

Jie Cui

List of Publications by Year in descending order

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73
papers

9,595
citations

168829

31
h-index

90395

73
g-index

86
all docs

86
docs citations

86
times ranked

18462
citing authors

#	ARTICLE	IF	CITATIONS
1	Viromes in marine ecosystems reveal remarkable invertebrate RNA virus diversity. <i>Science China Life Sciences</i> , 2022, 65, 426-437.	2.3	22
2	Human endogenous retroviruses in viral disease and therapy. <i>Clinical and Translational Discovery</i> , 2022, 2, .	0.2	2
3	Evolution and Genetic Diversity of the Retroviral Envelope in Anamniotes. <i>Journal of Virology</i> , 2022, 96, e0207221.	1.5	4
4	Origin and Deep Evolution of Human Endogenous Retroviruses in Pan-Primates. <i>Viruses</i> , 2022, 14, 1370.	1.5	9
5	Genetic Variation of Multiple Serotypes of Enteroviruses Associated with Hand, Foot and Mouth Disease in Southern China. <i>Virologica Sinica</i> , 2021, 36, 61-74.	1.2	11
6	Wildlife conservation and management in China: achievements, challenges and perspectives. <i>National Science Review</i> , 2021, 8, nwab042.	4.6	26
7	Human Endogenous Retroviruses as Biomedicine Markers. <i>Virologica Sinica</i> , 2021, 36, 852-858.	1.2	8
8	Multiple Infiltration and Cross-Species Transmission of Foamy Viruses across the Paleozoic to the Cenozoic Era. <i>Journal of Virology</i> , 2021, 95, e0048421.	1.5	7
9	Inhibition of viral suppressor of RNAi proteins by designer peptides protects from enteroviral infection in vivo. <i>Immunity</i> , 2021, 54, 2231-2244.e6.	6.6	23
10	Comparative study of the Malacostraca viromes between deep sea and shallow water. <i>Science Bulletin</i> , 2021, 66, 2458-2461.	4.3	3
11	Genetically Divergent Highly Pathogenic Avian Influenza A(H5N8) Viruses in Wild Birds, Eastern China. <i>Emerging Infectious Diseases</i> , 2021, 27, 2940-2943.	2.0	12
12	Different forms restrict localization of distinct tropomyosins on dorsal stress fibers in osteosarcoma cells. <i>Cytoskeleton</i> , 2020, 77, 16-24.	1.0	5
13	A PILOT CLINICAL TRIAL OUTCOME OF BIOSAFETY SYSTEM EVALUATION FOR PERV-C FREE PORCINE ISLET XENOTRANSPLANTATION BASED ON PRINCIPLE OF WHO "CHANGSHA COMMUNIQUE". <i>Transplantation</i> , 2020, 104, S9-S9.	0.5	0
14	A novel multistage antiplasmodial inhibitor targeting Plasmodium falciparum histone deacetylase 1. <i>Cell Discovery</i> , 2020, 6, 93.	3.1	23
15	Ancient origin and complex evolution of porcine endogenous retroviruses. <i>Biosafety and Health</i> , 2020, 2, 142-151.	1.2	7
16	Distinct Cell Transcriptomic Landscapes Upon Henipavirus Infections. <i>Frontiers in Microbiology</i> , 2020, 11, 986.	1.5	2
17	On the origin and continuing evolution of SARS-CoV-2. <i>National Science Review</i> , 2020, 7, 1012-1023.	4.6	1,248
18	Flavivirus induces and antagonizes antiviral RNA interference in both mammals and mosquitoes. <i>Science Advances</i> , 2020, 6, eaax7989.	4.7	60

