

Shuo Su

List of Publications by Year in descending order

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87
papers

5,370
citations

185998

28
h-index

91712

69
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89
all docs

89
docs citations

89
times ranked

8801
citing authors

#	ARTICLE	IF	CITATIONS
1	Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. Trends in Microbiology, 2016, 24, 490-502.	3.5	2,243
2	COVID-19: Epidemiology, Evolution, and Cross-Disciplinary Perspectives. Trends in Molecular Medicine, 2020, 26, 483-495.	3.5	470
3	Epidemiology, Evolution, and Recent Outbreaks of Avian Influenza Virus in China. Journal of Virology, 2015, 89, 8671-8676.	1.5	212
4	Epidemiology, Evolution, and Pathogenesis of H7N9 Influenza Viruses in Five Epidemic Waves since 2013 in China. Trends in Microbiology, 2017, 25, 713-728.	3.5	199
5	Comparison of Severe Acute Respiratory Syndrome Coronavirus 2 Spike Protein Binding to ACE2 Receptors from Human, Pets, Farm Animals, and Putative Intermediate Hosts. Journal of Virology, 2020, 94, .	1.5	148
6	Virome characterization of game animals in China reveals a spectrum of emerging pathogens. Cell, 2022, 185, 1117-1129.e8.	13.5	106
7	Novel Influenza D virus: Epidemiology, pathology, evolution and biological characteristics. Virulence, 2017, 8, 1580-1591.	1.8	101
8	Interspecies Transmission, Genetic Diversity, and Evolutionary Dynamics of Pseudorabies Virus. Journal of Infectious Diseases, 2019, 219, 1705-1715.	1.9	101
9	Origin, Genetic Diversity, and Evolutionary Dynamics of Novel Porcine Circovirus 3. Advanced Science, 2018, 5, 1800275.	5.6	92
10	MERS in South Korea and China: a potential outbreak threat?. Lancet, The, 2015, 385, 2349-2350.	6.3	78
11	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. Molecular Biology and Evolution, 2020, 37, 2641-2654.	3.5	76
12	First Evidence of H10N8 Avian Influenza Virus Infections among Feral Dogs in Live Poultry Markets in Guangdong Province, China. Clinical Infectious Diseases, 2014, 59, 748-750.	2.9	52
13	Bat-Origin Coronaviruses Expand Their Host Range to Pigs. Trends in Microbiology, 2018, 26, 466-470.	3.5	52
14	Insights into the genetic and host adaptability of emerging porcine circovirus 3. Virulence, 2018, 9, 1301-1313.	1.8	49
15	Virological and Epidemiological Evidence of Avian Influenza Virus Infections Among Feral Dogs in Live Poultry Markets, China: A Threat to Human Health?. Clinical Infectious Diseases, 2014, 58, 1644-1646.	2.9	48
16	Genotyping Porcine Circovirus 3 (PCV-3) Nowadays: Does It Make Sense?. Viruses, 2020, 12, 265.	1.5	47
17	BECN1-dependent CASP2 incomplete autophagy induction by binding to rabies virus phosphoprotein. Autophagy, 2017, 13, 739-753.	4.3	45
18	Development of a TaqMan-probe-based multiplex real-time PCR for the simultaneous detection of emerging and reemerging swine coronaviruses. Virulence, 2020, 11, 707-718.	1.8	42

