

# Yigang Tong

## List of Publications by Year in descending order

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218  
papers

7,571  
citations

87886

38  
h-index

76898

74  
g-index

225  
all docs

225  
docs citations

225  
times ranked

11578  
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.	3.0	6
2	A Novel Freshwater Cyanophage, Mae-Yong924-1, Reveals a New Family. <i>Viruses</i> , 2022, 14, 283.	3.3	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.	12.4	31
4	COVID-19 is a natural infectious disease. <i>Journal of Biosafety and Biosecurity</i> , 2022, 4, 38-42.	2.8	1
5	Importance of sample input volume for accurate SARS-CoV-2 qPCR testing. <i>Analytica Chimica Acta</i> , 2022, 1199, 339585.	5.4	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.	2.1	2
7	A Novel Wide-Range Freshwater Cyanophage MinS1 Infecting the Harmful Cyanobacterium <i>Microcystis aeruginosa</i> . <i>Viruses</i> , 2022, 14, 433.	3.3	9
8	Discovery and Characterization of Rubrinodin Provide Clues into the Evolution of Lasso Peptides. <i>Biochemistry</i> , 2022, 61, 595-607.	2.5	5
9	New Advances in Nanomaterial-Based Antiviral Strategies. <i>Small Structures</i> , 2022, 3, .	12.0	7
10	Characterization and Genomic Analysis of a Novel Drexleriophage IME268 with Lytic Activity Against <i>Klebsiella pneumoniae</i> . <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1533-1546.	2.7	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.	2.2	7
12	Biological characterization and genomic analysis of <i>Acinetobacter baumannii</i> phage BUCT628. <i>Archives of Virology</i> , 2022, 167, 1471-1474.	2.1	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.	2.2	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.	2.5	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.	4.1	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.	1.6	4
17	Human parainfluenza 3 and respiratory syncytial viruses detected in pangolins. <i>Emerging Microbes and Infections</i> , 2022, 11, 1657-1663.	6.5	3
18	Genomic Analysis of the <i>Serratia marcescens</i> Bacteriophage BUCT660. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	2

