Xiu-Feng Wan

List of Publications by Year
in descending order

129 papers	3,811 citations	159358 30 h-index	161609 54 g-index
139 all docs	139 docs citations	139 times ranked	4714 citing authors

#	Article	IF	Citations
1	Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?. PLoS Pathogens, 2020, 16, e1008421.	2.1	318
2	Avian-origin H3N2 canine influenza A viruses in Southern China. Infection, Genetics and Evolution, 2010, 10, 1286-1288.	1.0	150
3	Molecular Basis for Broad Neuraminidase Immunity: Conserved Epitopes in Seasonal and Pandemic H1N1 as Well as H5N1 Influenza Viruses. Journal of Virology, 2013, 87, 9290-9300.	1.5	141
4	Transcriptomic and Proteomic Characterization of the Fur Modulon in the Metal-Reducing Bacterium Shewanella oneidensis. Journal of Bacteriology, 2004, 186, 8385-8400.	1.0	134
5	Indications that Live Poultry Markets Are a Major Source of Human H5N1 Influenza Virus Infection in China. Journal of Virology, 2011, 85, 13432-13438.	1.5	128
6	Pathogenesis of Influenza D Virus in Cattle. Journal of Virology, 2016, 90, 5636-5642.	1.5	125
7	A Computational Framework for Influenza Antigenic Cartography. PLoS Computational Biology, 2010, 6, e1000949.	1.5	119
8	H3N2 Mismatch of 2014â€"15 Northern Hemisphere Influenza Vaccines and Head-to-head Comparison between Human and Ferret Antisera derived Antigenic Maps. Scientific Reports, 2015, 5, 15279.	1.6	118
9	Influenza D virus infection in Mississippi beef cattle. Virology, 2015, 486, 28-34.	1.1	115
10	Evolution of Highly Pathogenic H5N1 Avian Influenza Viruses in Vietnam between 2001 and 2007. PLoS ONE, 2008, 3, e3462.	1.1	112
11	Transport and fate of human expiratory dropletsâ€"A modeling approach. Physics of Fluids, 2020, 32, 083307.	1.6	101
12	Using Sequence Data To Infer the Antigenicity of Influenza Virus. MBio, 2013, 4, .	1.8	85
13	Placental SARSâ€CoVâ€2 in a pregnant woman with mild COVIDâ€19 disease. Journal of Medical Virology, 2021, 93, 1038-1044.	2.5	76
14	Identification of an H6N6 swine influenza virus in southern China. Infection, Genetics and Evolution, 2011, 11, 1174-1177.	1.0	71
15	Transcriptome Profiling of Shewanella oneidensis Gene Expression following Exposure to Acidic and Alkaline pH. Journal of Bacteriology, 2006, 188, 1633-1642.	1.0	62
16	The neuraminidase of A(H3N2) influenza viruses circulating since 2016 is antigenically distinct from the A/Hong Kong/4801/2014 vaccine strain. Nature Microbiology, 2019, 4, 2216-2225.	5.9	59
17	Serological evidence for high prevalence of Influenza D Viruses in Cattle, Nebraska, United States, 2003â€"2004. Virology, 2017, 501, 88-91.	1.1	52
18	Imprinting of Repeated Influenza A/H3 Exposures on Antibody Quantity and Antibody Quality: Implications for Seasonal Vaccine Strain Selection and Vaccine Performance. Clinical Infectious Diseases, 2018, 67, 1523-1532.	2.9	49

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19	Influenza D Virus Infection in Feral Swine Populations, United States. Emerging Infectious Diseases, 2018, 24, 1020-1028.	2.0	48
20	Nucleotide composition string selection in HIV-1 subtyping using whole genomes. Bioinformatics, 2007, 23, 1744-1752.	1.8	47
21	Phylogenetic analysis using complete signature information of whole genomes and clustered Neighbour-Joining method. International Journal of Bioinformatics Research and Applications, 2006, 2, 219.	0.1	45
