

# 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  
g-index

89  
all docs

89  
docs citations

89  
times ranked

8801  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | 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        |
| 2  | 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         |
| 3  | 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        |
| 4  | A new distinct geminivirus causes soybean stay-green disease. <i>Molecular Plant</i> , 2022, 15, 927-930.  | 3.9  | 17        |
| 5  | Virome characterization of game animals in China reveals a spectrum of emerging pathogens. <i>Cell</i> , 2022, 185, 1117-1129.e8.  | 13.5 | 106       |
| 6  | Emerging viruses: Cross-species transmission of coronaviruses, filoviruses, henipaviruses, and rotaviruses from bats. <i>Cell Reports</i> , 2022, 39, 110969.  | 2.9  | 29        |
| 7  | 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         |
| 8  | 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         |
| 9  | 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        |
| 10 | 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        |
| 11 | Emergence and adaptive evolution of influenza D virus. <i>Microbial Pathogenesis</i> , 2021, 160, 105193.  | 1.3  | 5         |
| 12 | 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         |
| 13 | Emergence and adaptive evolution of Nipah virus. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 121-132.   | 1.3  | 15        |
| 14 | 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        |
| 15 | Comparison of Severe Acute Respiratory Syndrome Coronavirus 2 Spike Protein Binding to ACE2 Receptors from Human, Pets, Farm Animals, and Putative Intermediate Hosts. <i>Journal of Virology</i> , 2020, 94, .                    | 1.5  | 148       |
| 16 | Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020, 37, 2641-2654.  | 3.5  | 76        |
| 17 | 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        |
| 18 | Long non-coding RNAs are associated with Seneca Valley virus infection. <i>Veterinary Microbiology</i> , 2020, 246, 108728.  | 0.8  | 8         |

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|----|---|-----|-----------|
| 19 | Development of a TaqMan-probe-based multiplex real-time PCR for the simultaneous detection of emerging and reemerging swine coronaviruses. <i>Virulence</i> , 2020, 11, 707-718.  | 1.8 | 42        |
| 20 | Epidemiology, genetic diversity and evolution of canine astrovirus. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2901-2910.   | 1.3 | 6         |
| 21 | COVID-19: Epidemiology, Evolution, and Cross-Disciplinary Perspectives. <i>Trends in Molecular Medicine</i> , 2020, 26, 483-495.  | 3.5 | 470       |
| 22 | Genotyping Porcine Circovirus 3 (PCV-3) Nowadays: Does It Make Sense?. <i>Viruses</i> , 2020, 12, 265.  | 1.5 | 47        |
| 23 | 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         |
| 24 | Adaption and parallel evolution of human-isolated H5 avian influenza viruses. <i>Journal of Infection</i> , 2020, 80, 630-638.  | 1.7 | 10        |
| 25 | Epidemiology and evolutionary analysis of Torque teno sus virus. <i>Veterinary Microbiology</i> , 2020, 244, 108668.  | 0.8 | 3         |
| 26 | 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        |
| 27 | 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         |
| 28 | Antiviral Effect of Lithium Chloride and Diammonium Glycyrrhizinate on Porcine Deltacoronavirus In Vitro. <i>Pathogens</i> , 2019, 8, 144.  | 1.2 | 25        |
| 29 | Comprehensive codon usage analysis of porcine deltacoronavirus. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106618.   | 1.2 | 13        |
| 30 | Genetic Analysis and Evolutionary Changes of the Torque teno sus Virus. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2881.  | 1.8 | 17        |
| 31 | Genetic analysis and evolutionary changes of Porcine circovirus 2. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106520.  | 1.2 | 36        |
| 32 | Generation of Monoclonal Antibodies against Variable Epitopes of the M Protein of Rabies Virus. <i>Viruses</i> , 2019, 11, 375.   | 1.5 | 5         |
| 33 | Genetic Evolution and Molecular Selection of the HE Gene of Influenza C Virus. <i>Viruses</i> , 2019, 11, 167.  | 1.5 | 27        |
| 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 | Antiviral Activity of Germacrone against Pseudorabies Virus in Vitro. <i>Pathogens</i> , 2019, 8, 258.  | 1.2 | 21        |
| 36 | Interspecies Transmission, Genetic Diversity, and Evolutionary Dynamics of Pseudorabies Virus. <i>Journal of Infectious Diseases</i> , 2019, 219, 1705-1715.  | 1.9 | 101       |

