

Changchun Tu

List of Publications by Year in descending order

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96
papers

2,746
citations

201674

27
h-index

233421

45
g-index

105
all docs

105
docs citations

105
times ranked

3312
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for SARS-CoV-2 related coronaviruses circulating in bats and pangolins in Southeast Asia. <i>Nature Communications</i> , 2021, 12, 972.	12.8	276
2	Identification of Diverse Alphacoronaviruses and Genomic Characterization of a Novel Severe Acute Respiratory Syndrome-Like Coronavirus from Bats in China. <i>Journal of Virology</i> , 2014, 88, 7070-7082.	3.4	125
3	Virome Profiling of Bats from Myanmar by Metagenomic Analysis of Tissue Samples Reveals More Novel Mammalian Viruses. <i>PLoS ONE</i> , 2013, 8, e61950.	2.5	113
4	Phylogenetic comparison of classical swine fever virus in China. <i>Virus Research</i> , 2001, 81, 29-37.	2.2	108
5	Evaluation of a multiplex real-time RT-PCR for quantitative and differential detection of wild-type viruses and C-strain vaccine of Classical swine fever virus. <i>Veterinary Microbiology</i> , 2008, 126, 1-10.	1.9	108
6	Virome characterization of game animals in China reveals a spectrum of emerging pathogens. <i>Cell</i> , 2022, 185, 1117-1129.e8.	28.9	106
7	Characterization of a Novel G3P[3] Rotavirus Isolated from a Lesser Horseshoe Bat: a Distant Relative of Feline/Canine Rotaviruses. <i>Journal of Virology</i> , 2013, 87, 12357-12366.	3.4	63
8	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	2.1	62
9	Genetically modified pigs are protected from classical swine fever virus. <i>PLoS Pathogens</i> , 2018, 14, e1007193.	4.7	60
10	Proteomic Alteration of PK-15 Cells after Infection by Classical Swine Fever Virus. <i>Journal of Proteome Research</i> , 2008, 7, 5263-5269.	3.7	54
11	Virome analysis of tick-borne viruses in Heilongjiang Province, China. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 412-420.	2.7	54
12	DNA-mediated protection against classical swine fever virus. <i>Vaccine</i> , 2001, 19, 1520-1525.	3.8	52
13	Filovirus RNA in Fruit Bats, China. <i>Emerging Infectious Diseases</i> , 2015, 21, 1675-1677.	4.3	51
14	Xi River virus, a new bat reovirus isolated in southern China. <i>Archives of Virology</i> , 2010, 155, 1295-1299.	2.1	49
15	Hepatitis Virus in Long-Fingered Bats, Myanmar. <i>Emerging Infectious Diseases</i> , 2013, 19, 638-640.	4.3	46
16	Bacteriophage T4 nanoparticle capsid surface SOC and HOC bipartite display with enhanced classical swine fever virus immunogenicity: A powerful immunological approach. <i>Journal of Virological Methods</i> , 2007, 139, 50-60.	2.1	44
17	Genetic diversity of subgenotype 2.1 isolates of classical swine fever virus. <i>Infection, Genetics and Evolution</i> , 2016, 41, 218-226.	2.3	43
18	Pigs immunized with a novel E2 subunit vaccine are protected from subgenotype heterologous classical swine fever virus challenge. <i>BMC Veterinary Research</i> , 2016, 12, 197.	1.9	43