22	A Triclade DNA Vaccine Designed on the Basis of a Comprehensive Serologic Study Elicits Neutralizing Antibody Responses against All Clades and Subclades of Highly Pathogenic Avian Influenza H5N1 Viruses. Journal of Virology, 2012, 86, 6970-6978.	1.5	45
23	AntigenMap 3D: an online antigenic cartography resource. Bioinformatics, 2012, 28, 1292-1293.	1.8	44
24	Identifying Antigenicity-Associated Sites in Highly Pathogenic H5N1 Influenza Virus Hemagglutinin by Using Sparse Learning. Journal of Molecular Biology, 2012, 422, 145-155.	2.0	43
25	Highly pathogenic avian influenza is an emerging disease threat to wild birds in North America. Journal of Wildlife Management, 2022, 86, .	0.7	43
26	Characterization of a highly pathogenic avian influenza H5N1 virus sublineage in poultry seized at ports of entry into Vietnam. Virology, 2009, 387, 250-256.	1.1	42
27	A Perspective on Multiple Waves of Influenza Pandemics. PLoS ONE, 2013, 8, e60343.	1.1	42
28	Mutation tryptophan to leucine at position 222 of haemagglutinin could facilitate H3N2 influenza A virus infection in dogs. Journal of General Virology, 2013, 94, 2599-2608.	1.3	38
29	Genotypic diversity of H5N1 highly pathogenic avian influenza viruses. Journal of General Virology, 2008, 89, 2182-2193.	1.3	37
30	Defining biological and biophysical properties of SARS-CoV-2 genetic material in wastewater. Science of the Total Environment, 2022, 807, 150786.	3.9	36
31	Antigenic Characterization of H3N2 Influenza A Viruses from Ohio Agricultural Fairs. Journal of Virology, 2013, 87, 7655-7667.	1.5	33
32	Influenza Neuraminidase: Underrated Role in Receptor Binding. Trends in Microbiology, 2019, 27, 477-479.	3.5	33
33	Extent of Antigenic Cross-Reactivity among Highly Pathogenic H5N1 Influenza Viruses. Journal of Clinical Microbiology, 2011, 49, 3531-3536.	1.8	28
34	Antigenic distance measurements for seasonal influenza vaccine selection. Vaccine, 2012, 30, 448-453.	1.7	28
35	SURVEY OF ARCTIC ALASKAN WILDLIFE FOR INFLUENZA A ANTIBODIES: LIMITED EVIDENCE FOR EXPOSURE OF MAMMALS. Journal of Wildlife Diseases, 2019, 55, 387.	0.3	28
36	Low-Pathogenic Influenza A Viruses in North American Diving Ducks Contribute to the Emergence of a Novel Highly Pathogenic Influenza A(H7N8) Virus. Journal of Virology, 2017, 91, .	1.5	27

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37	Mutation W222L at the Receptor Binding Site of Hemagglutinin Could Facilitate Viral Adaption from Equine Influenza A(H3N8) Virus to Dogs. Journal of Virology, 2018, 92, .	1.5	27
38	Influenza A Subtype H3 Viruses in Feral Swine, United States, 2011–2012. Emerging Infectious Diseases, 2014, 20, 839-842.	2.0	25
39	Computational Methods for Remote Homolog Identification. Current Protein and Peptide Science, 2005, 6, 527-546.	0.7	24
40	Transcriptome analysis reveals response regulator SO2426-mediated gene expression in Shewanella oneidensis MR-1 under chromate challenge. BMC Genomics, 2008, 9, 395.	1.2	24
41	Quartet-Net: A Quartet-Based Method to Reconstruct Phylogenetic Networks. Molecular Biology and Evolution, 2013, 30, 1206-1217.	3.5	24
42	Pathogenesis of co-infections of influenza D virus and Mannheimia haemolytica in cattle. Veterinary Microbiology, 2019, 231, 246-253.	0.8	24
43	A quantitative genotype algorithm reflecting H5N1 Avian influenza niches. Bioinformatics, 2007, 23, 2368-2375.	1.8	23
