

Identification of mammalian-adapting mutations in the H5N1 influenza virus

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Amino acid changes in PB2 and HA affect the growth of a recombinant influenza virus expressing a fluorescent reporter protein. <i>Scientific Reports</i> , 2016, 6, 19933.	1.6	8
2	First documented case of avian influenza (H5N1) virus infection in a lion. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-3.	3.0	15
3	Multiple Natural Substitutions in Avian Influenza A Virus PB2 Facilitate Efficient Replication in Human Cells. <i>Journal of Virology</i> , 2016, 90, 5928-5938.	1.5	47
4	Human-Animal Interface: The Case for Influenza Interspecies Transmission. <i>Advances in Experimental Medicine and Biology</i> , 2016, 972, 17-33.	0.8	26
5	Pathogen population bottlenecks and adaptive landscapes: overcoming the barriers to disease emergence. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160727.	1.2	46
6	Amino acid substitutions V63I or A37S/I61T/V63I/V100A in the PA N-terminal domain increase the virulence of H7N7 influenza A virus. <i>Scientific Reports</i> , 2016, 6, 37800.	1.6	25
7	Coupling high-throughput genetics with phylogenetic information reveals an epistatic interaction on the influenza A virus M segment. <i>BMC Genomics</i> , 2016, 17, 46.	1.2	24
8	Genomic Analysis of the Emergence, Evolution, and Spread of Human Respiratory RNA Viruses. <i>Annual Review of Genomics and Human Genetics</i> , 2016, 17, 193-218.	2.5	38
9	Rapid acquisition of polymorphic virulence markers during adaptation of highly pathogenic avian influenza H5N8 virus in the mouse. <i>Scientific Reports</i> , 2017, 7, 40667.	1.6	13
10	A Novel A(H7N2) Influenza Virus Isolated from a Veterinarian Caring for Cats in a New York City Animal Shelter Causes Mild Disease and Transmits Poorly in the Ferret Model. <i>Journal of Virology</i> , 2017, 91, .	1.5	35
11	Characterization of influenza A viruses with polymorphism in PB2 residues 701 and 702. <i>Scientific Reports</i> , 2017, 7, 11361.	1.6	9
12	Prerequisites for the acquisition of mammalian pathogenicity by influenza A virus with a prototypic avian PB2 gene. <i>Scientific Reports</i> , 2017, 7, 10205.	1.6	20
13	A brief summary of the epidemiology and genetic relatedness of avian influenza H9N2 virus in birds and mammals in the Middle East and North Africa. <i>Epidemiology and Infection</i> , 2017, 145, 3320-3333.	1.0	74
14	Understanding the complex evolution of rapidly mutating viruses with deep sequencing: Beyond the analysis of viral diversity. <i>Virus Research</i> , 2017, 239, 43-54.	1.1	19
15	H7N9 virulent mutants detected in chickens in China pose an increased threat to humans. <i>Cell Research</i> , 2017, 27, 1409-1421.	5.7	209
16	Phylogenetic Tree based Method for Uncovering Co-mutational Site-pairs in Influenza Viruses. , 2017, , .		0
17	The significance of avian influenza virus mouse-adaptation and its application in characterizing the efficacy of new vaccines and therapeutic agents. <i>Clinical and Experimental Vaccine Research</i> , 2017, 6, 83.	1.1	5
18	From Variation of Influenza Viral Proteins to Vaccine Development. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1554.	1.8	21

