

CARD 2020: antibiotic resistome surveillance with the CARD database

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The 27th annual Nucleic Acids Research database issue and molecular biology database collection. <i>Nucleic Acids Research</i> , 2020, 48, D1-D8.	6.5	470
2	<i>Latilactobacillus curvatus</i> : A Candidate Probiotic with Excellent Fermentation Properties and Health Benefits. <i>Foods</i> , 2020, 9, 1366.	1.9	24
3	Genomic Virulence Features of Two Novel Species <i>Nocardia bardulienensis</i> sp. nov. and <i>Nocardia gipuzkoensis</i> sp. nov., Isolated from Patients with Chronic Pulmonary Diseases. <i>Microorganisms</i> , 2020, 8, 1517.	1.6	24
4	Antibiotics Interfere with the Evolution of Plasmid Stability. <i>Current Biology</i> , 2020, 30, 3841-3847.e4.	1.8	37
5	Metagenomic Characterization of the Microbiome and Resistome of Retail Ground Beef Products. <i>Frontiers in Microbiology</i> , 2020, 11, 541972.	1.5	12
6	Predicting antimicrobial resistance using conserved genes. <i>PLoS Computational Biology</i> , 2020, 16, e1008319.	1.5	29
7	Complete Genome Sequences of Four Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Isolates from Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
8	Genomic characterization of a multidrug-resistant <i>Salmonella enterica</i> serovar Goldcoast sequence type 358 strain in China. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 23, 181-183.	0.9	3
9	Literature-Based Phenotype Survey and In Silico Genotype Investigation of Antibiotic Resistance in the Genus <i>Bifidobacterium</i> . <i>Current Microbiology</i> , 2020, 77, 4104-4113.	1.0	12
10	Exploration of the <i>Neisseria</i> Resistome Reveals Resistance Mechanisms in Commensals That May Be Acquired by <i>N. gonorrhoeae</i> through Horizontal Gene Transfer. <i>Antibiotics</i> , 2020, 9, 656.	1.5	33
11	Integrated genome-based probiotic relevance and safety evaluation of <i>Lactobacillus reuteri</i> PNW1. <i>PLoS ONE</i> , 2020, 15, e0235873.	1.1	36
12	Additives affect the distribution of metabolic profile, microbial communities and antibiotic resistance genes in high-moisture sweet corn kernel silage. <i>Bioresource Technology</i> , 2020, 315, 123821.	4.8	33
13	Metagenomic Profiling of Ocular Surface Microbiome Changes in Meibomian Gland Dysfunction. , 2020, 61, 22.		27
14	Experimental approaches to tracking mobile genetic elements in microbial communities. <i>FEMS Microbiology Reviews</i> , 2020, 44, 606-630.	3.9	23
15	The Effect of Iodine-Containing Nano-Micelles, FS-1, on Antibiotic Resistance, Gene Expression and Epigenetic Modifications in the Genome of Multidrug Resistant MRSA Strain <i>Staphylococcus aureus</i> ATCC BAA-39. <i>Frontiers in Microbiology</i> , 2020, 11, 581660.	1.5	9
16	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020, 11, 563975.	1.1	12
17	Genomic and Physiological Properties of a Facultative Methane-Oxidizing Bacterial Strain of <i>Methylocystis</i> sp. from a Wetland. <i>Microorganisms</i> , 2020, 8, 1719.	1.6	18
18	Living with sulfonamides: a diverse range of mechanisms observed in bacteria. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 10389-10408.	1.7	33

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19	Bacterial Whole Genome Sequencing on the Illumina iSeq 100 for Clinical and Public Health Laboratories. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 1419-1429.	1.2	8
20	Transcriptome-based design of antisense inhibitors potentiates carbapenem efficacy in CRE <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30699-30709.	3.3	20
21	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	1.7	82
22	Description of <i>Komagataeibacter melaceti</i> sp. nov. and <i>Komagataeibacter melomenus</i> sp. nov. Isolated from Apple Cider Vinegar. <i>Microorganisms</i> , 2020, 8, 1178.	1.6	34
23	Marine Plastics from Norwegian West Coast Carry Potentially Virulent Fish Pathogens and Opportunistic Human Pathogens Harboring New Variants of Antibiotic Resistance Genes. <i>Microorganisms</i> , 2020, 8, 1200.	1.6	56
