

Wei-Feng Shi

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97
papers

26,346
citations

31
h-index

101
g-index

101
ext. papers

33,894
ext. citations

12.3
avg, IF

7.35
L-index

#	Paper	IF	Citations
97	A Novel Coronavirus from Patients with Pneumonia in China, 2019. <i>New England Journal of Medicine</i> , 2020 , 382, 727-733	59.2	14511
96	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. <i>Lancet, The</i> , 2020 , 395, 565-574	40	6394
95	Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. <i>Trends in Microbiology</i> , 2016 , 24, 490-502	12.4	1599
94	Origin and diversity of novel avian influenza A H7N9 viruses causing human infection: phylogenetic, structural, and coalescent analyses. <i>Lancet, The</i> , 2013 , 381, 1926-32	40	436
93	Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. <i>Nature</i> , 2018 , 556, 255-258	50.4	369
92	A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. <i>Current Biology</i> , 2020 , 30, 2196-2203.e3	6.3	319
91	A single mutation in the prM protein of Zika virus contributes to fetal microcephaly. <i>Science</i> , 2017 , 358, 933-936	33.3	292
90	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016 , 20, 810-821	23.4	187
89	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015 , 524, 93-6	50.4	121
88	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014 , 5, 3142	17.4	120
87	Human infections with recently-emerging highly pathogenic H7N9 avian influenza virus in China. <i>Journal of Infection</i> , 2017 , 75, 71-75	18.9	115
86	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. <i>Cell</i> , 2021 , 184, 4380-4391.e14	56.2	99
85	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet, The</i> , 2014 , 383, 869	40	80
84	Two novel reassortants of avian influenza A (H5N6) virus in China. <i>Journal of General Virology</i> , 2015 , 96, 975-981	4.9	79
83	Hepatitis B virus subgenotyping: history, effects of recombination, misclassifications, and corrections. <i>Infection, Genetics and Evolution</i> , 2013 , 16, 355-61	4.5	75
82	Emergence and Adaptation of a Novel Highly Pathogenic H7N9 Influenza Virus in Birds and Humans from a 2013 Human-Infecting Low-Pathogenic Ancestor. <i>Journal of Virology</i> , 2018 , 92,	6.6	72
81	Origin and molecular characterization of the human-infecting H6N1 influenza virus in Taiwan. <i>Protein and Cell</i> , 2013 , 4, 846-53	7.2	71

80	Origin and Possible Genetic Recombination of the Middle East Respiratory Syndrome Coronavirus from the First Imported Case in China: Phylogenetics and Coalescence Analysis. <i>MBio</i> , 2015 , 6, e01280-13	7.8	70
79	Broad host range of SARS-CoV-2 and the molecular basis for SARS-CoV-2 binding to cat ACE2. <i>Cell Discovery</i> , 2020 , 6, 68	22.3	69
78	New Threats from H7N9 Influenza Virus: Spread and Evolution of High- and Low-Pathogenicity Variants with High Genomic Diversity in Wave Five. <i>Journal of Virology</i> , 2018 , 92,	6.6	67
77	Highly Pathogenic Avian Influenza A(H5N8) Virus in Wild Migratory Birds, Qinghai Lake, China. <i>Emerging Infectious Diseases</i> , 2017 , 23, 637-641	10.2	66
76	The evolution of Zika virus from Asia to the Americas. <i>Nature Reviews Microbiology</i> , 2019 , 17, 131-139	22.2	56
75	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016 , 1, 16151	26.6	54
74	Novel avian influenza A (H5N6) viruses isolated in migratory waterfowl before the first human case reported in China, 2014. <i>Scientific Reports</i> , 2016 , 6, 29888	4.9	46
73	Highly diversified Zika viruses imported to China, 2016. <i>Protein and Cell</i> , 2016 , 7, 461-4	7.2	46
72	The emergence, genomic diversity and global spread of SARS-CoV-2. <i>Nature</i> , 2021 ,	50.4	42
71	Identification of novel inter-genotypic recombinants of human hepatitis B viruses by large-scale phylogenetic analysis. <i>Virology</i> , 2012 , 427, 51-9	3.6	39
70	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015 , 5, 12986	4.9	38
69	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. <i>Clinical Infectious Diseases</i> , 2019 , 68, 1100-1109	11.6	35
68	Dominant subtype switch in avian influenza viruses during 2016-2019 in China. <i>Nature Communications</i> , 2020 , 11, 5909	17.4	35
67	A complete analysis of HA and NA genes of influenza A viruses. <i>PLoS ONE</i> , 2010 , 5, e14454	3.7	31
66	The first imported case of Rift Valley fever in China reveals a genetic reassortment of different viral lineages. <i>Emerging Microbes and Infections</i> , 2017 , 6, e4	18.9	30
65	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014-2015. <i>Virologica Sinica</i> , 2016 , 31, 300-5	6.4	28
64	Global and local persistence of influenza A(H5N1) virus. <i>Emerging Infectious Diseases</i> , 2014 , 20, 1287-95	10.2	28
63	Phylogenetics of varied subtypes of avian influenza viruses in China: potential threat to humans. <i>Protein and Cell</i> , 2014 , 5, 253-7	7.2	27

