

Yigang Tong

List of Publications by Year in descending order

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218
papers

7,571
citations

100601

38
h-index

87275

74
g-index

225
all docs

225
docs citations

225
times ranked

12507
citing authors

#	ARTICLE	IF	CITATIONS
1	A single nonsynonymous mutation on ZIKV E protein-coding sequences leads to markedly increased neurovirulence in vivo. <i>Virologica Sinica</i> , 2022, 37, 115-126.	1.2	6
2	A Novel Freshwater Cyanophage, Mae-Yong924-1, Reveals a New Family. <i>Viruses</i> , 2022, 14, 283.	1.5	3
3	Efficient disinfection of SARS-CoV-2-like coronavirus, pseudotyped SARS-CoV-2 and other coronaviruses using cold plasma induces spike protein damage. <i>Journal of Hazardous Materials</i> , 2022, 430, 128414.	6.5	31
4	COVID-19 is a natural infectious disease. <i>Journal of Biosafety and Biosecurity</i> , 2022, 4, 38-42.	1.4	1
5	Importance of sample input volume for accurate SARS-CoV-2 qPCR testing. <i>Analytica Chimica Acta</i> , 2022, 1199, 339585.	2.6	3
6	Genomic analysis of Acinetobacter phage BUCT629, a newly isolated member of the genus Obolenskvirus. <i>Archives of Virology</i> , 2022, 167, 1197-1199.	0.9	2
7	A Novel Wide-Range Freshwater Cyanophage MinS1 Infecting the Harmful Cyanobacterium <i>Microcystis aeruginosa</i> . <i>Viruses</i> , 2022, 14, 433.	1.5	9
8	Discovery and Characterization of Rubrinodin Provide Clues into the Evolution of Lasso Peptides. <i>Biochemistry</i> , 2022, 61, 595-607.	1.2	5
9	New Advances in Nanomaterial-Based Antiviral Strategies. <i>Small Structures</i> , 2022, 3, .	6.9	7
10	Characterization and Genomic Analysis of a Novel Drexleriviral Bacteriophage IME268 with Lytic Activity Against <i>Klebsiella pneumoniae</i> . <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1533-1546.	1.1	9
11	Characterization and genome analysis of a novel <i>Stenotrophomonas maltophilia</i> bacteriophage BUCT598 with extreme pH resistance. <i>Virus Research</i> , 2022, 314, 198751.	1.1	7
12	Biological characterization and genomic analysis of <i>Acinetobacter baumannii</i> phage BUCT628. <i>Archives of Virology</i> , 2022, 167, 1471-1474.	0.9	5
13	Characterization and Genomic Analysis of Bacteriophage vB_KpnM_IME346 Targeting Clinical <i>Klebsiella pneumoniae</i> Strain of the K63 Capsular Type. <i>Current Microbiology</i> , 2022, 79, 160.	1.0	3
14	Characterization and complete genome sequence analysis of a newly isolated phage against <i>Vibrio parahaemolyticus</i> from sick shrimp in Qingdao, China. <i>PLoS ONE</i> , 2022, 17, e0266683.	1.1	6
15	SARS-CoV-2-related pangolin coronavirus exhibits similar infection characteristics to SARS-CoV-2 and direct contact transmissibility in hamsters. <i>IScience</i> , 2022, 25, 104350.	1.9	13
16	Isolation and characterization of the novel bacteriophage vB_SmaS_BUCT626 against <i>Stenotrophomonas maltophilia</i> . <i>Virus Genes</i> , 2022, 58, 458-466.	0.7	4
17	Human parainfluenza 3 and respiratory syncytial viruses detected in pangolins. <i>Emerging Microbes and Infections</i> , 2022, 11, 1657-1663.	3.0	3
18	Genomic Analysis of the <i>Serratia marcescens</i> Bacteriophage BUCT660. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	2

