

List of Publications by Year in descending order

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76
papers

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citations

126708

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75
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78
all docs

78
docs citations

78
times ranked

60980
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging HxNy Influenza A Viruses. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a038406.	2.9	30
2	One-Year Sustained Cellular and Humoral Immunities in Coronavirus Disease 2019 (COVID-19) Convalescents. Clinical Infectious Diseases, 2022, 75, e1072-e1081.	2.9	48
3	Novel reassortment 2.3.4.4b H5N8 highly pathogenic avian influenza viruses circulating in Xinjiang, China. Preventive Veterinary Medicine, 2022, 199, 105564.	0.7	2
4	Rapid detection of the emerging tick-borne Tamdy virus by TaqMan-based real-time reverse transcription PCR. Journal of Virological Methods, 2022, 305, 114538.	1.0	0
5	Novel reassortant 2.3.4.4B H5N6 highly pathogenic avian influenza viruses circulating among wild, domestic birds in Xinjiang, Northwest China. Journal of Veterinary Science, 2021, 22, e43.	0.5	4
6	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. Briefings in Bioinformatics, 2021, 22, 631-641.	3.2	38
7	Re-emergence of H5N8 highly pathogenic avian influenza virus in wild birds, China. Emerging Microbes and Infections, 2021, 10, 1819-1823.	3.0	17
8	Emerging H5N8 avian influenza viruses. Science, 2021, 372, 784-786.	6.0	64
9	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. Cell, 2021, 184, 4380-4391.e14.	13.5	261
10	Ecology of avian influenza viruses in migratory birds wintering within the Yangtze River wetlands. Science Bulletin, 2021, 66, 2014-2024.	4.3	6
11	A reassortant highly pathogenic avian influenza H5N6 virus originating from the wildbird-origin H5N6 and the poultry H9N2/H7N9 viruses in Xinjiang, China. Medycyna Weterynaryjna, 2021, 77, 6532-2021.	0.0	2
12	The emergence, genomic diversity and global spread of SARS-CoV-2. Nature, 2021, 600, 408-418.	13.7	249
13	Rapid Emergence of the Reassortant 2.3.4.4b H5N2 Highly Pathogenic Avian Influenza Viruses in a Live Poultry Market in Xinjiang, Northwest China. Avian Diseases, 2021, 65, 578-583.	0.4	1
14	Broad host range of SARS-CoV-2 and the molecular basis for SARS-CoV-2 binding to cat ACE2. Cell Discovery, 2020, 6, 68.	3.1	132
15	Rapid humoral immune responses are required for recovery from haemorrhagic fever with renal syndrome patients. Emerging Microbes and Infections, 2020, 9, 2303-2314.	3.0	3
16	Dominant subtype switch in avian influenza viruses during 2016â€“2019 in China. Nature Communications, 2020, 11, 5909.	5.8	93
17	A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. Current Biology, 2020, 30, 2196-2203.e3.	1.8	480
18	Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5949-5954.	3.3	43

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19	A Novel Coronavirus from Patients with Pneumonia in China, 2019. <i>New England Journal of Medicine</i> , 2020, 382, 727-733.	13.9	21,542
20	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. <i>Lancet</i> , 2020, 395, 565-574.	6.3	9,430
21	Uncovering two phases of early intercontinental COVID-19 transmission dynamics. <i>Journal of Travel Medicine</i> , 2020, 27, .	1.4	28
22	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. <i>Clinical Infectious Diseases</i> , 2019, 68, 1100-1109.	2.9	56
23	Co-circulation and persistence of multiple A/H3N2 influenza variants in China. <i>Emerging Microbes and Infections</i> , 2019, 8, 1157-1167.	3.0	20
24	Tamdy Virus in <i>Ixodid</i> Ticks Infesting Bactrian Camels, Xinjiang, China, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 2136-2138.	2.0	21
25	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.	3.0	11
26	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. <i>Virologica Sinica</i> , 2019, 34, 1-8.	1.2	30
27	Effects of Acetylshikonin on the Infection and Replication of Coxsackievirus A16in Vitroandin Vivo. <i>Journal of Natural Products</i> , 2019, 82, 1089-1097.	1.5	7
28	Long noncoding RNAs: Novel regulators of virusâ€host interactions. <i>Reviews in Medical Virology</i> , 2019, 29, e2046.	3.9	38
29	Intra-host Ebola viral adaption during human infection. <i>Biosafety and Health</i> , 2019, 1, 14-24.	1.2	9
30	Avian Influenza A Viruses among Occupationally Exposed Populations, China, 2014â€2016. <i>Emerging Infectious Diseases</i> , 2019, 25, 2215-2225.	2.0	32
31	Continued reassortment of avian H6 influenza viruses from Southern China, 2014â€2016. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 592-598.	1.3	19
32	Sudden emergence of human infections with H7N9 avian influenza A virus in Hubei province, central China. <i>Scientific Reports</i> , 2018, 8, 2486.	1.6	4
33	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, .	1.5	92
34	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, .	1.5	99
35	Rapid detection of hand, foot and mouth disease enterovirus genotypes by multiplex PCR. <i>Journal of Virological Methods</i> , 2018, 258, 7-12.	1.0	16
36	Genomic characterizations of H4 subtype avian influenza viruses from live poultry markets in Sichuan province of China, 2014â€2015. <i>Science China Life Sciences</i> , 2018, 61, 1123-1126.	2.3	12