62	Recombination in hepatitis C virus: identification of four novel naturally occurring inter-subtype recombinants. <i>PLoS ONE</i> , 2012 , 7, e41997	3.7	25
61	Increasing genetic diversity of Zika virus in the Latin American outbreak. <i>Emerging Microbes and Infections</i> , 2016 , 5, e68	18.9	25
60	Epidemiological characteristics of hand, foot, and mouth disease in Shandong, China, 2009-2016. <i>Scientific Reports</i> , 2017 , 7, 8900	4.9	24
59	A Neonatal Murine Model of Coxsackievirus A6 Infection for Evaluation of Antiviral and Vaccine Efficacy. <i>Journal of Virology</i> , 2017 , 91,	6.6	23
58	Prospective of Genomics in Revealing Transmission, Reassortment and Evolution of Wildlife-Borne Avian Influenza A (H5N1) Viruses. <i>Current Genomics</i> , 2011 , 12, 466-74	2.6	23
57	A novel bat coronavirus reveals natural insertions at the S1/S2 cleavage site of the Spike protein and a possible recombinant origin of HCoV-19		22
56	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. <i>Virologica Sinica</i> , 2019 , 34, 1-8	6.4	21
55	Subgenotyping of genotype C hepatitis B virus: correcting misclassifications and identifying a novel subgenotype. <i>PLoS ONE</i> , 2012 , 7, e47271	3.7	21
54	Emerging H5N8 avian influenza viruses. <i>Science</i> , 2021 , 372, 784-786	33.3	20
53	Ecological dynamics of influenza A viruses: cross-species transmission and global migration. <i>Scientific Reports</i> , 2016 , 6, 36839	4.9	19
52	Subgenotype reclassification of genotype B hepatitis B virus. <i>BMC Gastroenterology</i> , 2012 , 12, 116	3	19
51	Avian Influenza A Viruses among Occupationally Exposed Populations, China, 2014-2016. <i>Emerging Infectious Diseases</i> , 2019 , 25, 2215-2225	10.2	19
50	A novel SARS-CoV-2 related coronavirus with complex recombination isolated from bats in Yunnan province, China. <i>Emerging Microbes and Infections</i> , 2021 , 10, 1683-1690	18.9	18
49	Protective Efficacies of Formaldehyde-Inactivated Whole-Virus Vaccine and Antivirals in a Murine Model of Coxsackievirus A10 Infection. <i>Journal of Virology</i> , 2017 , 91,	6.6	16
48	Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 5949-5954	11.5	16
47	Long noncoding RNAs: Novel regulators of virus-host interactions. <i>Reviews in Medical Virology</i> , 2019 , 29, e2046	11.7	15
46	Uncovering two phases of early intercontinental COVID-19 transmission dynamics. <i>Journal of Travel Medicine</i> , 2020 , 27,	12.9	14
45	One-year sustained cellular and humoral immunities of COVID-19 convalescents. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	14

