Lin-Fa Wang

List of Publications by Year
in descending order

352 papers	35,649 citations	3531 90 h-index	4991 167 g-index
401 all docs	401 docs citations	401 times ranked	35241 citing authors

#	Article	IF	Citations
1	Bats Are Natural Reservoirs of SARS-Like Coronaviruses. Science, 2005, 310, 676-679.	12.6	2,130
2	SARS-CoV-2-specific T cell immunity in cases of COVID-19 and SARS, and uninfected controls. Nature, 2020, 584, 457-462.	27.8	1,744
3	Epidemiologic Features and Clinical Course of Patients Infected With SARS-CoV-2 in Singapore. JAMA - Journal of the American Medical Association, 2020, 323, 1488.	7.4	1,700
4	Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. Nature, 2013, 503, 535-538.	27.8	1,439
5	A SARS-CoV-2 surrogate virus neutralization test based on antibody-mediated blockage of ACE2â€“spike proteinâ€“protein interaction. Nature Biotechnology, 2020, 38, 1073-1078.	17.5	1,042
6	Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. PLoS Pathogens, 2017, 13, e1006698.	4.7	797
7	Early induction of functional SARS-CoV-2-specific T cells associates with rapid viral clearance and mild disease in COVID-19 patients. Cell Reports, 2021, 34, 108728.	6.4	568
8	Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. Nature, 2018, 556, 255-258.	27.8	565
9	Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. Science, 2013, 339, 456-460.	12.6	522
10	Infectious disease in an era of global change. Nature Reviews Microbiology, 2022, 20, 193-205.	28.6	509
11	Taxonomy of the order Mononegavirales: update 2016. Archives of Virology, 2016, 161, 2351-2360.	2.1	407
12	From The Cover: Ephrin-B2 ligand is a functional receptor for Hendra virus and Nipah virus. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10652-10657.	7.1	395
13	Effects of a major deletion in the SARS-CoV-2 genome on the severity of infection and the inflammatory response: an observational cohort study. Lancet, The, 2020, 396, 603-611.	13.7	394
14	Duration of Antibody Responses after Severe Acute Respiratory Syndrome. Emerging Infectious Diseases, 2007, 13, 1562-1564.	4.3	381
15	Review of Bats and SARS. Emerging Infectious Diseases, 2006, 12, 1834-1840.	4.3	375
16	Ecological dynamics of emerging bat virus spillover. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20142124.	2.6	375
17	Hendra and Nipah viruses: different and dangerous. Nature Reviews Microbiology, 2006, 4, 23-35.	28.6	350
18	Bat origin of human coronaviruses. Virology Journal, 2015, 12, 221.	3.4	330

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19	Dynamics of SARS-CoV-2 neutralising antibody responses and duration of immunity: a longitudinal study. Lancet Microbe, The, 2021, 2, e240-e249.	7.3	322
20	Assessing Viral Shedding and Infectivity of Tears in Coronavirus Disease 2019 (COVID-19) Patients. Ophthalmology, 2020, 127, 977-979.	5.2	317
21	Potent cross-reactive neutralization of SARS coronavirus isolates by human monoclonal antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12123-12128.	7.1	276
22	Evidence for SARS-CoV-2 related coronaviruses circulating in bats and pangolins in Southeast Asia. Nature Communications, 2021, 12, 972.	12.8	276
23	Contraction of the type I IFN locus and unusual constitutive expression ofIFN-Î±in bats. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2696-2701.	7.1	272
24	Origin and cross-species transmission of bat coronaviruses in China. Nature Communications, 2020, 11, 4235.	12.8	264
25	Molecular biology of Hendra and Nipah viruses. Microbes and Infection, 2001, 3, 279-287.	1.9	259
26	Highly functional virus-specific cellular immune response in asymptomatic SARS-CoV-2 infection. Journal of Experimental Medicine, 2021, 218, .	8.5	259
