

# Yan Chen

## List of Publications by Year in descending order

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47  
papers

1,387  
citations

430874

18  
h-index

345221

36  
g-index

47  
all docs

47  
docs citations

47  
times ranked

1817  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epidemiology, evolution and cryptic susceptibility of methicillin-resistant <i>Staphylococcus aureus</i> in China: a whole-genome-based survey. <i>Clinical Microbiology and Infection</i> , 2022, 28, 85-92.	6.0	31
2	The Role of <i>mprF</i> Mutations in Seesaw Effect of Daptomycin-Resistant Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0129521.	3.2	9
3	Genetic Characteristics of Multiple Copies of Tn1546-Like Elements in <i>ermB</i> -Positive Methicillin-Resistant <i>Staphylococcus aureus</i> From Mainland China. <i>Frontiers in Microbiology</i> , 2022, 13, 814062.	3.5	1
4	The novel fosfomycin resistance gene <i>fosY</i> is present on a genomic island in CC1 methicillin-resistant <i>Staphylococcus aureus</i> . <i>Emerging Microbes and Infections</i> , 2022, 11, 1166-1173.	6.5	3
5	Staphylococcal cassette chromosome <i>mec</i> amplification as a mechanism for ceftobiprole resistance in clinical methicillin-resistant <i>Staphylococcus aureus</i> isolates. <i>Clinical Microbiology and Infection</i> , 2022, 28, 1151.e1-1151.e7.	6.0	3
6	High percentage of the ceftriaxone-resistant <i>Neisseria gonorrhoeae</i> FC428 clone among isolates from a single hospital in Hangzhou, China. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 936-939.	3.0	26
7	Household Transmission of Community-Associated Methicillin-Resistant <i>Staphylococcus Aureus</i> . <i>Frontiers in Public Health</i> , 2021, 9, 658638.	2.7	8
8	A random forest model based on core genome allelic profiles of MRSA for penicillin plus potassium clavulanate susceptibility prediction. <i>Microbial Genomics</i> , 2021, 7, .	2.0	3
9	Distribution of <i>erm</i> genes among MRSA isolates with resistance to clindamycin in a Chinese teaching hospital. <i>Infection, Genetics and Evolution</i> , 2021, 96, 105127.	2.3	5
10	Whole-genome sequencing for detecting linezolid resistance in a patient with persistent methicillin-resistant <i>Staphylococcus aureus</i> infection during linezolid exposure. <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105819.	2.5	2
11	Characterization of a community-acquired methicillin-resistant sequence type 338 <i>Staphylococcus aureus</i> strain containing a staphylococcal cassette chromosome <i>mec</i> type VT. <i>International Journal of Infectious Diseases</i> , 2020, 90, 181-187.	3.3	9
12	Tandem amplification of the <i>vanM</i> gene cluster drives vancomycin resistance in vancomycin-variable enterococci. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 283-291.	3.0	16
13	Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> ST59 in a Chinese Adult with Meningitis: A Case Report from China. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 2011-2016.	2.7	1
14	Phenotypic Variation and Carbapenem Resistance Potential in OXA-499-Producing <i>Acinetobacter pittii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1134.	3.5	5
15	Core Genome Allelic Profiles of Clinical <i>Klebsiella pneumoniae</i> Strains Using a Random Forest Algorithm Based on Multilocus Sequence Typing Scheme for Hypervirulence Analysis. <i>Journal of Infectious Diseases</i> , 2020, 221, S263-S271.	4.0	17
16	In-Host Evolution of Daptomycin Resistance and Heteroresistance in Methicillin-Resistant <i>Staphylococcus aureus</i> Strains From Three Endocarditis Patients. <i>Journal of Infectious Diseases</i> , 2020, 221, S243-S252.	4.0	16
17	Characterization of an ST5-SCCmec II-t311 methicillin-resistant <i>Staphylococcus aureus</i> strain with a widespread <i>cfr</i> -positive plasmid. <i>Journal of Infection and Chemotherapy</i> , 2020, 26, 699-705.	1.7	6
18	Increasing prevalence of <i>Neisseria gonorrhoeae</i> with decreased susceptibility to ceftriaxone and resistance to azithromycin in Hangzhou, China (2015-2017). <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 29-37.	3.0	17