44	Genetic Evidence Supports Sporadic and Independent Introductions of Subtype H5 Low-Pathogenic Avian Influenza A Viruses from Wild Birds to Domestic Poultry in North America. Journal of Virology, 2018, 92, .	1.5	23
45	A quantitative structure–activity relationship (QSAR) study on glycan array data to determine the specificities of glycan-binding proteins. Glycobiology, 2012, 22, 552-560.	1.3	22
46	Limited Antigenic Diversity in Contemporary H7 Avian-Origin Influenza A Viruses from North America. Scientific Reports, 2016, 6, 20688.	1.6	22
47	Differential Effects of Prior Influenza Exposures on H3N2 Cross-reactivity of Human Postvaccination Sera. Clinical Infectious Diseases, 2017, 65, 259-267.	2.9	22
48	Feral Swine in the United States Have Been Exposed to both Avian and Swine Influenza A Viruses. Applied and Environmental Microbiology, 2017, 83, .	1.4	22
49	Spatiotemporal Structure of Molecular Evolution of H5N1 Highly Pathogenic Avian Influenza Viruses in Vietnam. PLoS ONE, 2010, 5, e8631.	1.1	22
50	Detection of African swine fever virus-like sequences in ponds in the Mississippi Delta through metagenomic sequencing. Virus Genes, 2013, 46, 441-446.	0.7	21
51	Antigenic characterization of recent H5N1 highly pathogenic avian influenza viruses circulating in Egyptian poultry. Virology, 2013, 435, 350-356.	1.1	21
52	Sequence-Based Antigenic Change Prediction by a Sparse Learning Method Incorporating Co-Evolutionary Information. PLoS ONE, 2014, 9, e106660.	1.1	21
53	Antigenic and Genetic Evolution of Low-Pathogenicity Avian Influenza Viruses of Subtype H7N3 following Heterologous Vaccination. Vaccine Journal, 2014, 21, 603-612.	3.2	21
54	A Y161F Hemagglutinin Substitution Increases Thermostability and Improves Yields of 2009 H1N1 Influenza A Virus in Cells. Journal of Virology, 2018, 92, .	1.5	21

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55	Tissue tropisms opt for transmissible reassortants during avian and swine influenza A virus co-infection in swine. PLoS Pathogens, 2018, 14, e1007417.	2.1	21
56	Concepts and applications for influenza antigenic cartography. Influenza and Other Respiratory Viruses, 2011, 5, 204-7.	1.5	21
57	Computational Identification of Reassortments in Avian Influenza Viruses. Avian Diseases, 2007, 51, 434-439.	0.4	19
58	Pathogenicity and transmission of a swine influenza A(H6N6) virus. Emerging Microbes and Infections, 2017, 6, 1-13.	3.0	19
59	HA stabilization promotes replication and transmission of swine H1N1 gamma influenza viruses in ferrets. ELife, 2020, 9, .	2.8	19
60	Association analyses of large-scale glycan microarray data reveal novel host-specific substructures in influenza A virus binding glycans. Scientific Reports, 2015, 5, 15778.	1.6	18
61	Identification of the source of A (H10N8) virus causing human infection. Infection, Genetics and Evolution, 2015, 30, 159-163.	1.0	18
62	Intrauterine Fetal Demise in the Third Trimester of Pregnancy Associated With Mild Infection With the SARS-CoV-2 Delta Variant Without Protection From Vaccination. Journal of Infectious Diseases, 2022, 225, 748-753.	1.9	18
63	Quartet-based methods to reconstruct phylogenetic networks. BMC Systems Biology, 2014, 8, 21.	3.0	17
64	Error-prone pcr-based mutagenesis strategy for rapidly generating high-yield influenza vaccine candidates. Virology, 2015, 482, 234-243.	1.1	17
65	Aerosol Transmission of Gull-Origin Iceland Subtype H10N7 Influenza A Virus in Ferrets. Journal of Virology, 2019, 93, .	1.5	17
