

Biao Kan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5334884/publications.pdf>

Version: 2024-02-01

166
papers

4,970
citations

147566

31
h-index

123241

61
g-index

178
all docs

178
docs citations

178
times ranked

8063
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of an inactivated vaccine candidate for SARS-CoV-2. <i>Science</i> , 2020, 369, 77-81.	6.0	1,180
2	Molecular Evolution Analysis and Geographic Investigation of Severe Acute Respiratory Syndrome Coronavirus-Like Virus in Palm Civets at an Animal Market and on Farms. <i>Journal of Virology</i> , 2005, 79, 11892-11900.	1.5	291
3	<i>Streptococcus suis</i> Sequence Type 7 Outbreak, Sichuan, China. <i>Emerging Infectious Diseases</i> , 2006, 12, 1203-1208.	2.0	150
4	Bile salt-induced intermolecular disulfide bond formation activates <i>Vibrio cholerae</i> virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2348-2353.	3.3	147
5	Safety and Immunogenicity from a Phase I Trial of Inactivated Severe Acute Respiratory Syndrome Coronavirus Vaccine. <i>Antiviral Therapy</i> , 2007, 12, 1107-1114.	0.6	144
6	Construction and Evaluation of a Safe, Live, Oral <i>Vibrio cholerae</i> Vaccine Candidate, IEM108. <i>Infection and Immunity</i> , 2003, 71, 5498-5504.	1.0	92
7	Laboratory-Based Surveillance of Nontyphoidal <i>Salmonella</i> Infections in China. <i>Foodborne Pathogens and Disease</i> , 2011, 8, 921-927.	0.8	88
8	Identification and characterization of phosphodiesterases that specifically degrade 3'-cyclic GMP-AMP. <i>Cell Research</i> , 2015, 25, 539-550.	5.7	83
9	Epidemiologic and genomic insights on mcr-1-harboring <i>Salmonella</i> from diarrhoeal outpatients in Shanghai, China, 2006-2016. <i>EBioMedicine</i> , 2019, 42, 133-144.	2.7	80
10	The Role of China in the Global Spread of the Current Cholera Pandemic. <i>PLoS Genetics</i> , 2015, 11, e1005072.	1.5	73
11	<i>Streptococcus suis</i> sequence type 7 outbreak, Sichuan, China. <i>Emerging Infectious Diseases</i> , 2006, 12, 1203-8.	2.0	73
12	Genetic Diversity of Toxigenic and Nontoxigenic <i>Vibrio cholerae</i> Serogroups O1 and O139 Revealed by Array-Based Comparative Genomic Hybridization. <i>Journal of Bacteriology</i> , 2007, 189, 4837-4849.	1.0	66
13	Taxonomy, virulence genes and antimicrobial resistance of <i>Aeromonas</i> isolated from extra-intestinal and intestinal infections. <i>BMC Infectious Diseases</i> , 2019, 19, 158.	1.3	66
14	MCR-1.6, a New MCR Variant Carried by an IncP Plasmid in a Colistin-Resistant <i>Salmonella enterica</i> Serovar Typhimurium Isolate from a Healthy Individual. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	58
15	Enhanced Interaction of <i>Vibrio cholerae</i> Virulence Regulators TcpP and ToxR under Oxygen-Limiting Conditions. <i>Infection and Immunity</i> , 2014, 82, 1676-1682.	1.0	51
16	Functional RelBE-Family Toxin-Antitoxin Pairs Affect Biofilm Maturation and Intestine Colonization in <i>Vibrio cholerae</i> . <i>PLoS ONE</i> , 2015, 10, e0135696.	1.1	49
17	Variations in SXT elements in epidemic <i>Vibrio cholerae</i> O1 El Tor strains in China. <i>Scientific Reports</i> , 2016, 6, 22733.	1.6	49
18	Virulence regulator AphB enhances toxR transcription in <i>Vibrio cholerae</i> . <i>BMC Microbiology</i> , 2010, 10, 3.	1.3	46

