

Beiwen Zheng

List of Publications by Year in descending order

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92
papers

4,315
citations

236612

25
h-index

123241

61
g-index

93
all docs

93
docs citations

93
times ranked

6915
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid increase in occurrence of carbapenem-resistant Enterobacteriaceae in healthy rural residents in Shandong Province, China, from 2015 to 2017. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 28, 38-42.	0.9	5
2	Modulation of <i>Lactobacillus rhamnosus</i> GG on the gut microbiota and metabolism in mice with <i>Clostridioides difficile</i> infection. <i>Food and Function</i> , 2022, 13, 5667-5679.	2.1	4
3	Comparative Respiratory Tract Microbiome Between Carbapenem-Resistant <i>Acinetobacter baumannii</i> Colonization and Ventilator Associated Pneumonia. <i>Frontiers in Microbiology</i> , 2022, 13, 782210.	1.5	5
4	Co-Production of NDM-1 and OXA-10 β -Lactamase in <i>Citrobacter braakii</i> Strain Causing Urinary Tract Infection. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1127-1133.	1.1	3
5	Disordered Intestinal Microbial Communities During <i>Clostridioides difficile</i> Colonization and Subsequent Infection of Hepatic Cirrhosis Patients in a Tertiary Care Hospital in China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 825189.	1.8	0
6	The genetic feature and virulence determinant of highly virulent community-associated MRSA ST338-SCCmec Vb in China. <i>Emerging Microbes and Infections</i> , 2021, 10, 1052-1064.	3.0	14
7	Occurrence and distribution of antimicrobial resistance genes in the soil of an industrial park in China: A metagenomics survey. <i>Environmental Pollution</i> , 2021, 273, 116467.	3.7	8
8	Gut mycobiota alterations in patients with COVID-19 and H1N1 infections and their associations with clinical features. <i>Communications Biology</i> , 2021, 4, 480.	2.0	62
9	Characterizations of heavy metal contamination, microbial community, and resistance genes in a tailing of the largest copper mine in China. <i>Environmental Pollution</i> , 2021, 280, 116947.	3.7	80
10	Convergence of carbapenem resistance and hypervirulence in a highly-transmissible ST11 clone of <i>K. pneumoniae</i> : An epidemiological, genomic and functional study. <i>Virulence</i> , 2021, 12, 377-388.	1.8	24
11	Genomic Epidemiology and Characterization of Methicillin-Resistant <i>Staphylococcus aureus</i> from Bloodstream Infections in China. <i>MSystems</i> , 2021, 6, e0083721.	1.7	27
12	Rifaximin Modulates the Gut Microbiota to Prevent Hepatic Encephalopathy in Liver Cirrhosis Without Impacting the Resistome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 761192.	1.8	19
13	Confirmation of the Need for Reclassification of <i>Neisseria mucosa</i> and <i>Neisseria sicca</i> Using Average Nucleotide Identity Blast and Phylogenetic Analysis of Whole-Genome Sequencing: Hinted by Clinical Misclassification of a <i>Neisseria mucosa</i> Strain. <i>Frontiers in Microbiology</i> , 2021, 12, 780183.	1.5	3
14	MDR <i>Salmonella enterica</i> serovar Typhimurium ST34 carrying <i>mcr-1</i> isolated from cases of bloodstream and intestinal infection in children in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 92-95.	1.3	33
15	Emergence of KPC-2-Producing <i>Raoultella ornithinolytica</i> Isolated from a Hospital Wastewater Treatment Plant. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	7
16	Serotype Is Associated With High Rate of Colistin Resistance Among Clinical Isolates of <i>Salmonella</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 592146.	1.5	6
17	Comparative Analysis of Virulence and Toxin Expression of Vancomycin-Intermediate and Vancomycin-Sensitive <i>Staphylococcus aureus</i> Strains. <i>Frontiers in Microbiology</i> , 2020, 11, 596942.	1.5	6
18	Alterations of the Gut Microbiota in Patients With Coronavirus Disease 2019 or H1N1 Influenza. <i>Clinical Infectious Diseases</i> , 2020, 71, 2669-2678.	2.9	557