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19	Cepharanthine: A Promising Old Drug against SARS-CoV-2. <i>Advanced Biology</i> , 2022, 6, .	1.4	18
20	Identification and Molecular Characterization of a New Omono River Virus Isolated from <i>Culex Tritaeniorhynchus</i> in Yunnan, China. <i>Virologica Sinica</i> , 2021, 36, 152-154.	1.2	3
21	Topology engineering via protein catenane construction to strengthen an industrial biocatalyst. <i>Journal of Biotechnology</i> , 2021, 325, 271-279.	1.9	11
22	Complete genome analysis of an active prophage of <i>Vibrio alginolyticus</i> . <i>Archives of Virology</i> , 2021, 166, 891-896.	0.9	7
23	Transcriptome analysis of cepharanthine against a SARS-CoV-2-related coronavirus. <i>Briefings in Bioinformatics</i> , 2021, 22, 1378-1386.	3.2	39
24	Bacteriophage “A Promising Alternative Measure for Bacterial Biofilm Control. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 205-217.	1.1	53
25	Biological characteristics and genomic analysis of a <i>Stenotrophomonas maltophilia</i> phage vB_SmaS_BUCT548. <i>Virus Genes</i> , 2021, 57, 205-216.	0.7	20
26	All-in-one <i>in situ</i> colorimetric RT-LAMP assay for point-of-care testing of SARS-CoV-2. <i>Analyst, The</i> , 2021, 146, 6026-6034.	1.7	11
27	Genomic analysis of bacteriophage Xoo-sp13 infecting <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Archives of Virology</i> , 2021, 166, 1263-1265.	0.9	13
28	A Novel Singleton Giant Phage Yong-XC31 Lytic to the Pyropia Pathogen <i>Vibrio mediterranei</i> . <i>Applied Sciences (Switzerland)</i> , 2021, 11, 1602.	1.3	4
29	Ubiquitin-Modified Proteome of SARS-CoV-2-Infected Host Cells Reveals Insights into Virus-Host Interaction and Pathogenesis. <i>Journal of Proteome Research</i> , 2021, 20, 2224-2239.	1.8	38
30	The <i>Coxiella burnetii</i> QpH1 Plasmid Is a Virulence Factor for Colonizing Bone Marrow-Derived Murine Macrophages. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	9
31	Characterization and Genomic Analysis of BUCT549, a Novel Bacteriophage Infecting <i>Vibrio alginolyticus</i> With Flagella as Receptor. <i>Frontiers in Microbiology</i> , 2021, 12, 668319.	1.5	9
32	The zoonotic and natural foci characteristics of SARS-CoV-2. <i>Journal of Biosafety and Biosecurity</i> , 2021, 3, 51-55.	1.4	5
33	Computational design of ultrashort peptide inhibitors of the receptor-binding domain of the SARS-CoV-2 S protein. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
34	Isolation, Characterization, and Genome Sequence Analysis of a Novel Lytic Phage, Xoo-sp15 Infecting <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Current Microbiology</i> , 2021, 78, 3192-3200.	1.0	8
35	The Influence of Formulation Components and Environmental Humidity on Spray-Dried Phage Powders for Treatment of Respiratory Infections Caused by <i>Acinetobacter baumannii</i> . <i>Pharmaceutics</i> , 2021, 13, 1162.	2.0	9
36	Characterization and genome analysis of novel <i>Klebsiella</i> phage BUCT556A with lytic activity against carbapenemase-producing <i>Klebsiella pneumoniae</i> . <i>Virus Research</i> , 2021, 303, 198506.	1.1	11

