

Juan Li

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

7,704
citations

15
h-index

45
g-index

45
ext. papers

9,876
ext. citations

10.7
avg, IF

5.86
L-index

#	Paper	IF	Citations
44	Identification of a novel hepacivirus in Mongolian gerbil (<i>Meriones unguiculatus</i>) from Shaanxi, China.. <i>Virologica Sinica</i> , 2022 , 37, 307-307	6.4	0
43	The emergence, genomic diversity and global spread of SARS-CoV-2. <i>Nature</i> , 2021 ,	50.4	42
42	Novel reassortment 2.3.4.4b H5N8 highly pathogenic avian influenza viruses circulating in Xinjiang, China.. <i>Preventive Veterinary Medicine</i> , 2021 , 199, 105564	3.1	0
41	A Novel Virus of Associated with Sexual Precocity in. <i>MSystems</i> , 2021 , 6, e0000321	7.6	3
40	Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing. <i>Journal of Infection</i> , 2021 , 82, e44-e48	18.9	5
39	Novel reassortant 2.3.4.4B H5N6 highly pathogenic avian influenza viruses circulating among wild, domestic birds in Xinjiang, Northwest China. <i>Journal of Veterinary Science</i> , 2021 , 22, e43	1.6	3
38	Re-emergence of H5N8 highly pathogenic avian influenza virus in wild birds, China. <i>Emerging Microbes and Infections</i> , 2021 , 10, 1819-1823	18.9	4
37	Rescue of Senecavirus A to uncover mutation profiles of its progenies during 80 serial passages in vitro. <i>Veterinary Microbiology</i> , 2021 , 253, 108969	3.3	11
36	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. <i>Cell</i> , 2021 , 184, 4380-4391.e14	56.2	99
35	A reassortant highly pathogenic avian influenza H5N6 virus originating from the wildbird-origin H5N6 and the poultry H9N2/H7N9 viruses in Xinjiang, China. <i>Medycyna Weterynaryjna</i> , 2021 , 77, 6532-2021	1.4	2
34	Rapid Emergence of the Reassortant 2.3.4.4b H5N2 Highly Pathogenic Avian Influenza Viruses in a Live Poultry Market in Xinjiang, Northwest China.. <i>Avian Diseases</i> , 2021 , 65, 578-583	1.6	1
33	A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. <i>Current Biology</i> , 2020 , 30, 2196-2203.e3	6.3	319
32	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. <i>Lancet, The</i> , 2020 , 395, 565-574	40	6394
31	Uncovering two phases of early intercontinental COVID-19 transmission dynamics. <i>Journal of Travel Medicine</i> , 2020 , 27,	12.9	14
30	Amino acid substitutions in antigenic region B of hemagglutinin play a critical role in the antigenic drift of subclade 2.3.4.4 highly pathogenic H5NX influenza viruses. <i>Transboundary and Emerging Diseases</i> , 2020 , 67, 263-275	4.2	5
29	Dominant subtype switch in avian influenza viruses during 2016-2019 in China. <i>Nature Communications</i> , 2020 , 11, 5909	17.4	35
28	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. <i>Virologica Sinica</i> , 2019 , 34, 1-8	6.4	21

