

The Comprehensive Antibiotic Resistance Database

Antimicrobial Agents and Chemotherapy

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Innate Growth Bistability and Fitness Landscapes of Antibiotic-Resistant Bacteria. <i>Science</i> , 2013, 342, 1237435.	6.0	168
2	Draft Genome Sequence of Strain SA_ST125_MupR of Methicillin-Resistant <i>Staphylococcus aureus</i> ST125, a Major Clone in Spain. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
3	Draft Genome Sequence of a Multidrug-Resistant New Delhi Metallo- β -Lactamase-1 (NDM-1)-Producing <i>Escherichia coli</i> Isolate Obtained in Singapore. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
4	Draft Whole-Genome Sequence of VIM-1-Producing Multidrug-Resistant <i>Enterobacter cloacae</i> EC_38VIM1. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
5	Abundances of Tetracycline, Sulphonamide and Beta-Lactam Antibiotic Resistance Genes in Conventional Wastewater Treatment Plants (WWTPs) with Different Waste Load. <i>PLoS ONE</i> , 2014, 9, e103705.	1.1	144
6	Evaluation of a Hybrid Approach Using UBLAST and BLASTX for Metagenomic Sequences Annotation of Specific Functional Genes. <i>PLoS ONE</i> , 2014, 9, e110947.	1.1	36
7	Characterization of Antimicrobial Resistance Dissemination across Plasmid Communities Classified by Network Analysis. <i>Pathogens</i> , 2014, 3, 356-376.	1.2	26
8	CBMAR: a comprehensive β -lactamase molecular annotation resource. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau111.	1.4	36
9	Strategies for Circumventing Bacterial Resistance Mechanisms. , 2014, , 1-29.		0
10	Draft Whole-Genome Sequence of OXA-48-Producing Multidrug-Resistant <i>Klebsiella pneumoniae</i> KP_ST11_OXA-48. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
11	Prediction of <i>Staphylococcus aureus</i> Antimicrobial Resistance by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1182-1191.	1.8	303
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13	BacMet: antibacterial biocide and metal resistance genes database. <i>Nucleic Acids Research</i> , 2014, 42, D737-D743.	6.5	564
14	Abundant rifampin resistance genes and significant correlations of antibiotic resistance genes and plasmids in various environments revealed by metagenomic analysis. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5195-5204.	1.7	87
15	Barriers to the spread of resistance. <i>Nature</i> , 2014, 509, 567-568.	13.7	20
16	Bacterial phylogeny structures soil resistomes across habitats. <i>Nature</i> , 2014, 509, 612-616.	13.7	973
17	Energy storage wrapped up. <i>Nature</i> , 2014, 509, 568-569.	13.7	163
18	Antibiotic resistance gene discovery in food-producing animals. <i>Current Opinion in Microbiology</i> , 2014, 19, 25-29.	2.3	77

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20	Safety assessment of the butyrate-producing <i>Butyricoccus pullicaecorum</i> strain 25-3T, a potential probiotic for patients with inflammatory bowel disease, based on oral toxicity tests and whole genome sequencing. <i>Food and Chemical Toxicology</i> , 2014, 72, 129-137.	1.8	43
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25	Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. <i>Nature Communications</i> , 2014, 5, 4352.	5.8	195
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30	Antibiotic Resistance via Membrane Efflux Pumps. , 0, , 220-229.		0
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44	Antibiotics That Target DNA and RNA Information Transfer. , 0, , 148-162.		0
45	Antibiotics That Block Biosynthesis of the DNA Building Block Deoxythymidylate. , 0, , 164-176.		0
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69	Draft Genome Sequence of <i>Mycobacterium heraklionense</i> Strain Davo. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
70	Draft Genome Sequence of <i>Mycobacterium heckeshornense</i> Strain RLE. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
71	Complete Genome Sequencing of <i>Stenotrophomonas acidaminiphila</i> ZAC14D2_NAIMI4_2, a Multidrug-Resistant Strain Isolated from Sediments of a Polluted River in Mexico, Uncovers New Antibiotic Resistance Genes and a Novel Class-II Lasso Peptide Biosynthesis Gene Cluster. <i>Genome Announcements</i> , 2015, 3, .	0.8	18
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