

CARD 2017: expansion and model-centric curation of the resistance database

Nucleic Acids Research

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Rapid resistome mapping using nanopore sequencing. <i>Nucleic Acids Research</i> , 2017, 45, gkw1328.	6.5	62
2	Multidrug-resistant <i>Achromobacter animicus</i> causing wound infection in a street child in Mwanza, Tanzania. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 88, 58-61.	0.8	3
3	Mining prokaryotes for antimicrobial compounds: from diversity to function. <i>FEMS Microbiology Reviews</i> , 2017, 41, 417-429.	3.9	88
4	Whole-Genome Sequencing of Drug-Resistant <i>Salmonella enterica</i> Isolates from Dairy Cattle and Humans in New York and Washington States Reveals Source and Geographic Associations. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	89
5	IslandViewer 4: expanded prediction of genomic islands for larger-scale datasets. <i>Nucleic Acids Research</i> , 2017, 45, W30-W35.	6.5	1,251
6	MCR-1 and OXA-48 <i>In Vivo</i> Acquisition in KPC-Producing <i>Escherichia coli</i> after Colistin Treatment. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	74
7	Genome sequence of <i>Shigella flexneri</i> strain SP1, a diarrheal isolate that encodes an extended-spectrum β -lactamase (ESBL). <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2017, 16, 37.	1.7	7
8	Whole-Genome Sequencing Accurately Identifies Resistance to Extended-Spectrum β -Lactams for Major Gram-Negative Bacterial Pathogens. <i>Clinical Infectious Diseases</i> , 2017, 65, 738-745.	2.9	56
9	Draft Genome Sequence of a Strain of <i>Bacillus intestinalis</i> sp. nov., a New Member of Sporobiota Isolated from the Small Intestine of a Single Patient with Intestinal Cancer. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
10	Fine-Scale Structure Analysis Shows Epidemic Patterns of Clonal Complex 95, a Cosmopolitan <i>Escherichia coli</i> Lineage Responsible for Extraintestinal Infection. <i>MSphere</i> , 2017, 2, .	1.3	32
11	Comparative genomics of free-living Gammaproteobacteria: pathogenesis-related genes or interaction-related genes?. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	23
12	Genome sequencing and comparative analysis of an NDM-1-producing <i>Klebsiella pneumoniae</i> ST15 isolated from a refugee patient. <i>Pathogens and Global Health</i> , 2017, 111, 166-175.	1.0	18
13	Toward a Comprehensive Strategy to Mitigate Dissemination of Environmental Sources of Antibiotic Resistance. <i>Environmental Science & Technology</i> , 2017, 51, 13061-13069.	4.6	236
14	Antibiotic efficacy "context matters". <i>Current Opinion in Microbiology</i> , 2017, 39, 73-80.	2.3	71
15	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. <i>Clinical Microbiology Reviews</i> , 2017, 30, 1015-1063.	5.7	310
16	Draft Genome Sequence of <i>Acinetobacter johnsonii</i> C6, an Environmental Isolate Engaging in Interspecific Metabolic Interactions. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
17	Whole-Genome Sequencing and Concordance Between Antimicrobial Susceptibility Genotypes and Phenotypes of Bacterial Isolates Associated with Bovine Respiratory Disease. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3059-3071.	0.8	19
18	Genomic characterization of novel IncFII-type multidrug resistant plasmids p0716-KPC and p12181-KPC from <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2017, 7, 5830.	1.6	23

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19	Comparative genomics of a drug-resistant <i>Pseudomonas aeruginosa</i> panel and the challenges of antimicrobial resistance prediction from genomes. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	40
20	Insights from protein-protein interaction studies on bacterial pathogenesis. <i>Expert Review of Proteomics</i> , 2017, 14, 779-797.	1.3	11
21	Draft Genome Sequence of <i>Lactobacillus salivarius</i> L28 Isolated from Ground Beef. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
22	Complete Genome Sequence of <i>Enterococcus thailandicus</i> Strain a523 Isolated from Urban Raw Sewage. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