24	Antimicrobial resistance in enteric bacteria: current state and next-generation solutions. <i>Gut Microbes</i> , 2020, 12, 1799654.	4.3	41
25	Gene Duplications in the Genomes of Staphylococci and Enterococci. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 160.	1.6	6
26	Identification of Antimicrobial Resistance-Associated Genes through Whole Genome Sequencing of <i>Mycoplasma bovis</i> Isolates with Different Antimicrobial Resistances. <i>Pathogens</i> , 2020, 9, 588.	1.2	8
27	CeO ₂ Nanoparticles Regulate the Propagation of Antibiotic Resistance Genes by Altering Cellular Contact and Plasmid Transfer. <i>Environmental Science & Technology</i> , 2020, 54, 10012-10021.	4.6	73
28	Development of an NGS-Based Workflow for Improved Monitoring of Circulating Plasmids in Support of Risk Assessment of Antimicrobial Resistance Gene Dissemination. <i>Antibiotics</i> , 2020, 9, 503.	1.5	13
29	Selective concentrations for trimethoprim resistance in aquatic environments. <i>Environment International</i> , 2020, 144, 106083.	4.8	30
30	Systematic Investigation of Resistance Evolution to Common Antibiotics Reveals Conserved Collateral Responses across Common Human Pathogens. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	9
31	Complete genome sequence of a novel lytic phage infecting <i>Aeromonas hydrophila</i> , an infectious agent in striped catfish (<i>Pangasianodon hypophthalmus</i>). <i>Archives of Virology</i> , 2020, 165, 2973-2977.	0.9	15
32	Antibiotic Resistance: Moving From Individual Health Norms to Social Norms in One Health and Global Health. <i>Frontiers in Microbiology</i> , 2020, 11, 1914.	1.5	64
33	Outer Membrane Disruption Overcomes Intrinsic, Acquired, and Spontaneous Antibiotic Resistance. <i>MBio</i> , 2020, 11, .	1.8	51
34	Tracking Antimicrobial Resistance Determinants in Diarrheal Pathogens: A Cross-Institutional Pilot Study. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5928.	1.8	8
35	Overcoming Acquired and Native Macrolide Resistance with Bicarbonate. <i>ACS Infectious Diseases</i> , 2020, 6, 2709-2718.	1.8	18
36	Fecal Pollution Drives Antibiotic Resistance and Class 1 Integron Abundance in Aquatic Environments of the Bolivian Andes Impacted by Mining and Wastewater. <i>Microorganisms</i> , 2020, 8, 1122.	1.6	21

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37	Genomic epidemiology of <i>Campylobacter jejuni</i> associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008533.	1.3	20
38	Genomic Surveillance for One Health Antimicrobial Resistance: Understanding Human, Animal, and Environmental Reservoirs and Transmission. <i>Handbook of Environmental Chemistry</i> , 2020, , 71-100.	0.2	2
39	Pan-genome analysis of <i>Paenibacillus polymyxa</i> strains reveals the mechanism of plant growth promotion and biocontrol. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1539-1558.	0.7	17
40	Plant Species-Dependent Increased Abundance and Diversity of IncP-1 Plasmids in the Rhizosphere: New Insights Into Their Role and Ecology. <i>Frontiers in Microbiology</i> , 2020, 11, 590776.	1.5	17
41	The distribution of microbiomes and resistomes across farm environments in conventional and organic dairy herds in Pennsylvania. <i>Environmental Microbiomes</i> , 2020, 15, 21.	2.2	11
42	Raw Cow Milk Bacterial Consortium as Bioindicator of Circulating Anti-Microbial Resistance (AMR). <i>Animals</i> , 2020, 10, 2378.	1.0	11
43	Distribution of Important Probiotic Genes and Identification of the Biogenic Amines Produced by <i>Lactobacillus acidophilus</i> PNW3. <i>Foods</i> , 2020, 9, 1840.	1.9	5
44	A Novel Family of <i>Acinetobacter</i> Mega-Plasmids Are Disseminating Multi-Drug Resistance Across the Globe While Acquiring Location-Specific Accessory Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 605952.	1.5	18
45	Genome-Resolved Metagenomics and Antibiotic Resistance Genes Analysis in Reclaimed Water Distribution Systems. <i>Water (Switzerland)</i> , 2020, 12, 3477.	1.2	7