#	ARTICLE	IF	CITATIONS
19	Etiology of acute diarrhea due to enteropathogenic bacteria in Beijing, China. <i>Journal of Infection</i> , 2012, 65, 214-222.	1.7	46
20	Expansion of <i>Salmonella enterica</i> Serovar Typhimurium ST34 Clone Carrying Multiple Resistance Determinants in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 4599-4601.	1.4	46
21	Direct regulation of the natural competence regulator gene <i>tfoX</i> by cyclic AMP (cAMP) and cAMP receptor protein (CRP) in <i>Vibrios</i> . <i>Scientific Reports</i> , 2015, 5, 14921.	1.6	41
22	The prevalence of functional quorum-sensing systems in recently emerged <i>Vibrio cholerae</i> toxigenic strains. <i>Environmental Microbiology Reports</i> , 2011, 3, 218-222.	1.0	40
23	Dual Zinc Transporter Systems in <i>Vibrio cholerae</i> Promote Competitive Advantages over Gut Microbiome. <i>Infection and Immunity</i> , 2015, 83, 3902-3908.	1.0	40
24	Multiple Antibiotic Resistance of <i>Vibrio cholerae</i> Serogroup O139 in China from 1993 to 2009. <i>PLoS ONE</i> , 2012, 7, e38633.	1.1	38
25	Distribution, virulence-associated genes and antimicrobial resistance of <i>Aeromonas</i> isolates from diarrheal patients and water, China. <i>Journal of Infection</i> , 2015, 70, 600-608.	1.7	38
26	Functional Characterization and Conditional Regulation of the Type VI Secretion System in <i>Vibrio fluvialis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 528.	1.5	37
27	The emergence and outbreak of multidrug-resistant typhoid fever in China. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-6.	3.0	36
28	Differential Thiol-Based Switches Jump-Start <i>Vibrio cholerae</i> Pathogenesis. <i>Cell Reports</i> , 2016, 14, 347-354.	2.9	36
29	Growth Phase, Oxygen, Temperature, and Starvation Affect the Development of Viable but Non-culturable State of <i>Vibrio cholerae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 404.	1.5	35
30	The virulence phenotypes and molecular epidemiological characteristics of <i>Vibrio fluvialis</i> in China. <i>Gut Pathogens</i> , 2013, 5, 6.	1.6	34
31	Incl1 Plasmids Carrying Various <i>bla</i> _{CTX-M} Genes Contribute to Ceftriaxone Resistance in <i>Salmonella enterica</i> Serovar Enteritidis in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 982-989.	1.4	33
32	Gut microbiota community characteristics and disease-related microorganism pattern in a population of healthy Chinese people. <i>Scientific Reports</i> , 2019, 9, 1594.	1.6	33
33	Distribution of Virulence-Associated Genes and Genetic Relationships in Non-O1/O139 <i>Vibrio cholerae</i> Aquatic Isolates from China. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4987-4992.	1.4	32
34	Hypermutation-induced in vivo oxidative stress resistance enhances <i>Vibrio cholerae</i> host adaptation. <i>PLoS Pathogens</i> , 2018, 14, e1007413.	2.1	32
35	Molecular Epidemiology of <i>Vibrio cholerae</i> O139 in China: Polymorphism of Ribotypes and CTX Elements. <i>Journal of Clinical Microbiology</i> , 2003, 41, 2306-2310.	1.8	31
36	Identification of tetrodotoxin-producing <i>Shewanella</i> spp. from feces of food poisoning patients and food samples. <i>Gut Pathogens</i> , 2013, 5, 15.	1.6	31