66	Perspective on emergence and re-emergence of amantadine resistant influenza A viruses in domestic animals in China. Infection, Genetics and Evolution, 2013, 20, 298-303.	1.0	16
67	Variation in protection of four divergent avian influenza virus vaccine seed strains against eight clade 2.2.1 and 2.2.1.1. <scp>E</scp>gyptian <scp>H</scp>5<scp>N</scp>1 high pathogenicity variants in poultry. Influenza and Other Respiratory Viruses, 2014, 8, 654-662.	1.5	16
68	Measuring Site-specific Glycosylation Similarity between Influenza a Virus Variants with Statistical Certainty. Molecular and Cellular Proteomics, 2020, 19, 1533-1545.	2.5	16
69	Mutation from arginine to lysine at the position 189 of hemagglutinin contributes to the antigenic drift in H3N2 swine influenza viruses. Virology, 2013, 446, 225-229.	1.1	15
70	Zoonotic Risk, Pathogenesis, and Transmission of Avian-Origin H3N2 Canine Influenza Virus. Journal of Virology, 2017, 91, .	1.5	15
71	Rapid High-Throughput Whole-Genome Sequencing of SARS-CoV-2 by Using One-Step Reverse Transcription-PCR Amplification with an Integrated Microfluidic System and Next-Generation Sequencing. Journal of Clinical Microbiology, 2021, 59, .	1.8	15
72	Use of serological and mucosal immune responses to Mycoplasma hyopneumoniae antigens P97R1, P46 and P36 in the diagnosis of infection. Veterinary Journal, 2014, 202, 128-133.	0.6	14

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73	Graph-guided multi-task sparse learning model: a method for identifying antigenic variants of influenza A(H3N2) virus. Bioinformatics, 2019, 35, 77-87.	1.8	14
74	Dynamics of virus shedding and antibody responses in influenza A virus-infected feral swine. Journal of General Virology, 2015, 96, 2569-2578.	1.3	14
75	Revealing gene transcription and translation initiation patterns in archaea, using an interactive clustering model. Extremophiles, 2004, 8, 291-299.	0.9	13
76	Testing the Effect of Internal Genes Derived from a Wild-Bird-Origin H9N2 Influenza A Virus on the Pathogenicity of an A/H7N9 Virus. Cell Reports, 2015, 12, 1831-1841.	2.9	13
77	RNALL: AN EFFICIENT ALGORITHM FOR PREDICTING RNA LOCAL SECONDARY STRUCTURAL LANDSCAPE IN GENOMES. Journal of Bioinformatics and Computational Biology, 2006, 04, 1015-1031.	0.3	12
78	HA Triggers the Switch from MEK1 SUMOylation to Phosphorylation of the ERK Pathway in Influenza A Virus-Infected Cells and Facilitates Its Infection. Frontiers in Cellular and Infection Microbiology, 2017, 7, 27.	1.8	12
79	Reinfection with two genetically distinct SARS‐CoV‐2 viruses within 19 days. Journal of Medical Virology, 2021, 93, 5700-5703.	2.5	12
80	Intrinsic Terminator Prediction and Its Application in Synechococcus sp. WH8102. Journal of Computer Science and Technology, 2005, 20, 465-482.	0.9	11
81	Antigenic Characterization of H3 Subtypes of Avian Influenza A Viruses from North America. Avian Diseases, 2016, 60, 346.	0.4	11
82	Cross-Protection by Inactivated H5 Prepandemic Vaccine Seed Strains against Diverse Goose/Guangdong Lineage H5N1 Highly Pathogenic Avian Influenza Viruses. Journal of Virology, 2020, 94, .	1.5	11
83	Antibody Responses to SARS-CoV-2 Antigens in Humans and Animals. Vaccines, 2020, 8, 684.	2.1	11
84	Antigenic characterization of influenza and SARS-CoV-2 viruses. Analytical and Bioanalytical Chemistry, 2022, 414, 2841-2881.	1.9	11
85	Population-environment drivers of H5N1 avian influenza molecular change in Vietnam. Health and Place, 2012, 18, 1122-1131.	1.5	10
