

Wei-Feng Shi

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6566974/wei-feng-shi-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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
96	Global holiday datasets for understanding seasonal human mobility and population dynamics.. <i>Scientific Data</i> , 2022 , 9, 17	8.2	3
95	Identification of a Recombinant Equine Coronavirus in Donkey, China.. <i>Emerging Microbes and Infections</i> , 2022 , 1-16	18.9	0
94	Prevalence and genetic diversity of Dabieshan tick virus in Shandong Province, China.. <i>Journal of Infection</i> , 2022 ,	18.9	
93	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	
92	The emergence, genomic diversity and global spread of SARS-CoV-2. <i>Nature</i> , 2021 ,	50.4	42
91	Tick virome diversity in Hubei Province, China, and the influence of host ecology. <i>Virus Evolution</i> , 2021 , 7, veab089	3.7	1
90	A Novel Bunyavirus Discovered in Oriental Shrimp (). <i>Frontiers in Microbiology</i> , 2021 , 12, 751112	5.7	2
89	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
88	Intratumoral Virotherapy with Wild-Type Newcastle Disease Virus in Carcinoma Krebs-2 Cancer Model. <i>Viruses</i> , 2021 , 13,	6.2	1
87	Emerging H5N8 avian influenza viruses. <i>Science</i> , 2021 , 372, 784-786	33.3	20
86	A Novel Virus of Associated with Sexual Precocity in. <i>MSystems</i> , 2021 , 6, e0000321	7.6	3
85	Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing. <i>Journal of Infection</i> , 2021 , 82, e44-e48	18.9	5
84	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
83	One-year sustained cellular and humoral immunities of COVID-19 convalescents. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	14
82	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
81	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

80	Three Novel Avastroviruses Identified in Dead Wild Crows. <i>Virologica Sinica</i> , 2021 , 1	6.4	
79	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
78	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
77	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
76	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
75	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
74	A Novel Hepe-Like Virus from Farmed Giant Freshwater Prawn. <i>Viruses</i> , 2020 , 12,	6.2	6
73	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
72	A Novel Coronavirus from Patients with Pneumonia in China, 2019. <i>New England Journal of Medicine</i> , 2020 , 382, 727-733	59.2	14511
71	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
70	Uncovering two phases of early intercontinental COVID-19 transmission dynamics. <i>Journal of Travel Medicine</i> , 2020 , 27,	12.9	14
69	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 H5NX influenza viruses. <i>Transboundary and Emerging Diseases</i> , 2020 , 67, 263-275	4.2	5
68	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
67	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
66	Dominant subtype switch in avian influenza viruses during 2016-2019 in China. <i>Nature Communications</i> , 2020 , 11, 5909	17.4	35
65	Emerging HxNy Influenza A Viruses. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020 ,	5.4	11
64	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
63	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

62	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
61	Long noncoding RNAs: Novel regulators of virus-host interactions. <i>Reviews in Medical Virology</i> , 2019 , 29, e2046	11.7	15
60	Intra-host Ebola viral adaptation during human infection. <i>Biosafety and Health</i> , 2019 , 1, 14-24	4.7	7
59	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. <i>Clinical Infectious Diseases</i> , 2019 , 68, 1100-1109	11.6	35
58	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
57	Tamdy Virus in Ixodid Ticks Infesting Bactrian Camels, Xinjiang, China, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 2136-2138	10.2	9
56	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
55	Avian Influenza A Viruses among Occupationally Exposed Populations, China, 2014-2016. <i>Emerging Infectious Diseases</i> , 2019 , 25, 2215-2225	10.2	19
54	The evolution of Zika virus from Asia to the Americas. <i>Nature Reviews Microbiology</i> , 2019 , 17, 131-139	22.2	56
53	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
52	Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. <i>Nature</i> , 2018 , 556, 255-258	50.4	369
51	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
50	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
49	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
48	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
47	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
46	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
45	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

44	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
43	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
42	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
41	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
40	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
39	A single mutation in the prM protein of Zika virus contributes to fetal microcephaly. <i>Science</i> , 2017 , 358, 933-936	33.3	292
38	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
37	Epidemiological characteristics of hand, foot, and mouth disease in Shandong, China, 2009-2016. <i>Scientific Reports</i> , 2017 , 7, 8900	4.9	24
36	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
35	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
34	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
33	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016 , 1, 16151	26.6	54
32	Ecological dynamics of influenza A viruses: cross-species transmission and global migration. <i>Scientific Reports</i> , 2016 , 6, 36839	4.9	19
31	Highly diversified Zika viruses imported to China, 2016. <i>Protein and Cell</i> , 2016 , 7, 461-4	7.2	46
30	Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. <i>Trends in Microbiology</i> , 2016 , 24, 490-502	12.4	1599
29	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
28	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
27	Increasing genetic diversity of Zika virus in the Latin American outbreak. <i>Emerging Microbes and Infections</i> , 2016 , 5, e68	18.9	25

26	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016 , 20, 810-821	23.4	187
25	First documented case of avian influenza (H5N1) virus infection in a lion. <i>Emerging Microbes and Infections</i> , 2016 , 5, e125	18.9	11
24	Two novel reassortants of avian influenza A (H5N6) virus in China. <i>Journal of General Virology</i> , 2015 , 96, 975-981	4.9	79
23	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
22	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015 , 524, 93-6	50.4	121
21	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, e01280-15	7.8	70
20	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015 , 5, 12986	4.9	38
19	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014 , 5, 3142	17.4	120
18	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
17	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
16	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet, The</i> , 2014 , 383, 869	40	80
15	Global and local persistence of influenza A(H5N1) virus. <i>Emerging Infectious Diseases</i> , 2014 , 20, 1287-95	10.2	28
14	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
13	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
12	Hepatitis B virus subgenotyping: history, effects of recombination, misclassifications, and corrections. <i>Infection, Genetics and Evolution</i> , 2013 , 16, 355-61	4.5	75
11	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
10	MrBayes tgmcl: a tight GPU implementation of MrBayes. <i>PLoS ONE</i> , 2013 , 8, e60667	3.7	5
9	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

8	Subgenotype reclassification of genotype B hepatitis B virus. <i>BMC Gastroenterology</i> , 2012 , 12, 116	3	19
7	Recombination in hepatitis C virus: identification of four novel naturally occurring inter-subtype recombinants. <i>PLoS ONE</i> , 2012 , 7, e41997	3.7	25
6	Subgenotyping of genotype C hepatitis B virus: correcting misclassifications and identifying a novel subgenotype. <i>PLoS ONE</i> , 2012 , 7, e47271	3.7	21
5	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
4	A complete analysis of HA and NA genes of influenza A viruses. <i>PLoS ONE</i> , 2010 , 5, e14454	3.7	31
3	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
2	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses		9
1	A novel SARS-CoV-2 related virus with complex recombination isolated from bats in Yunnan province, China		6