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19	Detection and analysis of two cases of the internationally spreading ceftriaxone-resistant <i>Neisseria gonorrhoeae</i> FC428 clone in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3635-3636.	3.0	13
20	A Highly Efficient CRISPR-Cas9-Based Genome Engineering Platform in <i>Acinetobacter baumannii</i> to Understand the H <sub>2</sub> O <sub>2</sub> -Sensing Mechanism of OxyR. <i>Cell Chemical Biology</i> , 2019, 26, 1732-1742.e5.	5.2	55
21	Characterization of vanM carrying clinical <i>Enterococcus</i> isolates and diversity of the suppressed vanM gene cluster. <i>Infection, Genetics and Evolution</i> , 2019, 68, 145-152.	2.3	14
22	Surgical Site Infections Caused by Highly Virulent Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398, China. <i>Emerging Infectious Diseases</i> , 2019, 25, 157-160.	4.3	15
23	Molecular Epidemiology and Mechanism of Sulbactam Resistance in <i>Acinetobacter baumannii</i> Isolates with Diverse Genetic Backgrounds in China. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	35
24	Using Core-genome Multilocus Sequence Typing to Monitor the Changing Epidemiology of Methicillin-resistant <i>Staphylococcus aureus</i> in a Teaching Hospital. <i>Clinical Infectious Diseases</i> , 2018, 67, S241-S248.	5.8	21
25	Prevalence of Fosfomycin Resistance in Methicillin-Resistant <i>Staphylococcus aureus</i> Isolated from Patients in a University Hospital in China from 2013 to 2015. <i>Japanese Journal of Infectious Diseases</i> , 2018, 71, 312-314.	1.2	11
26	Predominance of ST5-II-t311 clone among healthcare-associated methicillin-resistant <i>Staphylococcus aureus</i> isolates recovered from Zhejiang, China. <i>International Journal of Infectious Diseases</i> , 2018, 71, 107-112.	3.3	17
27	Prevalence of mcr-1 in <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> recovered from bloodstream infections in China: a multicentre longitudinal study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 400-410.	9.1	177
28	Characterization of a PVL-negative community-acquired methicillin-resistant <i>Staphylococcus aureus</i> strain of sequence type 88 in China. <i>International Journal of Medical Microbiology</i> , 2017, 307, 346-352.	3.6	5
29	High prevalence of ESBL-producing <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> in community-onset bloodstream infections in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 273-280.	3.0	93
30	Glimpse into the genome sequence of a multidrug-resistant <i>Acinetobacter pittii</i> ST950 clinical isolate carrying the blaOXA-72 and blaOXA-533 genes in China. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2017, 112, 723-727.	1.6	3
31	Identification of Novel Conjugative Plasmids with Multiple Copies of fosB that Confer High-Level Fosfomycin Resistance to Vancomycin-Resistant <i>Enterococci</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1541.	3.5	21
32	Mechanism of Gene Regulation by a <i>Staphylococcus aureus</i> Toxin. <i>MBio</i> , 2016, 7, .	4.1	34
33	Spread of a common blaNDM-1-carrying plasmid among diverse <i>Acinetobacter</i> species. <i>Infection, Genetics and Evolution</i> , 2015, 32, 30-33.	2.3	9
34	ramR operon and lon play a central role in tigecycline resistance in <i>Klebsiella pneumoniae</i> . <i>Journal of Microbiology, Immunology and Infection</i> , 2015, 48, S106.	3.1	0
35	Basis of Virulence in a Pantone-Valentine Leukocidin-Negative Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Strain. <i>Journal of Infectious Diseases</i> , 2015, 211, 472-480.	4.0	29
36	Characterization of the Staphylococcal Cassette Chromosome Composite Island of <i>Staphylococcus haemolyticus</i> SH32, a Methicillin-Resistant Clinical Isolate from China. <i>PLoS ONE</i> , 2014, 9, e87346.	2.5	10

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37	Production of an Attenuated Phenol-Soluble Modulin Variant Unique to the MRSA Clonal Complex 30 Increases Severity of Bloodstream Infection. <i>PLoS Pathogens</i> , 2014, 10, e1004298.	4.7	51
38	Decreased susceptibility to tigecycline in <i>Acinetobacter baumannii</i> mediated by a mutation in <i>trm</i> encoding SAM-dependent methyltransferase. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 72-76.	3.0	72
39	Whole Genome Analysis of a Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> ST59 Isolate from a Case of Human Sepsis and Severe Pneumonia in China. <i>PLoS ONE</i> , 2014, 9, e89235.	2.5	19
40	Wide distribution of CC92 carbapenem-resistant and OXA-23-producing <i>Acinetobacter baumannii</i> in multiple provinces of China. <i>International Journal of Antimicrobial Agents</i> , 2013, 42, 322-328.	2.5	88
41	In vitro activity of sulbactam in combination with imipenem, meropenem, panipenem or cefoperazone against clinical isolates of <i>Acinetobacter baumannii</i> . <i>International Journal of Antimicrobial Agents</i> , 2013, 41, 400-401.	2.5	18
42	Emergence of <i>cfr</i> -harbouring coagulase-negative staphylococci among patients receiving linezolid therapy in two hospitals in China. <i>Journal of Medical Microbiology</i> , 2013, 62, 845-850.	1.8	29
43	Genetic characteristics of <i>bla</i> NDM-1-positive plasmid in <i>Citrobacter freundii</i> isolate separated from a clinical infectious patient. <i>Journal of Medical Microbiology</i> , 2013, 62, 1332-1337.	1.8	25
44	Complete Genome Sequence of a PantA <sup>3n</sup> -Valentine Leukocidin-Negative Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Strain of Sequence type 72 from Korea. <i>PLoS ONE</i> , 2013, 8, e72803.	2.5	22
45	Epidemiological characteristics and genetic structure of <i>bla</i> NDM-1 in non- <i>baumannii</i> <i>Acinetobacter</i> spp. in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 2114-2122.	3.0	98
46	Emergence of NDM-1-producing <i>Acinetobacter baumannii</i> in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1255-1259.	3.0	225
47	Community Origins of Healthcare-Associated CC59 Methicillin-Resistant <i>Staphylococcus aureus</i> in China. <i>Journal of Infectious Diseases</i> , 0, , .	4.0	0