

Xing-Yi Ge

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

6,185
citations

230014

27
h-index

150775

59
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64
all docs

64
docs citations

64
times ranked

10509
citing authors

#	ARTICLE	IF	CITATIONS
1	Epidemiology and evolution of novel deltacoronaviruses in birds in central China. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 632-644.	1.3	5
2	The phylogeny of the Anderson's White-bellied Rat (<i>Niviventer andersoni</i>) based on complete mitochondrial genomes. <i>Ecology and Evolution</i> , 2022, 12, e8663.	0.8	4
3	An atlas of human viruses provides new insights into diversity and tissue tropism of human viruses. <i>Bioinformatics</i> , 2022, 38, 3087-3093.	1.8	6
4	Prediction of coronavirus 3C-like protease cleavage sites using machine-learning algorithms. <i>Virologica Sinica</i> , 2022, 37, 437-444.	1.2	5
5	Characterization of Deltacoronavirus in Black-Headed Gulls (<i>Chroicocephalus ridibundus</i>) in South China Indicating Frequent Interspecies Transmission of the Virus in Birds. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
6	Receptor utilization of angiotensin-converting enzyme 2 (ACE2) indicates a narrower host range of SARS-CoV-2 than that of SARS-CoV. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 1046-1053.	1.3	15
7	Identification and characterization of circRNAs encoded by MERS-CoV, SARS-CoV-1 and SARS-CoV-2. <i>Briefings in Bioinformatics</i> , 2021, 22, 1297-1308.	3.2	37
8	The 442th amino acid residue of the spike protein is critical for the adaptation to bat hosts for SARS-related coronaviruses. <i>Virus Research</i> , 2021, 295, 198307.	1.1	5
9	The taxonomy, host range and pathogenicity of coronaviruses and other viruses in the Nidovirales order. <i>Animal Diseases</i> , 2021, 1, 5.	0.6	67
10	Characterization of Novel Rhabdoviruses in Chinese Bats. <i>Viruses</i> , 2021, 13, 64.	1.5	14
11	Innate Immunity Evasion Strategies of Highly Pathogenic Coronaviruses: SARS-CoV, MERS-CoV, and SARS-CoV-2. <i>Frontiers in Microbiology</i> , 2021, 12, 770656.	1.5	11
12	Genome Characterization of Bird-Related Rhabdoviruses Circulating in Africa. <i>Viruses</i> , 2021, 13, 2168.	1.5	1
13	Evaluation of the exposure risk of SARS-CoV-2 in different hospital environment. <i>Sustainable Cities and Society</i> , 2020, 61, 102413.	5.1	49
14	Special Features of Bat Microbiota Differ From Those of Terrestrial Mammals. <i>Frontiers in Microbiology</i> , 2020, 11, 1040.	1.5	17
15	A Unique Protease Cleavage Site Predicted in the Spike Protein of the Novel Pneumonia Coronavirus (2019-nCoV) Potentially Related to Viral Transmissibility. <i>Virologica Sinica</i> , 2020, 35, 337-339.	1.2	110
16	Predicting the angiotensin converting enzyme 2 (ACE2) utilizing capability as the receptor of SARS-CoV-2. <i>Microbes and Infection</i> , 2020, 22, 221-225.	1.0	180
17	Characterization of the First Genome of Porcine mastadenovirus B (HNU1 Strain) and Implications on Its Lymphoid and Special Origin. <i>Virologica Sinica</i> , 2020, 35, 528-537.	1.2	2
18	The ORF6, ORF8 and nucleocapsid proteins of SARS-CoV-2 inhibit type I interferon signaling pathway. <i>Virus Research</i> , 2020, 286, 198074.	1.1	371

