

MEGARes: an antimicrobial resistance database for high

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Genomic approaches to characterizing and reducing antimicrobial resistance in beef cattle production systems. <i>Canadian Journal of Animal Science</i> , 0, , .	0.7	0
3	Unexpected persistence of extended-spectrum β -lactamase-producing Enterobacteriaceae in the faecal microbiota of hospitalised patients treated with imipenem. <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 81-87.	1.1	23
4	Impact of "Raised without Antibiotics" Beef Cattle Production Practices on Occurrences of Antimicrobial Resistance. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	99
5	Establishing Genotype-to-Phenotype Relationships in Bacteria Causing Hospital-Acquired Pneumonia: A Prelude to the Application of Clinical Metagenomics. <i>Antibiotics</i> , 2017, 6, 30.	1.5	54
6	Metagenomics: The Next Culture-Independent Game Changer. <i>Frontiers in Microbiology</i> , 2017, 8, 1069.	1.5	230
7	Enrichment allows identification of diverse, rare elements in metagenomic resistome-virulome sequencing. <i>Microbiome</i> , 2017, 5, 142.	4.9	78
8	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017, 3, e000131.	1.0	478
9	Impact of sequencing depth on the characterization of the microbiome and resistome. <i>Scientific Reports</i> , 2018, 8, 5890.	1.6	174
10	ARGs-OAP v2.0 with an expanded SARG database and Hidden Markov Models for enhancement characterization and quantification of antibiotic resistance genes in environmental metagenomes. <i>Bioinformatics</i> , 2018, 34, 2263-2270.	1.8	375
11	MetaCherchant: analyzing genomic context of antibiotic resistance genes in gut microbiota. <i>Bioinformatics</i> , 2018, 34, 434-444.	1.8	31
12	Antimicrobial resistance in non-aureus staphylococci isolated from milk is associated with systemic but not intramammary administration of antimicrobials in dairy cattle. <i>Journal of Dairy Science</i> , 2018, 101, 7425-7436.	1.4	36
13	Complete genome sequence of <i>Bifidobacterium choerinum</i> FMB-1, a resistant starch-degrading bacterium. <i>Journal of Biotechnology</i> , 2018, 274, 28-32.	1.9	10
14	Antibiotic-Resistance Genes in Waste Water. <i>Trends in Microbiology</i> , 2018, 26, 220-228.	3.5	627
15	In vivo selection of a multidrug-resistant <i>Aeromonas salmonicida</i> during medicinal leech therapy. <i>New Microbes and New Infections</i> , 2018, 21, 23-27.	0.8	19
16	A fast and agnostic method for bacterial genome-wide association studies: Bridging the gap between k-mers and genetic events. <i>PLoS Genetics</i> , 2018, 14, e1007758.	1.5	144
17	Draft genome sequence of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain Fito_F321, an endophyte microorganism from <i>Vitis vinifera</i> with biocontrol potential. <i>Standards in Genomic Sciences</i> , 2018, 13, 30.	1.5	25
18	Genome-wide analysis of horizontally acquired genes in the genus <i>Mycobacterium</i> . <i>Scientific Reports</i> , 2018, 8, 14817.	1.6	21
19	<i>Bifidobacterial</i> Dominance of the Gut in Early Life and Acquisition of Antimicrobial Resistance. <i>MSphere</i> , 2018, 3, .	1.3	71