46	Genomic Analysis of <i>Aeromonas veronii</i> C198, a Novel Mcr-3.41-Harboring Isolate from a Patient with Septicemia in Thailand. <i>Pathogens</i> , 2020, 9, 1031.	1.2	14
47	Extended-Spectrum β -Lactamases in Human Isolates of Multidrug-Resistant Non-typhoidal <i>Salmonella enterica</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 592223.	1.5	10
48	Antibiotic-resistant <i>Acinetobacter baumannii</i> is a One Health problem. <i>Lancet Microbe</i> , The, 2020, 1, e279.	3.4	29
49	HARP: a database of structural impacts of systematic missense mutations in drug targets of <i>Mycobacterium leprae</i> . <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3692-3704.	1.9	16
50	Antimicrobial Resistance and Genomic Characterization of OXA-48- and CTX-M-15-Co-Producing Hypervirulent <i>Klebsiella pneumoniae</i> ST23 Recovered from Nosocomial Outbreak. <i>Antibiotics</i> , 2020, 9, 862.	1.5	27
51	Comparative Genome Analysis Reveals the Molecular Basis of Niche Adaptation of <i>Staphylococcus epidermidis</i> Strains. <i>Frontiers in Genetics</i> , 2020, 11, 566080.	1.1	5
52	Genomic basis of antimicrobial resistance in non-toxigenic <i>Clostridium difficile</i> in Southeast Asia. <i>Anaerobe</i> , 2020, 66, 102290.	1.0	16
53	Genome Sequences of Four <i>Shigella boydii</i> Strains Representative of the Major <i>S. boydii</i> Clades. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
54	Whole-Genome Draft Assemblies of Difficult-to-Classify <i>Escherichia coli</i> O157 and Non-O157 Isolates from Feces of Canadian Feedlot Cattle. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3

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55	Genomic profiling of antimicrobial resistance genes in clinical isolates of Salmonella Typhi from patients infected with Typhoid fever in India. <i>Scientific Reports</i> , 2020, 10, 8299.	1.6	41
56	Emerging Threat of Antimicrobial Resistance in \hat{I}^2 -Hemolytic Streptococci. <i>Frontiers in Microbiology</i> , 2020, 11, 797.	1.5	15
57	Antibiotic resistance: bioinformatics-based understanding as a functional strategy for drug design. <i>RSC Advances</i> , 2020, 10, 18451-18468.	1.7	45
58	Nanopore sequencing reveals genomic map of CTX-M-type extended-spectrum \hat{I}^2 -lactamases carried by <i>Escherichia coli</i> strains isolated from blue mussels (<i>Mytilus edulis</i>) in Norway. <i>BMC Microbiology</i> , 2020, 20, 134.	1.3	13
59	Whole-Genome Sequence of <i>Geobacillus thermoleovorans</i> ARTRW1, Isolated from Armutlu Geothermal Spring, Turkey. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
60	GC-MS analysis of the methanolic extracts of <i>Smilax china</i> and <i>Salix alba</i> and their antioxidant activity. <i>Turkish Journal of Chemistry</i> , 2020, 44, 352-363.	0.5	15
61	Exploring potential of vaginal <i>Lactobacillus</i> isolates from South African women for enhancing treatment for bacterial vaginosis. <i>PLoS Pathogens</i> , 2020, 16, e1008559.	2.1	31
62	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
63	Metagenomics as a Tool To Monitor Reclaimed-Water Quality. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	14
64	Broad-Spectrum Cephalosporin-Resistant <i>Klebsiella</i> spp. Isolated from Diseased Horses in Austria. <i>Animals</i> , 2020, 10, 332.	1.0	15
65	Draft Genome Sequence of <i>Bifidobacterium pseudocatenulatum</i> Bif4, Isolated from Healthy Infant Feces. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
66	Genomic characterisation of a multidrug-resistant <i>Mycoplasma hominis</i> isolate recovered from a synovial fluid sample in China. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 282-284.	0.9	1
67	Reservoirs of antimicrobial resistance genes in retail raw milk. <i>Microbiome</i> , 2020, 8, 99.	4.9	47
68	PSORTm: a bacterial and archaeal protein subcellular localization prediction tool for metagenomics data. <i>Bioinformatics</i> , 2020, 36, 3043-3048.	1.8	10
69	Draft whole-genome sequence of <i>Brevibacterium casei</i> strain isolated from a bloodstream infection. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 685-689.	0.8	8