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19	Bat origin of a new human coronavirus: there and back again. <i>Science China Life Sciences</i> , 2020, 63, 461-462.	2.3	91
20	GsmPlot: a web server to visualize epigenome data in NCBI. <i>BMC Bioinformatics</i> , 2020, 21, 55.	1.2	2
21	Evolutionary perspectives on novel coronaviruses identified in pneumonia cases in China. <i>National Science Review</i> , 2020, 7, 239-242.	4.6	50
22	Co-circulation of multiple reassortant H6 subtype avian influenza viruses in wild birds in eastern China, 2016â€“2017. <i>Virology Journal</i> , 2020, 17, 62.	1.4	8
23	High basal heat-shock protein expression in bats confers resistance to cellular heat/oxidative stress. <i>Cell Stress and Chaperones</i> , 2019, 24, 835-849.	1.2	35
24	A reptilian endogenous foamy virus sheds light on the early evolution of retroviruses. <i>Virus Evolution</i> , 2019, 5, vez001.	2.2	19
25	Geographical structure of bat SARS-related coronaviruses. <i>Infection, Genetics and Evolution</i> , 2019, 69, 224-229.	1.0	37
26	Zika virus infection induces RNAi-mediated antiviral immunity in human neural progenitors and brain organoids. <i>Cell Research</i> , 2019, 29, 265-273.	5.7	115
27	Discovery of endogenous retroviruses with mammalian envelopes in avian genomes uncovers long-term bird-mammal interaction. <i>Virology</i> , 2019, 530, 27-31.	1.1	6
28	Identification and evolution of avian endogenous foamy viruses. <i>Virus Evolution</i> , 2019, 5, vez049.	2.2	10
29	Origin and evolution of pathogenic coronaviruses. <i>Nature Reviews Microbiology</i> , 2019, 17, 181-192.	13.6	3,993
30	Dampened STING-Dependent Interferon Activation in Bats. <i>Cell Host and Microbe</i> , 2018, 23, 297-301.e4.	5.1	206
31	Differential Evolution of Antiretroviral Restriction Factors in Pteropid Bats as Revealed by APOBEC3 Gene Complexity. <i>Molecular Biology and Evolution</i> , 2018, 35, 1626-1637.	3.5	59
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	Genetic Analysis of Reemerging GII.P16-GII.2 Noroviruses in 2016â€“2017 in China. <i>Journal of Infectious Diseases</i> , 2018, 218, 133-143.	1.9	43
34	Serologic and viral genome prevalence of HSV, EBV, and HCMV among healthy adults in Wuhan, China. <i>Journal of Medical Virology</i> , 2018, 90, 571-581.	2.5	15
35	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
36	Why were so few people infected with H7N9 influenza A viruses in China from late 2017 to 2018?. <i>Science China Life Sciences</i> , 2018, 61, 1442-1444.	2.3	10

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37	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006738.	1.3	24
38	M Gene Reassortment in H9N2 Influenza Virus Promotes Early Infection and Replication: Contribution to Rising Virus Prevalence in Chickens in China. <i>Journal of Virology</i> , 2017, 91, .	1.5	41
39	Genetic properties and pathogenicity of a novel reassortant H10N5 influenza virus from wild birds. <i>Archives of Virology</i> , 2017, 162, 1349-1353.	0.9	4
40	Molecular Evolution and Emergence of H5N6 Avian Influenza Virus in Central China. <i>Journal of Virology</i> , 2017, 91, .	1.5	23
41	Epidemiology, Evolution, and Pathogenesis of H7N9 Influenza Viruses in Five Epidemic Waves since 2013 in China. <i>Trends in Microbiology</i> , 2017, 25, 713-728.	3.5	199
42	Bayesian evolutionary analysis for emerging infectious disease: an exemplified application for H7N9 avian influenza viruses. <i>Science China Life Sciences</i> , 2017, 60, 1392-1395.	2.3	6
43	Identification of Novel Long Non-coding and Circular RNAs in Human Papillomavirus-Mediated Cervical Cancer. <i>Frontiers in Microbiology</i> , 2017, 8, 1720.	1.5	44
44	Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. <i>PLoS Pathogens</i> , 2017, 13, e1006698.	2.1	797
45	Analysis of Dengue Serotype 4 in Sri Lanka during the 2012â€“2013 Dengue Epidemic. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 130-136.	0.6	12
46	Unique Loss of the PYHIN Gene Family in Bats Amongst Mammals: Implications for Inflammasome Sensing. <i>Scientific Reports</i> , 2016, 6, 21722.	1.6	113
47	Evolution and comparative analysis of the bat MHC-I region. <i>Scientific Reports</i> , 2016, 6, 21256.	1.6	56
48	Co-circulation of H5N6, H3N2, H3N8 and Emergence of Novel Reassortant H3N6 in a Local Community in Hunan Province in China. <i>Scientific Reports</i> , 2016, 6, 25549.	1.6	21
49	Contraction of the type I IFN locus and unusual constitutive expression of <i>IFN-Î±</i> in bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2696-2701.	3.3	272
50	Bats and Rodents Shape Mammalian Retroviral Phylogeny. <i>Scientific Reports</i> , 2015, 5, 16561.	1.6	31
51	Genomic Mining Reveals Deep Evolutionary Relationships between Bornaviruses and Bats. <i>Viruses</i> , 2015, 7, 5792-5800.	1.5	10
52	Endogenization of mouse mammary tumor virus (MMTV)-like elements in genomes of pikas (<i>Ochotona</i>) Tj ETQq0 0,0 rgBT /Oyerlock 10	1.1	8
53	Low frequency of paleoviral infiltration across the avian phylogeny. <i>Genome Biology</i> , 2014, 15, 539.	3.8	60
54	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895