#	ARTICLE	IF	CITATIONS
37	The Development and Evaluation of a Loop-Mediated Isothermal Amplification Method for the Rapid Detection of <i>Salmonella enterica</i> serovar Typhi. <i>PLoS ONE</i> , 2015, 10, e0124507.	1.1	31
38	OxyR-activated expression of Dps is important for <i>Vibrio cholerae</i> oxidative stress resistance and pathogenesis. <i>PLoS ONE</i> , 2017, 12, e0171201.	1.1	31
39	Enumeration of viable non-culturable <i>Vibrio cholerae</i> using propidium monoazide combined with quantitative PCR. <i>Journal of Microbiological Methods</i> , 2015, 115, 147-152.	0.7	28
40	Thiolase-based switch mechanism of virulence regulator AphB modulates oxidative stress response in <i>Vibrio cholerae</i> . <i>Molecular Microbiology</i> , 2016, 102, 939-949.	1.2	27
41	Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of <i>Salmonella</i> Paratyphi A. <i>PLoS ONE</i> , 2012, 7, e45346.	1.1	26
42	Expression of Hemolysin Is Regulated Under the Collective Actions of HapR, Fur, and HlyU in <i>Vibrio cholerae</i> El Tor Serogroup O1. <i>Frontiers in Microbiology</i> , 2018, 9, 1310.	1.5	26
43	Genome Sequencing Reveals Unique Mutations in Characteristic Metabolic Pathways and the Transfer of Virulence Genes between <i>V. mimicus</i> and <i>V. cholerae</i> . <i>PLoS ONE</i> , 2011, 6, e21299.	1.1	25
44	<i>Vibrio cholerae</i> Represses Polysaccharide Synthesis To Promote Motility in Mucosa. <i>Infection and Immunity</i> , 2015, 83, 1114-1121.	1.0	25
45	Time Course Transcriptome Changes in <i>Shewanella</i> algae in Response to Salt Stress. <i>PLoS ONE</i> , 2014, 9, e96001.	1.1	24
46	Development and evaluation of an up-converting phosphor technology-based lateral flow assay for the rapid, simultaneous detection of <i>Vibrio cholerae</i> serogroups O1 and O139. <i>PLoS ONE</i> , 2017, 12, e0179937.	1.1	24
47	Quorum Sensing Regulatory Cascades Control <i>Vibrio fluvialis</i> Pathogenesis. <i>Journal of Bacteriology</i> , 2013, 195, 3583-3589.	1.0	23
48	A Two-Tube Multiplex Reverse Transcription PCR Assay for Simultaneous Detection of Viral and Bacterial Pathogens of Infectious Diarrhea. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	23
49	Antibiotic resistance of <i>Vibrio cholerae</i> O1 El Tor strains from the seventh pandemic in China, 1961-2010. <i>International Journal of Antimicrobial Agents</i> , 2012, 40, 361-364.	1.1	22
50	Sequence polymorphisms of rfbT among the <i>Vibrio cholerae</i> O1 strains in the Ogawa and Inaba serotype shifts. <i>BMC Microbiology</i> , 2013, 13, 173.	1.3	22
51	A critical role for hemolysin in <i>Vibrio fluvialis</i> -induced IL-1 β secretion mediated by the NLRP3 inflammasome in macrophages. <i>Frontiers in Microbiology</i> , 2015, 6, 510.	1.5	21
52	The Outer Membrane Protein OmpW Enhanced <i>V. cholerae</i> Growth in Hypersaline Conditions by Transporting Carnitine. <i>Frontiers in Microbiology</i> , 2017, 8, 2703.	1.5	21
53	<i>Shewanella carassii</i> sp. nov., isolated from surface swabs of crucian carp and faeces of a diarrhoea patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5284-5289.	0.8	21
54	Transcript changes in <i>Vibrio cholerae</i> in response to salt stress. <i>Gut Pathogens</i> , 2014, 6, 47.	1.6	20

#	ARTICLE	IF	CITATIONS
55	Identifying Environmental Risk Factors of Cholera in a Coastal Area with Geospatial Technologies. <i>International Journal of Environmental Research and Public Health</i> , 2015, 12, 354-370.	1.2	20
56	Rapid and Sensitive <i>Salmonella</i> Typhi Detection in Blood and Fecal Samples Using Reverse Transcription Loop-Mediated Isothermal Amplification. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 778-786.	0.8	20
57	Sequences of a co-existing SXT element, a chromosomal integron (CI) and an IncA/C plasmid and their roles in multidrug resistance in a <i>Vibrio cholerae</i> O1 El Tor strain. <i>International Journal of Antimicrobial Agents</i> , 2016, 48, 305-309.	1.1	20
58	O Antigen Is the Receptor of <i>Vibrio cholerae</i> Serogroup O1 El Tor Typing Phage VP4. <i>Journal of Bacteriology</i> , 2013, 195, 798-806.	1.0	19
59	Population structural analysis of O1 El Tor <i>Vibrio cholerae</i> isolated in China among the seventh cholera pandemic on the basis of multilocus sequence typing and virulence gene profiles. <i>Infection, Genetics and Evolution</i> , 2014, 22, 72-80.	1.0	19
60	Colistin Resistance-Mediated Bacterial Surface Modification Sensitizes Phage Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	19
61	CitAB Two-Component System-Regulated Citrate Utilization Contributes to <i>Vibrio cholerae</i> Competitiveness with the Gut Microbiota. <i>Infection and Immunity</i> , 2019, 87, .	1.0	19
62	Fur Represses <i>Vibrio cholerae</i> Biofilm Formation via Direct Regulation of <i>vieSAB</i> , <i>cdgD</i> , <i>vpsU</i> , and <i>vpsA-K</i> Transcription. <i>Frontiers in Microbiology</i> , 2020, 11, 587159.	1.5	19
63	A Novel Strategy for the Detection of SARS-CoV-2 Variants Based on Multiplex PCR-Mass Spectrometry Minisequencing Technology. <i>Microbiology Spectrum</i> , 2021, 9, e0126721.	1.2	19
64	A Molecular Surveillance Reveals the Prevalence of <i>Vibrio cholerae</i> O139 Isolates in China from 1993 to 2012. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1146-1152.	1.8	18
65	IncA/C plasmids harboured in serious multidrug-resistant <i>Vibrio cholerae</i> serogroup O139 strains in China. <i>International Journal of Antimicrobial Agents</i> , 2015, 45, 249-254.	1.1	18
66	The Transmission and Antibiotic Resistance Variation in a Multiple Drug Resistance Clade of <i>Vibrio cholerae</i> Circulating in Multiple Countries in Asia. <i>PLoS ONE</i> , 2016, 11, e0149742.	1.1	18
67	Integration Host Factor Modulates the Expression and Function of T6SS2 in <i>Vibrio fluvialis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 962.	1.5	18
68	<i>Proteus columbae</i> sp. nov., isolated from a pigeon in Ma TM anshan, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 552-557.	0.8	18
69	Distribution and Genetic Characteristics of SXT/R391 Integrative Conjugative Elements in <i>Shewanella</i> spp. From China. <i>Frontiers in Microbiology</i> , 2018, 9, 920.	1.5	17
70	<i>Proteus alimentorum</i> sp. nov., isolated from pork and lobster in Ma TM anshan city, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1390-1395.	0.8	17
71	A Large-Scale Community-Based Outbreak of Paratyphoid Fever Caused by Hospital-Derived Transmission in Southern China. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003859.	1.3	17
72	The Core Oligosaccharide and Thioredoxin of <i>Vibrio cholerae</i> Are Necessary for Binding and Propagation of Its Typing Phage VP3. <i>Journal of Bacteriology</i> , 2009, 191, 2622-2629.	1.0	16