27	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. <i>Frontiers in Microbiology</i> , 2019 , 10, 1001	5.7	7
26	Effects of Acetylshikonin on the Infection and Replication of Coxsackievirus A16 in Vitro and in Vivo. <i>Journal of Natural Products</i> , 2019 , 82, 1089-1097	4.9	5
25	Long noncoding RNAs: Novel regulators of virus-host interactions. <i>Reviews in Medical Virology</i> , 2019 , 29, e2046	11.7	15
24	Multiplex one-step real-time PCR assay for rapid simultaneous detection of velogenic and mesogenic Newcastle disease virus and H5-subtype avian influenza virus. <i>Archives of Virology</i> , 2019 , 164, 1111-1119	2.6	6
23	Co-circulation and persistence of multiple A/H3N2 influenza variants in China. <i>Emerging Microbes and Infections</i> , 2019 , 8, 1157-1167	18.9	11
22	A neonatal murine model of coxsackievirus A4 infection for evaluation of vaccines and antiviral drugs. <i>Emerging Microbes and Infections</i> , 2019 , 8, 1445-1455	18.9	7
21	Continued reassortment of avian H6 influenza viruses from Southern China, 2014-2016. <i>Transboundary and Emerging Diseases</i> , 2019 , 66, 592-598	4.2	11
20	Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. <i>Nature</i> , 2018 , 556, 255-258	50.4	369
19	T160A mutation-induced deglycosylation at site 158 in hemagglutinin is a critical determinant of the dual receptor binding properties of clade 2.3.4.4 H5NX subtype avian influenza viruses. <i>Veterinary Microbiology</i> , 2018 , 217, 158-166	3.3	17
18	Genetic and biological characterization of three poultry-origin H5N6 avian influenza viruses with all internal genes from genotype S H9N2 viruses. <i>Archives of Virology</i> , 2018 , 163, 947-960	2.6	9
17	New Threats from H7N9 Influenza Virus: Spread and Evolution of High- and Low-Pathogenicity Variants with High Genomic Diversity in Wave Five. <i>Journal of Virology</i> , 2018 , 92,	6.6	67
16	Characteristics of the emerging chicken-origin highly pathogenic H7N9 viruses: A new threat to public health and poultry industry. <i>Journal of Infection</i> , 2018 , 76, 217-220	18.9	24
15	Genetic and biological characterization of two reassortant H5N2 avian influenza A viruses isolated from waterfowl in China in 2016. <i>Veterinary Microbiology</i> , 2018 , 224, 8-16	3.3	6
14	Characterization of an inactivated whole-virus bivalent vaccine that induces balanced protective immunity against coxsackievirus A6 and A10 in mice. <i>Vaccine</i> , 2018 , 36, 7095-7104	4.1	10
13	Rapid detection of hand, foot and mouth disease enterovirus genotypes by multiplex PCR. <i>Journal of Virological Methods</i> , 2018 , 258, 7-12	2.6	6
12	Novel sub-lineages, recombinants and reassortants of severe fever with thrombocytopenia syndrome virus. <i>Ticks and Tick-borne Diseases</i> , 2017 , 8, 385-390	3.6	13
11	A Neonatal Murine Model of Coxsackievirus A6 Infection for Evaluation of Antiviral and Vaccine Efficacy. <i>Journal of Virology</i> , 2017 , 91,	6.6	23
10	Protective Efficacies of Formaldehyde-Inactivated Whole-Virus Vaccine and Antivirals in a Murine Model of Coxsackievirus A10 Infection. <i>Journal of Virology</i> , 2017 , 91,	6.6	16

9	Pathogen genomic surveillance elucidates the origins, transmission and evolution of emerging viral agents in China. <i>Science China Life Sciences</i> , 2017 , 60, 1317-1330	8.5	8
8	Effects of the HN Antigenic Difference between the Vaccine Strain and the Challenge Strain of Newcastle Disease Virus on Virus Shedding and Transmission. <i>Viruses</i> , 2017 , 9,	6.2	12
7	Internal Gene Cassette from a Genotype S H9N2 Avian Influenza Virus Attenuates the Pathogenicity of H5 Viruses in Chickens and Mice. <i>Frontiers in Microbiology</i> , 2017 , 8, 1978	5.7	11
6	Phylogenetic and biological characterization of three K1203 (H5N8)-like avian influenza A virus reassortants in China in 2014. <i>Archives of Virology</i> , 2016 , 161, 289-302	2.6	20
5	Adaptive mutations in PB2 gene contribute to the high virulence of a natural reassortant H5N2 avian influenza virus in mice. <i>Virus Research</i> , 2015 , 210, 255-63	6.4	10
4	Novel reassortant H5N5 viruses bind to a human-type receptor as a factor in pandemic risk. <i>Veterinary Microbiology</i> , 2015 , 175, 356-61	3.3	7
3	A single amino acid mutation, R42A, in the Newcastle disease virus matrix protein abrogates its nuclear localization and attenuates viral replication and pathogenicity. <i>Journal of General Virology</i> , 2014 , 95, 1067-1073	4.9	13
2	A novel bat coronavirus reveals natural insertions at the S1/S2 cleavage site of the Spike protein and a possible recombinant origin of HCoV-19		22
1	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses		9