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55	An Allometric Relationship between the Genome Length and Virion Volume of Viruses. <i>Journal of Virology</i> , 2014, 88, 6403-6410.	1.5	62
56	Identification of diverse full-length endogenous betaretroviruses in megabats and microbats. <i>Retrovirology</i> , 2013, 10, 35.	0.9	45
57	Ancient invasion of an extinct gammaretrovirus in cetaceans. <i>Virology</i> , 2013, 441, 66-69.	1.1	5
58	Adaptive evolution of bat dipeptidyl peptidase 4 (dpp4): implications for the origin and emergence of Middle East respiratory syndrome coronavirus. <i>Virology Journal</i> , 2013, 10, 304.	1.4	47
59	Adaptation of Phenylalanine and Tyrosine Catabolic Pathway to Hibernation in Bats. <i>PLoS ONE</i> , 2013, 8, e62039.	1.1	23
60	Endogenous Hepadnaviruses in the Genome of the Budgerigar (<i>Melopsittacus undulatus</i>) and the Evolution of Avian Hepadnaviruses. <i>Journal of Virology</i> , 2012, 86, 7688-7691.	1.5	25
61	Evidence for an endogenous papillomavirus-like element in the platypus genome. <i>Journal of General Virology</i> , 2012, 93, 1362-1366.	1.3	5
62	Endogenous Lentiviruses in the Ferret Genome. <i>Journal of Virology</i> , 2012, 86, 3383-3385.	1.5	38
63	Discovery of Retroviral Homologs in Bats: Implications for the Origin of Mammalian Gammaretroviruses. <i>Journal of Virology</i> , 2012, 86, 4288-4293.	1.5	52
64	Identification of diverse groups of endogenous gammaretroviruses in mega- and microbats. <i>Journal of General Virology</i> , 2012, 93, 2037-2045.	1.3	48
65	Co-Circulation and Persistence of Genetically Distinct Saffold Viruses, Denmark. <i>Emerging Infectious Diseases</i> , 2012, 18, 1694-1696.	2.0	6
66	Endogenous RNA viruses of plants in insect genomes. <i>Virology</i> , 2012, 427, 77-79.	1.1	47
67	Progressive Pseudogenization: Vitamin C Synthesis and Its Loss in Bats. <i>Molecular Biology and Evolution</i> , 2011, 28, 1025-1031.	3.5	36
68	Recent Loss of Vitamin C Biosynthesis Ability in Bats. <i>PLoS ONE</i> , 2011, 6, e27114.	1.1	25
69	Positive Selection of the Bat Interferon Alpha Gene Family. <i>Biochemical Genetics</i> , 2010, 48, 840-846.	0.8	15
70	Accelerated evolution of PRRSV during recent outbreaks in China. <i>Virus Genes</i> , 2010, 41, 241-245.	0.7	32
71	Detection of Japanese Encephalitis Virus Antibodies in Bats in Southern China. <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 78, 1007-1011.	0.6	37
72	Detection of Japanese encephalitis virus antibodies in bats in Southern China. <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 78, 1007-11.	0.6	22

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73	Evolutionary Relationships between Bat Coronaviruses and Their Hosts. Emerging Infectious Diseases, 2007, 13, 1526-1532.	2.0	123