#	ARTICLE	IF	CITATIONS
73	Novel ctxB variants of <i>Vibrio cholerae</i> O1 isolates, China. <i>Infection, Genetics and Evolution</i> , 2013, 20, 48-53.	1.0	16
74	Molecular characterization and antibiotic resistance of clinical <i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> in Beijing, China. <i>Infection, Genetics and Evolution</i> , 2016, 40, 119-125.	1.0	16
75	Niche modeling predictions of the potential distribution of <i>Marmota himalayana</i> , the host animal of plague in Yushu County of Qinghai. <i>BMC Public Health</i> , 2016, 16, 183.	1.2	16
76	The outer-membrane protein TolC of <i>Vibrio cholerae</i> serves as a second cell-surface receptor for the VP3 phage. <i>Journal of Biological Chemistry</i> , 2018, 293, 4000-4013.	1.6	16
77	Optimization of Pulsed-Field Gel Electrophoresis for <i>Legionella pneumophila</i> Subtyping. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1334-1340.	1.4	15
78	<i>Proteus faecis</i> sp. nov., and <i>Proteus cibi</i> sp. nov., two new species isolated from food and clinical samples in China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 852-858.	0.8	15
79	Outer Membrane Protein OmpW Is the Receptor for Typing Phage VP5 in the <i>Vibrio cholerae</i> O1 El Tor Biotype. <i>Journal of Virology</i> , 2014, 88, 7109-7111.	1.5	14
80	Evaluation of PCR Based Assays for the Improvement of Proportion Estimation of Bacterial and Viral Pathogens in Diarrheal Surveillance. <i>Frontiers in Microbiology</i> , 2016, 7, 386.	1.5	14
81	Identification of diarrheagenic <i>Escherichia coli</i> by a new multiplex PCR assay and capillary electrophoresis. <i>Molecular and Cellular Probes</i> , 2020, 49, 101477.	0.9	14
82	CqsA/LuxS-HapR Quorum sensing circuit modulates type VI secretion system Vi γ , T6SS2 in <i>Vibrio fluvialis</i> . <i>Emerging Microbes and Infections</i> , 2021, 10, 589-601.	3.0	14
83	Identification of Genetic Bases of <i>Vibrio fluvialis</i> Species-Specific Biochemical Pathways and Potential Virulence Factors by Comparative Genomic Analysis. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2029-2037.	1.4	13
84	The evaluation and application of multilocus variable number tandem repeat analysis (MLVA) for the molecular epidemiological study of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Enteritidis</i> infection. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2016, 15, 4.	1.7	13
85	Transforming bacterial disease surveillance and investigation using whole-genome sequence to probe the trace. <i>Frontiers of Medicine</i> , 2018, 12, 23-33.	1.5	13
86	Multilocus Sequence Analysis, a Rapid and Accurate Tool for Taxonomic Classification, Evolutionary Relationship Determination, and Population Biology Studies of the Genus <i>Shewanella</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13
87	Super Dominant Pathobiontic Bacteria in the Nasopharyngeal Microbiota Cause Secondary Bacterial Infection in COVID-19 Patients. <i>Microbiology Spectrum</i> , 2022, 10, e0195621.	1.2	13
88	The Seventh Pandemic <i>Vibrio cholerae</i> O1 El Tor Isolate in China Has Undergone Genetic Shifts. <i>Journal of Clinical Microbiology</i> , 2014, 52, 964-967.	1.8	12
89	Application of digital PCR and next generation sequencing in the etiology investigation of a foodborne disease outbreak caused by <i>Vibrio parahaemolyticus</i> . <i>Food Microbiology</i> , 2019, 84, 103233.	2.1	12
90	Comparison of BioFire FilmArray gastrointestinal panel versus Luminex xTAG Gastrointestinal Pathogen Panel (xTAG GPP) for diarrheal pathogen detection in China. <i>International Journal of Infectious Diseases</i> , 2020, 99, 414-420.	1.5	12