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19	Cepharanthine: A Promising Old Drug against SARS-CoV-2. <i>Advanced Biology</i> , 2022, 6, .	2.5	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.	3.0	3
21	Topology engineering via protein catenane construction to strengthen an industrial biocatalyst. <i>Journal of Biotechnology</i> , 2021, 325, 271-279.	3.8	11
22	Complete genome analysis of an active prophage of <i>Vibrio alginolyticus</i> . <i>Archives of Virology</i> , 2021, 166, 891-896.	2.1	7
23	Transcriptome analysis of cepharanthine against a SARS-CoV-2-related coronavirus. <i>Briefings in Bioinformatics</i> , 2021, 22, 1378-1386.	6.5	39
24	Bacteriophage “A Promising Alternative Measure for Bacterial Biofilm Control. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 205-217.	2.7	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.	1.6	20
26	All-in-one <i>in situ</i> colorimetric RT-LAMP assay for point-of-care testing of SARS-CoV-2. <i>Analyst</i> , The, 2021, 146, 6026-6034.	3.5	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.	2.1	13
28	A Novel Singleton Giant Phage Yong-XC31 Lytic to the <i>Pyropia</i> Pathogen <i>Vibrio mediterranei</i> . <i>Applied Sciences (Switzerland)</i> , 2021, 11, 1602.	2.5	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.	3.7	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, .	2.2	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.	3.5	9
32	The zoonotic and natural foci characteristics of SARS-CoV-2. <i>Journal of Biosafety and Biosecurity</i> , 2021, 3, 51-55.	2.8	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, .	6.5	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.	2.2	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.	4.5	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.	2.2	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.	2.1	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.	2.1	24
39	Metatranscriptomic analysis identifies different viral-like sequences in two neotropical Mansoniini mosquito species. Virus Research, 2021, 301, 198455.	2.2	4
40	Biochemical and genomic characterization of a novel bacteriophage BUCT555 lysing Stenotrophomonas maltophilia. Virus Research, 2021, 301, 198465.	2.2	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.	3.9	28
42	Ultrafast multiplexed detection of SARS-CoV-2 RNA using a rapid droplet digital PCR system. Biosensors and Bioelectronics, 2021, 188, 113282.	10.1	52
43	Tracing the origins of SARS-CoV-2: lessons learned from the past. Cell Research, 2021, 31, 1139-1141.	12.0	25
44	The Benefits of Breastfeeding Still Outweigh the Risks of COVID-19 Transmission. Frontiers in Medicine, 2021, 8, 703950.	2.6	5
45	Isolation and characterization of a podovirus infecting the opportunist pathogen Vibrio alginolyticus and Vibrio parahaemolyticus. Virus Research, 2021, 302, 198481.	2.2	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.	10.1	44
47	The origins of viruses: discovery takes time, international resources, and cooperation. Lancet, The, 2021, 398, 1401-1402.	13.7	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.	1.1	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.	2.2	6
50	Emerging Aspects of Jumbo Bacteriophages. Infection and Drug Resistance, 2021, Volume 14, 5041-5055.	2.7	25
51	Perspective on taxonomic classification of uncultivated viruses. Current Opinion in Virology, 2021, 51, 207-215.	5.4	31
52	Multicenter assessment of shotgun metagenomics for pathogen detection. EBioMedicine, 2021, 74, 103649.	6.1	19
53	First Characterization of a Hafnia Phage Reveals Extraordinarily Large Burst Size and Unusual Plaque Polymorphism. Frontiers in Microbiology, 2021, 12, 754331.	3.5	14