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|----|--|-----|-----------|
| 37 | 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        |
| 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 | Genetic diversity of porcine circovirus type 2 in China between 1999–2017. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 599-605.   | 1.3 | 19        |
| 40 | 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         |
| 41 | Bat-Origin Coronaviruses Expand Their Host Range to Pigs. <i>Trends in Microbiology</i> , 2018, 26, 466-470.   | 3.5 | 52        |
| 42 | Genetic and evolutionary analysis of emerging H3N2 canine influenza virus. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-15.  | 3.0 | 34        |
| 43 | Origin, Genetic Diversity, and Evolutionary Dynamics of Novel Porcine Circovirus 3. <i>Advanced Science</i> , 2018, 5, 1800275.  | 5.6 | 92        |
| 44 | Insights into the genetic and host adaptability of emerging porcine circovirus 3. <i>Virulence</i> , 2018, 9, 1301-1313.   | 1.8 | 49        |
| 45 | Comprehensive Analysis of Codon Usage on Rabies Virus and Other Lyssaviruses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2397.   | 1.8 | 18        |
| 46 | 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        |
| 47 | BECN1-dependent CASP2 incomplete autophagy induction by binding to rabies virus phosphoprotein. <i>Autophagy</i> , 2017, 13, 739-753.  | 4.3 | 45        |
| 48 | One Health strategies for rabies control in rural areas of China. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 365-367.  | 4.6 | 31        |
| 49 | Identification and function analysis of canine stimulator of interferon gene (STING). <i>Microbial Pathogenesis</i> , 2017, 113, 202-208.  | 1.3 | 6         |
| 50 | Clinical Evaluation of Ebola Virus Disease Therapeutics. <i>Trends in Molecular Medicine</i> , 2017, 23, 820-830.  | 3.5 | 17        |
| 51 | 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       |
| 52 | Novel Influenza D virus: Epidemiology, pathology, evolution and biological characteristics. <i>Virulence</i> , 2017, 8, 1580-1591.   | 1.8 | 101       |
| 53 | Codon usage bias in the N gene of rabies virus. <i>Infection, Genetics and Evolution</i> , 2017, 54, 458-465.  | 1.0 | 19        |
| 54 | Evolutionary and genetic analysis of the VP2 gene of canine parvovirus. <i>BMC Genomics</i> , 2017, 18, 534.   | 1.2 | 38        |

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|----|---|-----|-----------|
| 55 | 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        |
| 56 | 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         |
| 57 | Rabies virus matrix protein induces apoptosis by targeting mitochondria. <i>Experimental Cell Research</i> , 2016, 347, 83-94.  | 1.2 | 28        |
| 58 | Spread of ZIKV and YFV to China: Potential implications. <i>Journal of Infection</i> , 2016, 73, 289-291.   | 1.7 | 3         |
| 59 | Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. <i>Trends in Microbiology</i> , 2016, 24, 490-502.  | 3.5 | 2,243     |
| 60 | Diagnostic strategies for Ebola virus detection. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 294-295.  | 4.6 | 6         |
| 61 | 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        |
| 62 | Identification of the IFN- $\gamma$ response in H3N2 canine influenza virus infection. <i>Journal of General Virology</i> , 2016, 97, 18-26.  | 1.3 | 9         |
| 63 | 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        |
| 64 | 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        |
| 65 | 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        |
| 66 | 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         |
| 67 | Epidemiology, Evolution, and Recent Outbreaks of Avian Influenza Virus in China. <i>Journal of Virology</i> , 2015, 89, 8671-8676.  | 1.5 | 212       |
| 68 | MERS in South Korea and China: a potential outbreak threat?. <i>Lancet</i> , The, 2015, 385, 2349-2350.   | 6.3 | 78        |
| 69 | 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        |
| 70 | 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        |
| 71 | Virological and Epidemiological Evidence of Avian Influenza Virus Infections Among Feral Dogs in Live Poultry Markets, China: A Threat to Human Health?. <i>Clinical Infectious Diseases</i> , 2014, 58, 1644-1646.     | 2.9 | 48        |
| 72 | 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        |

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|----|--|-----|-----------|
| 73 | 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        |
| 74 | 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        |
| 75 | First Evidence of H10N8 Avian Influenza Virus Infections among Feral Dogs in Live Poultry Markets in Guangdong Province, China. <i>Clinical Infectious Diseases</i> , 2014, 59, 748-750.             | 2.9 | 52        |
| 76 | 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        |
| 77 | 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        |
| 78 | Mutagenesis analysis of porcine reproductive and respiratory syndrome virus nonstructural protein 7. <i>Virus Genes</i> , 2013, 47, 467-477.   | 0.7 | 20        |
| 79 | 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         |
| 80 | 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        |
| 81 | 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        |
| 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 | 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        |
| 84 | Serologic Evidence of Pandemic Influenza Virus H1N1 2009 Infection in Cats in China. <i>Vaccine Journal</i> , 2013, 20, 115-117.   | 3.2 | 12        |
| 85 | 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        |
| 86 | 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        |
| 87 | 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        |