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19	Change in Antibiotic Use in Secondary and Tertiary Hospitals Nationwide After a National Antimicrobial Stewardship Campaign Was Launched in China, 2011–2016: An Observational Study. <i>Journal of Infectious Diseases</i> , 2020, 221, S148-S155.	1.9	23
20	Stool Samples of Acute Diarrhea Inpatients as a Reservoir of ST11 Hypervirulent KPC-2-Producing <i>Klebsiella pneumoniae</i> . <i>MSystems</i> , 2020, 5, .	1.7	42
21	<p>Effect of Short-Term Antimicrobial Therapy on the Tolerance and Antibiotic Resistance of Multidrug-Resistant Staphylococcus capitis </p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 2017-2026.	1.1	1
22	Comparative Genomic Analysis of 19 Clinical Isolates of Tigecycline-Resistant <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1321.	1.5	10
23	Genetic characterization and virulence of a carbapenem-resistant <i>Raoultella ornithinolytica</i> isolated from well water carrying a novel megaplasmid containing blaNDM-1. <i>Environmental Pollution</i> , 2020, 260, 114041.	3.7	19
24	<p>Complete-Genome Sequencing and Comparative Genomic Characterization of an IMP-4 Producing Citrobacter freundii Isolate from Patient with Diarrhea</p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1057-1065.	1.1	5
25	<p>Genomic and Phenotypic Diversity of Listeria monocytogenes Causing Pregnancy-Associated Listeriosis from Zhejiang Province, China, 2016–2018</p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1179-1184.	1.1	3
26	Bloodstream infections caused by Entero-bacteriaceae in China. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 810-811.	4.6	11
27	<p>Spinal brucellosis in Hulunbuir, China, 2011–2016</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 1565-1571.	1.1	22
28	Comprehensive Genome Analysis of Carbapenem-Resistant Strains of <i>Raoultella</i> Species, an Emerging Multidrug-Resistant Bacterium in Hospitals. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	2
29	<p>Genetic characterization of a novel sequence type of multidrug-resistant Citrobacter freundii strain recovered from wastewater treatment plant</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 2775-2779.	1.1	11
30	Whole Genome Sequencing of Extended-Spectrum Beta-Lactamase (ESBL)-Producing <i>Escherichia coli</i> Isolated From a Wastewater Treatment Plant in China. <i>Frontiers in Microbiology</i> , 2019, 10, 1797.	1.5	26
31	Emergence and Characterization of a Novel IncP-6 Plasmid Harboring blaKPC–2 and qnrS2 Genes in <i>Aeromonas taiwanensis</i> Isolates. <i>Frontiers in Microbiology</i> , 2019, 10, 2132.	1.5	17
32	<p>Genomic Analysis Of A KPC-2-Producing Klebsiella Pneumoniae ST11 Outbreak From A Teaching Hospital In Shandong Province, China</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 2961-2969.	1.1	16
33	<p>Simulating moxalactam dosage for extended-spectrum $\hat{1}^2$ -lactamase-producing Enterobacteriaceae using blood antimicrobial surveillance network data</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 1199-1208.	1.1	5
34	Complete genome sequence of an IMP-8, CTX-M-14, CTX-M-3 and QnrS1 co-producing <i>Enterobacter asburiae</i> isolate from a patient with wound infection. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 18, 52-54.	0.9	12
35	Detection and Genomic Characterization of a <i>Morganella morganii</i> Isolate From China That Produces NDM-5. <i>Frontiers in Microbiology</i> , 2019, 10, 1156.	1.5	30
36	Whole-Genome Sequence of <i>Brucella melitensis</i> Strain B7, Isolated from a Blood Sample of a Brucellosis Patient from Hulunbuir, Inner Mongolia, China. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0