27	A Neutralizing Human Monoclonal Antibody Protects against Lethal Disease in a New Ferret Model of Acute Nipah Virus Infection. PLoS Pathogens, 2009, 5, e1000642.	4.7	251
28	The Exceptionally Large Genome of Hendra Virus: Support for Creation of a New Genus within the FamilyParamyxoviridae. Journal of Virology, 2000, 74, 9972-9979.	3.4	249
29	Cedar Virus: A Novel Henipavirus Isolated from Australian Bats. PLoS Pathogens, 2012, 8, e1002836.	4.7	245
30	Dampened NLRP3-mediated inflammation in bats and implications for a special viral reservoir host. Nature Microbiology, 2019, 4, 789-799.	13.3	245
31	Discovery and Genomic Characterization of a 382-Nucleotide Deletion in ORF7b and ORF8 during the Early Evolution of SARS-CoV-2. MBio, 2020, 11, .	4.1	245
32	Bats and their virome: an important source of emerging viruses capable of infecting humans. Current Opinion in Virology, 2013, 3, 84-91.	5.4	235
33	Virological and serological kinetics of SARS-CoV-2 Delta variant vaccine breakthrough infections: a multicentre cohort study. Clinical Microbiology and Infection, 2022, 28, 612.e1-612.e7.	6.0	231
34	Connecting clusters of COVID-19: an epidemiological and serological investigation. Lancet Infectious Diseases, The, 2020, 20, 809-815.	9.1	229
35	Taxonomy of the order Mononegavirales: update 2019. Archives of Virology, 2019, 164, 1967-1980.	2.1	224
36	Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus. Journal of Virology, 2016, 90, 3253-3256.	3.4	221

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37	Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. Virologica Sinica, 2018, 33, 104-107.	3.0	219
38	Lessons from the host defences of bats, a unique viral reservoir. Nature, 2021, 589, 363-370.	27.8	217
39	ICTV Virus Taxonomy Profile: Pneumoviridae. Journal of General Virology, 2017, 98, 2912-2913.	2.9	215
40	Evidence of Henipavirus Infection in West African Fruit Bats. PLoS ONE, 2008, 3, e2739.	2.5	215
41	Dampened STING-Dependent Interferon Activation in Bats. Cell Host and Microbe, 2018, 23, 297-301.e4.	11.0	206
42	A previously unknown reovirus of bat origin is associated with an acute respiratory disease in humans. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11424-11429.	7.1	201
43	Viruses in bats and potential spillover to animals and humans. Current Opinion in Virology, 2019, 34, 79-89.	5.4	195
44	ICTV Virus Taxonomy Profile: Paramyxoviridae. Journal of General Virology, 2019, 100, 1593-1594.	2.9	194
45	Antibodies to SARS Coronavirus in Civets. Emerging Infectious Diseases, 2004, 10, 2244-2248.	4.3	192
46	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
47	SARS-CoV-2 seroprevalence and transmission risk factors among high-risk close contacts: a retrospective cohort study. Lancet Infectious Diseases, The, 2021, 21, 333-343.	9.1	183
48	Taxonomy of the order Mononegavirales: update 2017. Archives of Virology, 2017, 162, 2493-2504.	2.1	173
49	Feline Model of Acute Nipah Virus Infection and Protection with a Soluble Glycoprotein-Based Subunit Vaccine. Journal of Virology, 2006, 80, 12293-12302.	3.4	166
50	Mass extinctions, biodiversity and mitochondrial function: are bats â€˜specialâ€™ as reservoirs for emerging viruses?. Current Opinion in Virology, 2011, 1, 649-657.	5.4	163
51	Nipah Virus Infection. Journal of Clinical Microbiology, 2018, 56, .	3.9	162
52	Pan-Sarbecovirus Neutralizing Antibodies in BNT162b2-Immunized SARS-CoV-1 Survivors. New England Journal of Medicine, 2021, 385, 1401-1406.	27.0	161
53	Quantitative analysis of Nipah virus proteins released as virus-like particles reveals central role for the matrix protein. Virology Journal, 2007, 4, 1.	3.4	159
