Ning Dong

List of Publications by Year
in descending order

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53	2,198	361413	265206
papers	citations	20	42
		h-index	g-index

57	57	57	2249
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	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
3	Carbapenem Resistance-Encoding and Virulence-Encoding Conjugative Plasmids in Klebsiella pneumoniae. Trends in Microbiology, 2021, 29, 65-83.	7.7	133
4	Carriage of blaKPC-2 by a virulence plasmid in hypervirulent Klebsiella pneumoniae. Journal of Antimicrobial Chemotherapy, 2018, 73, 3317-3321.	3.0	67
5	Emergence of OXA-232 Carbapenemase-Producing Klebsiella pneumoniae That Carries a pLVPK-Like Virulence Plasmid among Elderly Patients in China. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	67
6	Tracking microevolution events among ST11 carbapenemase-producing hypervirulent Klebsiella pneumoniae outbreak strains. Emerging Microbes and Infections, 2018, 7, 1-8.	6.5	65
7	Klebsiella species: Taxonomy, hypervirulence and multidrug resistance. EBioMedicine, 2022, 79, 103998.	6.1	65
8	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
9	Widespread distribution of mcr-1-bearing bacteria in the ecosystem, 2015 to 2016. Eurosurveillance, 2017, 22, .	7.0	58
10	Genome analysis of clinical multilocus sequence Type 11 Klebsiella pneumoniae from China. Microbial Genomics, 2018, 4, .	2.0	52
11	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
12	Conjugation of Virulence Plasmid in Clinical Klebsiella pneumoniae Strains through Formation of a Fusion Plasmid. Advanced Biology, 2020, 4, e1900239.	3.0	49
13	Evolution of tigecycline- and colistin-resistant CRKP (carbapenem-resistant Klebsiella) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 1-11.	6.5	47
14	Epidemiological and phylogenetic analysis reveals Flavobacteriaceae as potential ancestral source of tigecycline resistance gene tet(X). Nature Communications, 2020, 11, 4648.	12.8	47
15	Genetic basis of chromosomally-encoded mcr-1 gene. International Journal of Antimicrobial Agents, 2018, 51, 578-585.	2.5	46
16	Clinical evolution of ST11 carbapenem resistant and hypervirulent Klebsiella pneumoniae. Communications Biology, 2021, 4, 650.	4.4	45
17	Colistin-resistance gene mcr in clinical carbapenem-resistant Enterobacteriaceae strains in China, 2014â€“2019. Emerging Microbes and Infections, 2020, 9, 237-245.	6.5	44
18	Transmission of ciprofloxacin resistance in Salmonella mediated by a novel type of conjugative helper plasmids. Emerging Microbes and Infections, 2019, 8, 857-865.	6.5	40

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19	Evolution of Carbapenem-Resistant Serotype K1 Hypervirulent Klebsiella pneumoniae by Acquisition of bla _{VIM-1} -Bearing Plasmid. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	26
20	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
21	Deinococcus antarcticus sp. nov., isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 331-335.	1.7	20
22	An IncR Plasmid Harbored by a Hypervirulent Carbapenem-Resistant Klebsiella pneumoniae Strain Possesses Five Tandem Repeats of the bla _{KPC-2} ::NTE _{KPC} -Id Fragment. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	20
23	Molecular Characterization of qnrVC Genes and Their Novel Alleles in Vibrio spp. Isolated from Food Products in China. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	19
24	Identification and Characterization of Conjugative Plasmids That Encode Ciprofloxacin Resistance in Salmonella. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	18
25	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
26	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
27	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
28	Bactericidal, anti-biofilm, and anti-virulence activity of vitamin C against carbapenem-resistant hypervirulent Klebsiella pneumoniae. IScience, 2022, 25, 103894.	4.1	17
29	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
30	Chromosomal and Plasmid-Borne Tigecycline Resistance Genes tet (X3) and tet (X4) in Dairy Cows on a Chinese Farm. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	16
31	Molecular epidemiology of carbapenem-resistant Klebsiella pneumoniae in China, 2016â€“20. Lancet Infectious Diseases, The, 2022, 22, 167-168.	9.1	16
32	Co-conjugation of Virulence Plasmid and KPC Plasmid in a Clinical Klebsiella pneumoniae Strain. Frontiers in Microbiology, 2021, 12, 739461.	3.5	15
33	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
34	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
35	Evolution of Ciprofloxacin Resistance-Encoding Genetic Elements in Salmonella. MSystems, 2020, 5, .	3.8	11
36	Leclercia adecarboxylata From Human Gut Flora Carries mcr-4.3 and blaIMP-4-Bearing Plasmids. Frontiers in Microbiology, 2019, 10, 2805.	3.5	9

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37	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
38	Transmission of pLVPK-like virulence plasmid in Klebsiella pneumoniae mediated by an IncI1 conjugative helper plasmid. IScience, 2022, 25, 104428.	4.1	8
39	Complete Genetic Analysis of Plasmids Carried by Two Nonclonal bla _{NDM-5} - and mcr-1 -Bearing Escherichia coli Strains: Insight into Plasmid Transmission among Foodborne Bacteria. Microbiology Spectrum, 2021, 9, e0021721.	3.0	6
40	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
41	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
42	Co-transfer of last-line antibiotic resistance and virulence operons by an IncFIBk-FII-X3-ColKP3 hybrid plasmid in Klebsiella pneumoniae. Journal of Antimicrobial Chemotherapy, 2022, 77, 1856-1861.	3.0	5
43	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
44	High-Resolution Metagenomics of Human Gut Microbiota Generated by Nanopore and Illumina Hybrid Metagenome Assembly. Frontiers in Microbiology, 2022, 13, .	3.5	4
45	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
46	Effectiveness of a double-carbapenem combinations against carbapenem-resistant Gram-negative bacteria. Saudi Pharmaceutical Journal, 2022, 30, 849-855.	2.7	3
47	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
48	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
49	Advanced Genetic Methodologies in Tracking Evolution and Spread of SARS-CoV-2. Methods in Molecular Biology, 2022, 2452, 33-43.	0.9	1
50	Emergence of Mobilized Colistin Resistance Gene mcr-8.2 in Multidrug-Resistant Enterobacter cloacae Isolated from a Patient in China. Microbiology Spectrum, 0, , .	3.0	1
51	Deciphering Evolutional Mechanisms of Non-K1/K2 Hypervirulent <i>Klebsiella pneumoniae</i>. SSRN Electronic Journal, 0, , .	0.4	0
52	Prevalence, Risk Factors, Treatment Outcome and Molecular Epidemiology of Gastrointestinal Carbapenem-Resistant Klebsiella Pneumoniae from Infections in China. SSRN Electronic Journal, 0, , .	0.4	0
53	Isolation, Molecular Characterization, and Antimicrobial Resistance of Selected Culturable Bacteria From Crayfish (Procambarus clarkii). Frontiers in Microbiology, 0, 13, .	3.5	0