

Biao Kan

List of Publications by Year in descending order

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166
papers

4,970
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147801

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docs citations

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8063
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.6	8
2	Cholera Caused by a New Clone of Serogroup O1 <i>Vibrio cholerae </i>â€™ Beijing Municipality, China, June 2021. <i>China CDC Weekly</i> , 2022, 4, 31-32.	2.3	2
3	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.	3.7	3
4	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.	2.3	2
5	Trans-Regional and Cross-Host Spread of <i>mcr</i>-Carrying Plasmids Revealed by Complete Plasmid Sequences â€™ 44 Countries, 1998â€™2020. <i>China CDC Weekly</i> , 2022, 4, 242-248.	2.3	6
6	Phylogenetic Analysis of Serogroup O5 <i>Vibrio cholerae</i> that Caused Successive Cholera Outbreaks â€™ Guangdong Province, China, 2020â€™2021. <i>China CDC Weekly</i> , 2022, 4, 238-241.	2.3	1
7	<i>Anaplasma bovis</i> Infection in Fever and Thrombocytopenia Patients â€™ Anhui Province, China, 2021. <i>China CDC Weekly</i> , 2022, 4, 249-253.	2.3	10
8	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.	10.0	3
9	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.	3.9	6
10	Filtration efficiency of face masks against aerosolized surrogate SARS-CoV-2 at different social distances. <i>Science Bulletin</i> , 2022, 67, 565-568.	9.0	9
11	High Carriage of Extended-Spectrum, Beta Lactamase-Producing, and Colistin-Resistant Enterobacteriaceae in Tibetan Outpatients with Diarrhea. <i>Antibiotics</i> , 2022, 11, 508.	3.7	2
12	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
13	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.	6.5	2
14	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.	3.3	2
15	Super Dominant Pathobiontic Bacteria in the Nasopharyngeal Microbiota Cause Secondary Bacterial Infection in COVID-19 Patients. <i>Microbiology Spectrum</i> , 2022, 10, e0195621.	3.0	13
16	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.	1.3	1
17	<i>Salmonella enterica</i> subsp. II serovar 4,5,12:a:- may cause gastroenteritis infections in humans. <i>Gut Microbes</i> , 2022, 14, .	9.8	4
18	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, .	3.0	7

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19	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.	2.1	12
20	CqsA/LuxS-HapR Quorum sensing circuit modulates type VI secretion system Vi-,T6SS2 in <i>Vibrio fluvialis</i> . <i>Emerging Microbes and Infections</i> , 2021, 10, 589-601.	6.5	14
21	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.	3.9	4
22	A PolyQ Membrane Protein of <i>Vibrio cholerae</i> Acts as the Receptor for Phage Infection. <i>Journal of Virology</i> , 2021, 95, .	3.4	1
23	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.	2.6	9
24	The Type II Secretory System Mediates Phage Infection in <i>Vibrio cholerae</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 662344.	3.9	1
25	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.	3.5	4
26	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.	1.8	6
27	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.	2.1	2
28	<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.	2.1	1
29	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.	0.9	2
30	Characterization of <i>bla</i> KPC-2-Carrying Plasmid pR31-KPC from a <i>Pseudomonas aeruginosa</i> Strain Isolated in China. <i>Antibiotics</i> , 2021, 10, 1234.	3.7	6
31	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.	3.9	6
32	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.	3.0	19
33	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
34	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.	2.1	14
35	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.	3.5	19
36	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.	6.5	3

