phylogenetic Analysis of RNA Viruses Is Highly Challenging but Not Meaningless. MBio, 2019, 10, .	4.1	18
159	A Lassa Virus Live-Attenuated Vaccine Candidate Based on Rearrangement of the Intergenic Region. MBio, 2020, 11, .	4.1	18
160	Leviviricetes: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. Microbial Genomics, 2021, 7, .	2.0	18
161	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. Systematic Biology, 2016, 66, syw096.	5.6	17
162	Programmed â^22/â^21 Ribosomal Frameshifting in Simarteriviruses: an Evolutionarily Conserved Mechanism. Journal of Virology, 2019, 93, .	3.4	17

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163	A Sarcina bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. Nature Communications, 2021, 12, 763.	12.8	17
164	Severe Acute Respiratory Syndrome Coronavirus Entry as a Target of Antiviral Therapies. Antiviral Therapy, 2007, 12, 639-650.	1.0	17
165	A small stem-loop structure of the Ebola virus trailer is essential for replication and interacts with heat-shock protein A8. Nucleic Acids Research, 2016, 44, gkw825.	14.5	16
166	Safety Precautions and Operating Procedures in an (A)BSL-4 Laboratory: 1. Biosafety Level 4 Suit Laboratory Suite Entry and Exit Procedures. Journal of Visualized Experiments, 2016, , .	0.3	16
167	Virus Taxonomy. , 2021, , 28-37.		16
168	Novel Filoviruses, Hantavirus, and Rhabdovirus in Freshwater Fish, Switzerland, 2017. Emerging Infectious Diseases, 2021, 27, 3082-3091.	4.3	16
169	<i>Jingchuvirales</i> : a New Taxonomical Framework for a Rapidly Expanding Order of Unusual Monjiviricete Viruses Broadly Distributed among Arthropod Subphyla. Applied and Environmental Microbiology, 2022, 88, AEM0195421.	3.1	16
170	ABSL-4 Aerobiology Biosafety and Technology at the NIH/NIAID Integrated Research Facility at Fort Detrick. Viruses, 2014, 6, 137-150.	3.3	15
171	Phylogenetic analysis of avian infectious bronchitis virus S1 glycoprotein regions reveals emergence of a new genotype in Moroccan broiler chicken flocks. Virology Journal, 2015, 12, 116.	3.4	14
172	Divergent Simian Arteriviruses Cause Simian Hemorrhagic Fever of Differing Severities in Macaques. MBio, 2016, 7, e02009-15.	4.1	14
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