#	ARTICLE	IF	CITATIONS
91	Comparative Genomics and Transcriptomics Analyses Reveal a Unique Environmental Adaptability of <i>Vibrio fujianensis</i> . <i>Microorganisms</i> , 2020, 8, 555.	1.6	12
92	A multiplex PCR assay for the detection of five human pathogenic <i>Vibrio</i> species and <i>Plesiomonas</i> . <i>Molecular and Cellular Probes</i> , 2021, 55, 101689.	0.9	12
93	<i>Vibrio fujianensis</i> sp. nov., isolated from aquaculture water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1146-1152.	0.8	12
94	Resistance of the cholera vaccine candidate IEM108 against CTX ϕ infection. <i>Vaccine</i> , 2006, 24, 1749-1755.	1.7	11
95	The Construction and Evaluation of Reference Spectra for the Identification of Human Pathogenic Microorganisms by MALDI-TOF MS. <i>PLoS ONE</i> , 2014, 9, e106312.	1.1	11
96	Population analysis of clinical and environmental <i>Vibrio parahaemolyticus</i> isolated from eastern provinces in China by removing the recombinant SNPs in the MLST loci. <i>Infection, Genetics and Evolution</i> , 2016, 45, 303-310.	1.0	11
97	<i>Vibrio cholerae</i> Colonization of Soft-Shelled Turtles. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	11
98	The Core Proteome and Pan Proteome of <i>Salmonella</i> Paratyphi A Epidemic Strains. <i>PLoS ONE</i> , 2014, 9, e89197.	1.1	11
99	District prediction of cholera risk in China based on environmental factors. <i>Science Bulletin</i> , 2013, 58, 2798-2804.	1.7	10
100	The Resistance of <i>Vibrio cholerae</i> O1 El Tor Strains to the Typing Phage 919TP, a Member of K139 Phage Family. <i>Frontiers in Microbiology</i> , 2016, 7, 726.	1.5	10
101	Multilocus sequence typing-based analysis of <i>Moraxella catarrhalis</i> population structure reveals clonal spreading of drug-resistant strains isolated from childhood pneumonia. <i>Infection, Genetics and Evolution</i> , 2017, 56, 117-124.	1.0	10
102	Rare <i>Shewanella</i> spp. associated with pulmonary and bloodstream infections of cancer patients, China: a case report. <i>BMC Infectious Diseases</i> , 2018, 18, 454.	1.3	10
103	<i>Vibrio parahaemolyticus</i> <i>cqsA</i> controls production of quorum sensing signal molecule 3-hydroxyundecan-4-one and regulates colony morphology. <i>Journal of Microbiology</i> , 2019, 57, 1105-1114.	1.3	10
104	Evaluation of the BioFire FilmArray Gastrointestinal Panel and Real-Time Polymerase Chain Reaction Assays for the Detection of Major Diarrheagenic Pathogens by a Multicenter Diarrheal Disease Surveillance Program in China. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 788-798.	0.8	10
105	Quorum sensing regulation confronts the development of a viable but non-culturable state in <i>Vibrio cholerae</i> . <i>Environmental Microbiology</i> , 2020, 22, 4314-4322.	1.8	10
106	Structural variation of the superintegron in the toxigenic <i>Vibrio cholerae</i> O1 El Tor. <i>Biomedical and Environmental Sciences</i> , 2011, 24, 579-92.	0.2	10
107	<i>Anaplasma bovis</i>; Infection in Fever and Thrombocytopenia Patients â€” Anhui Province, China, 2021. <i>China CDC Weekly</i> , 2022, 4, 249-253.	1.0	10
108	Comparison of different electrophoretic parameters of Pulse-Field Gel Electrophoresis for <i>Vibrio cholerae</i> subtyping. <i>Journal of Microbiological Methods</i> , 2007, 71, 15-22.	0.7	9