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19	The protective immune response induced by B cell epitope of classical swine fever virus glycoprotein E2. <i>Journal of Virological Methods</i> , 2006, 134, 125-129.	2.1	42
20	Nairobi Sheep Disease Virus RNA in Ixodid Ticks, China, 2013. <i>Emerging Infectious Diseases</i> , 2015, 21, 718-720.	4.3	39
21	Phylogenetic analysis using E2 gene of classical swine fever virus reveals a new subgenotype in China. <i>Infection, Genetics and Evolution</i> , 2013, 17, 231-238.	2.3	36
22	Characterization of a novel orthoreovirus isolated from fruit bat, China. <i>BMC Microbiology</i> , 2014, 14, 293.	3.3	36
23	Genomic expression profiling of peripheral blood leukocytes of pigs infected with highly virulent classical swine fever virus strain Shimen. <i>Journal of General Virology</i> , 2009, 90, 1670-1680.	2.9	35
24	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, .	8.9	35
25	A multiplex nested RT-PCR for the detection and differentiation of wild-type viruses from C-strain vaccine of classical swine fever virus. <i>Journal of Virological Methods</i> , 2007, 143, 16-22.	2.1	33
26	In vitro inhibition of classical swine fever virus replication by siRNAs targeting Npro and NS5B genes. <i>Antiviral Research</i> , 2008, 78, 188-193.	4.1	33
27	Annexin 2 is a host protein binding to classical swine fever virus E2 glycoprotein and promoting viral growth in PK-15 cells. <i>Virus Research</i> , 2015, 201, 16-23.	2.2	33
28	The complete genome sequence of a G3P[10] Chinese bat rotavirus suggests multiple bat rotavirus inter-host species transmission events. <i>Infection, Genetics and Evolution</i> , 2014, 28, 1-4.	2.3	29
29	Detection and characterization of diverse alpha- and betacoronaviruses from bats in China. <i>Virologica Sinica</i> , 2016, 31, 69-77.	3.0	29
30	Group A Rotaviruses in Chinese Bats: Genetic Composition, Serology, and Evidence for Bat-to-Human Transmission and Reassortment. <i>Journal of Virology</i> , 2017, 91, .	3.4	28
31	Animal Rabies Surveillance, China, 2004–2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 2825-2834.	4.3	27
32	Tick distribution in border regions of Northwestern China. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 665-669.	2.7	26
33	Sub-subgenotype 2.1c isolates of classical swine fever virus are dominant in Guangdong province of China, 2018. <i>Infection, Genetics and Evolution</i> , 2019, 68, 212-217.	2.3	26
34	Toll-Like Receptor 7 Enhances Rabies Virus-Induced Humoral Immunity by Facilitating the Formation of Germinal Centers. <i>Frontiers in Immunology</i> , 2019, 10, 429.	4.8	24
35	Identification of a novel orthohepadnavirus in pomona roundleaf bats in China. <i>Archives of Virology</i> , 2015, 160, 335-337.	2.1	23
36	<i>Brucella melitensis</i> and <i>B. abortus</i> in eggs, larvae and engorged females of <i>Dermacentor marginatus</i> . <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1045-1048.	2.7	23

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37	Inhibition of Rabies Virus by 1,2,3,4,6-Penta-O-galloyl- β -D-Glucose Involves mTOR-Dependent Autophagy. <i>Viruses</i> , 2018, 10, 201.	3.3	23
38	Isolation and characterization of Getah virus from pigs in Guangdong province of China. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2249.	3.0	23
39	In vitro inhibition of CSFV replication by multiple siRNA expression. <i>Antiviral Research</i> , 2011, 91, 209-216.	4.1	22
40	Novel hantavirus identified in black-bearded tomb bats, China. <i>Infection, Genetics and Evolution</i> , 2015, 31, 158-160.	2.3	22
41	Simultaneous detection of Classical swine fever virus and North American genotype Porcine reproductive and respiratory syndrome virus using a duplex real-time RT-PCR. <i>Journal of Virological Methods</i> , 2008, 151, 194-199.	2.1	21
42	Genomes and seroprevalence of severe fever with thrombocytopenia syndrome virus and Nairobi sheep disease virus in <i>Haemaphysalis longicornis</i> ticks and goats in Hubei, China. <i>Virology</i> , 2019, 529, 234-245.	2.4	21
43	The first molecular evidence of severe fever with thrombocytopenia syndrome virus in ticks in Jilin, Northeastern China. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 1280-1283.	2.7	20
44	Commercial E2 subunit vaccine provides full protection to pigs against lethal challenge with 4 strains of classical swine fever virus genotype 2. <i>Veterinary Microbiology</i> , 2019, 237, 108403.	1.9	20
45	Virome profiling of rodents in Xinjiang Uygur Autonomous Region, China: Isolation and characterization of a new strain of Wenzhou virus. <i>Virology</i> , 2019, 529, 122-134.	2.4	20
46	Quadruple antigenic epitope peptide producing immune protection against classical swine fever virus. <i>Vaccine</i> , 2006, 24, 7175-7180.	3.8	19
47	Antigenic differentiation of classical swine fever viruses in China by monoclonal antibodies. <i>Virus Research</i> , 2009, 142, 169-174.	2.2	19
48	Genetic diversity of porcine circovirus type 2 in China between 1999 and 2017. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 599-605.	3.0	19
49	A neutralizing monoclonal antibody-based competitive ELISA for classical swine fever C-strain post-vaccination monitoring. <i>BMC Veterinary Research</i> , 2020, 16, 14.	1.9	19
50	Cellular Hsp27 interacts with classical swine fever virus NS5A protein and negatively regulates viral replication by the NF- κ B signaling pathway. <i>Virology</i> , 2018, 518, 202-209.	2.4	18
51	A novel enterovirus species identified from severe diarrheal goats. <i>PLoS ONE</i> , 2017, 12, e0174600.	2.5	18
52	In vitro inhibition of CSFV replication by retroviral vector-mediated RNA interference. <i>Journal of Virological Methods</i> , 2010, 169, 316-321.	2.1	17
53	Pentagalloylglucose Inhibits the Replication of Rabies Virus via Mediation of the miR-455/SOCS3/STAT3/IL-6 Pathway. <i>Journal of Virology</i> , 2019, 93, .	3.4	17
54	Seroprevalence of Rabies Virus Antibodies in Bats from Southern China. <i>Vector-Borne and Zoonotic Diseases</i> , 2010, 10, 177-181.	1.5	16