23	Comparative genomics of type 1 IncC plasmids from China. <i>Future Microbiology</i> , 2017, 12, 1511-1522.	1.0	11
24	FMNH2-dependent monooxygenases initiate catabolism of sulfonamides in <i>Microbacterium</i> sp. strain BR1 subsisting on sulfonamide antibiotics. <i>Scientific Reports</i> , 2017, 7, 15783.	1.6	66
25	Draft Whole-Genome Sequences of Periodontal Pathobionts <i>Porphyromonas gingivalis</i> , <i>Prevotella intermedia</i> , and <i>Tannerella forsythia</i> Contain Phase-Variable Restriction-Modification Systems. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
26	Complete Genome Sequence of the <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> Strain DSM 16831. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
27	Using metagenomics to investigate human and environmental resistomes. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2690-2703.	1.3	87
28	Genomic characterization of environmental <i>Pseudomonas aeruginosa</i> isolated from dental unit waterlines revealed the insertion sequence ISPa11 as a chaotropic element. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	21
29	Whole metagenome profiles of particulates collected from the International Space Station. <i>Microbiome</i> , 2017, 5, 81.	4.9	54
30	Study of mesophilic <i>Aeromonas salmonicida</i> A527 strain sheds light on the species' lifestyles and taxonomic dilemma. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	24
31	Complete Genome Sequence of <i>Kluyvera intestini</i> sp. nov., Isolated from the Stomach of a Patient with Gastric Cancer. <i>Genome Announcements</i> , 2017, 5, .	0.8	26
32	Glimpse into the genome sequence of a multidrug-resistant <i>Acinetobacter pittii</i> ST950 clinical isolate carrying the blaOXA-72 and blaOXA-533 genes in China. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2017, 112, 723-727.	0.8	3
33	Current Status and Future Prospects of Marine Natural Products (MNPs) as Antimicrobials. <i>Marine Drugs</i> , 2017, 15, 272.	2.2	92
34	Sequencing of blaIMP-Carrying IncN2 Plasmids, and Comparative Genomics of IncN2 Plasmids Harboring Class 1 Integrons. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 102.	1.8	22
35	Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. <i>Frontiers in Microbiology</i> , 2017, 8, 909.	1.5	87
36	A Syst-OMICS Approach to Ensuring Food Safety and Reducing the Economic Burden of Salmonellosis. <i>Frontiers in Microbiology</i> , 2017, 8, 996.	1.5	42

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37	Metagenomics: The Next Culture-Independent Game Changer. <i>Frontiers in Microbiology</i> , 2017, 8, 1069.	1.5	230
38	Evolution of <i>Stenotrophomonas maltophilia</i> in Cystic Fibrosis Lung over Chronic Infection: A Genomic and Phenotypic Population Study. <i>Frontiers in Microbiology</i> , 2017, 8, 1590.	1.5	85
39	Probing Genomic Aspects of the Multi-Host Pathogen <i>Clostridium perfringens</i> Reveals Significant Pangenome Diversity, and a Diverse Array of Virulence Factors. <i>Frontiers in Microbiology</i> , 2017, 8, 2485.	1.5	70
40	Genomic analysis of vancomycin-resistant <i>Staphylococcus aureus</i> VRS3b and its comparison with other VRSA isolates. <i>Drug Discoveries and Therapeutics</i> , 2017, 11, 78-83.	0.6	15
41	In silico genomic insights into aspects of food safety and defense mechanisms of a potentially probiotic <i>Lactobacillus pentosus</i> MP-10 isolated from brines of naturally fermented Aloreña green table olives. <i>PLoS ONE</i> , 2017, 12, e0176801.	1.1	23
42	Antibiotic resistance: it's bad, but why isn't it worse?. <i>BMC Biology</i> , 2017, 15, 84.	1.7	60
43	Genetic characterization of novel class 1 Integrons In0, In1069 and In1287 to In1290, and the inference of In1069-associated integron evolution in Enterobacteriaceae. <i>Antimicrobial Resistance and Infection Control</i> , 2017, 6, 84.	1.5	8
44	Genome-resolved metaproteomic characterization of preterm infant gut microbiota development reveals species-specific metabolic shifts and variabilities during early life. <i>Microbiome</i> , 2017, 5, 72.	4.9	36
45	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. <i>Microbiome</i> , 2017, 5, 84.	4.9	247
46	Metagenomic characterization of ambulances across the USA. <i>Microbiome</i> , 2017, 5, 125.	4.9	32