54	Hendra Virus Vaccine, a One Health Approach to Protecting Horse, Human, and Environmental Health. Emerging Infectious Diseases, 2014, 20, 372-9.	4.3	159

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55	Receptor Binding, Fusion Inhibition, and Induction of Cross-Reactive Neutralizing Antibodies by a Soluble G Glycoprotein of Hendra Virus. Journal of Virology, 2005, 79, 6690-6702.	3.4	157
56	Potent Neutralization of Hendra and Nipah Viruses by Human Monoclonal Antibodies. Journal of Virology, 2006, 80, 891-899.	3.4	155
57	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	2.1	153
58	Difference in Receptor Usage between Severe Acute Respiratory Syndrome (SARS) Coronavirus and SARS-Like Coronavirus of Bat Origin. Journal of Virology, 2008, 82, 1899-1907.	3.4	145
59	Development of an Acute and Highly Pathogenic Nonhuman Primate Model of Nipah Virus Infection. PLoS ONE, 2010, 5, e10690.	2.5	145
60	Exceptionally Potent Cross-Reactive Neutralization of Nipah and Hendra Viruses by a Human Monoclonal Antibody. Journal of Infectious Diseases, 2008, 197, 846-853.	4.0	144
61	Viral Dynamics and Immune Correlates of Coronavirus Disease 2019 (COVID-19) Severity. Clinical Infectious Diseases, 2021, 73, e2932-e2942.	5.8	143
62	Establishment, Immortalisation and Characterisation of Pteropid Bat Cell Lines. PLoS ONE, 2009, 4, e8266.	2.5	143
63	Membrane Fusion Tropism and Heterotypic Functional Activities of the Nipah Virus and Hendra Virus Envelope Glycoproteins. Journal of Virology, 2002, 76, 11186-11198.	3.4	142
64	Hendra Virus V Protein Inhibits Interferon Signaling by Preventing STAT1 and STAT2 Nuclear Accumulation. Journal of Virology, 2003, 77, 11842-11845.	3.4	140
65	A recombinant Hendra virus G glycoprotein-based subunit vaccine protects ferrets from lethal Hendra virus challenge. Vaccine, 2011, 29, 5623-5630.	3.8	140
66	Tioman Virus, a Novel Paramyxovirus Isolated from Fruit Bats in Malaysia. Virology, 2001, 283, 215-229.	2.4	134
67	Long-Term Survival of an Urban Fruit Bat Seropositive for Ebola and Lagos Bat Viruses. PLoS ONE, 2010, 5, e11978.	2.5	132
68	Ebola Virus Antibodies in Fruit Bats, Bangladesh. Emerging Infectious Diseases, 2013, 19, 270-273.	4.3	129
69	Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats. PLoS Pathogens, 2020, 16, e1008758.	4.7	127
70	Ebola Virus Antibodies in Fruit Bats, Ghana, West Africa. Emerging Infectious Diseases, 2012, 18, 1207-1209.	4.3	126
71	Evolutionary Relationships between Bat Coronaviruses and Their Hosts. Emerging Infectious Diseases, 2007, 13, 1526-1532.	4.3	123
72	Neutralization assays for differential henipavirus serology using Bio-Plex Protein Array Systems. Journal of Virological Methods, 2007, 142, 29-40.	2.1	121

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73	Metagenomic study of the viruses of African straw-coloured fruit bats: Detection of a chiropteran poxvirus and isolation of a novel adenovirus. Virology, 2013, 441, 95-106.	2.4	121
74	Nipah virus dynamics in bats and implications for spillover to humans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29190-29201.	7.1	119
75	Host Range, Prevalence, and Genetic Diversity of Adenoviruses in Bats. Journal of Virology, 2010, 84, 3889-3897.	3.4	118
76	Civets Are Equally Susceptible to Experimental Infection by Two Different Severe Acute Respiratory Syndrome Coronavirus Isolates. Journal of Virology, 2005, 79, 2620-2625.	3.4	117
77	Characterization of a filovirus (MÄ›nglÃ virus) from Rousettus bats in China. Nature Microbiology, 2019, 4, 390-395.	13.3	116
78	Identification and Characterization of a New Orthoreovirus from Patients with Acute Respiratory Infections. PLoS ONE, 2008, 3, e3803.	2.5	116