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37	Characterization and genome sequence of the genetically unique Escherichia bacteriophage vB_EcoM_IME392. Archives of Virology, 2021, 166, 2505-2520.	0.9	8
38	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. Archives of Virology, 2021, 166, 3239-3244.	0.9	24
39	Metatranscriptomic analysis identifies different viral-like sequences in two neotropical Mansoniini mosquito species. Virus Research, 2021, 301, 198455.	1.1	4
40	Biochemical and genomic characterization of a novel bacteriophage BUCT555 lysing Stenotrophomonas maltophilia. Virus Research, 2021, 301, 198465.	1.1	16
41	Artemether, Artesunate, Arteannuin B, Echinatin, Licochalcone B and Andrographolide Effectively Inhibit SARS-CoV-2 and Related Viruses In Vitro. Frontiers in Cellular and Infection Microbiology, 2021, 11, 680127.	1.8	28
42	Ultrafast multiplexed detection of SARS-CoV-2 RNA using a rapid droplet digital PCR system. Biosensors and Bioelectronics, 2021, 188, 113282.	5.3	52
43	Tracing the origins of SARS-CoV-2: lessons learned from the past. Cell Research, 2021, 31, 1139-1141.	5.7	25
44	The Benefits of Breastfeeding Still Outweigh the Risks of COVID-19 Transmission. Frontiers in Medicine, 2021, 8, 703950.	1.2	5
45	Isolation and characterization of a podovirus infecting the opportunist pathogen Vibrio alginolyticus and Vibrio parahaemolyticus. Virus Research, 2021, 302, 198481.	1.1	17
46	Rapid and highly sensitive one-tube colorimetric RT-LAMP assay for visual detection of SARS-CoV-2 RNA. Biosensors and Bioelectronics, 2021, 187, 113330.	5.3	44
47	The origins of viruses: discovery takes time, international resources, and cooperation. Lancet, The, 2021, 398, 1401-1402.	6.3	12
48	A theoretical simulation of SARS-CoV-2 pooled testing: Pooled sample collection outperforms pooled RNA extraction. Clinica Chimica Acta, 2021, 521, 155-157.	0.5	0
49	Characteristics and genome analysis of a novel bacteriophage IME1323_01, the first temperate bacteriophage induced from Staphylococcus caprae. Virus Research, 2021, 305, 198569.	1.1	6
50	Emerging Aspects of Jumbo Bacteriophages. Infection and Drug Resistance, 2021, Volume 14, 5041-5055.	1.1	25
51	Perspective on taxonomic classification of uncultivated viruses. Current Opinion in Virology, 2021, 51, 207-215.	2.6	31
52	Multicenter assessment of shotgun metagenomics for pathogen detection. EBioMedicine, 2021, 74, 103649.	2.7	19
53	First Characterization of a Hafnia Phage Reveals Extraordinarily Large Burst Size and Unusual Plaque Polymorphism. Frontiers in Microbiology, 2021, 12, 754331.	1.5	14
54	Isolation and Characterization of a Novel Bacteriophage Infecting Carbapenem-Resistant Klebsiella pneumoniae. Current Microbiology, 2020, 77, 722-729.	1.0	14

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55	A novel freshwater cyanophage vB_MeS-Me-ZS1 infecting bloom-forming cyanobacterium <i>Microcystis elabens</i> . <i>Molecular Biology Reports</i> , 2020, 47, 7979-7989.	1.0	18
56	The effect of whey protein on viral infection and replication of SARS-CoV-2 and pangolin coronavirus in vitro. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 275.	7.1	40
57	Biological characteristics and genome analysis of a novel phage vB_KpnP_IME279 infecting <i>Klebsiella pneumoniae</i> . <i>Folia Microbiologica</i> , 2020, 65, 925-936.	1.1	7
58	A large-scale fatal outbreak of <i>Pasteurella multocida</i> among wild rodents in southwestern China. <i>Journal of Biosafety and Biosecurity</i> , 2020, 2, 91-98.	1.4	2
59	Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. <i>Nature</i> , 2020, 583, 282-285.	13.7	1,453
60	Phage-delivered sensitisation with subsequent antibiotic treatment reveals sustained effect against antimicrobial resistant bacteria. <i>Theranostics</i> , 2020, 10, 6310-6321.	4.6	16
61	Structural and functional insights into a novel two-component endolysin encoded by a single gene in <i>Enterococcus faecalis</i> phage. <i>PLoS Pathogens</i> , 2020, 16, e1008394.	2.1	24
62	New perspectives on the treatment of mycobacterial infections using antibiotics. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4197-4209.	1.7	8
63	Virome diversity analysis reveals novel enteroviruses and a human picobirnavirus in stool samples from African green monkeys with diarrhea. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104279.	1.0	4
64	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020, 165, 1253-1260.	0.9	144
65	Specific Integration of Temperate Phage Decreases the Pathogenicity of Host Bacteria. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 14.	1.8	25
66	Characteristics and complete genome sequence of the virulent <i>Vibrio alginolyticus</i> phage VAP7, isolated in Hainan, China. <i>Archives of Virology</i> , 2020, 165, 947-953.	0.9	7
67	Mining of epitopes on spike protein of SARS-CoV-2 from COVID-19 patients. <i>Cell Research</i> , 2020, 30, 702-704.	5.7	100
68	Clinical Multi-Omics Study on the Gut Microbiota in Critically Ill Patients After Cardiovascular Surgery Combined With Cardiopulmonary Bypass With or Without Sepsis (MUL-GM-CSCP Study): A Prospective Study Protocol. <i>Frontiers in Medicine</i> , 2020, 7, 269.	1.2	8
69	Structural Genomics of <i>repA</i> , <i>repB1</i> -Carrying IncFIB Family pA1705- <i>qnrS</i> , P911021- <i>tetA</i> , and P1642- <i>tetA</i> , Multidrug-Resistant Plasmids from <i>Klebsiella pneumoniae</i> . <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1889-1903.	1.1	12
70	High prevalence and viremia of human pegivirus 2 in the HIV-infected population in Honghe Prefecture, Yunnan Province. <i>Archives of Virology</i> , 2020, 165, 619-626.	0.9	2
71	Complete genome sequence of a novel bovine hepacivirus from Yunnan, China. <i>Archives of Virology</i> , 2020, 165, 1489-1494.	0.9	7
72	Classification of the Gut Microbiota of Patients in Intensive Care Units During Development of Sepsis and Septic Shock. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 696-707.	3.0	29