47	Whole genome sequencing-based detection of antimicrobial resistance and virulence in non-typhoidal <i>Salmonella enterica</i> isolated from wildlife. <i>Gut Pathogens</i> , 2017, 9, 66.	1.6	54
48	Antibiotics and antibiotic resistant bacteria and genes in northeastern dairy manure management systems: Project overview and preliminary findings from an 11 farm case study. <i>Antimicrob. Resist. Infect. Control</i> , 2017, 2, 1-11.		0
49	pSY153-MDR, a p12969-DIM-related mega plasmid carrying <i>bla</i> _{IMP-45} and <i>armA</i> , from clinical <i>Pseudomonas putida</i> . <i>Oncotarget</i> , 2017, 8, 68439-68447.	0.8	18
50	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017, 3, e000131.	1.0	478
51	Whole-Genome Analysis of an Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Strain XDR-BJ83: Insights into the Mechanisms of Resistance of an ST368 Strain from a Tertiary Care Hospital in China. <i>Microbial Drug Resistance</i> , 2018, 24, 1259-1270.	0.9	8
52	Impacts of zero valent iron, natural zeolite and Dnase on the fate of antibiotic resistance genes during thermophilic and mesophilic anaerobic digestion of swine manure. <i>Bioresource Technology</i> , 2018, 258, 135-141.	4.8	76
53	Serotype Diversity and Antimicrobial Resistance among <i>Salmonella enterica</i> Isolates from Patients at an Equine Referral Hospital. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	19
54	MARDy: Mycology Antifungal Resistance Database. <i>Bioinformatics</i> , 2018, 34, 3233-3234.	1.8	23

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55	Draft Genome Sequences of Interpatient and Inpatient Epidemiologically Linked <i>Neisseria gonorrhoeae</i> Isolates. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
56	Safety assessment and functional properties of four enterococci strains isolated from regional Argentinean cheese. <i>International Journal of Food Microbiology</i> , 2018, 277, 1-9.	2.1	16
57	Redefinition and Unification of the SXT/R391 Family of Integrative and Conjugative Elements. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	35
58	Whole-genome sequencing reveals the mechanisms for evolution of streptomycin resistance in <i>Lactobacillus plantarum</i> . <i>Journal of Dairy Science</i> , 2018, 101, 2867-2874.	1.4	14
59	Complex pollution of antibiotic resistance genes due to beta-lactam and aminoglycoside use in aquaculture farming. <i>Water Research</i> , 2018, 134, 200-208.	5.3	111
60	Detection of 16S rRNA and KPC Genes from Complex Matrix Utilizing a Molecular Inversion Probe Assay for Next-Generation Sequencing. <i>Scientific Reports</i> , 2018, 8, 2028.	1.6	9
61	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
62	Epidemic spread of <i>Escherichia coli</i> ST744 isolates carrying <i>mcr-3</i> and <i>blaCTX-M-55</i> in cattle in France. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 533-536.	1.3	60
63	Antibiotic resistance ABCF proteins reset the peptidyl transferase centre of the ribosome to counter translational arrest. <i>Nucleic Acids Research</i> , 2018, 46, 3753-3763.	6.5	71
65	A primer on microbial bioinformatics for nonbioinformaticians. <i>Clinical Microbiology and Infection</i> , 2018, 24, 342-349.	2.8	52
66	Simultaneous emergence and rapid spread of three OXA-23 producing <i>Acinetobacter baumannii</i> ST208 strains in intensive care units confirmed by whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2018, 58, 243-250.	1.0	6
67	Comparative study of sequence aligners for detecting antibiotic resistance in bacterial metagenomes. <i>Letters in Applied Microbiology</i> , 2018, 66, 162-168.	1.0	9
68	The complex resistomes of Paenibacillaceae reflect diverse antibiotic chemical ecologies. <i>ISME Journal</i> , 2018, 12, 885-897.	4.4	15
69	The evolution of substrate discrimination in macrolide antibiotic resistance enzymes. <i>Nature Communications</i> , 2018, 9, 112.	5.8	50
70	MetaCherchant: analyzing genomic context of antibiotic resistance genes in gut microbiota. <i>Bioinformatics</i> , 2018, 34, 434-444.	1.8	31
71	Methicillin-resistant <i>Staphylococcus pseudintermedius</i> among dogs in the description of novel SCCmec variants. <i>Veterinary Microbiology</i> , 2018, 213, 136-141.	0.8	12