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19	A Combination of HA and PA Mutations Enhances Virulence in a Mouse-Adapted H6N6 Influenza A Virus. <i>Journal of Virology</i> , 2014, 88, 14116-14125.	1.5	39
20	Evolutionary and genetic analysis of the VP2 gene of canine parvovirus. <i>BMC Genomics</i> , 2017, 18, 534.	1.2	38
21	Genetic analysis and evolutionary changes of Porcine circovirus 2. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106520.	1.2	36
22	Phylogeography Reveals Association between Swine Trade and the Spread of Porcine Epidemic Diarrhea Virus in China and across the World. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	35
23	Genetic and evolutionary analysis of emerging H3N2 canine influenza virus. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-15.	3.0	34
24	The Prevalence of Hepatitis E Virus Infections among Swine, Swine Farmers and the General Population in Guangdong Province, China. <i>PLoS ONE</i> , 2014, 9, e88106.	1.1	33
25	Hepatitis E Virus Serosurvey among Pet Dogs and Cats in Several Developed Cities in China. <i>PLoS ONE</i> , 2014, 9, e98068.	1.1	32
26	Complete Genome Sequence of an Avian-Like H4N8 Swine Influenza Virus Discovered in Southern China. <i>Journal of Virology</i> , 2012, 86, 9542-9542.	1.5	31
27	One Health strategies for rabies control in rural areas of China. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 365-367.	4.6	31
28	Multiple Incursions and Recurrent Epidemic Fade-Out of H3N2 Canine Influenza A Virus in the United States. <i>Journal of Virology</i> , 2018, 92, .	1.5	30
29	Avian-origin H3N2 canine influenza virus circulating in farmed dogs in Guangdong, China. <i>Infection, Genetics and Evolution</i> , 2013, 14, 444-449.	1.0	29
30	Blocking the PI3K/AKT pathway enhances mammalian reovirus replication by repressing IFN-stimulated genes. <i>Frontiers in Microbiology</i> , 2015, 6, 886.	1.5	29
31	Melatonin and other indoles show antiviral activities against swine coronaviruses in vitro at pharmacological concentrations. <i>Journal of Pineal Research</i> , 2021, 71, e12754.	3.4	29
32	Emerging viruses: Cross-species transmission of coronaviruses, filoviruses, henipaviruses, and rotaviruses from bats. <i>Cell Reports</i> , 2022, 39, 110969.	2.9	29
33	Rabies virus matrix protein induces apoptosis by targeting mitochondria. <i>Experimental Cell Research</i> , 2016, 347, 83-94.	1.2	28
34	A Shift in Porcine Circovirus 3 (PCV3) History Paradigm: Phylodynamic Analyses Reveal an Ancient Origin and Prolonged Undetected Circulation in the Worldwide Swine Population. <i>Advanced Science</i> , 2019, 6, 1901004.	5.6	28
35	Genetic Evolution and Molecular Selection of the HE Gene of Influenza C Virus. <i>Viruses</i> , 2019, 11, 167.	1.5	27
36	Seroepidemiological Evidence of Avian Influenza A Virus Transmission to Pigs in Southern China. <i>Journal of Clinical Microbiology</i> , 2013, 51, 601-602.	1.8	26

