Nobuhiro Takemae

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genetic Characterization of Influenza A Viruses in Japanese Swine in 2015 to 2019. Journal of Virology, 2020, 94, .	3.4	9
2	Isolation of highly pathogenic H5N6 avian influenza virus in Southern Vietnam with genetic similarity to those infecting humans in China. Transboundary and Emerging Diseases, 2019, 66, 2209-2217.	3.0	11
3	A novel H7N3 reassortant originating from the zoonotic H7N9 highly pathogenic avian influenza viruses that has adapted to ducks. Transboundary and Emerging Diseases, 2019, 66, 2342-2352.	3.0	10
4	Characterization of a novel reassortant H7N3 highly pathogenic avian influenza virus isolated from a poultry meat product taken on a passenger flight to Japan. Journal of Veterinary Medical Science, 2019, 81, 444-448.	0.9	10
5	Genetics and pathogenicity of H5N6 highly pathogenic avian influenza viruses isolated from wild birds and a chicken in Japan during winter 2017–2018. Virology, 2019, 533, 1-11.	2.4	21
6	Phylogeographic analysis of human influenza A and B viruses in Myanmar, 2010–2015. PLoS ONE, 2019, 14, e0210550.	2.5	14
7	Comparative pathogenicity of H5N6 subtype highly pathogenic avian influenza viruses in chicken, Pekin duck and Muscovy duck. Transboundary and Emerging Diseases, 2019, 66, 1227-1251.	3.0	24
8	Pathogenicity of two novel human-origin H7N9 highly pathogenic avian influenza viruses in chickens and ducks. Archives of Virology, 2019, 164, 535-545.	2.1	5
9	Appearance of reassortant European avian-origin H1 influenza A viruses of swine in Vietnam. Transboundary and Emerging Diseases, 2018, 65, 1110-1116.	3.0	6
10	Spatial transmission of H5N6 highly pathogenic avian influenza viruses among wild birds in Ibaraki Prefecture, Japan, 2016–2017. Archives of Virology, 2018, 163, 1195-1207.	2.1	10
11	Five distinct reassortants of H5N6 highly pathogenic avian influenza A viruses affected Japan during the winter of 2016–2017. Virology, 2017, 512, 8-20.	2.4	42
12	Susceptibility of chickens, quail, and pigeons to an H7N9 human influenza virus and subsequent egg-passaged strains. Archives of Virology, 2017, 162, 103-116.	2.1	7
13	Influenza A Viruses of Swine (IAV-S) in Vietnam from 2010 to 2015: Multiple Introductions of A(H1N1)pdm09 Viruses into the Pig Population and Diversifying Genetic Constellations of Enzootic IAV-S. Journal of Virology, 2017, 91, .	3.4	27
14	Community- and hospital-acquired infections with oseltamivir- and peramivir-resistant influenza A(H1N1)pdm09 viruses during the 2015–2016 season in Japan. Virus Genes, 2017, 53, 89-94.	1.6	7
15	Pathogenicity of H5N8 highly pathogenic avian influenza viruses isolated from a wild bird fecal specimen and a chicken in Japan in 2014. Microbiology and Immunology, 2016, 60, 243-252.	1.4	27
16	Intracontinental and intercontinental dissemination of Asian H5 highly pathogenic avian influenza virus (clade 2.3.4.4) in the winter of 2014–2015. Reviews in Medical Virology, 2015, 25, 388-405.	8.3	78
17	Characterization of an H5N8 influenza A virus isolated from chickens during an outbreak of severe avian influenza in Japan in April 2014. Archives of Virology, 2015, 160, 1629-1643.	2.1	65
18	Co-infection of influenza A viruses of swine contributes to effective shuffling of gene segments in a naturally reared pig. Virology, 2015, 484, 203-212.	2.4	13

#	Article	IF	CITATIONS
19	Genetics and infectivity of H5N1 highly pathogenic avian influenza viruses isolated from chickens and wild birds in Japan during 2010–11. Virus Research, 2012, 170, 109-117.	2.2	24
20	Genetic diversity of swine influenza viruses isolated from pigs during 2000 to 2005 in Thailand. Influenza and Other Respiratory Viruses, 2008, 2, 181-189.	3.4	51