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37	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.	3.3	12
38	Development of an inactivated vaccine candidate for SARS-CoV-2. <i>Science</i> , 2020, 369, 77-81.	12.6	1,180
39	Investigation of an imported cholera case in China with whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104362.	2.3	2
40	A novel pre-CTX prophage in the <i>Vibrio cholerae</i> serogroup O139 strain. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104238.	2.3	3
41	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.	3.5	9
42	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.	3.8	10
43	Comparative Genomics and Transcriptomics Analyses Reveal a Unique Environmental Adaptability of <i>Vibrio fujianensis</i> . <i>Microorganisms</i> , 2020, 8, 555.	3.6	12
44	Comparison of the Multiple Platforms to Identify Various <i>Aeromonas</i> Species. <i>Frontiers in Microbiology</i> , 2020, 11, 625961.	3.5	6
45	Co-existence of multiple distinct lineages in <i>Vibrio parahaemolyticus</i> serotype O4:K12. <i>Microbial Genomics</i> , 2020, 6, .	2.0	1
46	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.	3.4	0
47	<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.	2.8	10
48	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.	1.8	10
49	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.	2.1	1
50	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.	4.2	12
51	Expanding dynamics of the virulence-related gene variations in the toxigenic <i>Vibrio cholerae</i> serogroup O1. <i>BMC Genomics</i> , 2019, 20, 360.	2.8	9
52	Epidemiologic and genomic insights on <i>mcr-1</i> -harbouring <i>Salmonella</i> from diarrhoeal outpatients in Shanghai, China, 2006-2016. <i>EBioMedicine</i> , 2019, 42, 133-144.	6.1	80
53	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.	2.3	9
54	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, .	3.1	13

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55	Genomic comparison of serogroups O159 and O170 with other <i>Vibrio cholerae</i> serogroups. <i>BMC Genomics</i> , 2019, 20, 241.	2.8	9
56	Gut microbiota community characteristics and disease-related microorganism pattern in a population of healthy Chinese people. <i>Scientific Reports</i> , 2019, 9, 1594.	3.3	33
57	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.	2.9	66
58	Colistin Resistance-Mediated Bacterial Surface Modification Sensitizes Phage Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	19
59	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, .	2.2	19
60	<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.	1.7	15
61	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.	3.4	16
62	Transforming bacterial disease surveillance and investigation using whole-genome sequence to probe the trace. <i>Frontiers of Medicine</i> , 2018, 12, 23-33.	3.4	13
63	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.	3.3	7
64	Hypermutation-induced in vivo oxidative stress resistance enhances <i>Vibrio cholerae</i> host adaptation. <i>PLoS Pathogens</i> , 2018, 14, e1007413.	4.7	32
65	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.	2.9	10
66	Integration Host Factor Modulates the Expression and Function of T6SS2 in <i>Vibrio fluvialis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 962.	3.5	18
67	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.	3.5	8
68	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.	3.5	17
69	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.	3.5	26
70	<i>Proteus columbae</i> sp. nov., isolated from a pigeon in Ma'an shan, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 552-557.	1.7	18
71	<i>Vibrio fujianensis</i> sp. nov., isolated from aquaculture water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1146-1152.	1.7	12
72	<i>Proteus alimentorum</i> sp. nov., isolated from pork and lobster in Ma'an shan city, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1390-1395.	1.7	17

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73	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, .	3.2	58
74	<i>Vibrio cholerae</i> Colonization of Soft-Shelled Turtles. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	11
75	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.	2.3	10
76	Functional Characterization and Conditional Regulation of the Type VI Secretion System in <i>Vibrio fluvialis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 528.	3.5	37
77	Regional Transmission of <i>Salmonella</i> Paratyphi A, China, 1998–2012. <i>Emerging Infectious Diseases</i> , 2017, 23, 833-836.	4.3	9
78	Duplex Real-Time PCR Method for the Differentiation of <i>Cronobacter sakazakii</i> and <i>Cronobacter malonicus</i> . <i>Journal of Food Protection</i> , 2017, 80, 50-56.	1.7	5
79	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.	3.5	21
80	<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.	1.7	21
81	OxyR-activated expression of Dps is important for <i>Vibrio cholerae</i> oxidative stress resistance and pathogenesis. <i>PLoS ONE</i> , 2017, 12, e0171201.	2.5	31
82	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.	2.5	24
83	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.	3.5	14
84	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.	3.5	35
85	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.	3.5	10
86	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.	2.5	18
87	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.	2.3	16
88	Genotyping of <i>Salmonella</i> Typhi using 8-loci multi locus VNTR analysis. <i>Gut Pathogens</i> , 2016, 8, 14.	3.4	6
89	Thiol-based switch mechanism of virulence regulator AphB modulates oxidative stress response in <i>Vibrio cholerae</i> . <i>Molecular Microbiology</i> , 2016, 102, 939-949.	2.5	27
90	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.	2.3	5