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37	Genome Characteristics and Evolution of Pseudorabies Virus Strains in Eastern China from 2017 to 2019. <i>Virologica Sinica</i> , 2019, 34, 601-609.	1.2	26
38	Evolutionary changes of the novel Influenza D virus hemagglutinin-esterase fusion gene revealed by the codon usage pattern. <i>Virulence</i> , 2019, 10, 1-9.	1.8	26
39	Antiviral Effect of Lithium Chloride and Diammonium Glycyrrhizinate on Porcine Deltacoronavirus In Vitro. <i>Pathogens</i> , 2019, 8, 144.	1.2	25
40	Epidemiological and evolutionary characteristics of the PRRSV in Southern China from 2010 to 2013. <i>Microbial Pathogenesis</i> , 2014, 75, 7-15.	1.3	24
41	Evidence for Subclinical Influenza A(H1N1)pdm09 Virus Infection among Dogs in Guangdong Province, China. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1762-1765.	1.8	23
42	Comparative analysis of microRNAs from the lungs and trachea of dogs (<i>Canis familiaris</i>) infected with canine influenza virus. <i>Infection, Genetics and Evolution</i> , 2014, 21, 367-374.	1.0	21
43	Antiviral Activity of Germacrone against Pseudorabies Virus in Vitro. <i>Pathogens</i> , 2019, 8, 258.	1.2	21
44	Complete Genome Sequence of an Avian-Origin H3N2 Canine Influenza A Virus Isolated in Farmed Dogs in Southern China. <i>Journal of Virology</i> , 2012, 86, 10238-10238.	1.5	20
45	Mutagenesis analysis of porcine reproductive and respiratory syndrome virus nonstructural protein 7. <i>Virus Genes</i> , 2013, 47, 467-477.	0.7	20
46	Inhibition of porcine reproductive and respiratory syndrome virus by specific siRNA targeting Nsp9 gene. <i>Infection, Genetics and Evolution</i> , 2014, 28, 64-70.	1.0	20
47	Global and quantitative proteomic analysis of dogs infected by avian-like H3N2 canine influenza virus. <i>Frontiers in Microbiology</i> , 2015, 6, 228.	1.5	20
48	Codon usage bias in the N gene of rabies virus. <i>Infection, Genetics and Evolution</i> , 2017, 54, 458-465.	1.0	19
49	Genetic diversity of porcine circovirus type 2 in China between 1999 and 2017. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 599-605.	1.3	19
50	Characterization of H7N2 Avian Influenza Virus in Wild Birds and Pikas in Qinghai-Tibet Plateau Area. <i>Scientific Reports</i> , 2016, 6, 30974.	1.6	18
51	Comprehensive Analysis of Codon Usage on Rabies Virus and Other Lyssaviruses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2397.	1.8	18
52	Complete Genome Sequence of a Novel Avian-Like H3N2 Swine Influenza Virus Discovered in Southern China. <i>Journal of Virology</i> , 2012, 86, 9533-9533.	1.5	17
53	Clinical Evaluation of Ebola Virus Disease Therapeutics. <i>Trends in Molecular Medicine</i> , 2017, 23, 820-830.	3.5	17
54	Genetic Analysis and Evolutionary Changes of the Torque teno sus Virus. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2881.	1.8	17

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55	A new distinct geminivirus causes soybean stay-green disease. <i>Molecular Plant</i> , 2022, 15, 927-930.	3.9	17
56	Emergence and adaptive evolution of Nipah virus. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 121-132.	1.3	15
57	Microarray analysis of lncRNA expression in rabies virus infected human neuroblastoma cells. <i>Infection, Genetics and Evolution</i> , 2019, 67, 88-100.	1.0	14
58	Genetic variation, pathogenicity, and immunogenicity of highly pathogenic porcine reproductive and respiratory syndrome virus strain XH-GD at different passage levels. <i>Archives of Virology</i> , 2016, 161, 77-86.	0.9	13
59	Comprehensive codon usage analysis of porcine deltacoronavirus. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106618.	1.2	13
60	One-step multiplex TaqMan probe-based method for real-time PCR detection of four canine diarrhea viruses. <i>Molecular and Cellular Probes</i> , 2020, 53, 101618.	0.9	13
61	Serologic Evidence of Pandemic Influenza Virus H1N1 2009 Infection in Cats in China. <i>Vaccine Journal</i> , 2013, 20, 115-117.	3.2	12
62	Avian influenza A(H7N9) virus and mixed live poultry animal markets in Guangdong province: a perfect storm in the making?. <i>Emerging Microbes and Infections</i> , 2015, 4, 1-3.	3.0	12
63	Analysis of the Codon Usage Pattern of HA and NA Genes of H7N9 Influenza A Virus. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7129.	1.8	12
64	Expression Profiling and Bioinformatics Analysis of CircRNA in Mice Brain Infected with Rabies Virus. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6537.	1.8	12
65	Attenuation of Getah Virus by a Single Amino Acid Substitution at Residue 253 of the E2 Protein that Might Be Part of a New Heparan Sulfate Binding Site on Alphaviruses. <i>Journal of Virology</i> , 2022, 96, jvi0175121.	1.5	11
66	Lack of evidence of avian-to-human transmission of avian influenza A (H5N1) virus among veterinarians, Guangdong, China, 2012. <i>Journal of Clinical Virology</i> , 2013, 56, 365-366.	1.6	10
67	Adaption and parallel evolution of human-isolated H5 avian influenza viruses. <i>Journal of Infection</i> , 2020, 80, 630-638.	1.7	10
68	Host-range shift of H3N8 canine influenza virus: a phylodynamic analysis of its origin and adaptation from equine to canine host. <i>Veterinary Research</i> , 2019, 50, 87.	1.1	9
69	Emergence and adaptation of H3N2 canine influenza virus from avian influenza virus: An overlooked role of dogs in interspecies transmission. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 842-851.	1.3	9
70	Identification of the IFN- β response in H3N2 canine influenza virus infection. <i>Journal of General Virology</i> , 2016, 97, 18-26.	1.3	9
71	Long non-coding RNAs are associated with Seneca Valley virus infection. <i>Veterinary Microbiology</i> , 2020, 246, 108728.	0.8	8
72	Comprehensive analysis of the ubiquitome in rabies virus-infected brain tissue of <i>Mus musculus</i> . <i>Veterinary Microbiology</i> , 2020, 241, 108552.	0.8	8

