

Feng Wen

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

428
citations

759055

12
h-index

794469

19
g-index

35
all docs

35
docs citations

35
times ranked

831
citing authors

#	ARTICLE	IF	CITATIONS
1	Apolipoprotein E gene polymorphism and Alzheimer's disease in Chinese population: a meta-analysis. <i>Scientific Reports</i> , 2014, 4, 4383.	1.6	61
2	Identification of the hyper-variable genomic hotspot for the novel coronavirus SARS-CoV-2. <i>Journal of Infection</i> , 2020, 80, 671-693.	1.7	41
3	Influenza Neuraminidase: Underrated Role in Receptor Binding. <i>Trends in Microbiology</i> , 2019, 27, 477-479.	3.5	33
4	An M2e-based synthetic peptide vaccine for influenza A virus confers heterosubtypic protection from lethal virus challenge. <i>Virology Journal</i> , 2013, 10, 227.	1.4	29
5	Mutation W222L at the Receptor Binding Site of Hemagglutinin Could Facilitate Viral Adaption from Equine Influenza A(H3N8) Virus to Dogs. <i>Journal of Virology</i> , 2018, 92, .	1.5	27
6	Novel triple-reassortant H1N1 swine influenza viruses in pigs in Tianjin, Northern China. <i>Veterinary Microbiology</i> , 2016, 183, 85-91.	0.8	23
7	A Y161F Hemagglutinin Substitution Increases Thermostability and Improves Yields of 2009 H1N1 Influenza A Virus in Cells. <i>Journal of Virology</i> , 2018, 92, .	1.5	21
8	Molecular cloning and characterizations of porcine SAMHD1 and its roles in replication of highly pathogenic porcine reproductive and respiratory syndrome virus. <i>Developmental and Comparative Immunology</i> , 2014, 47, 234-246.	1.0	18
9	Identification of the source of A (H10N8) virus causing human infection. <i>Infection, Genetics and Evolution</i> , 2015, 30, 159-163.	1.0	18
10	Genetic characterization and phylogenetic analysis of porcine epidemic diarrhea virus in Guangdong, China, between 2018 and 2019. <i>PLoS ONE</i> , 2021, 16, e0253622.	1.1	18
11	Error-prone pcr-based mutagenesis strategy for rapidly generating high-yield influenza vaccine candidates. <i>Virology</i> , 2015, 482, 234-243.	1.1	17
12	Zoonotic Risk, Pathogenesis, and Transmission of Avian-Origin H3N2 Canine Influenza Virus. <i>Journal of Virology</i> , 2017, 91, .	1.5	15
13	Graph-guided multi-task sparse learning model: a method for identifying antigenic variants of influenza A(H3N2) virus. <i>Bioinformatics</i> , 2019, 35, 77-87.	1.8	14
14	Sex-specific patterns of gene expression following influenza vaccination. <i>Scientific Reports</i> , 2018, 8, 13517.	1.6	12
15	The role of PA-X C-terminal 20 residues of classical swine influenza virus in its replication and pathogenicity. <i>Veterinary Microbiology</i> , 2020, 251, 108916.	0.8	9
16	Pathogenicity and transmissibility of current H3N2 swine influenza virus in Southern China: A zoonotic potential. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 2052-2064.	1.3	9
17	Efficacy of a high-growth reassortant H1N1 influenza virus vaccine against the classical swine H1N1 subtype influenza virus in mice and pigs. <i>Archives of Virology</i> , 2014, 159, 2957-2967.	0.9	7
18	Genetic characterization of a novel genotype H9N2 avian influenza virus from chicken in South China. <i>Journal of Infection</i> , 2020, 81, 816-846.	1.7	7

#	ARTICLE	IF	CITATIONS
19	A meta-analysis identified genes responsible for distinct immune responses to trivalent inactivated and live attenuated influenza vaccines. <i>Journal of Cellular Physiology</i> , 2019, 234, 5196-5202.	2.0	6
20	A novel M2e-multiple antigenic peptide providing heterologous protection in mice. <i>Journal of Veterinary Science</i> , 2016, 17, 71.	0.5	5
21	Protective efficacy of a high-growth reassortant H1N1 influenza virus vaccine against the European Avian-like H1N1 swine influenza virus in mice and pigs. <i>Veterinary Microbiology</i> , 2018, 222, 75-84.	0.8	5
22	Re-emergence of highly pathogenic avian influenza A(H5N8) virus in domestic Goose, China. <i>Journal of Infection</i> , 2021, 83, 709-737.	1.7	5
23	The influence on oxidative stress markers, inflammatory factors and intestinal injury-related molecules in Wuhui pigeon induced by lipopolysaccharide. <i>PLoS ONE</i> , 2021, 16, e0251462.	1.1	4
24	A meta-analysis of transcriptomic characterization revealed extracellular matrix pathway involved in the H5N1 and H7N9 infections. <i>Oncotarget</i> , 2017, 8, 62561-62572.	0.8	4
25	Potential Threats to Human Health from Eurasian Avian-Like Swine Influenza A(H1N1) Virus and Its Reassortants. <i>Emerging Infectious Diseases</i> , 2022, 28, 1489-1493.	2.0	4
26	Genetic characterization of an H5N6 avian influenza virus from chickens in Guangdong, China. <i>Journal of Infection</i> , 2021, 82, 414-451.	1.7	3
27	A novel amino acid site of N protein could affect the PRRSV-2 replication by regulating the viral RNA transcription. <i>BMC Veterinary Research</i> , 2022, 18, 171.	0.7	3
28	Protective efficacy of a high-growth reassortant swine H3N2 inactivated vaccine constructed by reverse genetic manipulation. <i>Journal of Veterinary Science</i> , 2014, 15, 381.	0.5	2
29	Weighted gene co-expression network analysis revealed host transcriptional response to H1N1 influenza A virus infection. <i>Journal of Infection</i> , 2021, 82, e4-e7.	1.7	2
30	Genetic characterization of an H5N6 avian influenza virus with multiple origins from a chicken in southern China, October 2019. <i>BMC Veterinary Research</i> , 2021, 17, 200.	0.7	2
31	Identification of coevolution sites and evolution history for neuraminidase of human influenza A viruses. <i>Journal of Infection</i> , 2020, 80, 232-254.	1.7	1
32	Egg adaptive mutation patterns of H3N2 human influenza A viruses. <i>Journal of Infection</i> , 2020, 80, 232-254.	1.7	1
33	Letter to the editor: Sequencing bias for residue 28 of the neuraminidase of the recent highly pathogenic avian influenza virus A(H5N8). <i>Eurosurveillance</i> , 2021, 26, .	3.9	1
34	Second receptor binding site of influenza A virus neuraminidase: a key factor for virus host range?. <i>Future Virology</i> , 0, , .	0.9	0