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55	Livestock rabies outbreaks in Shanxi province, China. <i>Archives of Virology</i> , 2016, 161, 2851-2854.	2.1	16
56	The eukaryotic translation initiation factor 3 subunit E binds to classical swine fever virus NS5A and facilitates viral replication. <i>Virology</i> , 2018, 515, 11-20.	2.4	16
57	Virulence evaluation of classical swine fever virus subgenotype 2.1 and 2.2 isolates circulating in China. <i>Veterinary Microbiology</i> , 2019, 232, 114-120.	1.9	16
58	Proteomic analysis of primary porcine endothelial cells after infection by classical swine fever virus. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1882-1888.	2.3	15
59	Down-regulation of cellular protein heme oxygenase 1 inhibits proliferation of classical swine fever virus in PK-15 cells. <i>Virus Research</i> , 2013, 173, 315-320.	2.2	13
60	mTORC1 Negatively Regulates the Replication of Classical Swine Fever Virus Through Autophagy and IRES-Dependent Translation. <i>IScience</i> , 2018, 3, 87-101.	4.1	13
61	Proteomic Profiling of Purified Rabies Virus Particles. <i>Virologica Sinica</i> , 2020, 35, 143-155.	3.0	13
62	Interferon-inducible GTPase: a novel viral response protein involved in rabies virus infection. <i>Archives of Virology</i> , 2016, 161, 1285-1293.	2.1	12
63	Isolation and Characterization of Porcine Astrovirus 5 from a Classical Swine Fever Virus-Infected Specimen. <i>Journal of Virology</i> , 2020, 95, .	3.4	12
64	Extensive Genetic Diversity of Polyomaviruses in Sympatric Bat Communities: Host Switching versus Coevolution. <i>Journal of Virology</i> , 2020, 94, .	3.4	12
65	Genetic Diversity of <i>Echinococcus granulosus</i> Genotype G1 in Xinjiang, Northwest of China. <i>Korean Journal of Parasitology</i> , 2018, 56, 391-396.	1.3	12
66	Toward the development of a one-dose classical swine fever subunit vaccine: antigen titration, immunity onset, and duration of immunity. <i>Journal of Veterinary Science</i> , 2018, 19, 393.	1.3	11
67	Viral Metagenome-Based Precision Surveillance of Pig Population at Large Scale Reveals Viromic Signatures of Sample Types and Influence of Farming Management on Pig Virome. <i>MSystems</i> , 2021, 6, e0042021.	3.8	11
68	In vitro adaptation and genome analysis of a sub-subgenotype 2.1c isolate of classical swine fever virus. <i>Virus Genes</i> , 2016, 52, 651-659.	1.6	10
69	Seroprevalence, cross antigenicity and circulation sphere of bat-borne hantaviruses revealed by serological and antigenic analyses. <i>PLoS Pathogens</i> , 2019, 15, e1007545.	4.7	10
70	Autophagy is highly targeted among host comparative proteomes during infection with different virulent RABV strains. <i>Oncotarget</i> , 2017, 8, 21336-21350.	1.8	10
71	Complete Genome Sequences of Classical Swine Fever Virus Isolates Belonging to a New Subgenotype, 2.1c, from Hunan Province, China. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
72	The new <i>Haemaphysalis longicornis</i> genome provides insights into its requisite biological traits. <i>Genomics</i> , 2022, 114, 110317.	2.9	9

