Huachen Zhu

List of Publications by Year
in descending order

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		87888	62596
85	10,373	38	80
papers	citations	h-index	g-index

92	92	92	16233
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	<scp>ggtree</scp>: an <scp>r</scp> package for visualization and annotation of phylogenetic trees with their covariates and other associated data. Methods in Ecology and Evolution, 2017, 8, 28-36.	5.2	2,998
2	Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. Nature, 2020, 583, 282-285.	27.8	1,453
3	Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using Ggtree. Molecular Biology and Evolution, 2018, 35, 3041-3043.	8.9	535
4	The genesis and source of the H7N9 influenza viruses causing human infections in China. Nature, 2013, 502, 241-244.	27.8	429
5	Co-circulation of three camel coronavirus species and recombination of MERS-CoVs in Saudi Arabia. Science, 2016, 351, 81-84.	12.6	365
6	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. Molecular Biology and Evolution, 2020, 37, 599-603.	8.9	348
7	Reassortment of Pandemic H1N1/2009 Influenza A Virus in Swine. Science, 2010, 328, 1529-1529.	12.6	339
8	Nomenclature updates resulting from the evolution of avian influenza A(H5) virus clades 2.1.3.2a, 2.2.1, and 2.3.4 during 2013â€“2014. Influenza and Other Respiratory Viruses, 2015, 9, 271-276.	3.4	283
9	Infectivity, Transmission, and Pathology of Human-Isolated H7N9 Influenza Virus in Ferrets and Pigs. Science, 2013, 341, 183-186.	12.6	273
10	Epidemiology of avian influenza A H7N9 virus in human beings across five epidemics in mainland China, 2013â€“17: an epidemiological study of laboratory-confirmed case series. Lancet Infectious Diseases, The, 2017, 17, 822-832.	9.1	251
11	Long-term evolution and transmission dynamics of swine influenza A virus. Nature, 2011, 473, 519-522.	27.8	219
12	Dissemination, divergence and establishment of H7N9 influenza viruses in China. Nature, 2015, 522, 102-105.	27.8	201
13	Evidence for Antigenic Seniority in Influenza A (H3N2) Antibody Responses in Southern China. PLoS Pathogens, 2012, 8, e1002802.	4.7	184
14	Amino Acid Substitutions in Polymerase Basic Protein 2 Gene Contribute to the Pathogenicity of the Novel A/H7N9 Influenza Virus in Mammalian Hosts. Journal of Virology, 2014, 88, 3568-3576.	3.4	146
15	The emergence of pandemic influenza viruses. Protein and Cell, 2010, 1, 9-13.	11.0	140
16	Estimating the Life Course of Influenza A(H3N2) Antibody Responses from Cross-Sectional Data. PLoS Biology, 2015, 13, e1002082.	5.6	129
17	Detection of diverse astroviruses from bats in China. Journal of General Virology, 2009, 90, 883-887.	2.9	91
18	Resistance to Neuraminidase Inhibitors Conferred by an R292K Mutation in a Human Influenza Virus H7N9 Isolate Can Be Masked by a Mixed R/K Viral Population. MBio, 2013, 4, .	4.1	90

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19	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. Nature Communications, 2015, 6, 6553.	12.8	90
20	Novel Reassortment of Eurasian Avian-Like and Pandemic/2009 Influenza Viruses in Swine: Infectious Potential for Humans. Journal of Virology, 2011, 85, 10432-10439.	3.4	80
21	Expansion of Genotypic Diversity and Establishment of 2009 H1N1 Pandemic-Origin Internal Genes in Pigs in China. Journal of Virology, 2014, 88, 10864-10874.	3.4	79
22	Establishment and Lineage Replacement of H6 Influenza Viruses in Domestic Ducks in Southern China. Journal of Virology, 2012, 86, 6075-6083.	3.4	77
23	Pathogenicity of the Novel A/H7N9 Influenza Virus in Mice. MBio, 2013, 4, .	4.1	68
24	Detection and Phylogenetic Analysis of Group 1 Coronaviruses in South American Bats. Emerging Infectious Diseases, 2008, 14, 1890-1893.	4.3	66
25	Emergence and Evolution of Avian H5N2 Influenza Viruses in Chickens in Taiwan. Journal of Virology, 2014, 88, 5677-5686.	3.4	66
26	Dual E627K and D701N mutations in the PB2 protein of A(H7N9) influenza virus increased its virulence in mammalian models. Scientific Reports, 2015, 5, 14170.	3.3	66
27	Emergence and Evolution of H10 Subtype Influenza Viruses in Poultry in China. Journal of Virology, 2015, 89, 3534-3541.	3.4	61
28	Reassortment Events among Swine Influenza A Viruses in China: Implications for the Origin of the 2009 Influenza Pandemic. Journal of Virology, 2011, 85, 10279-10285.	3.4	57
29	A comparison of hemagglutination inhibition and neutralization assays for characterizing immunity to seasonal influenza A. Influenza and Other Respiratory Viruses, 2016, 10, 518-524.	3.4	57
30	Gender associates with both susceptibility to infection and pathogenesis of SARS-CoV-2 in Syrian hamster. Signal Transduction and Targeted Therapy, 2021, 6, 136.	17.1	57
31	Ferrets as Models for Influenza Virus Transmission Studies and Pandemic Risk Assessments. Emerging Infectious Diseases, 2018, 24, 965-971.	4.3	56
32	A recombinant spike protein subunit vaccine confers protective immunity against SARS-CoV-2 infection and transmission in hamsters. Science Translational Medicine, 2021, 13, .	12.4	56
33	Substitution of lysine at 627 position in PB2 protein does not change virulence of the 2009 pandemic H1N1 virus in mice. Virology, 2010, 401, 1-5.	2.4	55
34	Molecular epidemiology of human enterovirus 71 at the origin of an epidemic of fatal hand, foot and mouth disease cases in Cambodia. Emerging Microbes and Infections, 2016, 5, 1-9.	6.5	54
35	Emergence and Dissemination of a Swine H3N2 Reassortant Influenza Virus with 2009 Pandemic H1N1 Genes in Pigs in China. Journal of Virology, 2012, 86, 2375-2378.	3.4	52
36	Emergence and development of H7N9 influenza viruses in China. Current Opinion in Virology, 2016, 16, 106-113.	5.4	50