79	Neutralizing epitopes of the SARS-CoV S-protein cluster independent of repertoire, antigen structure or mAb technology. MAbs, 2010, 2, 53-66.	5.2	114
80	Unique Loss of the PYHIN Gene Family in Bats Amongst Mammals: Implications for Inflammasome Sensing. Scientific Reports, 2016, 6, 21722.	3.3	113
81	A Novel P/V/C Gene in a New Member of the Paramyxoviridae Family, Which Causes Lethal Infection in Humans, Horses, and Other Animals. Journal of Virology, 1998, 72, 1482-1490.	3.4	113
82	A treatment for and vaccine against the deadly Hendra and Nipah viruses. Antiviral Research, 2013, 100, 8-13.	4.1	111
83	Filovirus receptor NPC1 contributes to species-specific patterns of ebolavirus susceptibility in bats. ELife, 2015, 4, .	6.0	110
84	Antibodies to Nipah or Nipah-like Viruses in Bats, China. Emerging Infectious Diseases, 2008, 14, 1974-1976.	4.3	108
85	Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. Nature Communications, 2013, 4, 2770.	12.8	105
86	Ebola Reston Virus Infection of Pigs: Clinical Significance and Transmission Potential. Journal of Infectious Diseases, 2011, 204, S804-S809.	4.0	104
87	Hendra virus: an emerging paramyxovirus in Australia. Lancet Infectious Diseases, The, 2012, 12, 799-807.	9.1	104
88	The immune gene repertoire of an important viral reservoir, the Australian black flying fox. BMC Genomics, 2012, 13, 261.	2.8	104
89	A recombinant subunit vaccine formulation protects against lethal Nipah virus challenge in cats. Vaccine, 2008, 26, 3842-3852.	3.8	101
90	Infection of human Nasal Epithelial Cells with SARS-CoV-2 and a 382-nt deletion isolate lacking ORF8 reveals similar viral kinetics and host transcriptional profiles. PLoS Pathogens, 2020, 16, e1009130.	4.7	98

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91	Full-length genome sequences of two SARS-like coronaviruses in horseshoe bats and genetic variation analysis. Journal of General Virology, 2006, 87, 3355-3359.	2.9	96
92	Functional studies of host-specific ephrin-B ligands as Henipavirus receptors. Virology, 2008, 372, 357-371.	2.4	95
93	Chloroquine Administration Does Not Prevent Nipah Virus Infection and Disease in Ferrets. Journal of Virology, 2009, 83, 11979-11982.	3.4	95
94	Functional Expression and Membrane Fusion Tropism of the Envelope Glycoproteins of Hendra Virus. Virology, 2001, 290, 121-135.	2.4	94
95	Beilong virus, a novel paramyxovirus with the largest genome of non-segmented negative-stranded RNA viruses. Virology, 2006, 346, 219-228.	2.4	94
96	Emerging Viruses: Coming in on a Wrinkled Wing and a Prayer. Clinical Infectious Diseases, 2007, 44, 711-717.	5.8	94
97	Improved rapid amplification of cDNA ends (RACE) for mapping both the 5â€² and 3â€² terminal sequences of paramyxovirus genomes. Journal of Virological Methods, 2005, 130, 154-156.	2.1	91
98	Serological evidence of ebolavirus infection in bats, China. Virology Journal, 2012, 9, 236.	3.4	91
99	Accelerated viral dynamics in bat cell lines, with implications for zoonotic emergence. ELife, 2020, 9, .	6.0	91
100	Type III IFNs in Pteropid Bats: Differential Expression Patterns Provide Evidence for Distinct Roles in Antiviral Immunity. Journal of Immunology, 2011, 186, 3138-3147.	0.8	90
101	Lack of cross-neutralization by SARS patient sera towards SARS-CoV-2. Emerging Microbes and Infections, 2020, 9, 900-902.	6.5	89
102	Serological differentiation between COVID-19 and SARS infections. Emerging Microbes and Infections, 2020, 9, 1497-1505.	6.5	89
103	Rapid measurement of SARS-CoV-2 spike T cells in whole blood from vaccinated and naturally infected individuals. Journal of Clinical Investigation, 2021, 131, .	8.2	89
104	Identifying Hendra Virus Diversity in Pteropid Bats. PLoS ONE, 2011, 6, e25275.	2.5	88