72	Oli2go: an automated multiplex oligonucleotide design tool. <i>Nucleic Acids Research</i> , 2018, 46, W252-W256.	6.5	30
73	<i>Klebsiella pneumoniae</i> as a key trafficker of drug resistance genes from environmental to clinically important bacteria. <i>Current Opinion in Microbiology</i> , 2018, 45, 131-139.	2.3	337

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74	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
75	Complete Genome Sequence of <i>Listeria monocytogenes</i> Strain MR310, Isolated from a Pastured-Flock Poultry Farm System. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
76	The human clone ST22 SCCmec IV methicillin-resistant <i>Staphylococcus aureus</i> isolated from swine herds and wild primates in Nepal: is man the common source?. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	26
77	Highlighting Clinical Metagenomics for Enhanced Diagnostic Decision-making: A Step Towards Wider Implementation. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 108-120.	1.9	79
78	Adaptation in toxic environments: comparative genomics of loci carrying antibiotic resistance genes derived from acid mine drainage waters. <i>Environmental Science and Pollution Research</i> , 2018, 25, 1470-1483.	2.7	16
79	Antibiotic-Resistance Genes in Waste Water. <i>Trends in Microbiology</i> , 2018, 26, 220-228.	3.5	627
80	Coexistence of two novel resistance plasmids, <i>bla</i> _{KPC-2} -carrying p14057A and <i>tetA</i> (A)-carrying p14057B, in <i>Pseudomonas aeruginosa</i> . <i>Virulence</i> , 2018, 9, 306-311.	1.8	18
81	Toxoid Vaccination against Bacterial Infection Using Cell Membrane-Coated Nanoparticles. <i>Bioconjugate Chemistry</i> , 2018, 29, 604-612.	1.8	46
82	Genome-based analysis of virulence determinants of a <i>Serratia marcescens</i> strain from soft tissues following a snake bite. <i>Future Microbiology</i> , 2018, 13, 331-343.	1.0	5
83	Co-occurrence of 3 different resistance plasmids in a multi-drug resistant <i>Cronobacter sakazakii</i> isolate causing neonatal infections. <i>Virulence</i> , 2018, 9, 110-120.	1.8	36
84	Complete Closed Genome Sequences of Three <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Dublin Strains Isolated from Cattle at Harvest. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
85	MDAD: A Special Resource for Microbe-Drug Associations. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 424.	1.8	57
86	Human Resistome Study with Metagenomic Sequencing Data. <i>Hanyang Medical Reviews</i> , 2018, 38, 73.	0.4	1
87	Genotypic and Phenotypic Characterization of <i>Salmonella</i> Isolated from Fresh Ground Meats Obtained from Retail Grocery Stores in the Brookings, South Dakota, Area. <i>Journal of Food Protection</i> , 2018, 81, 1526-1534.	0.8	5
88	Hospitalized Pets as a Source of Carbapenem-Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 2872.	1.5	47
89	Read cloud sequencing elucidates microbiome dynamics in a hematopoietic cell transplant patient. , 2018, 2018, 234-241.		2
90	Metagenomic Next-Generation Sequencing for Pathogen Detection and Identification. , 2018, , 617-632.		0
91	Complete Genome Sequence of the Hydrocarbon-Degrading Strain <i>Achromobacter</i> sp. B7, Isolated during Petroleum Hydrocarbon Bioremediation in the Valparaiso Region, Chile. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4

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92	Impact of Amoxicillin-Clavulanate followed by Autologous Fecal Microbiota Transplantation on Fecal Microbiome Structure and Metabolic Potential. <i>MSphere</i> , 2018, 3, .	1.3	17
93	Antibiotics and Resistance in the Environment. , 2018, , 383-407.		3
94	The gill-associated microbiome is the main source of wood plant polysaccharide hydrolases and secondary metabolite gene clusters in the mangrove shipworm <i>Neoteredo reynei</i> . <i>PLoS ONE</i> , 2018, 13, e0200437.	1.1	18
95	Emergence of dominant multidrug-resistant bacterial clades: Lessons from history and whole-genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12872-12877.	3.3	67
96	Use of omics methods for the advancement of food quality and food safety. <i>Animal Frontiers</i> , 2018, 8, 33-41.	0.8	19