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37	History of Swine Influenza Viruses in Asia. Current Topics in Microbiology and Immunology, 2011, 370, 57-68.	1.1	47
38	H7N9 Incident, immune status, the elderly and a warning of an influenza pandemic. Journal of Infection in Developing Countries, 2013, 7, 302-307.	1.2	43
39	Multiannual patterns of influenza A transmission in Chinese live bird market systems. Influenza and Other Respiratory Viruses, 2013, 7, 97-107.	3.4	41
40	A Combination of HA and PA Mutations Enhances Virulence in a Mouse-Adapted H6N6 Influenza A Virus. Journal of Virology, 2014, 88, 14116-14125.	3.4	39
41	Genomic Analysis of the Emergence, Evolution, and Spread of Human Respiratory RNA Viruses. Annual Review of Genomics and Human Genetics, 2016, 17, 193-218.	6.2	38
42	Location-specific patterns of exposure to recent pre-pandemic strains of influenza A in southern China. Nature Communications, 2011, 2, 423.	12.8	36
43	Possible Role of Songbirds and Parakeets in Transmission of Influenza A(H7N9) Virus to Humans. Emerging Infectious Diseases, 2014, 20, 380-5.	4.3	32
44	Infectivity and Transmissibility of Avian H9N2 Influenza Viruses in Pigs. Journal of Virology, 2016, 90, 3506-3514.	3.4	29
45	Tropism and innate host responses of influenza A/H5N6 virus: an analysis ofexÂvivoandin vitrocultures of the human respiratory tract. European Respiratory Journal, 2017, 49, 1601710.	6.7	27
46	The recombinant origin of emerging human norovirus GII.4/2008: intra-genotypic exchange of the capsid P2 domain. Journal of General Virology, 2012, 93, 817-822.	2.9	24
47	Insect resistance toNilaparvata lugens andCnaphalocrocis medinalis in transgenic indica rice and the inheritance ofgna+sbti transgenes. Pest Management Science, 2005, 61, 390-396.	3.4	23
48	Quantifying within-host diversity of H5N1 influenza viruses in humans and poultry in Cambodia. PLoS Pathogens, 2020, 16, e1008191.	4.7	22
49	Enhancing disease resistances of Super Hybrid Rice with four antifungal genes. Science in China Series C: Life Sciences, 2007, 50, 31-39.	1.3	20
50	Global and quantitative proteomic analysis of dogs infected by avian-like H3N2 canine influenza virus. Frontiers in Microbiology, 2015, 6, 228.	3.5	20
51	Dexamethasone ameliorates severe pneumonia but slightly enhances viral replication in the lungs of SARS-CoV-2-infected Syrian hamsters. Cellular and Molecular Immunology, 2022, 19, 290-292.	10.5	17
52	Minimizing the threat of pandemic emergence from avian influenza in poultry systems. BMC Infectious Diseases, 2013, 13, 592.	2.9	16
53	Molecular Detection of Human H7N9 Influenza A Virus Causing Outbreaks in China. Clinical Chemistry, 2013, 59, 1062-1067.	3.2	15
54	Genetic characterization of highly pathogenic H5 influenza viruses from poultry in Taiwan, 2015. Infection, Genetics and Evolution, 2016, 38, 96-100.	2.3	15