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73	Sequence Analysis of a Jumbo Bacteriophage, <i>Xoo-sp14</i> , That Infects <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	11
74	Genomic characterization of Inc _{pA1763-KPC} : IncFII _{K7} type plasmids p13294-KPC and pA1966-NR from <i>Klebsiella pneumoniae</i> . <i>Future Microbiology</i> , 2020, 15, 713-721.	1.0	0
75	Title is missing!. , 2020, 16, e1008394.		0
76	Title is missing!. , 2020, 16, e1008394.		0
77	Title is missing!. , 2020, 16, e1008394.		0
78	Title is missing!. , 2020, 16, e1008394.		0
79	Title is missing!. , 2020, 16, e1008394.		0
80	Title is missing!. , 2020, 16, e1008394.		0
81	Identification and characterization of <i>Clostridium botulinum</i> strains associated with an infant botulism case in China. <i>Anaerobe</i> , 2019, 55, 1-7.	1.0	10
82	Genomic and biological characterization of the <i>Vibrio alginolyticus</i> -infecting <i>Podoviridae</i> bacteriophage, vB_ValP_IME271. <i>Virus Genes</i> , 2019, 55, 218-226.	0.7	25
83	Characterization of a NDM-1- Encoding Plasmid pHFK418-NDM From a Clinical <i>Proteus mirabilis</i> Isolate Harboring Two Novel Transposons, Tn6624 and Tn6625. <i>Frontiers in Microbiology</i> , 2019, 10, 2030.	1.5	14
84	Complete genome analysis of a novel temperate bacteriophage induced from <i>Corynebacterium striatum</i> . <i>Archives of Virology</i> , 2019, 164, 2877-2880.	0.9	7
85	Genome sequence of <i>Bacillus anthracis</i> typing phage AP631. <i>Archives of Virology</i> , 2019, 164, 917-921.	0.9	3
86	Complete genome sequence of a novel negevirus isolated from <i>Culex tritaeniorhynchus</i> in China. <i>Archives of Virology</i> , 2019, 164, 907-911.	0.9	9
87	Characterization and complete genome sequence analysis of phage GP4, a novel lytic Bcep22-like podovirus. <i>Archives of Virology</i> , 2019, 164, 2339-2343.	0.9	28
88	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. <i>Frontiers in Microbiology</i> , 2019, 10, 1001.	1.5	12
89	Screening of Polyvalent Phage-Resistant <i>Escherichia coli</i> Strains Based on Phage Receptor Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 850.	1.5	33
90	Characterization and genome analysis of a novel bacteriophage vB_SpuP_Spp16 that infects <i>Salmonella enterica</i> serovar pullorum. <i>Virus Genes</i> , 2019, 55, 532-540.	0.7	22