97	Genetic exchanges are more frequent in bacteria encoding capsules. <i>PLoS Genetics</i> , 2018, 14, e1007862.	1.5	31
98	Complete Genome Sequence of <i>Streptacidiphilus</i> sp. Strain 15-057A, Obtained from Bronchial Lavage Fluid. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
99	Genomic Analysis of Consecutive <i>Acinetobacter baumannii</i> Strains From a Single Patient. <i>Frontiers in Microbiology</i> , 2018, 9, 2840.	1.5	7
100	Metagenomic Sequencing of Wastewater from a South African Research Farm. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
101	The chicken gut metagenome and the modulatory effects of plant-derived benzyloquinoline alkaloids. <i>Microbiome</i> , 2018, 6, 211.	4.9	204
102	Genomic Study of a <i>Clostridium difficile</i> Multidrug Resistant Outbreak-Related Clone Reveals Novel Determinants of Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 2994.	1.5	25
103	Genome-wide analysis of horizontally acquired genes in the genus <i>Mycobacterium</i> . <i>Scientific Reports</i> , 2018, 8, 14817.	1.6	21
104	Comparative genomics of five different resistance plasmids coexisting in a clinical multi-drug resistant <i>Citrobacter freundii</i> isolate. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1447-1460.	1.1	15
105	Comparative genome analysis provides deep insights into <i>Aeromonas hydrophila</i> taxonomy and virulence-related factors. <i>BMC Genomics</i> , 2018, 19, 712.	1.2	26
106	Bifidobacterial Dominance of the Gut in Early Life and Acquisition of Antimicrobial Resistance. <i>MSphere</i> , 2018, 3, .	1.3	71
107	Metagenomic Insights Into the Contribution of Phages to Antibiotic Resistance in Water Samples Related to Swine Feedlot Wastewater Treatment. <i>Frontiers in Microbiology</i> , 2018, 9, 2474.	1.5	39
108	T cell dynamics and response of the microbiota after gene therapy to treat X-linked severe combined immunodeficiency. <i>Genome Medicine</i> , 2018, 10, 70.	3.6	28
109	Sources of Antibiotic Resistance Genes in a Rural River System. <i>Journal of Environmental Quality</i> , 2018, 47, 997-1005.	1.0	24

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110	Transcriptional and Functional Analysis of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Exposure to Tetracycline. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	22
111	Discovering novel hydrolases from hot environments. <i>Biotechnology Advances</i> , 2018, 36, 2077-2100.	6.0	38
112	Detection of the carbapenemase gene blaVIM-5 in members of the <i>Pseudomonas putida</i> group isolated from polluted Nigerian wetlands. <i>Scientific Reports</i> , 2018, 8, 15116.	1.6	20
113	Comparative Genomics of <i>Aspergillus flavus</i> S and L Morphotypes Yield Insights into Niche Adaptation. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3915-3930.	0.8	23
114	Draft Genome Sequences of bla KPC -Containing <i>Enterobacter aerogenes</i> , <i>Citrobacter freundii</i> , and <i>Citrobacter koseri</i> Strains. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
115	Comparative genomics of clinical strains of <i>Pseudomonas aeruginosa</i> strains isolated from different geographic sites. <i>Scientific Reports</i> , 2018, 8, 15668.	1.6	61
116	Insights into the genome sequence of ovine <i>Pasteurella multocida</i> type A strain associated with pneumonic pasteurellosis. <i>Small Ruminant Research</i> , 2018, 169, 167-175.	0.6	5
117	BacCapSeq: a Platform for Diagnosis and Characterization of Bacterial Infections. <i>MBio</i> , 2018, 9, .	1.8	42
118	Comparative analysis of bla _{KPC-2} and bla _{rmtB} -carrying IncFII-family pKPC-LK30/pHN7A8 hybrid plasmids from <i>Klebsiella pneumoniae</i> CG258 strains disseminated among multiple Chinese hospitals. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1783-1793.	1.1	20
119	<i>Cupriavidus metallidurans</i> Strains with Different Mobilomes and from Distinct Environments Have Comparable Phenomes. <i>Genes</i> , 2018, 9, 507.	1.0	21
120	Genomic Characterization of <i>Lactobacillus delbrueckii</i> TUA4408L and Evaluation of the Antiviral Activities of its Extracellular Polysaccharides in Porcine Intestinal Epithelial Cells. <i>Frontiers in Immunology</i> , 2018, 9, 2178.	2.2	56