54	Isolation and Characterization of a Novel Bacteriophage Infecting Carbapenem-Resistant Klebsiella pneumoniae. Current Microbiology, 2020, 77, 722-729.	2.2	14

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55	A novel freshwater cyanophage vB_MelS-Me-ZS1 infecting bloom-forming cyanobacterium <i>Microcystis elabens</i> . <i>Molecular Biology Reports</i> , 2020, 47, 7979-7989.	2.3	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.	17.1	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.	2.3	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.	2.8	2
59	Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. <i>Nature</i> , 2020, 583, 282-285.	27.8	1,453
60	Phage-delivered sensitisation with subsequent antibiotic treatment reveals sustained effect against antimicrobial resistant bacteria. <i>Theranostics</i> , 2020, 10, 6310-6321.	10.0	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.	4.7	24
62	New perspectives on the treatment of mycobacterial infections using antibiotics. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4197-4209.	3.6	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.	2.3	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.	2.1	144
65	Specific Integration of Temperate Phage Decreases the Pathogenicity of Host Bacteria. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 14.	3.9	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.	2.1	7
67	Mining of epitopes on spike protein of SARS-CoV-2 from COVID-19 patients. <i>Cell Research</i> , 2020, 30, 702-704.	12.0	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.	2.6	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.	2.7	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.	2.1	2
71	Complete genome sequence of a novel bovine hepacivirus from Yunnan, China. <i>Archives of Virology</i> , 2020, 165, 1489-1494.	2.1	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.	6.9	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> . Microbiology Resource Announcements, 2020, 9, .	0.6	11
74	Genomic characterization of Inc <sub>pA1763-KPC</sub> : IncFII <sub>K7</sub> type plasmids p13294-KPC and pA1966-NR from <i>Klebsiella pneumoniae</i> . Future Microbiology, 2020, 15, 713-721.	2.0	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. Anaerobe, 2019, 55, 1-7.	2.1	10
82	Genomic and biological characterization of the <i>Vibrio alginolyticus</i> -infecting <i>Podoviridae</i> bacteriophage, vB_ValP_IME271. Virus Genes, 2019, 55, 218-226.	1.6	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. Frontiers in Microbiology, 2019, 10, 2030.	3.5	14
84	Complete genome analysis of a novel temperate bacteriophage induced from <i>Corynebacterium striatum</i> . Archives of Virology, 2019, 164, 2877-2880.	2.1	7
85	Genome sequence of <i>Bacillus anthracis</i> typing phage AP631. Archives of Virology, 2019, 164, 917-921.	2.1	3
86	Complete genome sequence of a novel negevirus isolated from <i>Culex tritaeniorhynchus</i> in China. Archives of Virology, 2019, 164, 907-911.	2.1	9
87	Characterization and complete genome sequence analysis of phage GP4, a novel lytic Bcep22-like podovirus. Archives of Virology, 2019, 164, 2339-2343.	2.1	28
88	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. Frontiers in Microbiology, 2019, 10, 1001.	3.5	12
89	Screening of Polyvalent Phage-Resistant <i>Escherichia coli</i> Strains Based on Phage Receptor Analysis. Frontiers in Microbiology, 2019, 10, 850.	3.5	33
90	Characterization and genome analysis of a novel bacteriophage vB_SpuP_Spp16 that infects <i>Salmonella enterica</i> serovar pullorum. Virus Genes, 2019, 55, 532-540.	1.6	22