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91	The Fast Track for Microbiome Research. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 1-3.	3.0	2
92	Lassomycin and lariatins as suitable antibiotics for combating mycobacterial infections: current state of biosynthesis and perspectives for production. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3931-3940.	1.7	12
93	Intra-host Ebola viral adaptation during human infection. <i>Biosafety and Health</i> , 2019, 1, 14-24.	1.2	9
94	The Characteristics and Genome Analysis of vB_AviM_AVP, the First Phage Infecting <i>Aerococcus viridans</i> . <i>Viruses</i> , 2019, 11, 104.	1.5	24
95	Identification of <i>Histoplasma</i> causing an unexplained disease cluster in Matthews Ridge, Guyana. <i>Biosafety and Health</i> , 2019, 1, 150-154.	1.2	6
96	Genome sequencing and analysis of <i>Alcaligenes faecalis</i> subsp. <i>phenolicus</i> MB207. <i>Scientific Reports</i> , 2018, 8, 3616.	1.6	35
97	Sequencing of pT5282-CTXM, p13190-KPC and p30860-NR, and comparative genomics analysis of IncX8 plasmids. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 210-217.	1.1	13
98	Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. <i>Nature</i> , 2018, 556, 255-258.	13.7	565
99	Contact reductions from live poultry market closures limit the epidemic of human infections with H7N9 influenza. <i>Journal of Infection</i> , 2018, 76, 295-304.	1.7	9
100	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	0.9	172
101	Coexistence of two novel resistance plasmids, <i>bla</i> _{KPC-2} -carrying p14057A and <i>tetA</i> (A)-carrying p14057B, in <i>Pseudomonas aeruginosa</i> . <i>Virulence</i> , 2018, 9, 306-311.	1.8	18
102	Analyzing Genome Termini of Bacteriophage Through High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1681, 139-163.	0.4	15
103	Co-occurrence of 3 different resistance plasmids in a multi-drug resistant <i>Cronobacter sakazakii</i> isolate causing neonatal infections. <i>Virulence</i> , 2018, 9, 110-120.	1.8	36
104	Comparative genomics of five different resistance plasmids coexisting in a clinical multi-drug resistant <i>Citrobacter freundii</i> isolate. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1447-1460.	1.1	15
105	Comparative analysis of <i>bla</i> _{KPC-2} - and <i>rmtB</i> -carrying IncFII-family pKPC-LK30/pHN7A8 hybrid plasmids from <i>Klebsiella pneumoniae</i> CG258 strains disseminated among multiple Chinese hospitals. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1783-1793.	1.1	20
106	Characterization and genome analysis of novel phage vB_EfaP_IME195 infecting <i>Enterococcus faecalis</i> . <i>Virus Genes</i> , 2018, 54, 804-811.	0.7	28
107	Novel phage-host interactions and evolution as revealed by a cyanomyovirus isolated from an estuarine environment. <i>Environmental Microbiology</i> , 2018, 20, 2974-2989.	1.8	30
108	Discovery of two novel totiviruses from <i>Culex tritaeniorhynchus</i> classifiable in a distinct clade with arthropod-infecting viruses within the family Totiviridae. <i>Archives of Virology</i> , 2018, 163, 2899-2902.	0.9	12

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109	Dissemination of KPC-2-Encoding IncX6 Plasmids Among Multiple Enterobacteriaceae Species in a Single Chinese Hospital. <i>Frontiers in Microbiology</i> , 2018, 9, 478.	1.5	26
110	Comparison of Bacterial Diversity Between Two Traditional Starters and the Round-Koji-Maker Starter for Traditional Cantonese Chi-Flavor Liquor Brewing. <i>Frontiers in Microbiology</i> , 2018, 9, 1053.	1.5	33
111	Three <i>Salmonella enterica</i> serovar Enteritidis bacteriophages from the <i>Siphoviridae</i> family are promising candidates for phage therapy. <i>Canadian Journal of Microbiology</i> , 2018, 64, 865-875.	0.8	30
112	vB_EcoS_IME347 a novel T1-like <i>Escherichia coli</i> bacteriophage. <i>Journal of Basic Microbiology</i> , 2018, 58, 968-976.	1.8	4
113	Sequencing and Genomic Diversity Analysis of IncHI5 Plasmids. <i>Frontiers in Microbiology</i> , 2018, 9, 3318.	1.5	30
114	Isolation and characterization of a novel phage Xoo-sp2 that infects <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Journal of General Virology</i> , 2018, 99, 1453-1462.	1.3	35
115	Novel sub-lineages, recombinants and reassortants of severe fever with thrombocytopenia syndrome virus. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 385-390.	1.1	18
116	A novel mosquito-borne reassortant orbivirus isolated from Xishuangbanna, China. <i>Virologica Sinica</i> , 2017, 32, 159-162.	1.2	11
117	First complete genome sequence of a virulent bacteriophage infecting the opportunistic pathogen <i>Serratia rubidaea</i> . <i>Archives of Virology</i> , 2017, 162, 2021-2028.	0.9	8
118	Complete genome sequence of Menghai flavivirus, a novel insect-specific flavivirus from China. <i>Archives of Virology</i> , 2017, 162, 1435-1439.	0.9	10
119	Model-informed risk assessment for Zika virus outbreaks in the Asia-Pacific regions. <i>Journal of Infection</i> , 2017, 74, 484-491.	1.7	23
120	A Neonatal Murine Model of Coxsackievirus A6 Infection for Evaluation of Antiviral and Vaccine Efficacy. <i>Journal of Virology</i> , 2017, 91, .	1.5	32
121	Sequencing and comparative genomics analysis of the IncHI2 plasmids pT5282-mphA and p112298-cata and the IncHI5 plasmid pYNKP001-dfrA. <i>International Journal of Antimicrobial Agents</i> , 2017, 49, 709-718.	1.1	60
122	Protective Efficacies of Formaldehyde-Inactivated Whole-Virus Vaccine and Antivirals in a Murine Model of Coxsackievirus A10 Infection. <i>Journal of Virology</i> , 2017, 91, .	1.5	30
123	Features of Ebola Virus Disease at the Late Outbreak Stage in Sierra Leone: Clinical, Virological, Immunological, and Evolutionary Analyses. <i>Journal of Infectious Diseases</i> , 2017, 215, 1107-1110.	1.9	8
124	Complete Genome Sequence of a Novel Multidrug-Resistant <i>Klebsiella pneumoniae</i> Phage, vB_Kpn_IME260. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
125	Characterization and complete genome sequence analysis of a novel virulent <i>Siphoviridae</i> phage against <i>Staphylococcus aureus</i> isolated from bovine mastitis in Xinjiang, China. <i>Virus Genes</i> , 2017, 53, 464-476.	0.7	35
126	Complete genome sequence of Menghai rhabdovirus, a novel mosquito-borne rhabdovirus from China. <i>Archives of Virology</i> , 2017, 162, 1103-1106.	0.9	9