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73	Diagnostic strategies for Ebola virus detection. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 294-295.	4.6	6
74	Identification and function analysis of canine stimulator of interferon gene (STING). <i>Microbial Pathogenesis</i> , 2017, 113, 202-208.	1.3	6
75	Epidemiology, genetic diversity and evolution of canine astrovirus. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2901-2910.	1.3	6
76	Development of Monoclonal Antibodies for Detection of Conserved and Variable Epitopes of Large Protein of Rabies Virus. <i>Viruses</i> , 2021, 13, 220.	1.5	6
77	Short communication: isolation and phylogenetic analysis of an avian-origin H3N2 canine influenza virus in dog shelter, China. <i>Virus Genes</i> , 2013, 46, 554-557.	0.7	5
78	Beagle dogs have low susceptibility to BJ94-like H9N2 avian influenza virus. <i>Infection, Genetics and Evolution</i> , 2015, 31, 216-220.	1.0	5
79	Generation of Monoclonal Antibodies against Variable Epitopes of the M Protein of Rabies Virus. <i>Viruses</i> , 2019, 11, 375.	1.5	5
80	Emergence and adaptive evolution of influenza D virus. <i>Microbial Pathogenesis</i> , 2021, 160, 105193.	1.3	5
81	Spatiotemporal Associations and Molecular Evolution of Highly Pathogenic Avian Influenza A H7N9 Virus in China from 2017 to 2021. <i>Viruses</i> , 2021, 13, 2524.	1.5	5
82	Detection of Antibodies against Avian Influenza Virus Subtypes H7 and H9 among Veterinarians in Guangdong Province, China. <i>Journal of Clinical Microbiology</i> , 2013, 51, 4272-4274.	1.8	4
83	Spread of ZIKV and YFV to China: Potential implications. <i>Journal of Infection</i> , 2016, 73, 289-291.	1.7	3
84	Epidemiology and evolutionary analysis of Torque teno sus virus. <i>Veterinary Microbiology</i> , 2020, 244, 108668.	0.8	3
85	Divergent Viruses Discovered in Swine Alter the Understanding of Evolutionary History and Genetic Diversity of the <i>Respirovirus</i> Genus and Related Porcine Parainfluenza Viruses. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
86	Human infections by avian influenza virus H5N6: Increasing risk by dynamic reassortment?. <i>Infection, Genetics and Evolution</i> , 2016, 42, 46-48.	1.0	2
87	Structural and functional analysis of the roles of Influenza C virus membrane proteins in assembly and budding. <i>Journal of Biological Chemistry</i> , 2022, , 101727.	1.6	1