44	Novel sub-lineages, recombinants and reassortants of severe fever with thrombocytopenia syndrome virus. <i>Ticks and Tick-borne Diseases</i> , 2017 , 8, 385-390	3.6	13
43	High genetic diversity and frequent genetic reassortment of avian influenza A(H9N2) viruses along the East Asian-Australian migratory flyway. <i>Infection, Genetics and Evolution</i> , 2016 , 39, 325-329	4.5	13
42	Continuous reassortments with local chicken H9N2 virus underlie the human-infecting influenza A (H7N9) virus in the new influenza season, Guangdong, China. <i>Protein and Cell</i> , 2014 , 5, 878-82	7.2	12
41	Co-circulation and persistence of multiple A/H3N2 influenza variants in China. <i>Emerging Microbes and Infections</i> , 2019 , 8, 1157-1167	18.9	11
40	Emerging HxNy Influenza A Viruses. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020 ,	5.4	11
39	First documented case of avian influenza (H5N1) virus infection in a lion. <i>Emerging Microbes and Infections</i> , 2016 , 5, e125	18.9	11
38	Continued reassortment of avian H6 influenza viruses from Southern China, 2014-2016. <i>Transboundary and Emerging Diseases</i> , 2019 , 66, 592-598	4.2	11
37	Characterization of an inactivated whole-virus bivalent vaccine that induces balanced protective immunity against coxsackievirus A6 and A10 in mice. <i>Vaccine</i> , 2018 , 36, 7095-7104	4.1	10
36	Tamdy Virus in Ixodid Ticks Infesting Bactrian Camels, Xinjiang, China, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 2136-2138	10.2	9
35	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses		9
34	Pathogen genomic surveillance elucidates the origins, transmission and evolution of emerging viral agents in China. <i>Science China Life Sciences</i> , 2017 , 60, 1317-1330	8.5	8
33	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. <i>Frontiers in Microbiology</i> , 2019 , 10, 1001	5.7	7
32	Intra-host Ebola viral adaption during human infection. <i>Biosafety and Health</i> , 2019 , 1, 14-24	4.7	7
31	A neonatal murine model of coxsackievirus A4 infection for evaluation of vaccines and antiviral drugs. <i>Emerging Microbes and Infections</i> , 2019 , 8, 1445-1455	18.9	7
30	A Novel Hepe-Like Virus from Farmed Giant Freshwater Prawn. <i>Viruses</i> , 2020 , 12,	6.2	6
29	Genomic characterizations of H4 subtype avian influenza viruses from live poultry markets in Sichuan province of China, 2014-2015. <i>Science China Life Sciences</i> , 2018 , 61, 1123-1126	8.5	6
28	Substitution rates of the internal genes in the novel avian H7N9 influenza virus. <i>Clinical Infectious Diseases</i> , 2013 , 57, 1213-5	11.6	6
27	A novel SARS-CoV-2 related virus with complex recombination isolated from bats in Yunnan province, China		6