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37	Dissemination of extended-spectrum β -lactamase-producing <i>Escherichia coli</i> carrying <i>mcr-1</i> among multiple environmental sources in rural China and associated risk to human health. <i>Environmental Pollution</i> , 2019, 251, 619-627.	3.7	28
38	Characterization of Clinically Relevant Strains of Extended-Spectrum β -Lactamase-Producing <i>Klebsiella pneumoniae</i> Occurring in Environmental Sources in a Rural Area of China by Using Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2019, 10, 211.	1.5	25
39	MCR-1-producing <i>Salmonella</i> Typhimurium ST34 links animal foods to human community infections. <i>EBioMedicine</i> , 2019, 42, 10-11.	2.7	11
40	Evaluating Dissemination Mechanisms of Antibiotic-Resistant Bacteria in Rural Environments in China by Using CTX-M-Producing <i>Escherichia coli</i> as an Indicator. <i>Microbial Drug Resistance</i> , 2019, 25, 975-984.	0.9	16
41	Antagonistic effect between tigecycline and meropenem: successful management of KPC-producing <i>Klebsiella pneumoniae</i> infection. <i>Infection</i> , 2019, 47, 497-500.	2.3	13
42	Occurrence and Genomic Characterization of Two MCR-1-Producing <i>Escherichia coli</i> Isolates from the Same Mink Farmer. <i>MSphere</i> , 2019, 4, .	1.3	13
43	Emergence and Comparative Genomics Analysis of Extended-Spectrum β -Lactamase-Producing <i>Escherichia coli</i> Carrying <i>mcr-1</i> in Fennec Fox Imported from Sudan to China. <i>MSphere</i> , 2019, 4, .	1.3	15
44	Emergence of NDM-1- and CTX-M-3-Producing <i>Raoultella ornithinolytica</i> in Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2019, 10, 2678.	1.5	11
45	Detection and characterization of ESBL-producing <i>Escherichia coli</i> expressing <i>mcr-1</i> from dairy cows in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 321-325.	1.3	41
46	First detection and genomics analysis of KPC-2-producing <i>Citrobacter</i> isolates from river sediments. <i>Environmental Pollution</i> , 2018, 235, 931-937.	3.7	42
47	Identification and genomic characterization of a KPC-2-, NDM-1- and NDM-5-producing <i>Klebsiella michiganensis</i> isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 536-538.	1.3	40
48	Complete nucleotide sequences of two KPC-2-encoding plasmids from the same <i>Citrobacter freundii</i> isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 531-533.	1.3	15
49	Study protocol for One Health data collections, analyses and intervention of the Sino-Swedish integrated multisectoral partnership for antibiotic resistance containment (IMPACT). <i>BMJ Open</i> , 2018, 8, e017832.	0.8	26
50	Discovery and characterisation of an <i>Escherichia coli</i> ST206 strain producing NDM-5 and MCR-1 from a patient with acute diarrhoea in China. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 273-275.	1.1	38
51	Low prevalence of MCR-1-producing <i>Klebsiella pneumoniae</i> in bloodstream infections in China. <i>Clinical Microbiology and Infection</i> , 2018, 24, 205-206.	2.8	19
52	Retrospective comparative analysis of risk factors and outcomes in patients with carbapenem resistant <i>Acinetobacter baumannii</i> bloodstream infections: cefoperazone–sulbactam associated with resistance and tigecycline increased the mortality. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2021-2030.	1.1	26
53	Protective Effect of <i>Pediococcus pentosaceus</i> LI05 Against <i>Clostridium difficile</i> Infection in a Mouse Model. <i>Frontiers in Microbiology</i> , 2018, 9, 2396.	1.5	26
54	First genome sequence of a blaKPC-2-carrying <i>Citrobacter koseri</i> isolate collected from a patient with diarrhoea. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 15, 166-168.	0.9	7