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20	Discovering novel hydrolases from hot environments. <i>Biotechnology Advances</i> , 2018, 36, 2077-2100.	6.0	38
21	Investigating Effects of Tulathromycin Metaphylaxis on the Fecal Resistome and Microbiome of Commercial Feedlot Cattle Early in the Feeding Period. <i>Frontiers in Microbiology</i> , 2018, 9, 1715.	1.5	78
22	An Environmental Science and Engineering Framework for Combating Antimicrobial Resistance. <i>Environmental Engineering Science</i> , 2018, 35, 1005-1011.	0.8	47
23	Indexed variation graphs for efficient and accurate resistome profiling. <i>Bioinformatics</i> , 2018, 34, 3601-3608.	1.8	55
24	Whole-Genome Shotgun Sequencing of Three <i>Listeria monocytogenes</i> Strains Isolated from a Ready-to-Eat Salad-Producing Facility in Switzerland. <i>Genome Announcements</i> , 2018, 6, .	0.8	7
25	Whole-genome sequencing identification of a multidrug-resistant <i>Listeria monocytogenes</i> serotype 1/2a isolated from fresh mixed sausage in southern Brazil. <i>Infection, Genetics and Evolution</i> , 2018, 65, 127-130.	1.0	9
26	Prevalence and Genetic Basis of Antimicrobial Resistance in Non-aureus Staphylococci Isolated from Canadian Dairy Herds. <i>Frontiers in Microbiology</i> , 2018, 9, 256.	1.5	52
27	Effects of Ceftiofur and Chlortetracycline on the Resistomes of Feedlot Cattle. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	50
28	DeepARG: a deep learning approach for predicting antibiotic resistance genes from metagenomic data. <i>Microbiome</i> , 2018, 6, 23.	4.9	462
29	Antimicrobial Resistance in the Environment. <i>Water Environment Research</i> , 2018, 90, 865-884.	1.3	11
30	Using Genomics to Track Global Antimicrobial Resistance. <i>Frontiers in Public Health</i> , 2019, 7, 242.	1.3	263
31	Genomic and Ecogenomic Characterization of <i>Proteus mirabilis</i> Bacteriophages. <i>Frontiers in Microbiology</i> , 2019, 10, 1783.	1.5	13
32	Shifts in the Human Gut Microbiota Structure Caused by Quadruple <i>Helicobacter pylori</i> Eradication Therapy. <i>Frontiers in Microbiology</i> , 2019, 10, 1902.	1.5	39
33	Integrated genomic epidemiology and phenotypic profiling of <i>Clostridium difficile</i> across intra-hospital and community populations in Colombia. <i>Scientific Reports</i> , 2019, 9, 11293.	1.6	12
34	Gut microbiome alteration in MORDOR I: a community-randomized trial of mass azithromycin distribution. <i>Nature Medicine</i> , 2019, 25, 1370-1376.	15.2	90
35	Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. <i>Communications Biology</i> , 2019, 2, 294.	2.0	31
36	Characterization of the Microbial Resistome in Conventional and "Raised Without Antibiotics" Beef and Dairy Production Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 1980.	1.5	58
37	Investigation of tylosin in feed of feedlot cattle and effects on liver abscess prevalence, and fecal and soil microbiomes and resistomes ¹ . <i>Journal of Animal Science</i> , 2019, 97, 4567-4578.	0.2	21

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38	CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. <i>Nucleic Acids Research</i> , 2020, 48, D517-D525.	6.5	1,605
39	mNGS in clinical microbiology laboratories: on the road to maturity. <i>Critical Reviews in Microbiology</i> , 2019, 45, 668-685.	2.7	172
40	Comparative genomic analysis of the <i>Hafnia</i> genus reveals an explicit evolutionary relationship between the species <i>alvei</i> and <i>paralvei</i> and provides insights into pathogenicity. <i>BMC Genomics</i> , 2019, 20, 768.	1.2	19
41	Metagenomics: aid to combat antimicrobial resistance in diarrhea. <i>Gut Pathogens</i> , 2019, 11, 47.	1.6	34
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43	Diagnostic Optical Sequencing. <i>ACS Applied Materials & Interfaces</i> , 2019, 11, 35587-35596.	4.0	6
44	Fecal Transplant in Children With <i>Clostridioides difficile</i> Gives Sustained Reduction in Antimicrobial Resistance and Potential Pathogen Burden. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz379.	0.4	32
45	The fecal resistome of dairy cattle is associated with diet during nursing. <i>Nature Communications</i> , 2019, 10, 4406.	5.8	100
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48	Macrolide Resistance in MORDOR I – A Cluster-Randomized Trial in Niger. <i>New England Journal of Medicine</i> , 2019, 380, 2271-2273.	13.9	67
49	Linking the resistome and plasmidome to the microbiome. <i>ISME Journal</i> , 2019, 13, 2437-2446.	4.4	183
50	BOCS: DNA k-mer content and scoring for rapid genetic biomarker identification at low coverage. <i>Computers in Biology and Medicine</i> , 2019, 110, 196-206.	3.9	9
51	Genetic characterization of susceptible and multi-drug resistant <i>Mannheimia haemolytica</i> isolated from high-risk stocker calves prior to and after antimicrobial metaphylaxis. <i>Veterinary Microbiology</i> , 2019, 235, 110-117.	0.8	11
52	Effects of Dairy Manure-Based Amendments and Soil Texture on Lettuce- and Radish-Associated Microbiota and Resistomes. <i>MSphere</i> , 2019, 4, .	1.3	35
53	Integrating Whole-Genome Sequencing Data Into Quantitative Risk Assessment of Foodborne Antimicrobial Resistance: A Review of Opportunities and Challenges. <i>Frontiers in Microbiology</i> , 2019, 10, 1107.	1.5	73
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55	Application of Next-Generation Sequencing for Characterization of Surveillance and Clinical Trial Isolates: Analysis of the Distribution of β -lactamase Resistance Genes and Lineage Background in the United States. <i>Open Forum Infectious Diseases</i> , 2019, 6, S69-S78.	0.4	45

