

Di Liu

List of Publications by Year in descending order

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140
papers

12,282
citations

41344

49
h-index

27406

106
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149
all docs

149
docs citations

149
times ranked

19496
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Infection in Children. <i>New England Journal of Medicine</i> , 2020, 382, 1663-1665.	27.0	1,970
2	Emergence of Fatal PRRSV Variants: Unparalleled Outbreaks of Atypical PRRS in China and Molecular Dissection of the Unique Hallmark. <i>PLoS ONE</i> , 2007, 2, e526.	2.5	841
3	First-wave COVID-19 transmissibility and severity in China outside Hubei after control measures, and second-wave scenario planning: a modelling impact assessment. <i>Lancet, The</i> , 2020, 395, 1382-1393.	13.7	703
4	Metagenome-wide analysis of antibiotic resistance genes in a large cohort of human gut microbiota. <i>Nature Communications</i> , 2013, 4, 2151.	12.8	606
5	Origin and diversity of novel avian influenza A H7N9 viruses causing human infection: phylogenetic, structural, and coalescent analyses. <i>Lancet, The</i> , 2013, 381, 1926-1932.	13.7	516
6	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
7	DATF: a database of Arabidopsis transcription factors. <i>Bioinformatics</i> , 2005, 21, 2568-2569.	4.1	296
8	Duck Egg-Drop Syndrome Caused by BYD Virus, a New Tembusu-Related Flavivirus. <i>PLoS ONE</i> , 2011, 6, e18106.	2.5	296
9	Fatty Liver Disease Caused by High-Alcohol-Producing <i>Klebsiella pneumoniae</i> . <i>Cell Metabolism</i> , 2019, 30, 675-688.e7.	16.2	294
10	Genesis, Evolution and Prevalence of H5N6 Avian Influenza Viruses in China. <i>Cell Host and Microbe</i> , 2016, 20, 810-821.	11.0	257
11	A Glimpse of Streptococcal Toxic Shock Syndrome from Comparative Genomics of <i>S. suis</i> 2 Chinese Isolates. <i>PLoS ONE</i> , 2007, 2, e315.	2.5	244
12	Autophagy is involved in influenza A virus replication. <i>Autophagy</i> , 2009, 5, 321-328.	9.1	229
13	Isolation and analyses of genes preferentially expressed during early cotton fiber development by subtractive PCR and cDNA array. <i>Nucleic Acids Research</i> , 2003, 31, 2534-2543.	14.5	226
14	Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1375-1386.	3.1	206
15	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.	7.7	199
16	SARS-CoV-2 infection induces sustained humoral immune responses in convalescent patients following symptomatic COVID-19. <i>Nature Communications</i> , 2021, 12, 1813.	12.8	198
17	Ginseng polysaccharides alter the gut microbiota and kynurenine/tryptophan ratio, potentiating the antitumour effect of antiprogrammed cell death 1/programmed cell death ligand 1 (anti-PD-1/PD-L1) immunotherapy. <i>Gut</i> , 2022, 71, 734-745.	12.1	177
18	An Annotation Update via cDNA Sequence Analysis and Comprehensive Profiling of Developmental, Hormonal or Environmental Responsiveness of the Arabidopsis AP2/EREBP Transcription Factor Gene Family. <i>Plant Molecular Biology</i> , 2005, 59, 853-868.	3.9	170