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73	Detection and Characterization of a Novel Norovirus in Bats, China. <i>Virologica Sinica</i> , 2018, 33, 100-103.	3.0	8
74	Low-dose Norfloxacin-treated leptospirases induce less IL-1 β release in J774A.1 cells following discrepant leptospiral gene expression. <i>Microbial Pathogenesis</i> , 2018, 119, 125-130.	2.9	8
75	Molecular characterization of a novel bat-associated circovirus with a poly-T tract in the 3' intergenic region. <i>Virus Research</i> , 2018, 250, 95-103.	2.2	8
76	Seroepidemiological Investigation of Crimean-Congo Hemorrhagic Fever Virus in Sheep and Camels of Inner Mongolia of China. <i>Vector-Borne and Zoonotic Diseases</i> , 2020, 20, 461-467.	1.5	8
77	Comprehensive Evaluation of RNA and DNA Viromic Methods Based on Species Richness and Abundance Analyses Using Marmot Rectal Samples. <i>MSystems</i> , 2022, 7, .	3.8	8
78	Complete genome sequence of a novel sub-subgenotype 2.1g isolate of classical swine fever virus from China. <i>Archives of Virology</i> , 2016, 161, 2613-2617.	2.1	7
79	Construction of an HRP-streptavidin bound antigen and its application in an ELISA for porcine circovirus 2 antibodies. <i>AMB Express</i> , 2017, 7, 177.	3.0	7
80	Isolation and evolutionary analysis of Senecavirus A isolates from Guangdong province, China. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104819.	2.3	7
81	Seroreactive Profiling of Filoviruses in Chinese Bats Reveals Extensive Infection of Diverse Viruses. <i>Journal of Virology</i> , 2020, 94, .	3.4	6
82	Mammalian birnaviruses identified in pigs infected by classical swine fever virus. <i>Virus Evolution</i> , 2021, 7, veab084.	4.9	6
83	Evaluation of monoclonal antibody-based direct, rapid immunohistochemical test for rabies diagnosis. <i>Journal of Virological Methods</i> , 2018, 256, 12-16.	2.1	5
84	Molecular detection and sequence characterization of diverse rhabdoviruses in bats, China. <i>Virus Research</i> , 2018, 244, 208-212.	2.2	5
85	Genetic diversity of bat orthohepadnaviruses in China and a proposed new nomenclature. <i>Infection, Genetics and Evolution</i> , 2018, 63, 135-143.	2.3	5
86	Different clinical presentations of subgenotype 2.1 strain of classical swine fever infection in weaned piglets and adults, and long-term cross-protection conferred by a C-strain vaccine. <i>Veterinary Microbiology</i> , 2021, 253, 108915.	1.9	5
87	Diversity of rabies virus detected in Inner Mongolia, China, 2019-2021. <i>Transboundary and Emerging Diseases</i> , 2022, , .	3.0	5
88	Identification of cleavage of NS5A of C-strain classical swine fever virus. <i>Archives of Virology</i> , 2017, 162, 391-400.	2.1	4
89	Identification of two novel ephemeroviruses in pigs infected by classical swine fever virus. <i>Infection, Genetics and Evolution</i> , 2022, 100, 105273.	2.3	4
90	Determination of antibody induction by highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV) vaccine: A comparison of two ELISA kits. <i>Journal of Veterinary Medical Science</i> , 2019, 81, 1173-1176.	0.9	3

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91	A novel combined vaccine against classical swine fever and porcine epidemic diarrhea viruses elicits a significant Th2-favored humoral response in mice. <i>Vaccine</i> , 2021, 39, 4573-4576.	3.8	3
92	Genetic characterization of hepatitis E virus from wild boar in China. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	2
93	Evaluation of a Universal Nested Reverse Transcription Polymerase Chain Reaction for the Detection of Lyssaviruses. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	1
94	Characterization of monoclonal antibodies that specifically differentiate field isolates from vaccine strains of classical swine fever virus. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	1
95	Complete Genome Sequence of a Sub-Subgenotype 2.1i Isolate of Classical Swine Fever Virus from China. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
96	A Novel Competitive ELISA for Specifically Measuring and Differentiating Immune Responses to Classical Swine Fever C-Strain Vaccine in Pigs. <i>Viruses</i> , 2022, 14, 1544.	3.3	0