105	Use of a gene-targeted phage display random epitope library to map an antigenic determinant on the bluetongue virus outer capsid protein VP5. Journal of Immunological Methods, 1995, 178, 1-12.	1.4	86
106	Transmission Routes for Nipah Virus from Malaysia and Bangladesh. Emerging Infectious Diseases, 2012, 18, 1983-1993.	4.3	85
107	Identification of Hendra Virus G Glycoprotein Residues That Are Critical for Receptor Binding. Journal of Virology, 2007, 81, 5893-5901.	3.4	84
108	ACE2 receptor usage reveals variation in susceptibility to SARS-CoV and SARS-CoV-2 infection among bat species. Nature Ecology and Evolution, 2021, 5, 600-608.	7.8	83

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109	Studying immunity to zoonotic diseases in the natural host â€" keeping it real. Nature Reviews Immunology, 2013, 13, 851-861.	22.7	82
110	The Complete Genome Sequence of J Virus Reveals a Unique Genome Structure in the Family Paramyxoviridae. Journal of Virology, 2005, 79, 10690-10700.	3.4	78
111	Investigation of a Potential Zoonotic Transmission of Orthoreovirus Associated with Acute Influenza-Like Illness in an Adult Patient. PLoS ONE, 2011, 6, e25434.	2.5	78
112	Molecular characterization of the first Australian isolate of Japanese encephalitis virus, the FU strain. Journal of General Virology, 2000, 81, 2471-2480.	2.9	78
113	Molecular Characterization of Menangle Virus, a Novel Paramyxovirus which Infects Pigs, Fruit Bats, and Humans. Virology, 2001, 283, 358-373.	2.4	76
114	Angiotensin-converting enzyme 2 (ACE2) proteins of different bat species confer variable susceptibility to SARS-CoV entry. Archives of Virology, 2010, 155, 1563-1569.	2.1	76
115	Novel Phlebovirus with Zoonotic Potential Isolated from Ticks, Australia. Emerging Infectious Diseases, 2014, 20, 1040-1043.	4.3	76
116	Novel, Potentially Zoonotic Paramyxoviruses from the African Straw-Colored Fruit Bat Eidolon helvum. Journal of Virology, 2013, 87, 1348-1358.	3.4	75
117	Residues in the Stalk Domain of the Hendra Virus G Glycoprotein Modulate Conformational Changes Associated with Receptor Binding. Journal of Virology, 2008, 82, 11398-11409.	3.4	74
118	Hendra and Nipah viruses: why are they so deadly?. Current Opinion in Virology, 2012, 2, 242-247.	5.4	74
119	From Hendra to Wuhan: what has been learned in responding to emerging zoonotic viruses. Lancet, The, 2020, 395, e33-e34.	13.7	74
120	Discovery of Bat Coronaviruses through Surveillance and Probe Capture-Based Next-Generation Sequencing. MSphere, 2020, 5, .	2.9	73
121	The IFN Response in Bats Displays Distinctive IFN-Stimulated Gene Expression Kinetics with Atypical RNASEL Induction. Journal of Immunology, 2018, 200, 209-217.	0.8	73
122	Antibodies to Henipavirus or Henipa-Like Viruses in Domestic Pigs in Ghana, West Africa. PLoS ONE, 2011, 6, e25256.	2.5	72
123	Aligning bona fide dendritic cell populations across species. Cellular Immunology, 2014, 291, 3-10.	3.0	72
124	Inhibition of Henipavirus fusion and infection by heptad-derived peptides of the Nipah virus fusion glycoprotein. Virology Journal, 2005, 2, 57.	3.4	71
125	Experimental Infection of Horses with Hendra Virus/Australia/Horse/2008/Redlands. Emerging Infectious Diseases, 2011, 17, 2232-8.	4.3	71
126	Henipavirus Neutralising Antibodies in an Isolated Island Population of African Fruit Bats. PLoS ONE, 2012, 7, e30346.	2.5	71

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127	Molecular evidence of Ebola Reston virus infection in Philippine bats. Virology Journal, 2015, 12, 107.	3.4	71
128	Taxonomy of the order Mononegavirales: second update 2018. Archives of Virology, 2019, 164, 1233-1244.	2.1	70