#	ARTICLE	IF	CITATIONS
109	Regional Transmission of <i>Salmonella</i> Paratyphi A, China, 1998–2012. <i>Emerging Infectious Diseases</i> , 2017, 23, 833-836.	2.0	9
110	Expanding dynamics of the virulence-related gene variations in the toxigenic <i>Vibrio cholerae</i> serogroup O1. <i>BMC Genomics</i> , 2019, 20, 360.	1.2	9
111	Distribution and characteristics of SGI1/PGI2 genomic island from <i>Proteus</i> strains in China. <i>Infection, Genetics and Evolution</i> , 2019, 70, 123-130.	1.0	9
112	Genomic comparison of serogroups O159 and O170 with other <i>Vibrio cholerae</i> serogroups. <i>BMC Genomics</i> , 2019, 20, 241.	1.2	9
113	Direct Binding and Regulation by Fur and HapR of the Intermediate Regulator and Virulence Factor Genes Within the ToxR Virulence Regulon in <i>Vibrio cholerae</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 709.	1.5	9
114	Case Report: Identification of SARS-CoV-2 in Cerebrospinal Fluid by Ultrahigh-Depth Sequencing in a Patient With Coronavirus Disease 2019 and Neurological Dysfunction. <i>Frontiers in Medicine</i> , 2021, 8, 629828.	1.2	9
115	Filtration efficiency of face masks against aerosolized surrogate SARS-CoV-2 at different social distances. <i>Science Bulletin</i> , 2022, 67, 565-568.	4.3	9
116	High prevalence and diversity of pre-CTX ϕ alleles in the environmental <i>Vibrio cholerae</i> O1 and O139 strains in the Zhujiang River estuary. <i>Environmental Microbiology Reports</i> , 2014, 6, 251-258.	1.0	8
117	Comparison and Evaluation of the Molecular Typing Methods for Toxigenic <i>Vibrio cholerae</i> in Southwest China. <i>Frontiers in Microbiology</i> , 2018, 9, 905.	1.5	8
118	Development and evaluation of a sensitive recombinase aided amplification assay for rapid detection of <i>Vibrio parahaemolyticus</i> . <i>Journal of Microbiological Methods</i> , 2022, 193, 106404.	0.7	8
119	Proteins involved in difference of sorbitol fermentation rates of the toxigenic and nontoxigenic <i>Vibrio cholerae</i> El Tor strains revealed by comparative proteome analysis. <i>BMC Microbiology</i> , 2009, 9, 135.	1.3	7
120	The genome of VP3, a T7-like phage used for the typing of <i>Vibrio cholerae</i> . <i>Archives of Virology</i> , 2013, 158, 1865-1876.	0.9	7
121	The Hybrid Pre-CTX ϕ -RS1 Prophage Genome and Its Regulatory Function in Environmental <i>Vibrio cholerae</i> O1 Strains. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7171-7177.	1.4	7
122	Bacterial pathogen spectrum of acute diarrheal outpatients in an urbanized rural district in Southwest China. <i>International Journal of Infectious Diseases</i> , 2018, 70, 59-64.	1.5	7
123	Absolute Quantification of Viable but Nonculturable <i>Vibrio cholerae</i> Using Droplet Digital PCR with Oil-Enveloped Bacterial Cells. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
124	Optimization of pulse-field gel electrophoresis for <i>Bartonella</i> subtyping. <i>Journal of Microbiological Methods</i> , 2009, 76, 6-11.	0.7	6
125	Genotyping of <i>Salmonella</i> Typhi using 8-loci multi locus VNTR analysis. <i>Gut Pathogens</i> , 2016, 8, 14.	1.6	6
126	Comparison of the Multiple Platforms to Identify Various <i>Aeromonas</i> Species. <i>Frontiers in Microbiology</i> , 2020, 11, 625961.	1.5	6