86	Potency, Efficacy, and Antigenic Mapping of H7 Avian Influenza Virus Vaccines Against the 2012 H7N3 Highly Pathogenic Avian Influenza Virus from Mexico. Avian Diseases, 2014, 58, 359-366.	0.4	10
87	Prediction of DNA-binding proteins by interaction fusion feature representation and selective ensemble. Knowledge-Based Systems, 2019, 163, 598-610.	4.0	10
88	Multi-task learning sparse group lasso: a method for quantifying antigenicity of influenza A(H1N1) virus using mutations and variations in glycosylation of Hemagglutinin. BMC Bioinformatics, 2020, 21, 182.	1.2	10
89	UBIQUITOUS REASSORTMENTS IN INFLUENZA A VIRUSES. Journal of Bioinformatics and Computational Biology, 2008, 06, 981-999.	0.3	9
90	Comprehensive N‐and O‐glycosylation mapping of human coagulation factor V. Journal of Thrombosis and Haemostasis, 2020, 18, 1884-1892.	1.9	9

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91	The Ribosomal Shunt Translation Strategy of Cauliflower Mosaic Virus Has Evolved from Ancient Long Terminal Repeats. Journal of Virology, 2006, 80, 3811-3822.	1.5	8
92	Identifying a few foot-and-mouth disease virus signature nucleotide strings for computational genotyping. BMC Bioinformatics, 2008, 9, 279.	1.2	8
93	Genetic Variation of Highly Pathogenic H5N1 Avian Influenza Viruses in Vietnam Shows Both Species-Specific and Spatiotemporal Associations. Avian Diseases, 2011, 55, 659-666.	0.4	8
94	Individual-Level Antibody Dynamics Reveal Potential Drivers of Influenza A Seasonality in Wild Pig Populations. Integrative and Comparative Biology, 2019, 59, 1231-1242.	0.9	8
95	Limited Cross-Protection Provided by Prior Infection Contributes to High Prevalence of Influenza D Viruses in Cattle. Journal of Virology, 2020, 94, .	1.5	8
96	Terminal Epitope-Dependent Branch Preference of Siglecs Toward N-Glycans. Frontiers in Molecular Biosciences, 2021, 8, 645999.	1.6	8
97	Site-Specific N- and O-Glycosylation Analysis of Human Plasma Fibronectin. Frontiers in Chemistry, 2021, 9, 691217.	1.8	8
98	Ascovirus and its evolution. Virologica Sinica, 2007, 22, 137-147.	1.2	7
99	Tissue Tropisms of Avian Influenza A Viruses Affect Their Spillovers from Wild Birds to Pigs. Journal of Virology, 2020, 94, .	1.5	7
100	SARS‑CoV‑2 show no infectivity at later stages in a prolonged COVID‑19 patient despite positivity in RNA testing. Journal of Medical Virology, 2021, 93, 4570-4575.	2.5	7
101	Systematic synthesis of bisected *N*-glycans and unique recognitions by glycan-binding proteins. Chemical Science, 2022, 13, 7644-7656.	3.7	7
102	Generalized Hierarchical Sparse Model for Arbitrary-Order Interactive Antigenic Sites Identification in Flu Virus Data. , 2016, 2016, 865-874.		6
103	Evolutionary pathway for the 2017 emergence of a novel highly pathogenic avian influenza A(H7N9) virus among domestic poultry in Tennessee, United States. Virology, 2018, 525, 32-39.	1.1	6
104	Inferring seasonal infection risk at population and regional scales from serology samples. Ecology, 2020, 101, e02882.	1.5	6
105	A review on medical management of inflammatory bowel disease during the coronavirus disease 2019 pandemic. Journal of Gastroenterology and Hepatology (Australia), 2021, 36, 918-926.	1.4	6
106	Characterization of Subtype H6 Avian Influenza A Viruses Isolated From Wild Birds in Poyang Lake, China. Frontiers in Veterinary Science, 2021, 8, 685399.	0.9	6