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19	The 2009 pandemic H1N1 neuraminidase N1 lacks the 150-cavity in its active site. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1266-1268.	8.2	160
20	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015, 524, 93-96.	27.8	150
21	Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. <i>Nature Communications</i> , 2014, 5, 3142.	12.8	145
22	HTQC: a fast quality control toolkit for Illumina sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 33.	2.6	142
23	SalK/SalR, a Two-Component Signal Transduction System, Is Essential for Full Virulence of Highly Invasive <i>Streptococcus suis</i> Serotype 2. <i>PLoS ONE</i> , 2008, 3, e2080.	2.5	132
24	Poultry carrying H9N2 act as incubators for novel human avian influenza viruses. <i>Lancet</i> , The, 2014, 383, 869.	13.7	113
25	Porcine Respiratory and Reproductive Syndrome Virus Variants, Vietnam and China, 2007. <i>Emerging Infectious Diseases</i> , 2008, 14, 1774-1776.	4.3	112
26	H5N1 avian influenza re-emergence of Lake Qinghai: phylogenetic and antigenic analyses of the newly isolated viruses and roles of migratory birds in virus circulation. <i>Journal of General Virology</i> , 2008, 89, 697-702.	2.9	100
27	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, .	3.4	99
28	Metagenomic Insights into the Fibrolytic Microbiome in Yak Rumen. <i>PLoS ONE</i> , 2012, 7, e40430.	2.5	98
29	Crystal structure of the swine-origin A (H1N1)-2009 influenza A virus hemagglutinin (HA) reveals similar antigenicity to that of the 1918 pandemic virus. <i>Protein and Cell</i> , 2010, 1, 459-467.	11.0	94
30	Human Infection with Influenza Virus A(H10N8) from Live Poultry Markets, China, 2014. <i>Emerging Infectious Diseases</i> , 2014, 20, 2076-9.	4.3	94
31	A Bat-Derived Putative Cross-Family Recombinant Coronavirus with a Reovirus Gene. <i>PLoS Pathogens</i> , 2016, 12, e1005883.	4.7	92
32	Autophagy protects LNCaP cells under androgen deprivation conditions. <i>Autophagy</i> , 2008, 4, 54-60.	9.1	90
33	Two novel reassortants of avian influenza A (H5N6) virus in China. <i>Journal of General Virology</i> , 2015, 96, 975-981.	2.9	89
34	Glucosyltransferase-mediated horizontal transfer of the 89K pathogenicity island in epidemic <i>Streptococcus suis</i> serotype 2. <i>Molecular Microbiology</i> , 2011, 79, 1670-1683.	2.5	86
35	Origin and molecular characterization of the human-infecting H6N1 influenza virus in Taiwan. <i>Protein and Cell</i> , 2013, 4, 846-853.	11.0	86
36	Origin and Possible Genetic Recombination of the Middle East Respiratory Syndrome Coronavirus from the First Imported Case in China: Phylogenetics and Coalescence Analysis. <i>MBio</i> , 2015, 6, e01280-15.	4.1	86

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37	Genesis of the novel human-infecting influenza A(H10N8) virus and potential genetic diversity of the virus in poultry, China. <i>Eurosurveillance</i> , 2014, 19, .	7.0	83
38	Highly Pathogenic Avian Influenza A(H5N8) Virus in Wild Migratory Birds, Qinghai Lake, China. <i>Emerging Infectious Diseases</i> , 2017, 23, 637-641.	4.3	82
39	Environmental connections of novel avian-origin H7N9 influenza virus infection and virus adaptation to the human. <i>Science China Life Sciences</i> , 2013, 56, 485-492.	4.9	81
40	Reverse-Transcription Recombinase-Aided Amplification Assay for Rapid Detection of the 2019 Novel Coronavirus (SARS-CoV-2). <i>Analytical Chemistry</i> , 2020, 92, 9699-9705.	6.5	74
41	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016, 1, 16151.	13.3	70
42	Phylogenetics, Genomic Recombination, and NSP2 Polymorphic Patterns of Porcine Reproductive and Respiratory Syndrome Virus in China and the United States in 2014â€“2018. <i>Journal of Virology</i> , 2020, 94, .	3.4	69
43	The involvement of sortase A in high virulence of STSS-causing <i>Streptococcus suis</i> serotype 2. <i>Archives of Microbiology</i> , 2009, 191, 23-33.	2.2	65
44	H7N9: a low pathogenic avian influenza A virus infecting humans. <i>Current Opinion in Virology</i> , 2014, 5, 91-97.	5.4	65
45	SARS-like virus in the Middle East: A truly bat-related coronavirus causing human diseases. <i>Protein and Cell</i> , 2012, 3, 803-805.	11.0	64
46	Novel avian influenza A (H5N6) viruses isolated in migratory waterfowl before the first human case reported in China, 2014. <i>Scientific Reports</i> , 2016, 6, 29888.	3.3	57
47	Clinical and Immunological Characteristics of Human Infections With H5N6 Avian Influenza Virus. <i>Clinical Infectious Diseases</i> , 2019, 68, 1100-1109.	5.8	56
48	Network pharmacology based investigation into the effect and mechanism of Modified Sijunzi Decoction against the subtypes of chronic atrophic gastritis. <i>Pharmacological Research</i> , 2019, 144, 158-166.	7.1	56
49	Identification and Characterization of Bmi-1-responding Element within the Human p16 Promoter*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33219-33229.	3.4	51
50	Highly Pathogenic Avian Influenza A(H5N1) Virus Struck Migratory Birds in China in 2015. <i>Scientific Reports</i> , 2015, 5, 12986.	3.3	47
51	TCRklass: A New K-Stringâ€“Based Algorithm for Human and Mouse TCR Repertoire Characterization. <i>Journal of Immunology</i> , 2015, 194, 446-454.	0.8	43
52	Assessing the role of live poultry trade in community-structured transmission of avian influenza in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5949-5954.	7.1	43
53	Interaction of Hsp40 with influenza virus M2 protein: implications for PKR signaling pathway. <i>Protein and Cell</i> , 2010, 1, 944-955.	11.0	41
54	The efficient hemostatic effect of Antarctic krill chitosan is related to its hydration property. <i>Carbohydrate Polymers</i> , 2015, 132, 295-303.	10.2	41