#	ARTICLE	IF	CITATIONS
127	Rapid Identification of Plasmid Replicon Type and Coexisting Plasmid-Borne Antimicrobial Resistance Genes by S1-Pulsed-Field Gel Electrophoresis-Droplet Digital Polymerase Chain Reaction. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 298-305.	0.8	6
128	Characterization of blaKPC-2-Carrying Plasmid pR31-KPC from a <i>Pseudomonas aeruginosa</i> Strain Isolated in China. <i>Antibiotics</i> , 2021, 10, 1234.	1.5	6
129	Enumeration of Viable Non-Culturable <i>Vibrio cholerae</i> Using Droplet Digital PCR Combined With Propidium Monoazide Treatment. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 753078.	1.8	6
130	Trans-Regional and Cross-Host Spread of ϕ CR1-Carrying Plasmids Revealed by Complete Plasmid Sequences in 44 Countries, 1998–2020. <i>China CDC Weekly</i> , 2022, 4, 242-248.	1.0	6
131	Visual Identification and Serotyping of Toxigenic <i>Vibrio cholerae</i> Serogroups O1 and O139 With CARID. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 863435.	1.8	6
132	Whole Genome PCR Scanning Reveals the Syntenic Genome Structure of Toxigenic <i>Vibrio cholerae</i> Strains in the O1/O139 Population. <i>PLoS ONE</i> , 2011, 6, e24267.	1.1	5
133	A Three-Loci Variable Number of Tandem Repeats Analysis for Molecular Subtyping of <i>Vibrio cholerae</i> O1 and O139. <i>Foodborne Pathogens and Disease</i> , 2013, 10, 723-730.	0.8	5
134	Survival and proliferation of the lysogenic bacteriophage CTX ϕ in <i>Vibrio cholerae</i> . <i>Virologica Sinica</i> , 2015, 30, 19-25.	1.2	5
135	The complete genomic analysis of an imported <i>Vibrio cholerae</i> from Myanmar in southwest China. <i>Infection, Genetics and Evolution</i> , 2016, 44, 272-277.	1.0	5
136	Duplex Real-Time PCR Method for the Differentiation of <i>Cronobacter sakazakii</i> and <i>Cronobacter malonaticus</i> . <i>Journal of Food Protection</i> , 2017, 80, 50-56.	0.8	5
137	Characterization of environmental <i>Vibrio cholerae</i> serogroups O1 and O139 in the Pearl River Estuary, China. <i>Canadian Journal of Microbiology</i> , 2016, 62, 139-147.	0.8	4
138	Development of a Rapid and Fully Automated Multiplex Real-Time PCR Assay for Identification and Differentiation of <i>Vibrio cholerae</i> and <i>Vibrio parahaemolyticus</i> on the BD MAX Platform. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 639473.	1.8	4
139	Prevalence of 16S rRNA Methylation Enzyme Gene <i>armA</i> in <i>Salmonella</i> From Outpatients and Food. <i>Frontiers in Microbiology</i> , 2021, 12, 663210.	1.5	4
140	<i>Salmonella enterica</i> subsp. II serovar 4,5,12:a:- may cause gastroenteritis infections in humans. <i>Gut Microbes</i> , 2022, 14, .	4.3	4
141	Comparison of Amplified Fragment Length Polymorphism and Pulsed-Field Gel Electrophoresis for Subtyping of <i>Vibrio cholerae</i> Serogroups O1 and O139. <i>Foodborne Pathogens and Disease</i> , 2011, 8, 291-298.	0.8	3
142	Whole-genome sequencing of rough <i>Brucella melitensis</i> in China provides insights into its genetic features. <i>Emerging Microbes and Infections</i> , 2020, 9, 2147-2156.	3.0	3
143	A novel pre-CTX prophage in the <i>Vibrio cholerae</i> serogroup O139 strain. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104238.	1.0	3
144	Incidence, aetiology, and environmental risk factors of community-acquired pneumonia requiring hospitalization in China: a 3-year, prospective, age-stratified, multi-centre case-control study. <i>Open Forum Infectious Diseases</i> , 0, , .	0.4	3