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55	Antibacterial effect evaluation of moxalactam against extended-spectrum β -lactamase-producing <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> with in vitro pharmacokinetics/pharmacodynamics simulation. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 103-112.	1.1	9
56	Complete genome sequencing of <i>Comamonas kerstersii</i> 8943, a causative agent for peritonitis. <i>Scientific Data</i> , 2018, 5, 180222.	2.4	12
57	Occurrence of <i>bla</i> _{KPC-2} , <i>bla</i> _{CTX-M} , and <i>mcr-1</i> in Enterobacteriaceae from Well Water in Rural China. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	68
58	Genome sequence of <i>Shigella flexneri</i> strain SP1, a diarrheal isolate that encodes an extended-spectrum β -lactamase (ESBL). <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2017, 16, 37.	1.7	7
59	Community-associated methicillin-resistant <i>Staphylococcus aureus</i> pneumonia in China. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 26.	4.6	6
60	Complete nucleotide sequence of pSKLX3330, an IncI1 plasmid carrying <i>bla</i> _{CTX-M-55} isolated from community-onset <i>Escherichia coli</i> infection. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 11, 120-122.	0.9	1
61	Genome characterization of two bile-isolated <i>Vibrio fluvialis</i> strains: an insight into pathogenicity and bile salt adaption. <i>Scientific Reports</i> , 2017, 7, 11827.	1.6	14
62	Hospital-acquired <i>Clostridium difficile</i> infection in Mainland China: A seven-year (2009–2016) retrospective study in a large university hospital. <i>Scientific Reports</i> , 2017, 7, 9645.	1.6	27
63	In vitro antibacterial activity of fosfomycin combined with other antimicrobials against KPC-producing <i>Klebsiella pneumoniae</i> . <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 237-241.	1.1	31
64	Complete genome sequencing and genomic characterization of two <i>Escherichia coli</i> strains co-producing MCR-1 and NDM-1 from bloodstream infection. <i>Scientific Reports</i> , 2017, 7, 17885.	1.6	35
65	Complete Genome Sequence and Comparative Analysis of <i>Staphylococcus condimentii</i> DSM 11674, a Potential Starter Culture Isolated from Soy Sauce Mash. <i>Frontiers in Bioengineering and Biotechnology</i> , 2017, 5, 56.	2.0	1
66	Occurrence and Genomic Characterization of ESBL-Producing, MCR-1-Harboring <i>Escherichia coli</i> in Farming Soil. <i>Frontiers in Microbiology</i> , 2017, 8, 2510.	1.5	56
67	High Prevalence of ESBL-Producing <i>Klebsiella pneumoniae</i> Causing Community-Onset Infections in China. <i>Frontiers in Microbiology</i> , 2016, 7, 1830.	1.5	50
68	First Draft Genome Sequence of <i>Staphylococcus condimentii</i> F-2 ^T . <i>Genome Announcements</i> , 2016, 4, .	0.8	0
69	A case of multiple recurrence of <i>Clostridium difficile</i> infection with severe hematochezia in an immunocompromised host. <i>Anaerobe</i> , 2016, 42, 31-32.	1.0	2
70	Building bridges to operationalise one health – A Sino-Swedish collaboration to tackle antibiotic resistance. <i>One Health</i> , 2016, 2, 139-143.	1.5	18
71	Retrospective survey of the efficacy of mandatory implementation of the Essential Medicine Policy in the primary healthcare setting in China: failure to promote the rational use of antibiotics in clinics. <i>International Journal of Antimicrobial Agents</i> , 2016, 48, 409-414.	1.1	24
72	Active site analysis of sortase A from <i>Staphylococcus simulans</i> indicates function in cleavage of putative cell wall proteins. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 1653-1659.	1.0	4