70	Characteristics of the antibiotic resistance genes in the soil of medical waste disposal sites. <i>Science of the Total Environment</i> , 2020, 730, 139042.	3.9	14
71	Complete Genome Sequences of Four Isolates of Vancomycin-Resistant <i>Enterococcus faecium</i> with the <i>vanA</i> Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
72	Platforms for elucidating antibiotic resistance in single genomes and complex metagenomes. <i>Environment International</i> , 2020, 138, 105667.	4.8	48

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73	Interregional spread in Spain of linezolid-resistant <i>Enterococcus</i> spp. isolates carrying the <i>optrA</i> and <i>poxA</i> genes. <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105977.	1.1	33
74	Restoring carbapenem efficacy: a novel carbapenem companion targeting metallo- β -lactamases in carbapenem-resistant <i>Enterobacterales</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 460-466.	1.3	11
75	Initial safety evaluation of <i>Enterococcus faecium</i> LBB.E81. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 11-17.	0.5	4
76	β -Lactamase-Producing, Ciprofloxacin-Resistant <i>Neisseria meningitidis</i> Isolated From a 5-Month-Old Boy in the United States. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, 379-381.	0.6	4
77	Distribution of Beta-Lactamase Producing Gram-Negative Bacterial Isolates in Isabela River of Santo Domingo, Dominican Republic. <i>Frontiers in Microbiology</i> , 2021, 11, 519169.	1.5	2
78	Genome sequences of antibiotic-resistant <i>Streptococcus suis</i> strains isolated from human patients and diseased and asymptomatic pigs in Thailand. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104674.	1.0	9
79	Fate and removal of bacteria and antibiotic resistance genes in horizontal subsurface constructed wetlands: Effect of mixed vegetation and substrate type. <i>Science of the Total Environment</i> , 2021, 759, 144193.	3.9	30
80	Genome analysis reveals probiotic propensities of <i>Paenibacillus polymyxa</i> HK4. <i>Genomics</i> , 2021, 113, 861-873.	1.3	27
81	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
82	Closed Genome and Plasmid Sequences of <i>Legionella pneumophila</i> AW-13-4, Isolated from a Hot Water Loop System of a Large Occupational Building. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
83	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	15
84	Analysis of Genome Sequences of Coagulase-Negative <i>Staphylococci</i> Isolates from South Africa and Nigeria Highlighted Environmentally Driven Heterogeneity. <i>Journal of Genomics</i> , 2021, 9, 26-37.	0.6	0
85	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
86	Train-the-Trainer as an Effective Approach to Building Global Networks of Experts in Genomic Surveillance of Antimicrobial Resistance (AMR). <i>Clinical Infectious Diseases</i> , 2021, 73, S283-S289.	2.9	8
87	Peeling the Layers Away: The Genomic Characterization of <i>Bacillus pumilus</i> 64-1, an Isolate With Antimicrobial Activity From the Marine Sponge <i>Plakina cyanorosea</i> (Porifera, Homoscleromorpha). <i>Frontiers in Microbiology</i> , 2020, 11, 592735.	1.5	9
88	Genomic Characterization of VIM and MCR Co-Producers: The First Two Clinical Cases, in Italy. <i>Diagnostics</i> , 2021, 11, 79.	1.3	15
90	Comparative Genomics of <i>Leuconostoc carnosum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 605127.	1.5	11
92	Genome-wide comparison of four MRSA clinical isolates from Germany and Hungary. <i>PeerJ</i> , 2021, 9, e10185.	0.9	6

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93	Antibiotic resistance: Time of synthesis in a post-genomic age. Computational and Structural Biotechnology Journal, 2021, 19, 3110-3124.	1.9	28
94	Complete genome sequence of Salmonella enterica strain K_SA184, multidrug resistance bacterium isolated from lamb (<i>Ovis aries</i>). Journal of Animal Science and Technology, 2021, 63, 194-197.	0.8	3