26	Rapid detection of hand, foot and mouth disease enterovirus genotypes by multiplex PCR. <i>Journal of Virological Methods</i> , 2018 , 258, 7-12	2.6	6
25	Effects of Acetylshikonin on the Infection and Replication of Coxsackievirus A16 in Vitro and in Vivo. <i>Journal of Natural Products</i> , 2019 , 82, 1089-1097	4.9	5
24	MrBayes tgMCL: a tight GPU implementation of MrBayes. <i>PLoS ONE</i> , 2013 , 8, e60667	3.7	5
23	Amino acid substitutions in antigenic region B of hemagglutinin play a critical role in the antigenic drift of subclade 2.3.4.4 highly pathogenic H5N1 influenza viruses. <i>Transboundary and Emerging Diseases</i> , 2020 , 67, 263-275	4.2	5
22	Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing. <i>Journal of Infection</i> , 2021 , 82, e44-e48	18.9	5
21	Sudden emergence of human infections with H7N9 avian influenza A virus in Hubei province, central China. <i>Scientific Reports</i> , 2018 , 8, 2486	4.9	4
20	Re-emergence of H5N8 highly pathogenic avian influenza virus in wild birds, China. <i>Emerging Microbes and Infections</i> , 2021 , 10, 1819-1823	18.9	4
19	Non-coding regions of the Ebola virus genome contain indispensable phylogenetic and evolutionary information. <i>Science China Life Sciences</i> , 2015 , 58, 682-6	8.5	3
18	MrBayes tgMC++: A High Performance and Resource-Efficient GPU-Oriented Phylogenetic Analysis Method. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016 , 13, 845-854	3	3
17	Global holiday datasets for understanding seasonal human mobility and population dynamics.. <i>Scientific Data</i> , 2022 , 9, 17	8.2	3
16	A Novel Virus of Associated with Sexual Precocity in. <i>MSystems</i> , 2021 , 6, e0000321	7.6	3
15	Novel reassortant 2.3.4.4B H5N6 highly pathogenic avian influenza viruses circulating among wild, domestic birds in Xinjiang, Northwest China. <i>Journal of Veterinary Science</i> , 2021 , 22, e43	1.6	3
14	A Novel Bunyavirus Discovered in Oriental Shrimp (). <i>Frontiers in Microbiology</i> , 2021 , 12, 751112	5.7	2
13	Ecology of avian influenza viruses in migratory birds wintering within the Yangtze River wetlands. <i>Science Bulletin</i> , 2021 , 66, 2014-2024	10.6	2
12	A reassortant highly pathogenic avian influenza H5N6 virus originating from the wildbird-origin H5N6 and the poultry H9N2/H7N9 viruses in Xinjiang, China. <i>Medycyna Weterynaryjna</i> , 2021 , 77, 6532-2021	1.4	2
11	Tick virome diversity in Hubei Province, China, and the influence of host ecology. <i>Virus Evolution</i> , 2021 , 7, veab089	3.7	1
10	Murine model of acute myocarditis and cerebral cortical neuron edema induced by coxsackievirus B4. <i>Zoological Research</i> , 2018 , 39, 52-57	3.4	1
9	Rapid humoral immune responses are required for recovery from haemorrhagic fever with renal syndrome patients. <i>Emerging Microbes and Infections</i> , 2020 , 9, 2303-2314	18.9	1

8	Intratumoral Virotherapy with Wild-Type Newcastle Disease Virus in Carcinoma Krebs-2 Cancer Model. <i>Viruses</i> , 2021 , 13,	6.2	1
7	Rapid Emergence of the Reassortant 2.3.4.4b H5N2 Highly Pathogenic Avian Influenza Viruses in a Live Poultry Market in Xinjiang, Northwest China.. <i>Avian Diseases</i> , 2021 , 65, 578-583	1.6	1
6	Identification of a novel hepacivirus in Mongolian gerbil (<i>Meriones unguiculatus</i>) from Shaanxi, China.. <i>Virologica Sinica</i> , 2022 , 37, 307-307	6.4	0
5	Novel reassortment 2.3.4.4b H5N8 highly pathogenic avian influenza viruses circulating in Xinjiang, China.. <i>Preventive Veterinary Medicine</i> , 2021 , 199, 105564	3.1	0
4	Identification of a Recombinant Equine Coronavirus in Donkey, China.. <i>Emerging Microbes and Infections</i> , 2022 , 1-16	18.9	0
3	Three Novel Avastroviruses Identified in Dead Wild Crows. <i>Virologica Sinica</i> , 2021 , 1	6.4	
2	Prevalence and genetic diversity of Dabieshan tick virus in Shandong Province, China.. <i>Journal of Infection</i> , 2022 ,	18.9	
1	Rapid detection of the emerging tick-borne Tamdy virus by TaqMan-based real-time reverse transcription PCR.. <i>Journal of Virological Methods</i> , 2022 , 305, 114538	2.6	