

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	Alterations of the human gut microbiome in liver cirrhosis. <i>Nature</i> , 2014, 513, 59-64.	13.7	1,782
2	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
3	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. <i>BMC Infectious Diseases</i> , 2014, 14, 659.	1.3	139
4	Influence of H7N9 virus infection and associated treatment on human gut microbiota. <i>Scientific Reports</i> , 2015, 5, 14771.	1.6	88
5	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
6	Transcriptome analysis of the biofilm formed by methicillin-susceptible <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2015, 5, 11997.	1.6	75
7	Identification of key taxa that favor intestinal colonization of <i>Clostridium difficile</i> in an adult Chinese population. <i>Microbes and Infection</i> , 2016, 18, 30-38.	1.0	73
8	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
9	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
10	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
11	Molecular Epidemiology and Genetic Diversity of Fluoroquinolone-Resistant <i>Escherichia coli</i> Isolates from Patients with Community-Onset Infections in 30 Chinese County Hospitals. <i>Journal of Clinical Microbiology</i> , 2015, 53, 766-770.	1.8	54
12	Emergence of <i>Raoultella ornithinolytica</i> Coproducing IMP-4 and KPC-2 Carbapenemases in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 7086-7089.	1.4	50
13	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
14	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
15	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
16	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
17	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
18	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

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19	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
20	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
21	Analysis of tigecycline resistance development in clinical <i>Acinetobacter baumannii</i> isolates through a combined genomic and transcriptomic approach. <i>Scientific Reports</i> , 2016, 6, 26930.	1.6	31
22	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
23	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
24	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
25	Structural and functional analysis of an anchorless fibronectin-binding protein FBPS from Gram-positive bacterium <i>Streptococcus suis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13869-13874.	3.3	27
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	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
34	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
35	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
36	Spinal brucellosis in Hulunbuir, China, 2011–2016. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 1565-1571.	1.1	22

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37	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
38	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
39	The Effect of Probiotic Treatment on Patients Infected with the H7N9 Influenza Virus. <i>PLoS ONE</i> , 2016, 11, e0151976.	1.1	19
40	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
41	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
42	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
43	Genomic Analysis Of A KPC-2-Producing <i>Klebsiella pneumoniae</i> ST11 Outbreak From A Teaching Hospital In Shandong Province, China. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 2961-2969.	1.1	16
44	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
45	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
46	Emergence and Comparative Genomics Analysis of Extended-Spectrum- β -Lactamase-Producing <i>Escherichia coli</i> Carrying mcr-1 in Fennec Fox Imported from Sudan to China. <i>MSphere</i> , 2019, 4, .	1.3	15
47	Genome sequencing and genomic characterization of a tigecycline-resistant <i>Klebsiella pneumoniae</i> strain isolated from the bile samples of a cholangiocarcinoma patient. <i>Gut Pathogens</i> , 2014, 6, 40.	1.6	14
48	Genome characterization of two bile-isolated <i>Vibrio fluvialis</i> strains: an insight into pathogenicity and bile salt adaptation. <i>Scientific Reports</i> , 2017, 7, 11827.	1.6	14
49	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
50	Severe infective endocarditis with systemic embolism due to community associated methicillin-resistant <i>Staphylococcus aureus</i> ST630. <i>Brazilian Journal of Infectious Diseases</i> , 2015, 19, 85-89.	0.3	13
51	Whole genome sequencing uncovers a novel IND-16 metallo- β -lactamase from an extensively drug-resistant <i>Chryseobacterium indologenes</i> strain J31. <i>Gut Pathogens</i> , 2016, 8, 47.	1.6	13
52	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
53	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
54	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

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55	Complete genome sequencing of <i>Comamonas kerstersii</i> 8943, a causative agent for peritonitis. <i>Scientific Data</i> , 2018, 5, 180222.	2.4	12
56	Bloodstream infections caused by Entero-bacteriaceae in China. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 810-811.	4.6	11
57	Genetic characterization of a novel sequence type of multidrug-resistant <i>Citrobacter freundii</i> strain recovered from wastewater treatment plant. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 2775-2779.	1.1	11
58	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
59	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
60	Draft Genome Sequence of <i>Staphylococcus sciuri</i> subsp. <i>sciuri</i> Strain Z8, Isolated from Human Skin. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
61	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
62	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
63	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
64	Characterization of a novel metallo- β -lactamases fold hydrolase from <i>Pelagibacterium halotolerans</i> , a marine halotolerant bacterium isolated from East China Sea. <i>Extremophiles</i> , 2016, 20, 37-44.	0.9	8
65	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
66	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
67	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
68	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
69	Community-associated methicillin-resistant <i>Staphylococcus aureus</i> pneumonia in China. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 26.	4.6	6
70	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
71	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
72	Identification and characterization of cfr-positive <i>Staphylococcus aureus</i> isolates from community-onset infectious patients in a county hospital in China. <i>Journal of Medical Microbiology</i> , 2015, 64, 910-915.	0.7	6

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73	Whole-Genome Sequence of Multidrug-Resistant <i>Staphylococcus caprae</i> Strain 9557, Isolated from Cerebrospinal Fluid. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
74	Simulating moxalactam dosage for extended-spectrum β -lactamase-producing <i>Enterobacteriaceae</i> using blood antimicrobial surveillance network data. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 1199-1208.	1.1	5
75	Complete-Genome Sequencing and Comparative Genomic Characterization of an IMP-4 Producing <i>Citrobacter freundii</i> Isolate from Patient with Diarrhea. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1057-1065.	1.1	5
76	Rapid increase in occurrence of carbapenem-resistant <i>Enterobacteriaceae</i> 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
77	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
78	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
79	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
80	Complete genome sequence of <i>Lactobacillus heilongjiangensis</i> DSM 28069T: Insight into its probiotic potential. <i>Journal of Biotechnology</i> , 2015, 216, 65-66.	1.9	3
81	Genomic and Phenotypic Diversity of <i>Listeria monocytogenes</i> Causing Pregnancy-Associated Listeriosis from Zhejiang Province, China, 2016–2018. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1179-1184.	1.1	3
82	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
83	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
84	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
85	Draft genome sequence of <i>Paenibacillus</i> sp. strain A2. <i>Standards in Genomic Sciences</i> , 2016, 11, 9.	1.5	2
86	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
87	Complete nucleotide sequence of pSKLX3330, an IncI1 plasmid carrying bla 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
88	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
89	Effect of Short-Term Antimicrobial Therapy on the Tolerance and Antibiotic Resistance of Multidrug-Resistant <i>Staphylococcus capitis</i> . <i>Infection and Drug Resistance</i> , 2020, Volume 13, 2017-2026.	1.1	1
90	First Draft Genome Sequence of <i>Staphylococcus condimentii</i> F-2. <i>Genome Announcements</i> , 2016, 4, .	0.8	0

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91	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
92	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