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58	Nasal Resistome Development in Infants With Cystic Fibrosis in the First Year of Life. <i>Frontiers in Microbiology</i> , 2019, 10, 212.	1.5	10
59	In Silico Drug Repurposing for MDR Bacteria: Opportunities and Challenges. , 2019, , 781-799.		2
60	Lower Respiratory Tract Microbiome and Resistome of Bovine Respiratory Disease Mortalities. <i>Microbial Ecology</i> , 2019, 78, 446-456.	1.4	46
61	The dynamics of the antibiotic resistome in the feces of freshly weaned pigs following therapeutic administration of oxytetracycline. <i>Scientific Reports</i> , 2019, 9, 4062.	1.6	45
62	Long-Term Azithromycin Reduces <i>Haemophilus influenzae</i> and Increases Antibiotic Resistance in Severe Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 309-317.	2.5	121
63	Bacterial colonization and antimicrobial resistance genes in neonatal enteral feeding tubes. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	9
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65	Effects of a <i>Saccharomyces cerevisiae</i> fermentation product on liver abscesses, fecal microbiome, and resistome in feedlot cattle raised without antibiotics. <i>Scientific Reports</i> , 2019, 9, 2559.	1.6	41
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70	A Cautionary Report for Pathogen Identification Using Shotgun Metagenomics; A Comparison to Aerobic Culture and Polymerase Chain Reaction for <i>Salmonella enterica</i> Identification. <i>Frontiers in Microbiology</i> , 2019, 10, 2499.	1.5	27
71	Gut uropathogen abundance is a risk factor for development of bacteriuria and urinary tract infection. <i>Nature Communications</i> , 2019, 10, 5521.	5.8	123
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73	Bioinformatics Workflows With NoSQL Database in Cloud Computing. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431988997.	0.6	4
74	Mobilome and Resistome Reconstruction from Genomes Belonging to Members of the <i>Bifidobacterium</i> Genus. <i>Microorganisms</i> , 2019, 7, 638.	1.6	25

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75	Genomic Diversity of Common Sequence Types of <i>Listeria monocytogenes</i> Isolated from Ready-to-Eat Products of Animal Origin in South Africa. <i>Genes</i> , 2019, 10, 1007.	1.0	8
77	Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	221
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80	Gut Resistome After Oral Antibiotics in Preschool Children in Burkina Faso: A Randomized, Controlled Trial. <i>Clinical Infectious Diseases</i> , 2020, 70, 525-527.	2.9	20
81	MEGARes 2.0: a database for classification of antimicrobial drug, biocide and metal resistance determinants in metagenomic sequence data. <i>Nucleic Acids Research</i> , 2020, 48, D561-D569.	6.5	227
82	Antimicrobial Resistance in Bacteria: Mechanisms, Evolution, and Persistence. <i>Journal of Molecular Evolution</i> , 2020, 88, 26-40.	0.8	324
83	Antimicrobial Resistance Following Azithromycin Mass Drug Administration: Potential Surveillance Strategies to Assess Public Health Impact. <i>Clinical Infectious Diseases</i> , 2020, 70, 1501-1508.	2.9	25
84	The microbial community of a biofilm lining the wall of a pristine cave in Western New Guinea. <i>Microbiological Research</i> , 2020, 241, 126584.	2.5	20
85	Metagenomic Characterization of the Microbiome and Resistome of Retail Ground Beef Products. <i>Frontiers in Microbiology</i> , 2020, 11, 541972.	1.5	12
86	Concordance of disk diffusion, broth microdilution, and whole-genome sequencing for determination of in vitro antimicrobial susceptibility of <i>Mannheimia haemolytica</i> . <i>Journal of Veterinary Internal Medicine</i> , 2020, 34, 2158-2168.	0.6	4
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91	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	1.7	82
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93	Bacterial Genome Wide Association Studies (bGWAS) and Transcriptomics Identifies Cryptic Antimicrobial Resistance Mechanisms in <i>Acinetobacter baumannii</i> . <i>Frontiers in Public Health</i> , 2020, 8, 451.	1.3	9