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55	Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014–2015. <i>Virologica Sinica</i> , 2016, 31, 300-305.	3.0	39
56	Clade 2.3.2 Avian Influenza Virus (H5N1), Qinghai Lake Region, China, 2009–2010. <i>Emerging Infectious Diseases</i> , 2011, 17, 560-562.	4.3	38
57	The Genome Characteristics and Predicted Function of Methyl-Group Oxidation Pathway in the Obligate Aceticlastic Methanogens, <i>Methanosaeta</i> spp. <i>PLoS ONE</i> , 2012, 7, e36756.	2.5	38
58	Phylogeography, Transmission, and Viral Proteins of Nipah Virus. <i>Virologica Sinica</i> , 2018, 33, 385-393.	3.0	37
59	Endogenous Retroviruses Function as Gene Expression Regulatory Elements During Mammalian Pre-implantation Embryo Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 790.	4.1	37
60	Cadmium chloride-induced transgenerational neurotoxicity in zebrafish development. <i>Environmental Toxicology and Pharmacology</i> , 2021, 81, 103545.	4.0	36
61	Cancer attributable to human papillomavirus infection in China: Burden and trends. <i>Cancer</i> , 2020, 126, 3719-3732.	4.1	35
62	Existence and characterization of allelic variants of Sao, a newly identified surface protein from <i>Streptococcus suis</i> . <i>FEMS Microbiology Letters</i> , 2007, 275, 80-88.	1.8	34
63	An unexpected similarity between antibiotic-resistant NDM-1 and beta-lactamase II from <i>Erythrobacter litoralis</i> . <i>Protein and Cell</i> , 2011, 2, 250-258.	11.0	34
64	Identification of climate factors related to human infection with avian influenza A H7N9 and H5N1 viruses in China. <i>Scientific Reports</i> , 2015, 5, 18094.	3.3	33
65	Interspecies transmission and host restriction of avian H5N1 influenza virus. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 428-438.	1.3	32
66	Avian influenza virus, <i>Streptococcus suis</i> serotype 2, severe acute respiratory syndrome-coronavirus and beyond: molecular epidemiology, ecology and the situation in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 2725-2737.	4.0	31
67	Phylogenetics of varied subtypes of avian influenza viruses in China: potential threat to humans. <i>Protein and Cell</i> , 2014, 5, 253-257.	11.0	31
68	Avian influenza A (H7N9) virus: from low pathogenic to highly pathogenic. <i>Frontiers of Medicine</i> , 2021, 15, 507-527.	3.4	30
69	In silico characterization of the functional and structural modules of the hemagglutinin protein from the swine-origin influenza virus A (H1N1)-2009. <i>Science China Life Sciences</i> , 2010, 53, 633-642.	4.9	29
70	Serological Surveillance of Influenza A Virus Infection in Swine Populations in Fujian Province, China: No Evidence of Naturally Occurring H5N1 Infection in Pigs. <i>Zoonoses and Public Health</i> , 2010, 57, 291-298.	2.2	28
71	Whole-Genome Sequences of Four <i>Mycobacterium bovis</i> BCG Vaccine Strains. <i>Journal of Bacteriology</i> , 2011, 193, 3152-3153.	2.2	28
72	BMP2 gene delivery to bone mesenchymal stem cell by chitosan-g-PEI nonviral vector. <i>Nanoscale Research Letters</i> , 2015, 10, 203.	5.7	28