129	Immunoglobulin heavy chain diversity in Pteropid bats: evidence for a diverse and highly specific antigen binding repertoire. Immunogenetics, 2010, 62, 173-184.	2.4	68
130	The Attachment Protein of Hendra Virus Has High Structural Similarity but Limited Primary Sequence Homology Compared with Viruses in the GenusParamyxovirus. Virology, 1998, 251, 227-233.	2.4	65
131	Bats and Viruses: Friend or Foe?. PLoS Pathogens, 2013, 9, e1003651.	4.7	65
132	Genetically Diverse Filoviruses in Rousettus and Eonycteris spp. Bats, China, 2009 and 2015. Emerging Infectious Diseases, 2017, 23, 482-486.	4.3	64
133	Interferon Production and Signaling Pathways Are Antagonized during Henipavirus Infection of Fruit Bat Cell Lines. PLoS ONE, 2011, 6, e22488.	2.5	64
134	The YPLGVG sequence of the Nipah virus matrix protein is required for budding. Virology Journal, 2008, 5, 137.	3.4	63
135	Molecular characterisation of Toll-like receptors in the black flying fox Pteropus alecto. Developmental and Comparative Immunology, 2011, 35, 7-18.	2.3	63
136	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
137	Novel Paramyxoviruses in Free-Ranging European Bats. PLoS ONE, 2012, 7, e38688.	2.5	61
138	Full-length genome sequence of Mossman virus, a novel paramyxovirus isolated from rodents in Australia. Virology, 2003, 317, 330-344.	2.4	60
139	Safety, tolerability, pharmacokinetics, and immunogenicity of a human monoclonal antibody targeting the G glycoprotein of henipaviruses in healthy adults: a first-in-human, randomised, controlled, phase 1 study. Lancet Infectious Diseases, The, 2020, 20, 445-454.	9.1	60
140	Differential Evolution of Antiretroviral Restriction Factors in Pteropid Bats as Revealed by APOBEC3 Gene Complexity. Molecular Biology and Evolution, 2018, 35, 1626-1637.	8.9	59
141	Crystal Structure of the Pre-fusion Nipah Virus Fusion Glycoprotein Reveals a Novel Hexamer-of-Trimers Assembly. PLoS Pathogens, 2015, 11, e1005322.	4.7	59
142	Vaccine Potential of Nipah Virus-Like Particles. PLoS ONE, 2011, 6, e18437.	2.5	58
143	SARS-CoV-2 neutralizing antibodies in patients with varying severity of acute COVID-19 illness. Scientific Reports, 2021, 11, 2062.	3.3	58
144	Serological Evidence of Henipavirus Exposure in Cattle, Goats and Pigs in Bangladesh. PLoS Neglected Tropical Diseases, 2014, 8, e3302.	3.0	57

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145	Broome virus, a new fusogenic Orthoreovirus species isolated from an Australian fruit bat. Virology, 2010, 402, 26-40.	2.4	56
146	Evolution and comparative analysis of the bat MHC-I region. Scientific Reports, 2016, 6, 21256.	3.3	56
147	WHO international standard for SARS-CoV-2 antibodies to determine markers of protection. Lancet Microbe, The, 2022, 3, e81-e82.	7.3	56
148	A neutralization test for specific detection of Nipah virus antibodies using pseudotyped vesicular stomatitis virus expressing green fluorescent protein. Journal of Virological Methods, 2009, 160, 7-13.	2.1	55
149	A New Model for Hendra Virus Encephalitis in the Mouse. PLoS ONE, 2012, 7, e40308.	2.5	55
150	SARS-CoV-2 neutralizing antibody levels are correlated with severity of COVID-19 pneumonia. Biomedicine and Pharmacotherapy, 2020, 130, 110629.	5.6	55
151	Biochemical, Conformational, and Immunogenic Analysis of Soluble Trimeric Forms of Henipavirus Fusion Glycoproteins. Journal of Virology, 2012, 86, 11457-11471.	3.4	54
152	Promotion of Hendra Virus Replication by MicroRNA 146a. Journal of Virology, 2013, 87, 3782-3791.	3.4	54
153	Evidence of bat origin for Menangle virus, a zoonotic paramyxovirus first isolated from diseased pigs. Journal of General Virology, 2012, 93, 2590-2594.	2.9	53