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95	Detection of Antimicrobial Resistance Genes in the Milk Production Environment: Impact of Host DNA and Sequencing Depth. <i>Frontiers in Microbiology</i> , 2020, 11, 1983.	1.5	21
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97	Oral Microbial Species and Virulence Factors Associated with Oral Squamous Cell Carcinoma. <i>Microbial Ecology</i> , 2021, 82, 1030-1046.	1.4	29
98	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	1.6	18
99	Dissemination of Quinolone-Resistant <i>Escherichia coli</i> in the Norwegian Broiler and Pig Production Chains and Possible Persistence in the Broiler Production Environment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
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103	The novel and transferable <i>erm</i> (51) gene confers macrolides, lincosamides and streptogramins B (MLS) Tj ETQq1 1 0.784314 rgBT /Ov 2858-2869.	1.8	15
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105	Survey of drug resistance associated gene mutations in <i>Mycobacterium tuberculosis</i> , ESKAPE and other bacterial species. <i>Scientific Reports</i> , 2020, 10, 8957.	1.6	37
106	Interest of bacterial pangenome analyses in clinical microbiology. <i>Microbial Pathogenesis</i> , 2020, 149, 104275.	1.3	12
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113	Mobilization of Antibiotic Resistance: Are Current Approaches for Colocalizing Resistomes and Mobilomes Useful?. Frontiers in Microbiology, 2020, 11, 1376.	1.5	33
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115	Reservoirs of antimicrobial resistance genes in retail raw milk. Microbiome, 2020, 8, 99.	4.9	47
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129	Taking the next-gen step: Comprehensive antimicrobial resistance detection from Burkholderia pseudomallei. EBioMedicine, 2021, 63, 103152.	2.7	18

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131	ResistoXplorer: a web-based tool for visual, statistical and exploratory data analysis of resistome data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab018.	1.5	9
132	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	15
133	Nanopore sequencing and its application to the study of microbial communities. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1497-1511.	1.9	106
134	WGS for Bacterial Identification and Susceptibility Testing in the Clinical Lab. , 2021, , 25-44.		1
135	Antibiotic resistance: Time of synthesis in a post-genomic age. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3110-3124.	1.9	28
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138	Monitoring the microbiome for food safety and quality using deep shotgun sequencing. <i>Npj Science of Food</i> , 2021, 5, 3.	2.5	22
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142	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
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145	Whole genome-based characterisation of antimicrobial resistance and genetic diversity in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> from ruminants. <i>Scientific Reports</i> , 2021, 11, 8998.	1.6	25
146	Importance of beta-lactam pharmacokinetics and pharmacodynamics on the recovery of microbial diversity in the airway of persons with cystic fibrosis. <i>Journal of Investigative Medicine</i> , 2021, 69, 1350-1359.	0.7	6
147	Gut Resistome of Preschool Children After Prolonged Mass Azithromycin Distribution: A Cluster-randomized Trial. <i>Clinical Infectious Diseases</i> , 2021, 73, 1292-1295.	2.9	6
148	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164

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150	Prevalence and mechanisms of antibiotic resistance in <i>Escherichia coli</i> isolated from mastitic dairy cattle in Canada. <i>BMC Microbiology</i> , 2021, 21, 222.	1.3	22
151	KARGA: Multi-platform Toolkit for k-mer-based Antibiotic Resistance Gene Analysis of High-throughput Sequencing Data. , 2021, 2021, .		8
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153	Horizontal Gene Transfer Is the Main Driver of Antimicrobial Resistance in Broiler Chicks Infected with <i>Salmonella enterica</i> Serovar Heidelberg. <i>MSystems</i> , 2021, 6, e0072921.	1.7	8
155	Characterisation of Early Positive <i>mcr-1</i> Resistance Gene and Plasmidome in <i>Escherichia coli</i> Pathogenic Strains Associated with Variable Phylogroups under Colistin Selection. <i>Antibiotics</i> , 2021, 10, 1041.	1.5	7
156	Computational resources in the management of antibiotic resistance: Speeding up drug discovery. <i>Drug Discovery Today</i> , 2021, 26, 2138-2151.	3.2	11
157	The Diagnostic Value of Metagenomic Next-Generation Sequencing in Lower Respiratory Tract Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 694756.	1.8	42
158	First report from Bangladesh on genetic diversity of multidrug-resistant <i>Pasteurella multocida</i> type B:2 in fowl cholera. <i>Veterinary World</i> , 2021, 14, 2527-2542.	0.7	7
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