## Ning Dong

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	Prevalence, transmission, and molecular epidemiology of tet(X)-positive bacteria among humans, animals, and environmental niches in China: An epidemiological, and genomic-based study. Science of the Total Environment, 2022, 818, 151767.	8.0	18
2	Molecular epidemiology of carbapenem-resistant Klebsiella pneumoniae in China, 2016–20. Lancet Infectious Diseases, The, 2022, 22, 167-168.	9.1	16
3	Bactericidal, anti-biofilm, and anti-virulence activity of vitamin C against carbapenem-resistant hypervirulent Klebsiella pneumoniae. IScience, 2022, 25, 103894.	4.1	17
4	Co-transfer of last-line antibiotic resistance and virulence operons by an IncFIBk-FII-X3-ColKP3 hybrid plasmid in <i>Klebsiella pneumoniae</i> . Journal of Antimicrobial Chemotherapy, 2022, 77, 1856-1861.	3.0	5
5	Phenotypic Changes Associated With In Vivo Evolution of Colistin Resistance in ST11 Carbapenem-Resistant Klebsiella pneumoniae. Frontiers in Cellular and Infection Microbiology, 2022, 12, 841748.	3.9	2
6	Effectiveness of a double-carbapenem combinations against carbapenem-resistant Gram-negative bacteria. Saudi Pharmaceutical Journal, 2022, 30, 849-855.	2.7	3
7	Emergence of an ST1326 (CG258) Multi-Drug Resistant Klebsiella pneumoniae Co-harboring mcr-8.2, ESBL Genes, and the Resistance-Nodulation-Division Efflux Pump Gene Cluster tmexCD1-toprJ1 in China. Frontiers in Microbiology, 2022, 13, 800993.	3.5	5
8	Klebsiella species: Taxonomy, hypervirulence and multidrug resistance. EBioMedicine, 2022, 79, 103998.	6.1	65
9	Advanced Genetic Methodologies in Tracking Evolution and Spread of SARS-CoV-2. Methods in Molecular Biology, 2022, 2452, 33-43.	0.9	1
10	High-Resolution Metagenomics of Human Gut Microbiota Generated by Nanopore and Illumina Hybrid Metagenome Assembly. Frontiers in Microbiology, 2022, 13, .	3.5	4
11	The Rapid Emergence of Ceftazidime-Avibactam Resistance Mediated by KPC Variants in Carbapenem-Resistant Klebsiella pneumoniae in Zhejiang Province, China. Antibiotics, 2022, 11, 731.	3.7	6
12	Transmission of pLVPK-like virulence plasmid in Klebsiella pneumoniae mediated by an Incl1 conjugative helper plasmid. IScience, 2022, 25, 104428.	4.1	8
13	Presence of tet(X4)-positive Citrobacter freundii in a cancer patient with chemotherapy-induced persistent diarrhoea. Journal of Global Antimicrobial Resistance, 2021, 24, 88-89.	2.2	8
14	Clinical evolution of ST11 carbapenem resistant and hypervirulent Klebsiella pneumoniae. Communications Biology, 2021, 4, 650.	4.4	45
15	Complete Genetic Analysis of Plasmids Carried by Two Nonclonal <i>bla</i> <sub>NDM-5</sub> - and <i>mcr-1</i> -Bearing Escherichia coli Strains: Insight into Plasmid Transmission among Foodborne Bacteria. Microbiology Spectrum, 2021, 9, e0021721.	3.0	6
16	Carbapenem Resistance-Encoding and Virulence-Encoding Conjugative Plasmids in Klebsiella pneumoniae. Trends in Microbiology, 2021, 29, 65-83.	7.7	133
17	Emergence of ST63 Pandrug-Resistant Acinetobacter pittii Isolated From an AECOPD Patient in China. Frontiers in Cellular and Infection Microbiology, 2021, 11, 739211.	3.9	6
18	Co-conjugation of Virulence Plasmid and KPC Plasmid in a Clinical Klebsiella pneumoniae Strain. Frontiers in Microbiology, 2021, 12, 739461.	3.5	15