95	Unearthing Antibiotic Resistance Associated with Disturbance-Induced Permafrost Thaw in Interior Alaska. Microorganisms, 2021, 9, 116.	1.6	15
96	Genomic characterization of four <i>Escherichia coli</i> strains isolated from oral lichen planus biopsies. Journal of Oral Microbiology, 2021, 13, 1905958.	1.2	5
97	The repertoire of ABC proteins in <i>Clostridioides difficile</i> . Computational and Structural Biotechnology Journal, 2021, 19, 2905-2920.	1.9	5
98	Whole-Genome Sequencing of Clinically Isolated Carbapenem-Resistant Enterobacterales Harboring mcr Genes in Thailand, 2016–2019. Frontiers in Microbiology, 2020, 11, 586368.	1.5	24
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101	Genomic Characterization of Multidrug-Resistant <i>Escherichia coli</i> BH100 Sub-strains. Frontiers in Microbiology, 2020, 11, 549254.	1.5	5
102	ApmA Is a Unique Aminoglycoside Antibiotic Acetyltransferase That Inactivates Apramycin. MBio, 2021, 12, .	1.8	12
103	Genotypic and Phenotypic Characterization of <i>Staphylococcus aureus</i> Isolates from the Respiratory Tract in Mechanically-Ventilated Patients. Toxins, 2021, 13, 122.	1.5	6
104	Comparative Genomic Analysis of Three <i>Pseudomonas</i> Species Isolated from the Eastern Oyster (<i>Crassostrea virginica</i>) Tissues, Mantle Fluid, and the Overlying Estuarine Water Column. Microorganisms, 2021, 9, 490.	1.6	7
105	Hypo- and Hyper-Virulent <i>Listeria monocytogenes</i> Clones Persisting in Two Different Food Processing Plants of Central Italy. Microorganisms, 2021, 9, 376.	1.6	25
106	Complete Genome Sequencing of <i>Acinetobacter baumannii</i> AC1633 and <i>Acinetobacter nosocomialis</i> AC1530 Unveils a Large Multidrug-Resistant Plasmid Encoding the NDM-1 and OXA-58 Carbapenemases. MSphere, 2021, 6, .	1.3	14
107	Modern View on <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> Resistance Mechanisms to Antibiotics. Antibiotiki I Khimioterapiya, 2021, 65, 38-48.	0.1	1
108	Antimicrobial resistance and interspecies gene transfer in <i>Campylobacter coli</i> and <i>Campylobacter jejuni</i> isolated from food animals, poultry processing, and retail meat in North Carolina, 2018–2019. PLoS ONE, 2021, 16, e0246571.	1.1	34
109	Isolation and characterization of a novel <i>Escherichia coli</i> Kayfunavirus phage DY1. Virus Research, 2021, 293, 198274.	1.1	16
110	The Emergence of Invasive <i>Streptococcus pneumoniae</i> Serotype 24F in Lebanon: Complete Genome Sequencing Reveals High Virulence and Antimicrobial Resistance Characteristics. Frontiers in Microbiology, 2021, 12, 637813.	1.5	10

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111	Exploring Antibiotic Resistance Diversity in <i>Leuconostoc</i> spp. by a Genome-Based Approach: Focus on the <i>IsaA</i> Gene. <i>Microorganisms</i> , 2021, 9, 491.	1.6	8
112	Comparative genomics reveals broad genetic diversity, extensive recombination and nascent ecological adaptation in <i>Micrococcus luteus</i> . <i>BMC Genomics</i> , 2021, 22, 124.	1.2	15
113	Genomic Investigation of Virulence Potential in Shiga Toxin <i>Escherichia coli</i> (STEC) Strains From a Semi-Hard Raw Milk Cheese. <i>Frontiers in Microbiology</i> , 2020, 11, 629189.	1.5	5
115	Draft Genome Sequence of Invasive <i>Salmonella enterica</i> Serovar Cannstatt Harboring <i>mcr-1.1</i> , Isolated from a Fatal Sepsis Case. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
116	The Antibiotic Resistome: A Guide for the Discovery of Natural Products as Antimicrobial Agents. <i>Chemical Reviews</i> , 2021, 121, 3464-3494.	23.0	114
117	Genomic islands mediate environmental adaptation and the spread of antibiotic resistance in multiresistant <i>Enterococci</i> - evidence from genomic sequences. <i>BMC Microbiology</i> , 2021, 21, 55.	1.3	14
118	<i>Janthinobacterium tructae</i> sp. nov., Isolated from Kidney of Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>Pathogens</i> , 2021, 10, 229.	1.2	11
119	Epidemiological analysis of pneumococcal strains isolated at Yangon Children's Hospital in Myanmar via whole-genome sequencing-based methods. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