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73	Structural and functional analysis of an anchorless fibronectin-binding protein FBPS from Gram-positive bacterium <i>Streptococcus suis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13869-13874.	3.3	27
74	Analysis of tigecycline resistance development in clinical <i>Acinetobacter baumannii</i> isolates through a combined genomic and transcriptomic approach. Scientific Reports, 2016, 6, 26930.	1.6	31
75	Whole genome sequencing uncovers a novel IND-16 metallo- β -lactamase from an extensively drug-resistant <i>Chryseobacterium indologenes</i> strain J31. Gut Pathogens, 2016, 8, 47.	1.6	13
76	Draft genome sequence of <i>Paenibacillus</i> sp. strain A2. Standards in Genomic Sciences, 2016, 11, 9.	1.5	2
77	Characterization of a novel metallo- β -lactamases fold hydrolase from <i>Pelagibacterium halotolerans</i> , a marine halotolerant bacterium isolated from East China Sea. Extremophiles, 2016, 20, 37-44.	0.9	8
78	Identification of key taxa that favor intestinal colonization of <i>Clostridium difficile</i> in an adult Chinese population. Microbes and Infection, 2016, 18, 30-38.	1.0	73
79	The Effect of Probiotic Treatment on Patients Infected with the H7N9 Influenza Virus. PLoS ONE, 2016, 11, e0151976.	1.1	19
80	Influence of H7N9 virus infection and associated treatment on human gut microbiota. Scientific Reports, 2015, 5, 14771.	1.6	88
81	Draft Genome Sequence of <i>Staphylococcus sciuri</i> subsp. <i>sciuri</i> Strain Z8, Isolated from Human Skin. Genome Announcements, 2015, 3, .	0.8	10
82	Severe infective endocarditis with systemic embolism due to community associated methicillin-resistant <i>Staphylococcus aureus</i> ST630. Brazilian Journal of Infectious Diseases, 2015, 19, 85-89.	0.3	13
83	Molecular Epidemiology and Genetic Diversity of Fluoroquinolone-Resistant <i>Escherichia coli</i> Isolates from Patients with Community-Onset Infections in 30 Chinese County Hospitals. Journal of Clinical Microbiology, 2015, 53, 766-770.	1.8	54
84	Transcriptome analysis of the biofilm formed by methicillin-susceptible <i>Staphylococcus aureus</i> . Scientific Reports, 2015, 5, 11997.	1.6	75
85	Whole-Genome Sequence of Multidrug-Resistant <i>Staphylococcus caprae</i> Strain 9557, Isolated from Cerebrospinal Fluid. Genome Announcements, 2015, 3, .	0.8	5
86	Emergence of <i>Raoultella ornithinolytica</i> Coproducing IMP-4 and KPC-2 Carbapenemases in China. Antimicrobial Agents and Chemotherapy, 2015, 59, 7086-7089.	1.4	50
87	Complete genome sequence of <i>Lactobacillus heilongjiangensis</i> DSM 28069T: Insight into its probiotic potential. Journal of Biotechnology, 2015, 216, 65-66.	1.9	3
88	Identification and characterization of cfr-positive <i>Staphylococcus aureus</i> isolates from community-onset infectious patients in a county hospital in China. Journal of Medical Microbiology, 2015, 64, 910-915.	0.7	6
89	Nationwide high prevalence of CTX-M and an increase of CTX-M-55 in <i>Escherichia coli</i> isolated from patients with community-onset infections in Chinese county hospitals. BMC Infectious Diseases, 2014, 14, 659.	1.3	139
90	Genome sequencing and genomic characterization of a tigecycline-resistant <i>Klebsiella pneumoniae</i> strain isolated from the bile samples of a cholangiocarcinoma patient. Gut Pathogens, 2014, 6, 40.	1.6	14

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91	Alterations of the human gut microbiome in liver cirrhosis. <i>Nature</i> , 2014, 513, 59-64.	13.7	1,782
92	High quality draft genome sequence of <i>Staphylococcus cohnii</i> subsp. <i>cohnii</i> strain hu-01. <i>Standards in Genomic Sciences</i> , 2014, 9, 755-762.	1.5	8