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91	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.	2.5	20
92	Variations in SXT elements in epidemic <i>Vibrio cholerae</i> O1 El Tor strains in China. <i>Scientific Reports</i> , 2016, 6, 22733.	3.3	49
93	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.	2.3	11
94	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.	2.9	16
95	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.	3.8	13
96	The emergence and outbreak of multidrug-resistant typhoid fever in China. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-6.	6.5	36
97	Incl1 Plasmids Carrying Various bla _{CTX-M} Genes Contribute to Ceftriaxone Resistance in <i>Salmonella enterica</i> Serovar <i>Enteritidis</i> in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 982-989.	3.2	33
98	Differential Thiol-Based Switches Jump-Start <i>Vibrio cholerae</i> Pathogenesis. <i>Cell Reports</i> , 2016, 14, 347-354.	6.4	36
99	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.	1.7	4
100	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.	3.3	41
101	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.	2.6	20
102	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.	3.5	21
103	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.	2.5	31
104	Functional RelBE-Family Toxin-Antitoxin Pairs Affect Biofilm Maturation and Intestine Colonization in <i>Vibrio cholerae</i> . <i>PLoS ONE</i> , 2015, 10, e0135696.	2.5	49
105	Survival and proliferation of the lysogenic bacteriophage CTX ϕ in <i>Vibrio cholerae</i> . <i>Virologica Sinica</i> , 2015, 30, 19-25.	3.0	5
106	The Role of China in the Global Spread of the Current Cholera Pandemic. <i>PLoS Genetics</i> , 2015, 11, e1005072.	3.5	73
107	Dual Zinc Transporter Systems in <i>Vibrio cholerae</i> Promote Competitive Advantages over Gut Microbiome. <i>Infection and Immunity</i> , 2015, 83, 3902-3908.	2.2	40
108	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.	1.6	28

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109	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.	2.5	18
110	<i>Vibrio cholerae</i> Represses Polysaccharide Synthesis To Promote Motility in Mucosa. <i>Infection and Immunity</i> , 2015, 83, 1114-1121.	2.2	25
111	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.	1.8	20
112	Identification and characterization of phosphodiesterases that specifically degrade 3'-cyclic GMP-AMP. <i>Cell Research</i> , 2015, 25, 539-550.	12.0	83
113	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.	3.1	7
114	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.	3.3	38
115	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.	3.0	17
116	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.	2.5	11
117	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.	1.9	23
118	Transcript changes in <i>Vibrio cholerae</i> in response to salt stress. <i>Gut Pathogens</i> , 2014, 6, 47.	3.4	20
119	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.	2.2	51
120	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.	3.4	14
121	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.	3.1	13
122	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.	2.3	19
123	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.	3.9	18
124	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.	3.9	12
125	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.	3.1	32
126	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.	2.4	8

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139	Quorum Sensing Regulatory Cascades Control <i>Vibrio fluvialis</i> Pathogenesis. <i>Journal of Bacteriology</i> , 2013, 195, 3583-3589.	2.2	23
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143	Etiology of acute diarrhea due to enteropathogenic bacteria in Beijing, China. <i>Journal of Infection</i> , 2012, 65, 214-222.	3.3	46
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162	<i>Streptococcus suis</i> Sequence Type 7 Outbreak, Sichuan, China. Emerging Infectious Diseases, 2006, 12, 1203-1208.	4.3	150

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