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73	Naturally Occurring Single Mutations in Ebola Virus Observably Impact Infectivity. <i>Journal of Virology</i> , 2019, 93, .	3.4	28
74	Characterization of human $\hat{1}\hat{2}$ TCR repertoire and discovery of D-D fusion in TCR $\hat{1}^2$ chains. <i>Protein and Cell</i> , 2014, 5, 603-615.	11.0	27
75	Comparative Analysis of Gene Expression Profiles Between Cortex and Thalamus in Chinese Fatal Familial Insomnia Patients. <i>Molecular Neurobiology</i> , 2013, 48, 36-48.	4.0	26
76	Genomic surveillance of COVID-19 cases in Beijing. <i>Nature Communications</i> , 2020, 11, 5503.	12.8	26
77	Phylogenomic analysis unravels evolution of yellow fever virus within hosts. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006738.	3.0	24
78	Simplified amino acid alphabets based on deviation of conditional probability from random background. <i>Physical Review E</i> , 2002, 66, 021906.	2.1	23
79	Analyses of the Similarity and Difference of Global Gene Expression Profiles in Cortex Regions of Three Neurodegenerative Diseases: Sporadic Creutzfeldt-Jakob Disease (sCJD), Fatal Familial Insomnia (FFI), and Alzheimer's Disease (AD). <i>Molecular Neurobiology</i> , 2014, 50, 473-481.	4.0	23
80	Transcription profile of human endogenous retroviruses in response to dengue virus serotype 2 infection. <i>Virology</i> , 2020, 544, 21-30.	2.4	22
81	Deep sequencing of hepatitis B virus basal core promoter and precore mutants in HBeAg-positive chronic hepatitis B patients. <i>Scientific Reports</i> , 2015, 5, 17950.	3.3	21
82	Nanopore sequencing of African swine fever virus. <i>Science China Life Sciences</i> , 2020, 63, 160-164.	4.9	18
83	Rapid Acquisition of High-Quality SARS-CoV-2 Genome via Amplicon-Oxford Nanopore Sequencing. <i>Virologica Sinica</i> , 2021, 36, 901-912.	3.0	18
84	Continuous reassortments with local chicken H9N2 virus underlie the human-infecting influenza A (H7N9) virus in the new influenza season, Guangdong, China. <i>Protein and Cell</i> , 2014, 5, 878-882.	11.0	17
85	aKMT Catalyzes Extensive Protein Lysine Methylation in the Hyperthermophilic Archaeon <i>Sulfolobus islandicus</i> but is Dispensable for the Growth of the Organism. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2908-2923.	3.8	16
86	Three amino acid substitutions in the NS1 protein change the virus replication of H5N1 influenza virus in human cells. <i>Virology</i> , 2018, 519, 64-73.	2.4	16
87	Light stimulates anoxic and oligotrophic growth of glacial <i>Flavobacterium</i> strains that produce zeaxanthin. <i>ISME Journal</i> , 2021, 15, 1844-1857.	9.8	16
88	Rapid and Specific Detection of All Known Nipah virus Strains' Sequences With Reverse Transcription-Loop-Mediated Isothermal Amplification. <i>Frontiers in Microbiology</i> , 2019, 10, 418.	3.5	15
89	Transcriptome Analyses Implicate Endogenous Retroviruses Involved in the Host Antiviral Immune System through the Interferon Pathway. <i>Virologica Sinica</i> , 2021, 36, 1315-1326.	3.0	15
90	Global transcriptional profiling of the postmortem brain of a patient with G114V genetic Creutzfeldt-Jakob disease. <i>International Journal of Molecular Medicine</i> , 2013, 31, 676-688.	4.0	14