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37	The first imported case of Rift Valley fever in China reveals a genetic reassortment of different viral lineages. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-7.	3.0	40
38	Novel sub-lineages, recombinants and reassortants of severe fever with thrombocytopenia syndrome virus. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 385-390.	1.1	18
39	A Neonatal Murine Model of Coxsackievirus A6 Infection for Evaluation of Antiviral and Vaccine Efficacy. <i>Journal of Virology</i> , 2017, 91, .	1.5	32
40	Human infections with recently-emerging highly pathogenic H7N9 avian influenza virus in China. <i>Journal of Infection</i> , 2017, 75, 71-75.	1.7	143
41	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, .	1.5	30
42	A single mutation in the prM protein of Zika virus contributes to fetal microcephaly. <i>Science</i> , 2017, 358, 933-936.	6.0	399
43	Epidemiological characteristics of hand, foot, and mouth disease in Shandong, China, 2009â€“2016. <i>Scientific Reports</i> , 2017, 7, 8900.	1.6	35
44	CASCIRE surveillance network and work on avian influenza viruses. <i>Science China Life Sciences</i> , 2017, 60, 1386-1391.	2.3	12
45	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.	2.3	10
46	Highly Pathogenic Avian Influenza A(H5N8) Virus in Wild Migratory Birds, Qinghai Lake, China. <i>Emerging Infectious Diseases</i> , 2017, 23, 637-641.	2.0	82
47	Increasing genetic diversity of Zika virus in the Latin American outbreak. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-3.	3.0	28
48	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	5.1	257
49	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
50	Novel avian influenza A (H5N6) viruses isolated in migratory waterfowl before the first human case reported in China, 2014. <i>Scientific Reports</i> , 2016, 6, 29888.	1.6	57
51	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014â€“2015. <i>Virologica Sinica</i> , 2016, 31, 300-305.	1.2	39
52	Ecological dynamics of influenza A viruses: cross-species transmission and global migration. <i>Scientific Reports</i> , 2016, 6, 36839.	1.6	36
53	Highly diversified Zika viruses imported to China, 2016. <i>Protein and Cell</i> , 2016, 7, 461-464.	4.8	48
54	Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. <i>Trends in Microbiology</i> , 2016, 24, 490-502.	3.5	2,243

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55	High genetic diversity and frequent genetic reassortment of avian influenza A(H9N2) viruses along the East Asian–Australian migratory flyway. <i>Infection, Genetics and Evolution</i> , 2016, 39, 325-329.	1.0	18
56	MrBayes tgmC ³ & bold; A High Performance and Resource-Efficient GPU-Oriented Phylogenetic Analysis Method. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 845-854.	1.9	4
57	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015, 5, 12986.	1.6	47
58	Two novel reassortants of avian influenza A (H5N6) virus in China. <i>Journal of General Virology</i> , 2015, 96, 975-981.	1.3	89
59	Non-coding regions of the Ebola virus genome contain indispensable phylogenetic and evolutionary information. <i>Science China Life Sciences</i> , 2015, 58, 682-686.	2.3	3
60	Origin and Possible Genetic Recombination of the Middle East Respiratory Syndrome Coronavirus from the First Imported Case in China: Phylogenetics and Coalescence Analysis. <i>MBio</i> , 2015, 6, e01280-15.	1.8	86
61	Global and Local Persistence of Influenza A(H5N1) Virus. <i>Emerging Infectious Diseases</i> , 2014, 20, 1287-1295.	2.0	49
62	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014, 5, 3142.	5.8	145
63	Continuous reassortments with local chicken H9N2 virus underlie the human-infecting influenza A (H7N9) virus in the new influenza season, Guangdong, China. <i>Protein and Cell</i> , 2014, 5, 878-882.	4.8	17
64	Phylogenetics of varied subtypes of avian influenza viruses in China: potential threat to humans. <i>Protein and Cell</i> , 2014, 5, 253-257.	4.8	31
65	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet, The</i> , 2014, 383, 869.	6.3	113
66	Origin and molecular characterization of the human-infecting H6N1 influenza virus in Taiwan. <i>Protein and Cell</i> , 2013, 4, 846-853.	4.8	86
67	Origin and diversity of novel avian influenza A H7N9 viruses causing human infection: phylogenetic, structural, and coalescent analyses. <i>Lancet, The</i> , 2013, 381, 1926-1932.	6.3	516
68	Hepatitis B virus subgenotyping: History, effects of recombination, misclassifications, and corrections. <i>Infection, Genetics and Evolution</i> , 2013, 16, 355-361.	1.0	89
69	Substitution Rates of the Internal Genes in the Novel Avian H7N9 Influenza Virus. <i>Clinical Infectious Diseases</i> , 2013, 57, 1213-1215.	2.9	8
70	MrBayes tgmC3: A Tight GPU Implementation of MrBayes. <i>PLoS ONE</i> , 2013, 8, e60667.	1.1	10
71	Subgenotype reclassification of genotype B hepatitis B virus. <i>BMC Gastroenterology</i> , 2012, 12, 116.	0.8	20
72	Identification of novel inter-genotypic recombinants of human hepatitis B viruses by large-scale phylogenetic analysis. <i>Virology</i> , 2012, 427, 51-59.	1.1	44

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73	Recombination in Hepatitis C Virus: Identification of Four Novel Naturally Occurring Inter-Subtype Recombinants. PLoS ONE, 2012, 7, e41997.	1.1	27
74	Subgenotyping of Genotype C Hepatitis B Virus: Correcting Misclassifications and Identifying a Novel Subgenotype. PLoS ONE, 2012, 7, e47271.	1.1	26
75	Prospective of Genomics in Revealing Transmission, Reassortment and Evolution of Wildlife-Borne Avian Influenza A (H5N1) Viruses. Current Genomics, 2011, 12, 466-474.	0.7	28
76	A Complete Analysis of HA and NA Genes of Influenza A Viruses. PLoS ONE, 2010, 5, e14454.	1.1	38