154	Experimental Infection and Response to Rechallenge of Alpacas with Middle East Respiratory Syndrome Coronavirus. Emerging Infectious Diseases, 2016, 22, 1071-1074.	4.3	53
155	Comprehensive mapping of SARS-CoV-2 interactions in vivo reveals functional virus-host interactions. Nature Communications, 2021, 12, 5113.	12.8	53
156	Discovery of Retroviral Homologs in Bats: Implications for the Origin of Mammalian Gammaretroviruses. Journal of Virology, 2012, 86, 4288-4293.	3.4	52
157	A rapid immune plaque assay for the detection of Hendra and Nipah viruses and anti-virus antibodies. Journal of Virological Methods, 2002, 99, 41-51.	2.1	51
158	Molecular characterisation of RIG-I-like helicases in the black flying fox, Pteropus alecto. Developmental and Comparative Immunology, 2012, 36, 657-664.	2.3	51
159	Phenotypic and functional characterization of the major lymphocyte populations in the fruit-eating bat Pteropus alecto. Scientific Reports, 2016, 6, 37796.	3.3	51
160	Complementary regulation of caspase-1 and IL-1Î² reveals additional mechanisms of dampened inflammation in bats. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28939-28949.	7.1	51
161	IRF7 in the Australian Black Flying Fox, Pteropus alecto: Evidence for a Unique Expression Pattern and Functional Conservation. PLoS ONE, 2014, 9, e103875.	2.5	51
162	Use of cross-reactive serological assays for detecting novel pathogens in wildlife: Assessing an appropriate cutoff for henipavirus assays in African bats. Journal of Virological Methods, 2013, 193, 295-303.	2.1	50

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163	Hendra and Nipah Viruses: Pathogenesis and Therapeutics. Current Molecular Medicine, 2005, 5, 805-816.	1.3	49
164	Synchronous shedding of multiple bat paramyxoviruses coincides with peak periods of Hendra virus spillover. Emerging Microbes and Infections, 2019, 8, 1314-1323.	6.5	49
165	Ecological Aspects of Hendra Virus. Current Topics in Microbiology and Immunology, 2012, 359, 11-23.	1.1	48
166	Identification of diverse groups of endogenous gammaretroviruses in mega- and microbats. Journal of General Virology, 2012, 93, 2037-2045.	2.9	48
167	The Distribution of Henipaviruses in Southeast Asia and Australasia: Is Wallaceâ€™s Line a Barrier to Nipah Virus?. PLoS ONE, 2013, 8, e61316.	2.5	48
168	Genome Sequence Conservation of Hendra Virus Isolates during Spillover to Horses, Australia. Emerging Infectious Diseases, 2010, 16, 1767-1769.	4.3	47
169	Prevalence of Henipavirus and Rubulavirus Antibodies in Pteropid Bats, Papua New Guinea. Emerging Infectious Diseases, 2010, 16, 1997-1999.	4.3	47
170	Adaptive evolution of bat dipeptidyl peptidase 4 (dpp4): implications for the origin and emergence of Middle East respiratory syndrome coronavirus. Virology Journal, 2013, 10, 304.	3.4	47
171	Serological Evidence of Possible Human Infection withTioman virus,a Newly Described Paramyxovirus of Bat Origin. Journal of Infectious Diseases, 2007, 196, 884-886.	4.0	46
172	Identification of diverse full-length endogenous betaretroviruses in megabats and microbats. Retrovirology, 2013, 10, 35.	2.0	45
173	Serologic Evidence of Fruit Bat Exposure to Filoviruses, Singapore, 2011â€“2016. Emerging Infectious Diseases, 2018, 24, 114-117.	4.3	44
174	The cleavage activation and sites of glycosylation in the fusion protein of Hendra virus. Virus Research, 2000, 69, 83-93.	2.2	43
175	Interferon Signaling Remains Functional during Henipavirus Infection of Human Cell Lines. Journal of Virology, 2011, 85, 4031-4034.	3.4	43
176	Isolation of multiple novel paramyxoviruses from pteropid bat urine. Journal of General Virology, 2015, 96, 24-29.	2.9	43
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