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91	A global assessment of the impact of school closure in reducing COVID-19 spread. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2022, 380, 20210124.	3.4	13
92	Interaction between DAHP synthase and chorismate mutase endows new regulation on DAHP synthase activity in <i>Corynebacterium glutamicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 10373-10380.	3.6	12
93	Web Resources for Microbial Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 69-72.	6.9	12
94	Two reassortant types of highly pathogenic H5N8 avian influenza virus from wild birds in Central China in 2016. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-8.	6.5	12
95	Pan-Genomic Analysis of African Swine Fever Virus. <i>Virologica Sinica</i> , 2020, 35, 662-665.	3.0	12
96	Visualization and Analysis of Gene Expression in Stanford Type A Aortic Dissection Tissue Section by Spatial Transcriptomics. <i>Frontiers in Genetics</i> , 2021, 12, 698124.	2.3	12
97	High-Throughput Analysis of the T Cell Receptor Beta Chain Repertoire in PBMCs from Chronic Hepatitis B Patients with HBeAg Seroconversion. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016, 2016, 1-7.	1.9	11
98	Two genetically diverse H7N7 avian influenza viruses isolated from migratory birds in central China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	6.5	11
99	Nanopore sequencing: a rapid solution for infectious disease epidemics. <i>Science China Life Sciences</i> , 2019, 62, 1101-1103.	4.9	11
100	Integrated characterization of SARS-CoV-2 genome, microbiome, antibiotic resistance and host response from single throat swabs. <i>Cell Discovery</i> , 2021, 7, 19.	6.7	11
101	Molecular evolution and genetic diversity analysis of SFTS virus based on next-generation sequencing. <i>Biosafety and Health</i> , 2021, 3, 105-115.	2.7	11
102	A large scale comparative genomic analysis reveals insertion sites for newly acquired genomic islands in bacterial genomes. <i>BMC Microbiology</i> , 2011, 11, 135.	3.3	10
103	A Replicating Modified Vaccinia TianTan Strain Expressing an Avian-Derived Influenza H5N1 Hemagglutinin Induce Broadly Neutralizing Antibodies and Cross-Clade Protective Immunity in Mice. <i>PLoS ONE</i> , 2013, 8, e83274.	2.5	10
104	Distribution of sialic acid receptors and experimental infections with different subtypes of influenza A viruses in Qinghai-Tibet plateau wild pika. <i>Virology Journal</i> , 2015, 12, 63.	3.4	10
105	Synergistic effect of the responses of different tissues against African swine fever virus. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	10
106	Website for avian flu information and bioinformatics. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 470-473.	1.3	9
107	A new reassortment of influenza A (H7N9) virus causing human infection in Beijing, 2014. <i>Scientific Reports</i> , 2016, 6, 26624.	3.3	9
108	Intra-host Ebola viral adaption during human infection. <i>Biosafety and Health</i> , 2019, 1, 14-24.	2.7	9

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109	Genomic epidemiological characteristics of dengue fever in Guangdong province, China from 2013 to 2017. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008049.	3.0	9
110	OsHT, a Rice Gene Encoding for a Plasma-Membrane Localized Histidine Transporter. <i>Journal of Integrative Plant Biology</i> , 2005, 47, 92-99.	8.5	8
111	Molecular characterization and phylogenetics of a reassortant H13N8 influenza virus isolated from gulls in Mongolia. <i>Virus Genes</i> , 2014, 49, 237-249.	1.6	8
112	The new emerging H7N9 influenza virus indicates poultry as new mixing vessels. <i>Science China Life Sciences</i> , 2014, 57, 731-732.	4.9	8
113	The triphibious warfare against viruses. <i>Science China Life Sciences</i> , 2017, 60, 1295-1298.	4.9	8
114	A Promising IFN-Deficient System to Manufacture IFN-Sensitive Influenza Vaccine Virus. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 127.	3.9	8
115	Analysis of ACE2 Gene-Encoded Proteins Across Mammalian Species. <i>Frontiers in Veterinary Science</i> , 2020, 7, 457.	2.2	7
116	Human Adenovirus Type 7 Infections in Hubei, China During 2018-2019: Epidemic Features and Genetic Characterization of the Detected Viruses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 684606.	3.9	7
117	Cost-effectiveness of strategies for preventing paediatric lower respiratory infections associated with respiratory syncytial virus in eight Chinese cities. <i>Vaccine</i> , 2021, 39, 5490-5498.	3.8	7
118	Circulation, Evolution and Transmission of H5N8 virus, 2016-2018. <i>Journal of Infection</i> , 2019, 79, 363-372.	3.3	6
119	Potential m6A and m5C Methylations within the Genome of A Chinese African Swine Fever Virus Strain. <i>Virologica Sinica</i> , 2021, 36, 321-324.	3.0	6
120	Computational predicting the human infectivity of H7N9 influenza viruses isolated from avian hosts. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 846-856.	3.0	6
121	Ecology of avian influenza viruses in migratory birds wintering within the Yangtze River wetlands. <i>Science Bulletin</i> , 2021, 66, 2014-2024.	9.0	6
122	Bioinformatics analysis raises candidate genes in blood for early screening of Parkinson's disease. <i>Biomedical and Environmental Sciences</i> , 2014, 27, 462-5.	0.2	6
123	Mapping the clinical outcomes and genetic evolution of Ebola virus in Sierra Leone. <i>JCI Insight</i> , 2017, 2, .	5.0	5
124	Sudden emergence of human infections with H7N9 avian influenza A virus in Hubei province, central China. <i>Scientific Reports</i> , 2018, 8, 2486.	3.3	4
125	Vaccination with Consensus H7 Elicits Broadly Reactive and Protective Antibodies against Eurasian and North American Lineage H7 Viruses. <i>Vaccines</i> , 2020, 8, 143.	4.4	4
126	Development of a highly sensitive digital PCR assay to quantify long non-coding RNA MYU in urine samples which exhibited great potential as an alternative diagnostic biomarker for prostate cancer. <i>Translational Andrology and Urology</i> , 2021, 10, 3815-3825.	1.4	4

