

List of Publications by Year in descending order

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76
papers

37,999
citations

126708

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h-index

74018

75
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78
all docs

78
docs citations

78
times ranked

60980
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. <i>Lancet, The</i> , 2020, 395, 565-574.	6.3	9,430
3	Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. <i>Trends in Microbiology</i> , 2016, 24, 490-502.	3.5	2,243
4	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
5	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.	1.8	480
6	A single mutation in the prM protein of Zika virus contributes to fetal microcephaly. <i>Science</i> , 2017, 358, 933-936.	6.0	399
7	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.	13.5	261
8	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	5.1	257
9	The emergence, genomic diversity and global spread of SARS-CoV-2. <i>Nature</i> , 2021, 600, 408-418.	13.7	249
10	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014, 5, 3142.	5.8	145
11	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
12	Broad host range of SARS-CoV-2 and the molecular basis for SARS-CoV-2 binding to cat ACE2. <i>Cell Discovery</i> , 2020, 6, 68.	3.1	132
13	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet, The</i> , 2014, 383, 869.	6.3	113
14	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
15	Dominant subtype switch in avian influenza viruses during 2016â€“2019 in China. <i>Nature Communications</i> , 2020, 11, 5909.	5.8	93
16	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
17	Hepatitis B virus subgenotyping: History, effects of recombination, misclassifications, and corrections. <i>Infection, Genetics and Evolution</i> , 2013, 16, 355-361.	1.0	89
18	Two novel reassortants of avian influenza A (H5N6) virus in China. <i>Journal of General Virology</i> , 2015, 96, 975-981.	1.3	89

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19	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
20	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
21	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
22	Emerging H5N8 avian influenza viruses. <i>Science</i> , 2021, 372, 784-786.	6.0	64
23	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
24	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. <i>Clinical Infectious Diseases</i> , 2019, 68, 1100-1109.	2.9	56
25	Global and Local Persistence of Influenza A(H5N1) Virus. <i>Emerging Infectious Diseases</i> , 2014, 20, 1287-1295.	2.0	49
26	Highly diversified Zika viruses imported to China, 2016. <i>Protein and Cell</i> , 2016, 7, 461-464.	4.8	48
27	One-Year Sustained Cellular and Humoral Immunities in Coronavirus Disease 2019 (COVID-19) Convalescents. <i>Clinical Infectious Diseases</i> , 2022, 75, e1072-e1081.	2.9	48
28	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015, 5, 12986.	1.6	47
29	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
30	Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5949-5954.	3.3	43
31	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
32	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014–2015. <i>Virologica Sinica</i> , 2016, 31, 300-305.	1.2	39
33	A Complete Analysis of HA and NA Genes of Influenza A Viruses. <i>PLoS ONE</i> , 2010, 5, e14454.	1.1	38
34	Long noncoding RNAs: Novel regulators of virus–host interactions. <i>Reviews in Medical Virology</i> , 2019, 29, e2046.	3.9	38
35	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	3.2	38
36	Ecological dynamics of influenza A viruses: cross-species transmission and global migration. <i>Scientific Reports</i> , 2016, 6, 36839.	1.6	36

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37	Epidemiological characteristics of hand, foot, and mouth disease in Shandong, China, 2009–2016. <i>Scientific Reports</i> , 2017, 7, 8900.	1.6	35
38	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
39	Avian Influenza A Viruses among Occupationally Exposed Populations, China, 2014–2016. <i>Emerging Infectious Diseases</i> , 2019, 25, 2215-2225.	2.0	32
40	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
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	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
43	Emerging HxNy Influenza A Viruses. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2022, 12, a038406.	2.9	30
44	Increasing genetic diversity of Zika virus in the Latin American outbreak. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-3.	3.0	28
45	Uncovering two phases of early intercontinental COVID-19 transmission dynamics. <i>Journal of Travel Medicine</i> , 2020, 27, .	1.4	28
46	Prospective of Genomics in Revealing Transmission, Reassortment and Evolution of Wildlife-Borne Avian Influenza A (H5N1) Viruses. <i>Current Genomics</i> , 2011, 12, 466-474.	0.7	28
47	Recombination in Hepatitis C Virus: Identification of Four Novel Naturally Occurring Inter-Subtype Recombinants. <i>PLoS ONE</i> , 2012, 7, e41997.	1.1	27
48	Subgenotyping of Genotype C Hepatitis B Virus: Correcting Misclassifications and Identifying a Novel Subgenotype. <i>PLoS ONE</i> , 2012, 7, e47271.	1.1	26
49	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
50	Subgenotype reclassification of genotype B hepatitis B virus. <i>BMC Gastroenterology</i> , 2012, 12, 116.	0.8	20
51	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
52	Continued reassortment of avian H6 influenza viruses from Southern China, 2014–2016. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 592-598.	1.3	19
53	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
54	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

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55	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
56	Re-emergence of H5N8 highly pathogenic avian influenza virus in wild birds, China. <i>Emerging Microbes and Infections</i> , 2021, 10, 1819-1823.	3.0	17
57	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
58	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
59	CASCIRE surveillance network and work on avian influenza viruses. <i>Science China Life Sciences</i> , 2017, 60, 1386-1391.	2.3	12
60	Genomic characterizations of H4 subtype avian influenza viruses from live poultry markets in Sichuan province of China, 2014-2015. <i>Science China Life Sciences</i> , 2018, 61, 1123-1126.	2.3	12
61	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
62	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
63	MrBayes tgMC3: A Tight GPU Implementation of MrBayes. <i>PLoS ONE</i> , 2013, 8, e60667.	1.1	10
64	Intra-host Ebola viral adaptation during human infection. <i>Biosafety and Health</i> , 2019, 1, 14-24.	1.2	9
65	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
66	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.	1.5	7
67	Ecology of avian influenza viruses in migratory birds wintering within the Yangtze River wetlands. <i>Science Bulletin</i> , 2021, 66, 2014-2024.	4.3	6
68	MrBayes tgMC ³ & bold; ++ & /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
69	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
70	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.	0.5	4
71	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
72	Rapid humoral immune responses are required for recovery from haemorrhagic fever with renal syndrome patients. <i>Emerging Microbes and Infections</i> , 2020, 9, 2303-2314.	3.0	3

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73	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.	0.0	2
74	Novel reassortment 2.3.4.4b H5N8 highly pathogenic avian influenza viruses circulating in Xinjiang, China. <i>Preventive Veterinary Medicine</i> , 2022, 199, 105564.	0.7	2
75	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.	0.4	1
76	Rapid detection of the emerging tick-borne Tamdy virus by TaqMan-based real-time reverse transcription PCR. <i>Journal of Virological Methods</i> , 2022, 305, 114538.	1.0	0