#	ARTICLE	IF	CITATIONS
145	High Carriage Rate of the Multiple Resistant Plasmids Harboring Quinolone Resistance Genes in <i>Enterobacter</i> spp. Isolated from Healthy Individuals. <i>Antibiotics</i> , 2022, 11, 15.	1.5	3
146	Inhibitor screening using microarray identifies the high capacity of neutralizing antibodies to Spike variants in SARS-CoV-2 infection and vaccination. <i>Theranostics</i> , 2022, 12, 2519-2534.	4.6	3
147	Investigation of an imported cholera case in China with whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104362.	1.0	2
148	Transcriptional regulation of the mannitol phosphotransferase system operon by the ferric uptake regulator (Fur) in <i>Vibrio cholerae</i> El Tor serogroup O1. <i>Research in Microbiology</i> , 2021, 172, 103848.	1.0	2
149	Correlation between prevalence of selected enteropathogens and diarrhea in children: a case-control study in China. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab445.	0.4	2
150	Cholera Caused by a New Clone of Serogroup O1 & Vibrio cholerae &” Beijing Municipality, China, June 2021. <i>China CDC Weekly</i> , 2022, 4, 31-32.	1.0	2
151	Co-Localization of Sampling and Sequencing for Zoonotic Pathogen Identification in the Field Monitoring Using Mobile Laboratories. <i>China CDC Weekly</i> , 2022, 4, 259-263.	1.0	2
152	High Carriage of Extended-Spectrum, Beta Lactamase-Producing, and Colistin-Resistant Enterobacteriaceae in Tibetan Outpatients with Diarrhea. <i>Antibiotics</i> , 2022, 11, 508.	1.5	2
153	Comparative Study of the Genetic Diversity, Antimicrobial Resistance, and Pathogenicity of Isolates from Clinical Patients and Healthy Individuals. <i>Biomedical and Environmental Sciences</i> , 2021, 34, 454-464.	0.2	2
154	Molecular diagnostics and next-generation sequencing reveal real etiological characteristics of invasive <i>Salmonella</i> infection in febrile illness in Freetown, Sierra Leone. <i>Emerging Microbes and Infections</i> , 2022, 11, 1416-1424.	3.0	2
155	A duplex droplet digital PCR assay for <i>Salmonella</i> and <i>Shigella</i> and its application in diarrheal and non-diarrheal samples. <i>International Journal of Infectious Diseases</i> , 2022, 120, 210-216.	1.5	2
156	Conserved alanine rich protein Rv3878 in <i>Mycobacterium tuberculosis</i> contains sequence polymorphisms. <i>Tuberculosis</i> , 2014, 94, 245-251.	0.8	1
157	The purifying trend in the chromosomal integron in <i>Vibrio cholerae</i> strains during the seventh pandemic. <i>Infection, Genetics and Evolution</i> , 2014, 26, 241-249.	1.0	1
158	Serotype-shifting gene <i>rfbT</i> is a direct transcriptional target of cAMP receptor protein (CRP) in <i>V. cholerae</i> O1. <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 874-879.	1.0	1
159	A PolyQ Membrane Protein of <i>Vibrio cholerae</i> Acts as the Receptor for Phage Infection. <i>Journal of Virology</i> , 2021, 95, .	1.5	1
160	The Type II Secretory System Mediates Phage Infection in <i>Vibrio cholerae</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 662344.	1.8	1
161	<i>vgrG</i> is separately transcribed from <i>hcp</i> in T6SS orphan clusters and is under the regulation of IHF and HapR. <i>Biochemical and Biophysical Research Communications</i> , 2021, 559, 15-20.	1.0	1
162	Co-existence of multiple distinct lineages in <i>Vibrio parahaemolyticus</i> serotype O4:K12. <i>Microbial Genomics</i> , 2020, 6, .	1.0	1

#	ARTICLE	IF	CITATIONS
163	Phylogenetic Analysis of Serogroup O5 <i>Vibrio cholerae</i> that Caused Successive Cholera Outbreaks in Guangdong Province, China, 2020–2021. <i>China CDC Weekly</i> , 2022, 4, 238-241.	1.0	1
164	VfqI-VfqR quorum sensing circuit modulates type VI secretion system VfiT6SS2 in <i>Vibrio fluvialis</i> . <i>Biochemistry and Biophysics Reports</i> , 2022, 31, 101282.	0.7	1
165	Nonhemolysis of epidemic El Tor biotype strains of <i>Vibrio cholerae</i> is related to multiple functional deficiencies of hemolysin A. <i>Gut Pathogens</i> , 2019, 11, 38.	1.6	0
166	Master Quorum Sensing Regulator HapR Acts as A Repressor of the Mannitol Phosphotransferase System Operon in .. <i>Biomedical and Environmental Sciences</i> , 2022, 35, 69-72.	0.2	0