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127	Circulation, genomic characteristics, and evolutionary dynamics of class I Newcastle disease virus in China. <i>Virulence</i> , 2022, 13, 414-427.	4.4	4
128	Hemagglutinin Gene Variation Rate of H9N2 Avian Influenza Virus by Vaccine Intervention in China. <i>Viruses</i> , 2022, 14, 1043.	3.3	4
129	An Assessment of Amplicon-Sequencing Based Method for Viral Intra-host Analysis. <i>Virologica Sinica</i> , 2018, 33, 557-560.	3.0	3
130	Association of C-reactive Protein with Cardiovascular Outcomes: A Mendelian Randomization Study in the Japanese Population.. <i>Biomedical and Environmental Sciences</i> , 2022, 35, 126-132.	0.2	3
131	Discriminating Clonotypes of Influenza A Virus Genes by Nanopore Sequencing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10069.	4.1	2
132	T4SP: a novel tool and database for type IV secretion systems in bacterial genomes. <i>Biomedical and Environmental Sciences</i> , 2013, 26, 614-7.	0.2	2
133	Assessment of the Causal Effect of IgG N-Glycosylation Level on Risk of Dementia: A 2-Sample Mendelian Randomization Study. <i>Journal of Alzheimer's Disease</i> , 2022, 88, 1435-1441.	2.6	2
134	Biological data processing based on bio-processor unit (BPU), a new concept for next generation computational biology. <i>Science China Life Sciences</i> , 2018, 61, 597-598.	4.9	1
135	Integration of biosafety surveillance through Biosafety Surveillance Conceptual Data Model. <i>Biosafety and Health</i> , 2019, 1, 98-104.	2.7	1
136	Low Pathogenic Avian Influenza A (H5N7) Virus Isolated from a Domestic Duck in Dongting Lake Wetland of China, 2016. <i>Virologica Sinica</i> , 2019, 34, 97-101.	3.0	1
137	Partial recovery of disturbed V-J pairing profiles of T-cell receptor in people living with HIV receiving long-term antiretroviral therapy. <i>Science China Life Sciences</i> , 2021, 64, 152-161.	4.9	1
138	Stable non-synonymous substitutions on NS gene (NS1 and NS2 proteins) of Qinghai Lake H5N1 influenza virus (Clade 2.2) after successive passages in Muscovy ducks. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 847-853.	1.3	0
139	Functional Genomic Analysis of Taxonomic and Typing Loci for Pathogenic Bacteria Based on Orthologous Genes. <i>Scientia Sinica Vitae</i> , 2011, 41, 640-648.	0.3	0
140	Identifying Japanese Encephalitis Virus Using Metatranscriptomic Sequencing, Xinjiang Province, China. <i>Emerging Infectious Diseases</i> , 2022, 28, .	4.3	0