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127	Virus-like particle vaccine by intranasal vaccination elicits protective immunity against respiratory syncytial viral infection in mice. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 74-82.	0.9	22
128	Structural genomics of pNDM-BTR harboring <i>In191</i> and <i>Tn6360</i> , and other <i>bla</i> _{NDM} -carrying <i>IncN1</i> plasmids. <i>Future Microbiology</i> , 2017, 12, 1271-1281.	1.0	18
129	Complete sequences of two novel <i>bla</i> NDM-1-harboring plasmids from two <i>Acinetobacter towneri</i> isolates in China associated with the acquisition of <i>Tn125</i> . <i>Scientific Reports</i> , 2017, 7, 9405.	1.6	19
130	Genomic characterization of novel <i>IncFII</i> -type multidrug resistant plasmids p0716-KPC and p12181-KPC from <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2017, 7, 5830.	1.6	23
131	Complete genome sequence of a novel, virulent <i>Ahjdlikevirus</i> bacteriophage that infects <i>Enterococcus faecium</i> . <i>Archives of Virology</i> , 2017, 162, 3843-3847.	0.9	25
132	Characterization of <i>cis</i> -Acting RNA Elements of Zika Virus by Using a Self-Splicing Ribozyme-Dependent Infectious Clone. <i>Journal of Virology</i> , 2017, 91, .	1.5	46
133	Comparative genomics of type 1 <i>IncC</i> plasmids from China. <i>Future Microbiology</i> , 2017, 12, 1511-1522.	1.0	11
134	Intranasal infection and contact transmission of Zika virus in guinea pigs. <i>Nature Communications</i> , 2017, 8, 1648.	5.8	47
135	Investigation on Mosquito-Borne Viruses at Lancang River and Nu River Watersheds in Southwestern China. <i>Vector-Borne and Zoonotic Diseases</i> , 2017, 17, 804-812.	0.6	13
136	A Novel <i>Roseosiphophage</i> Isolated from the Oligotrophic South China Sea. <i>Viruses</i> , 2017, 9, 109.	1.5	41
137	Removal of Integrated Hepatitis B Virus DNA Using CRISPR-Cas9. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 91.	1.8	96
138	Sequencing of <i>bla</i> IMP-Carrying <i>IncN2</i> Plasmids, and Comparative Genomics of <i>IncN2</i> Plasmids Harboring Class 1 Integrons. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 102.	1.8	22
139	Dynamic Forecasting of Zika Epidemics Using Google Trends. <i>PLoS ONE</i> , 2017, 12, e0165085.	1.1	137
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