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91	The Fast Track for Microbiome Research. Genomics, Proteomics and Bioinformatics, 2019, 17, 1-3.	6.9	2
92	Lassomycin and lariat in lasso peptides as suitable antibiotics for combating mycobacterial infections: current state of biosynthesis and perspectives for production. Applied Microbiology and Biotechnology, 2019, 103, 3931-3940.	3.6	12
93	Intra-host Ebola viral adaption during human infection. Biosafety and Health, 2019, 1, 14-24.	2.7	9
94	The Characteristics and Genome Analysis of vB_AviM_AVP, the First Phage Infecting Aerococcus viridans. Viruses, 2019, 11, 104.	3.3	24
95	Identification of Histoplasma causing an unexplained disease cluster in Matthews Ridge, Guyana. Biosafety and Health, 2019, 1, 150-154.	2.7	6
96	Genome sequencing and analysis of Alcaligenes faecalis subsp. phenolicus MB207. Scientific Reports, 2018, 8, 3616.	3.3	35
97	Sequencing of pT5282-CTXM, p13190-KPC and p30860-NR, and comparative genomics analysis of IncX8 plasmids. International Journal of Antimicrobial Agents, 2018, 52, 210-217.	2.5	13
98	Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. Nature, 2018, 556, 255-258.	27.8	565
99	Contact reductions from live poultry market closures limit the epidemic of human infections with H7N9 influenza. Journal of Infection, 2018, 76, 295-304.	3.3	9
100	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. Archives of Virology, 2018, 163, 1125-1129.	2.1	172
101	Coexistence of two novel resistance plasmids, <i>bla</i> <sub>KPC-2</sub> -carrying p14057A and <i>tetA</i> (A)-carrying p14057B, in <i>Pseudomonas aeruginosa</i> . Virulence, 2018, 9, 306-311.	4.4	18
102	Analyzing Genome Termini of Bacteriophage Through High-Throughput Sequencing. Methods in Molecular Biology, 2018, 1681, 139-163.	0.9	15
103	Co-occurrence of 3 different resistance plasmids in a multi-drug resistant Cronobacter sakazakii isolate causing neonatal infections. Virulence, 2018, 9, 110-120.	4.4	36
104	Comparative genomics of five different resistance plasmids coexisting in a clinical multi-drug resistant <i>Citrobacter freundii</i> isolate. Infection and Drug Resistance, 2018, Volume 11, 1447-1460.	2.7	15
105	Comparative analysis of <i>bla</i> <sub>KPC-2</sub> - and <i>rmtB</i> -carrying IncFII-family pKPC-LK30/pHN7A8 hybrid plasmids from <i>Klebsiella pneumoniae</i> CG258 strains disseminated among multiple Chinese hospitals. Infection and Drug Resistance, 2018, Volume 11, 1783-1793.	2.7	20
106	Characterization and genome analysis of novel phage vB_EfaP_IME195 infecting Enterococcus faecalis. Virus Genes, 2018, 54, 804-811.	1.6	28
107	Novel phage-host interactions and evolution as revealed by a cyanomyovirus isolated from an estuarine environment. Environmental Microbiology, 2018, 20, 2974-2989.	3.8	30
108	Discovery of two novel totiviruses from Culex tritaeniorhynchus classifiable in a distinct clade with arthropod-infecting viruses within the family Totiviridae. Archives of Virology, 2018, 163, 2899-2902.	2.1	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.	3.5	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.	3.5	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.	1.7	30
112	vB_EcoS_IME347 a novel T1-like <i>Escherichia coli</i> bacteriophage. <i>Journal of Basic Microbiology</i> , 2018, 58, 968-976.	3.3	4
113	Sequencing and Genomic Diversity Analysis of IncHI5 Plasmids. <i>Frontiers in Microbiology</i> , 2018, 9, 3318.	3.5	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.	2.9	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.	2.7	18
116	A novel mosquito-borne reassortant orbivirus isolated from Xishuangbanna, China. <i>Virologica Sinica</i> , 2017, 32, 159-162.	3.0	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.	2.1	8
118	Complete genome sequence of Menghai flavivirus, a novel insect-specific flavivirus from China. <i>Archives of Virology</i> , 2017, 162, 1435-1439.	2.1	10
119	Model-informed risk assessment for Zika virus outbreaks in the Asia-Pacific regions. <i>Journal of Infection</i> , 2017, 74, 484-491.	3.3	23
120	A Neonatal Murine Model of Coxsackievirus A6 Infection for Evaluation of Antiviral and Vaccine Efficacy. <i>Journal of Virology</i> , 2017, 91, .	3.4	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.	2.5	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, .	3.4	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.	4.0	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.	1.6	35
126	Complete genome sequence of Menghai rhabdovirus, a novel mosquito-borne rhabdovirus from China. <i>Archives of Virology</i> , 2017, 162, 1103-1106.	2.1	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.	2.0	22
128	Structural genomics of pNDM-BTR harboring <i>In191</i> and <i>Tn6360</i> , and other <i>bla</i> <sub>NDM</sub> -carrying <i>IncN1</i> plasmids. <i>Future Microbiology</i> , 2017, 12, 1271-1281.	2.0	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.	3.3	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.	3.3	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.	2.1	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, .	3.4	46
133	Comparative genomics of type 1 <i>IncC</i> plasmids from China. <i>Future Microbiology</i> , 2017, 12, 1511-1522.	2.0	11
134	Intranasal infection and contact transmission of Zika virus in guinea pigs. <i>Nature Communications</i> , 2017, 8, 1648.	12.8	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.	1.5	13
136	A Novel <i>Roseosiphophage</i> Isolated from the Oligotrophic South China Sea. <i>Viruses</i> , 2017, 9, 109.	3.3	41
137	Removal of Integrated Hepatitis B Virus DNA Using CRISPR-Cas9. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 91.	3.9	96
138	Sequencing of <i>bla</i> IMP-Carrying <i>IncN2</i> Plasmids, and Comparative Genomics of <i>IncN2</i> Plasmids Harboring Class 1 Integrins. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 102.	3.9	22
139	Dynamic Forecasting of Zika Epidemics Using Google Trends. <i>PLoS ONE</i> , 2017, 12, e0165085.	2.5	137
140	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
141	An Effective Molecular Target Site in Hepatitis B Virus S Gene for Cas9 Cleavage and Mutational Inactivation. <i>International Journal of Biological Sciences</i> , 2016, 12, 1104-1113.	6.4	41
142	Increasing genetic diversity of Zika virus in the Latin American outbreak. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-3.	6.5	28
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