

Jiahao Zhang

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	The PB2 coadaptation of H10N8 avian influenza virus increases the pathogenicity to chickens and mice. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 1794-1803.	3.0	6
2	Combined insertion of basic and non-basic amino acids at hemagglutinin cleavage site of highly pathogenic H7N9 virus promotes replication and pathogenicity in chickens and mice. <i>Virologica Sinica</i> , 2022, 37, 38-47.	3.0	3
3	Survivability of H5N8 mixed wild bird droppings in different conditions. <i>Lancet Microbe</i> , The, 2022, 3, e332.	7.3	1
4	The Genomic Evolution and the Transmission Dynamics of H6N2 Avian Influenza A Viruses in Southern China. <i>Viruses</i> , 2022, 14, 1154.	3.3	4
5	Resurgence of H5N6 avian influenza virus in 2021 poses new threat to public health. <i>Lancet Microbe</i> , The, 2022, 3, e558.	7.3	8
6	Genomic evolution, transmission dynamics, and pathogenicity of avian influenza A (H5N8) viruses emerging in China, 2020. <i>Virus Evolution</i> , 2021, 7, veab046.	4.9	20
7	A risk marker of tribasic hemagglutinin cleavage site in influenza A (H9N2) virus. <i>Communications Biology</i> , 2021, 4, 71.	4.4	10
8	Generation of recombinant influenza virus bearing strep tagged PB2 and effective identification of interactional host factors. <i>Veterinary Microbiology</i> , 2021, 254, 108985.	1.9	0
9	Japanese encephalitis virus manipulates lysosomes membrane for RNA replication and utilizes autophagy components for intracellular growth. <i>Veterinary Microbiology</i> , 2021, 255, 109025.	1.9	8
10	Avian influenza H10 subtype viruses continuously pose threat to public health in China. <i>Journal of Infection</i> , 2021, 83, 607-635.	3.3	6
11	Genetic diversity, phylogeography, and evolutionary dynamics of highly pathogenic avian influenza A (H5N6) viruses. <i>Virus Evolution</i> , 2020, 6, veaa079.	4.9	23
12	Evolution and Antigenic Drift of Influenza A (H7N9) Viruses, China, 2017–2019. <i>Emerging Infectious Diseases</i> , 2020, 26, 1906-1911.	4.3	19
13	Continuous Reassortment of Clade 2.3.4.4 H5N6 Highly Pathogenic Avian Influenza Viruses Demonstrating High Risk to Public Health. <i>Pathogens</i> , 2020, 9, 670.	2.8	13
14	Insights into the cross-species evolution of 2019 novel coronavirus. <i>Journal of Infection</i> , 2020, 80, 671-693.	3.3	13
15	The continuous evolution and dissemination of 2019 novel human coronavirus. <i>Journal of Infection</i> , 2020, 80, 671-693.	3.3	12
16	Genetic diversity and dissemination pathways of highly pathogenic H5N6 avian influenza viruses from birds in Southwestern China along the East Asian–Australian migration flyway. <i>Journal of Infection</i> , 2018, 76, 418-422.	3.3	8
17	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, .	3.4	99
18	Divergent Reassortment and Transmission Dynamics of Highly Pathogenic Avian Influenza A(H5N8) Virus in Birds of China During 2021. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	4