120	Genetic Plurality of OXA/NDM-Encoding Features Characterized From <i>Enterobacterales</i> Recovered From Czech Hospitals. <i>Frontiers in Microbiology</i> , 2021, 12, 641415.	1.5	21
121	Tracking the Origin of Austrian Human Brucellosis Cases Using Whole Genome Sequencing. <i>Frontiers in Medicine</i> , 2021, 8, 635547.	1.2	14
122	Ruminal resistome of dairy cattle is individualized and the resistotypes are associated with milking traits. <i>Animal Microbiome</i> , 2021, 3, 18.	1.5	14
123	Dissemination of Extended-Spectrum- β -Lactamase-Producing <i>Enterobacter cloacae</i> Complex from a Hospital to the Nearby Environment in Guadeloupe (French West Indies): ST114 Lineage Coding for a Successful <i>InchI2/ST1</i> Plasmid. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	9
124	Sequence characterisation and novel insights into bovine mastitis-associated <i>Streptococcus uberis</i> in dairy herds. <i>Scientific Reports</i> , 2021, 11, 3046.	1.6	16
127	PathoFact: a pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. <i>Microbiome</i> , 2021, 9, 49.	4.9	81
128	Metagenomic Quantification of Genes with Internal Standards. <i>MBio</i> , 2021, 12, .	1.8	18
129	Draft Genome Sequences of 27 Northern Maine Clinical Isolates. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
130	Gentamicin Adsorption onto Soil Particles Prevents Overall Short-Term Effects on the Soil Microbiome and Resistome. <i>Antibiotics</i> , 2021, 10, 191.	1.5	3
131	Impact of Probiotic <i>B. infantis</i> EVC001 Feeding in Premature Infants on the Gut Microbiome, Nosocomially Acquired Antibiotic Resistance, and Enteric Inflammation. <i>Frontiers in Pediatrics</i> , 2021, 9, 618009.	0.9	38

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132	Genomic Background and Phylogeny of <i>cfiA</i> -Positive <i>Bacteroides fragilis</i> Strains Resistant to Meropenem-EDTA. <i>Antibiotics</i> , 2021, 10, 304.	1.5	8
133	Whole-genome analysis of probiotic product isolates reveals the presence of genes related to antimicrobial resistance, virulence factors, and toxic metabolites, posing potential health risks. <i>BMC Genomics</i> , 2021, 22, 210.	1.2	30
134	Identification of Microbiome Etiology Associated With Drug Resistance in Pleural Empyema. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 637018.	1.8	16
135	Genomic insights into evolution of pathogenicity and resistance of multidrug-resistant <i>Raoultella ornithinolytica</i> WM1. <i>Annals of the New York Academy of Sciences</i> , 2021, 1497, 74-90.	1.8	7
136	Market Chickens as a Source of Antibiotic-Resistant <i>Escherichia coli</i> in a Peri-Urban Community in Lima, Peru. <i>Frontiers in Microbiology</i> , 2021, 12, 635871.	1.5	27
137	Genome analysis and antimicrobial resistance characteristics of <i>Chryseobacterium aquaticum</i> isolated from farmed salmonids. <i>Aquaculture</i> , 2021, 535, 736364.	1.7	11
138	Comparison of three species of <i>Elizabethkingia</i> genus by whole-genome sequence analysis. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	6
139	Resistance Determinants and Their Genetic Context in Enterobacteria from a Longitudinal Study of Pigs Reared under Various Husbandry Conditions. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
140	Prevalence and Genetic Diversity of <i>Listeria monocytogenes</i> Isolated From Retail Pork in Wuhan, China. <i>Frontiers in Microbiology</i> , 2021, 12, 620482.	1.5	13
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1016	KARGAMobile: Android app for portable, real-time, easily interpretable analysis of antibiotic resistance genes via nanopore sequencing. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	1
1017	Effect of Thermophilic Microbial Agents on Antibiotic Resistance Genes and Microbial Communities during Co-Composting of Pig Manure and Tea Stalks. <i>Sustainability</i> , 2022, 14, 12593.	1.6	3

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