107	Exposure of white-tailed deer in North America to influenza D virus. Virology, 2022, 573, 111-117.	1.1	6
108	Highly Pathogenic H5N1 Avian Influenza Viruses Exhibit Few Barriers to Gene Flow in Vietnam. EcoHealth, 2012, 9, 60-69.	0.9	5

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109	Detection of influenza antigenic variants directly from clinical samples using polyclonal antibody based proximity ligation assays. Virology, 2015, 476, 151-158.	1.1	5
110	Identification and Initial Characterization of a Putative Mycoplasma gallinarum Leucine Aminopeptidase Gene. Current Microbiology, 2004, 48, 32-38.	1.0	4
111	Detection of Avian H7N9 Influenza A Viruses in the Yangtze Delta Region of China During Early H7N9 Outbreaks. Avian Diseases, 2015, 60, 118.	0.4	4
112	Reduced Influenza B–Specific Postvaccination Antibody Cross-reactivity in the B/Victoria Lineage–Predominant 2019/20 Season. Clinical Infectious Diseases, 2021, 72, e776-e783.	2.9	4
113	Variations outside the conserved motifs of PB1 catalytic active site may affect replication efficiency of the RNP complex of influenza A virus. Virology, 2021, 559, 145-155.	1.1	4
114	Time-Dependent Proinflammatory Responses Shape Virus Interference during Coinfections of Influenza A Virus and Influenza D Virus. Viruses, 2022, 14, 224.	1.5	4
115	Proteomics inference of genes involved in host adaptation of Mycoplasma gallinarum. Veterinary Microbiology, 2010, 145, 177-184.	0.8	3
116	A Joint Matrix Completion and Filtering Model for Influenza Serological Data Integration. PLoS ONE, 2013, 8, e69842.	1.1	3
117	A quantitative RT-PCR assay for rapid detection of Eurasian-lineage H10 subtype influenza A virus. Virologica Sinica, 2016, 31, 444-447.	1.2	3
118	Detection of Antigenic Variants of Subtype H3 Swine Influenza A Viruses from Clinical Samples. Journal of Clinical Microbiology, 2017, 55, 1037-1045.	1.8	3
119	Cell-Adapted Mutations and Antigenic Diversity of Influenza B Viruses in Missouri, 2019–2020 Season. Viruses, 2021, 13, 1896.	1.5	3
120	Triple reassortment increases compatibility among viral ribonucleoprotein genes of contemporary avian and human influenza A viruses. PLoS Pathogens, 2021, 17, e1009962.	2.1	3
121	Serologic Evidence for Influenza a Virus Exposure in Three Loon Species Breeding in Alaska, USA. Journal of Wildlife Diseases, 2019, 55, 862.	0.3	2
122	WHOLE GENOME COMPOSITION DISTANCE FOR HIV-1 GENOTYPING. , 2006, , .		1
123	H7N1 Low Pathogenicity Avian Influenza Viruses in Poultry in the United States During 2018. Avian Diseases, 2020, 65, 59-62.	0.4	1
124	IPMiner: a progenitor gene identifier for influenza A virus. Influenza and Other Respiratory Viruses, 2011, 5, 413-5.	1.5	1
125	Mixture model analysis reflecting dynamics of the population diversity of 2009 pandemic H1N1 influenza virus. In Silico Biology, 2011, 11, 225-36.	0.4	1
126	Exploring Core/Periphery Structures in Protein Interaction Networks Provides Structure-Property Relation Insights. , 2008, , .		0

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127	SO2426 is a positive regulator of siderophore expression in Shewanella oneidensis MR-1. BMC Microbiology, 2011, 11, 125.	1.3	0
128	Serologic Evidence for Influenza A Virus Exposure in Three Loon Species Breeding in Alaska, USA. Journal of Wildlife Diseases, 2019, 55, 862-867.	0.3	0
129	Influenza Virus Infections in Polarized Cells. Viruses, 2022, 14, 1307.	1.5	0