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19	Emergence of an Empedobacter falsenii strain harbouring a tet(X)-variant-bearing novel plasmid conferring resistance to tigecycline. Journal of Antimicrobial Chemotherapy, 2020, 75, 531-536.	3.0	16
20	A hybrid plasmid formed by recombination of a virulence plasmid and a resistance plasmid in Klebsiella pneumoniae. Journal of Global Antimicrobial Resistance, 2020, 23, 466-470.	2.2	13
21	Detection and genetic characterization of the colistin resistance gene mcr-3.3 in an Aeromonas veronii strain isolated from alligator faeces. Journal of Global Antimicrobial Resistance, 2020, 22, 860-861.	2.2	2
22	Chromosomal and Plasmid-Borne Tigecycline Resistance Genes <i>tet</i> (X3) and <i>tet</i> (X4) in Dairy Cows on a Chinese Farm. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	16
23	Epidemiological and phylogenetic analysis reveals Flavobacteriaceae as potential ancestral source of tigecycline resistance gene tet(X). Nature Communications, 2020, 11, 4648.	12.8	47
24	Genetic cluster analysis of SARS-CoV-2 and the identification of those responsible for the major outbreaks in various countries. Emerging Microbes and Infections, 2020, 9, 1287-1299.	6.5	51
25	Prevalence and molecular epidemiology of mcr-1-positive Klebsiella pneumoniae in healthy adults from China. Journal of Antimicrobial Chemotherapy, 2020, 75, 2485-2494.	3.0	17
26	Conjugation of Virulence Plasmid in Clinical <i>Klebsiella pneumoniae</i> Strains through Formation of a Fusion Plasmid. Advanced Biology, 2020, 4, e1900239.	3.0	49
27	Colistin-resistance gene <i>mcr</i> in clinical carbapenem-resistant <i>Enterobacteriaceae</i> strains in China, 2014–2019. Emerging Microbes and Infections, 2020, 9, 237-245.	6.5	44
28	Evolution of Ciprofloxacin Resistance-Encoding Genetic Elements in <i>Salmonella</i> . MSystems, 2020, 5, .	3.8	11
29	Evolution of Carbapenem-Resistant Serotype K1 Hypervirulent Klebsiella pneumoniae by Acquisition of <i>bla</i> <sub>VIM-1</sub> -Bearing Plasmid. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	26
30	Transmission of ciprofloxacin resistance in <i>Salmonella</i> mediated by a novel type of conjugative helper plasmids. Emerging Microbes and Infections, 2019, 8, 857-865.	6.5	40
31	Application of CRISPR/Cas9-Based Genome Editing in Studying the Mechanism of Pandrug Resistance in Klebsiella pneumoniae. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	24
32	Leclercia adecarboxylata From Human Gut Flora Carries mcr-4.3 and blaIMP-4-Bearing Plasmids. Frontiers in Microbiology, 2019, 10, 2805.	3.5	9
33	Emergence of OXA-232 Carbapenemase-Producing <i>Klebsiella pneumoniae</i> That Carries a pLVPK-Like Virulence Plasmid among Elderly Patients in China. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	67
34	An IncR Plasmid Harbored by a Hypervirulent Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strain Possesses Five Tandem Repeats of the <i>bla</i> <sub>KPC-2</sub> ::NTE <sub>KPC</sub> -ld Fragment. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	20
35	Molecular Characterization of <i>qnrVC</i> Genes and Their Novel Alleles in Vibrio spp. Isolated from Food Products in China. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	19
36	Efficient generation of complete sequences of MDR-encoding plasmids by rapid assembly of MinION barcoding sequencing data. GigaScience, 2018, 7, 1-9.	6.4	140

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37	A fatal outbreak of ST11 carbapenem-resistant hypervirulent Klebsiella pneumoniae in a Chinese hospital: a molecular epidemiological study. Lancet Infectious Diseases, The, 2018, 18, 37-46.	9.1	683
38	Genetic basis of chromosomally-encoded mcr-1 gene. International Journal of Antimicrobial Agents, 2018, 51, 578-585.	2.5	46
39	Genome analysis of clinical multilocus sequence Type 11 Klebsiella pneumoniae from China. Microbial Genomics, 2018, 4, .	2.0	52
40	Carriage of blaKPC-2 by a virulence plasmid in hypervirulent Klebsiella pneumoniae. Journal of Antimicrobial Chemotherapy, 2018, 73, 3317-3321.	3.0	67
41	Identification and Characterization of Conjugative Plasmids That Encode Ciprofloxacin Resistance in Salmonella. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	18
42	Evolution of tigecycline- and colistin-resistant CRKP (carbapenem-resistant <i>Klebsiella) Tj ETQq0 0 0 rgBT /Over 1-11.</i>	lock 10 Tf 6.5	50 547 Td ( 47
43	Tracking microevolution events among ST11 carbapenemase-producing hypervirulent <i>Klebsiella pneumoniae</i> outbreak strains. Emerging Microbes and Infections, 2018, 7, 1-8.	6.5	65
44	Widespread distribution of mcr-1-bearing bacteria in the ecosystem, 2015 to 2016. Eurosurveillance, 2017, 22, .	7.0	58
45	Deinococcus antarcticus sp. nov., isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 331-335.	1.7	20
46	Phylogenetic Diversity and Biological Activity of Actinobacteria Isolated from the Chukchi Shelf Marine Sediments in the Arctic Ocean. Marine Drugs, 2014, 12, 1281-1297.	4.6	58
47	Overexpression of mltA in Edwardsiella tarda reduces resistance to antibiotics and enhances lethality in zebra fish. Journal of Applied Microbiology, 2012, 112, 1075-1085.	3.1	14
48	Genomic and protein structure modelling analysis depicts the origin and pathogenicity of 2019-nCoV, a new coronavirus which caused a pneumonia outbreak in Wuhan, China. F1000Research, 0, 9, 121.	1.6	3
49	Genomic and protein structure modelling analysis depicts the origin and pathogenicity of 2019-nCoV, a new coronavirus which caused a pneumonia outbreak in Wuhan, China. F1000Research, 0, 9, 121.	1.6	17
50	Deciphering Evolutional Mechanisms of Non-K1/K2 Hypervirulent <i>Klebsiella pneumoniae</i> . SSRN Electronic Journal, 0, , .	0.4	0
51	Prevalence, Risk Factors, Treatment Outcome and Molecular Epidemiology of Gastrointestinal Carbapenem-Resistant <i>Klebsiella Pneumoniae</i> from Infections in China. SSRN Electronic Journal, 0, , .	0.4	0
52	Isolation, Molecular Characterization, and Antimicrobial Resistance of Selected Culturable Bacteria From Crayfish (Procambarus clarkii). Frontiers in Microbiology, 0, 13, .	3.5	0
53	Emergence of Mobilized Colistin Resistance Gene <i>mcr-8.2</i> in Multidrug-Resistant Enterobacter cloacae Isolated from a Patient in China. Microbiology Spectrum, 0, , .	3.0	1