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55	Dysregulated T-Helper Type 1 (Th1):Th2 Cytokine Profile and Poor Immune Response in Pregnant Ferrets Infected With 2009 Pandemic Influenza A(H1N1) Virus. Journal of Infectious Diseases, 2018, 217, 438-442.	4.0	15
56	Inhibition of autophagy enhances adenosineâ€'induced apoptosis in human hepatoblastoma HepG2 cells. Oncology Reports, 2019, 41, 829-838.	2.6	15
57	Life course exposures continually shape antibody profiles and risk of seroconversion to influenza. PLoS Pathogens, 2020, 16, e1008635.	4.7	15
58	Cross-species tropism and antigenic landscapes of circulating SARS-CoV-2 variants. Cell Reports, 2022, 38, 110558.	6.4	15
59	Seroconversion to Pandemic (H1N1) 2009 Virus and Cross-Reactive Immunity to Other Swine Influenza Viruses. Emerging Infectious Diseases, 2011, 17, 1897-1899.	4.3	14
60	Puzzling Origins of the Ebola Outbreak in the Democratic Republic of the Congo, 2014. Journal of Virology, 2015, 89, 10130-10132.	3.4	14
61	The PB2 mutation with lysine at 627 enhances the pathogenicity of avian influenza (H7N9) virus which belongs to a non-zoonotic lineage. Scientific Reports, 2017, 7, 2352.	3.3	13
62	Influenza virus surveillance in migratory ducks and sentinel ducks at Poyang Lake, China. Influenza and Other Respiratory Viruses, 2011, 5, 65-8.	3.4	12
63	Female sex hormone, progesterone, ameliorates the severity of SARS-CoV-2-caused pneumonia in the Syrian hamster model. Signal Transduction and Targeted Therapy, 2022, 7, 47.	17.1	12
64	Cohort Profile: A study of influenza immunity in the urban and rural Guangzhou region of China: the Fluscape Study. International Journal of Epidemiology, 2017, 46, dyv353.	1.9	11
65	The persistence of multiple strains of avian influenza in live bird markets. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170715.	2.6	11
66	A fieldâ€deployable insulated isothermal RTâ€PCR assay for identification of influenza A (H7N9) shows good performance in the laboratory. Influenza and Other Respiratory Viruses, 2019, 13, 610-617.	3.4	10
67	SARS-CoV-2 infection and disease outcomes in non-human primate models: advances and implications. Emerging Microbes and Infections, 2021, 10, 1881-1889.	6.5	10
68	Anticipating the Prevalence of Avian Influenza Subtypes H9 and H5 in Live-Bird Markets. PLoS ONE, 2013, 8, e56157.	2.5	10
69	Oncolytic Activity of Wild-type Newcastle Disease Virus HK84 Against Hepatocellular Carcinoma Associated with Activation of Type I Interferon Signaling. Journal of Clinical and Translational Hepatology, 2022, 10, 284-296.	1.4	10
70	Specificity, kinetics and longevity of antibody responses to avian influenza A(H7N9) virus infection in humans. Journal of Infection, 2020, 80, 310-319.	3.3	9
71	Genetic diversity of the 2013â€“14 human isolates of influenza H7N9 in China. BMC Infectious Diseases, 2015, 15, 109.	2.9	8
72	Using serological measures to estimate influenza incidence in the presence of secular trends in exposure and immunoâ€modulation of antibody response. Influenza and Other Respiratory Viruses, 2021, 15, 235-244.	3.4	8

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73	A SCID mouse-human lung xenograft model of SARS-CoV-2 infection. Theranostics, 2021, 11, 6607-6615.	10.0	8
74	Cohort profile: the China Ageing REespiratory infections Study (CARES), a prospective cohort study in older adults in Eastern China. BMJ Open, 2017, 7, e017503.	1.9	7
75	Safety and immunogenicity of an 8 year interval heterologous prime-boost influenza A/H7N7-H7N9 vaccination. Vaccine, 2019, 37, 2561-2568.	3.8	6
76	Persisting lung pathogenesis and minimum residual virus in hamster after acute COVID-19. Protein and Cell, 2022, 13, 72-77.	11.0	6
77	Pathogenicity and transmissibility of the pandemic H1N1 2009-related influenza viruses in mice, ferrets, and pigs. Influenza and Other Respiratory Viruses, 2011, 5, 82-4.	3.4	3
78	Use of fractional factorial design to study the compatibility of viral ribonucleoprotein gene segments of human H7N9 virus and circulating human influenza subtypes. Influenza and Other Respiratory Viruses, 2014, 8, 580-584.	3.4	2
79	A7â€ƒEvolution of influenza A(H7N9) viruses from waves I to IV. Virus Evolution, 2017, 3, .	4.9	1
80	A24â€ƒApplication of large-scale sequencing and data analysis to research on emerging infectious diseases. Virus Evolution, 2017, 3, .	4.9	0
81	A38â€‚Prevalence and evolution of avian H1 subtype influenza A viruses in Southern China. Virus Evolution, 2018, 4, .	4.9	0
82	Life course exposures continually shape antibody profiles and risk of seroconversion to influenza. , 2020, 16, e1008635.		0
83	Life course exposures continually shape antibody profiles and risk of seroconversion to influenza. , 2020, 16, e1008635.		0
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