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19	In silico thermodynamic stability of mammalian adaptation and virulence determinants in polymerase complex proteins of H9N2 virus. <i>Journal of Genetic Engineering and Biotechnology</i> , 2018, 16, 757-767.	1.5	5
20	Genome-wide identification of interferon-sensitive mutations enables influenza vaccine design. <i>Science</i> , 2018, 359, 290-296.	6.0	64
21	H5N1 Influenza A Virus PB1-F2 Relieves HAX-1-Mediated Restriction of Avian Virus Polymerase PA in Human Lung Cells. <i>Journal of Virology</i> , 2018, 92, .	1.5	17
22	Altered virulence of Highly Pathogenic Avian Influenza (HPAI) H5N8 reassortant viruses in mammalian models. <i>Virulence</i> , 2018, 9, 133-148.	1.8	13
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24	Multiple polymerase gene mutations for human adaptation occurring in Asian H5N1 influenza virus clinical isolates. <i>Scientific Reports</i> , 2018, 8, 13066.	1.6	17
25	Characterization of H9N2 avian influenza viruses from the Middle East demonstrates heterogeneity at amino acid position 226 in the hemagglutinin and potential for transmission to mammals. <i>Virology</i> , 2018, 518, 195-201.	1.1	41
26	Differential Responses of Plants to Biotic Stress and the Role of Metabolites. , 2018, , 69-87.		13
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28	PB2 mutations arising during H9N2 influenza evolution in the Middle East confer enhanced replication and growth in mammals. <i>PLoS Pathogens</i> , 2019, 15, e1007919.	2.1	34
29	Insights into the Acquisition of Virulence of Avian Influenza Viruses during a Single Passage in Ferrets. <i>Viruses</i> , 2019, 11, 915.	1.5	3
30	Multiple amino acid substitutions involved in the adaption of three avian-origin H7N9 influenza viruses in mice. <i>Virology Journal</i> , 2019, 16, 3.	1.4	10
31	Tropism and Infectivity of a Seasonal A(H1N1) and a Highly Pathogenic Avian A(H5N1) Influenza Virus in Primary Differentiated Ferret Nasal Epithelial Cell Cultures. <i>Journal of Virology</i> , 2019, 93, .	1.5	20
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33	Genetic Compatibility of Reassortants between Avian H5N1 and H9N2 Influenza Viruses with Higher Pathogenicity in Mammals. <i>Journal of Virology</i> , 2019, 93, .	1.5	24
34	Characterization of H7N9 avian influenza viruses isolated from duck meat products. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 792-798.	1.3	6
35	PA Mutations Inherited during Viral Evolution Act Cooperatively To Increase Replication of Contemporary H5N1 Influenza Virus with an Expanded Host Range. <i>Journal of Virology</i> , 2020, 95, .	1.5	11
36	Full-length genome sequences of the first H9N2 avian influenza viruses isolated in the Northeast of Algeria. <i>Virology Journal</i> , 2020, 17, 108.	1.4	12

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38	Suppression of Cytotoxic T Cell Functions and Decreased Levels of Tissue-Resident Memory T Cells during H5N1 Infection. Journal of Virology, 2020, 94, .	1.5	9
39	Host Innate Immune Response of Geese Infected with Clade 2.3.4.4 H5N6 Highly Pathogenic Avian Influenza Viruses. Microorganisms, 2020, 8, 224.	1.6	2
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51	First field evidence of the evolution from a non-virulent HPR0 to a virulent HPR-deleted infectious salmon anaemia virus. Journal of General Virology, 2017, 98, 595-606.	1.3	33
52	Y-Box-Binding Protein 3 (YBX3) Restricts Influenza A Virus by Interacting with Viral Ribonucleoprotein Complex and Impairing its Function. Journal of General Virology, 2020, 101, 385-398.	1.3	6
55	Novel Polymerase Gene Mutations for Human Adaptation in Clinical Isolates of Avian H5N1 Influenza Viruses. PLoS Pathogens, 2016, 12, e1005583.	2.1	59
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60	Emergence, prevalence, and evolution of H5N8 avian influenza viruses in central China, 2020. <i>Emerging Microbes and Infections</i> , 2022, 11, 73-82.	3.0	15
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63	Emergence of H3N8 avian influenza viruses possessing tri-basic hemagglutinin cleavage sites in China. <i>Journal of Infection</i> , 2022, 85, e112-e114.	1.7	7
64	Phylogeography and Biological Characterizations of H12 Influenza A Viruses. <i>Viruses</i> , 2022, 14, 2251.	1.5	1
65	Highly Pathogenic Avian Influenza H5N1 Virus Infections in Wild Red Foxes (<i>Vulpes vulpes</i>) Show Neurotropism and Adaptive Virus Mutations. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	21
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