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19	The complete mitochondrial genome of Uruguayan native cattle (<i>Bos taurus</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 443-444.	0.2	4
20	The epidemic of 2019-novel-coronavirus (2019-nCoV) pneumonia and insights for emerging infectious diseases in the future. <i>Microbes and Infection</i> , 2020, 22, 80-85.	1.0	296
21	BioAider: An efficient tool for viral genome analysis and its application in tracing SARS-CoV-2 transmission. <i>Sustainable Cities and Society</i> , 2020, 63, 102466.	5.1	63
22	Cell membrane proteins with high N-glycosylation, high expression and multiple interaction partners are preferred by mammalian viruses as receptors. <i>Bioinformatics</i> , 2019, 35, 723-728.	1.8	31
23	Expression Profile and Function Analysis of Long Non-coding RNAs in the Infection of Coxsackievirus B3. <i>Virologica Sinica</i> , 2019, 34, 618-630.	1.2	10
24	Genomic characterization of a novel astrovirus identified in Amur tigers from a zoo in China. <i>Archives of Virology</i> , 2019, 164, 3151-3155.	0.9	5
25	Detection and genome characterization of two novel papillomaviruses and a novel polyomavirus in tree shrew (<i>Tupaia belangeri chinensis</i>) in China. <i>Virology Journal</i> , 2019, 16, 35.	1.4	7
26	Genomic characterization and pathogenicity of porcine deltacoronavirus strain CHN-HG-2017 from China. <i>Archives of Virology</i> , 2019, 164, 413-425.	0.9	26
27	Predicting the receptor-binding domain usage of the coronavirus based on kmer frequency on spike protein. <i>Infection, Genetics and Evolution</i> , 2018, 61, 183-184.	1.0	55
28	Genetic Evidence of Middle East Respiratory Syndrome Coronavirus (MERS-Cov) and Widespread Seroprevalence among Camels in Kenya. <i>Virologica Sinica</i> , 2018, 33, 484-492.	1.2	42
29	Detection and genome characterization of four novel bat hepadnaviruses and a hepevirus in China. <i>Virology Journal</i> , 2017, 14, 40.	1.4	50
30	Molecular detection of viruses in Kenyan bats and discovery of novel astroviruses, caliciviruses and rotaviruses. <i>Virologica Sinica</i> , 2017, 32, 101-114.	1.2	54
31	Coexistence of multiple genotypes of porcine epidemic diarrhea virus with novel mutant S genes in the Hubei Province of China in 2016. <i>Virologica Sinica</i> , 2017, 32, 298-306.	1.2	7
32	Characterization of a Minimal Type of Promoter Containing the σ^{10} Element and a Guanine at the σ^{14} or σ^{13} Position in Mycobacteria. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	16
33	Cross-neutralization of SARS coronavirus-specific antibodies against bat SARS-like coronaviruses. <i>Science China Life Sciences</i> , 2017, 60, 1399-1402.	2.3	33
34	Detection of alpha- and betacoronaviruses in rodents from Yunnan, China. <i>Virology Journal</i> , 2017, 14, 98.	1.4	48
35	Complete Genome Sequence of a Novel Strain of Infectious Bronchitis Virus, Isolated from Chickens in China in 2016. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
36	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

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37	Novel bat adenoviruses with low G+C content shed new light on the evolution of adenoviruses. <i>Journal of General Virology</i> , 2017, 98, 739-748.	1.3	23
38	Bat Severe Acute Respiratory Syndrome-Like Coronavirus WIV1 Encodes an Extra Accessory Protein, ORFX, Involved in Modulation of the Host Immune Response. <i>Journal of Virology</i> , 2016, 90, 6573-6582.	1.5	57
39	Chemical Targeting of a G-Quadruplex RNA in the Ebola Virus L Gene. <i>Cell Chemical Biology</i> , 2016, 23, 1113-1122.	2.5	107
40	Fugong virus, a novel hantavirus harbored by the small oriental vole (<i>Eothenomys eleusis</i>) in China. <i>Virology Journal</i> , 2016, 13, 27.	1.4	16
41	Coexistence of multiple coronaviruses in several bat colonies in an abandoned mineshaft. <i>Virologica Sinica</i> , 2016, 31, 31-40.	1.2	117
42	Longitudinal surveillance of SARS-like coronaviruses in bats by quantitative real-time PCR. <i>Virologica Sinica</i> , 2016, 31, 78-80.	1.2	20
43	Isolation and Characterization of a Novel Bat Coronavirus Closely Related to the Direct Progenitor of Severe Acute Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2016, 90, 3253-3256.	1.5	221
44	Novel bat adenoviruses with an extremely large E3 gene. <i>Journal of General Virology</i> , 2016, 97, 1625-1635.	1.3	21
45	Cloning, expression, and antiviral activity of interferon β from the Chinese microbat, <i>Myotis davidii</i> . <i>Virologica Sinica</i> , 2015, 30, 425-432.	1.2	7
46	Bat origin of human coronaviruses. <i>Virology Journal</i> , 2015, 12, 221.	1.4	330
47	Coronavirus nsp10/nsp16 Methyltransferase Can Be Targeted by nsp10-Derived Peptide <i>In Vitro</i> and <i>In Vivo</i> To Reduce Replication and Pathogenesis. <i>Journal of Virology</i> , 2015, 89, 8416-8427.	1.5	138
48	Identification of a novel strain of influenza A (H9N2) virus in chicken. <i>Virologica Sinica</i> , 2015, 30, 309-312.	1.2	2
49	A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. <i>Nature Medicine</i> , 2015, 21, 1508-1513.	15.2	753
50	Isolation and identification of bat viruses closely related to human, porcine and mink orthoreoviruses. <i>Journal of General Virology</i> , 2015, 96, 3525-3531.	1.3	41
51	Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. <i>Nature</i> , 2013, 503, 535-538.	13.7	1,439
52	Viral metagenomics analysis of planktonic viruses in East Lake, Wuhan, China. <i>Virologica Sinica</i> , 2013, 28, 280-290.	1.2	23
53	Metagenomic Analysis of Viruses from Bat Fecal Samples Reveals Many Novel Viruses in Insectivorous Bats in China. <i>Journal of Virology</i> , 2012, 86, 4620-4630.	1.5	185
54	Genetic diversity of novel circular ssDNA viruses in bats in China. <i>Journal of General Virology</i> , 2011, 92, 2646-2653.	1.3	101

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55	Host Range, Prevalence, and Genetic Diversity of Adenoviruses in Bats. <i>Journal of Virology</i> , 2010, 84, 3889-3897.	1.5	118