121	Integrative metagenomic and biochemical studies on rifamycin ADP-ribosyltransferases discovered in the sediment microbiome. <i>Scientific Reports</i> , 2018, 8, 12143.	1.6	7
122	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265.	5.9	483
123	Antibiotic multidrug resistance in the cystic fibrosis airway microbiome is associated with decreased diversity. <i>Heliyon</i> , 2018, 4, e00795.	1.4	31
124	OXA-48 type carbapenemase in <i>Klebsiella pneumoniae</i> producing extended spectrum B-lactamases (ESBL) in Senegal. <i>African Journal of Microbiology Research</i> , 2018, 12, 413-418.	0.4	3
125	Multi-Year Persistence of Verotoxigenic <i>Escherichia coli</i> (VTEC) in a Closed Canadian Beef Herd: A Cohort Study. <i>Frontiers in Microbiology</i> , 2018, 9, 2040.	1.5	15
126	Co-production of MCR-1 and NDM-5 in <i>Escherichia coli</i> ; isolated from a colonization case of inpatient. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1157-1161.	1.1	15
127	Comparative Genomic Studies of <i>Salmonella Heidelberg</i> Isolated From Chicken- and Turkey-Associated Farm Environmental Samples. <i>Frontiers in Microbiology</i> , 2018, 9, 1841.	1.5	21

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128	Hotspot mutations and ColE1 plasmids contribute to the fitness of Salmonella Heidelberg in poultry litter. PLoS ONE, 2018, 13, e0202286.	1.1	34
129	Therapeutic target database update 2018: enriched resource for facilitating bench-to-clinic research of targeted therapeutics. Nucleic Acids Research, 2018, 46, D1121-D1127.	6.5	462
130	RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Research, 2018, 46, D851-D860.	6.5	749
131	Draft Genome Sequence of the First Documented Clinical Siccibacter turicensis Isolate in Austria. Genome Announcements, 2018, 6, .	0.8	3
132	Metagenomic analysis reveals the prevalence and persistence of antibiotic- and heavy metal-resistance genes in wastewater treatment plant. Journal of Microbiology, 2018, 56, 408-415.	1.3	69
133	Self-Resistance of Natural Product Producers: Past, Present, and Future Focusing on Self-Resistant Protein Variants. ACS Chemical Biology, 2018, 13, 1426-1437.	1.6	66
134	Indexed variation graphs for efficient and accurate resistome profiling. Bioinformatics, 2018, 34, 3601-3608.	1.8	55
135	A pan-genome-based machine learning approach for predicting antimicrobial resistance activities of the <i>Escherichia coli</i> strains. Bioinformatics, 2018, 34, i89-i95.	1.8	72
136	Transcriptome Analysis of Neisseria gonorrhoeae during Natural Infection Reveals Differential Expression of Antibiotic Resistance Determinants between Men and Women. MSphere, 2018, 3, .	1.3	26
137	Environmental superbugs: The case study of Pedobacter spp.. Environmental Pollution, 2018, 241, 1048-1055.	3.7	54
138	Genome of <i>Serratia nematodiphila</i> MB307 offers unique insights into its diverse traits. Genome, 2018, 61, 469-476.	0.9	15
139	Past and Present Perspectives on β -Lactamases. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	554
140	PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. BMC Bioinformatics, 2018, 19, 246.	1.2	9
141	Metagenome analysis of Russian and Georgian Pyophage cocktails and a placebo-controlled safety trial of single phage versus phage cocktail in healthy <i>Staphylococcus aureus</i> carriers. Environmental Microbiology, 2018, 20, 3278-3293.	1.8	75
142	Plasmid and chromosomal integration of four novel blaIMP-carrying transposons from Pseudomonas aeruginosa, Klebsiella pneumoniae and an Enterobacter sp.. Journal of Antimicrobial Chemotherapy, 2018, 73, 3005-3015.	1.3	41
143	Construction and Characterization of Synthetic Bacterial Community for Experimental Ecology and Evolution. Frontiers in Genetics, 2018, 9, 312.	1.1	28
144	Antimicrobial Resistance and Respiratory Infections. Chest, 2018, 154, 1202-1212.	0.4	56
145	Comparative Genomic Analysis of a Clinical Isolate of Klebsiella quasipneumoniae subsp. similipneumoniae, a KPC-2 and OKP-B-6 Beta-Lactamases Producer Harboring Two Drug-Resistance Plasmids from Southeast Brazil. Frontiers in Microbiology, 2018, 9, 220.	1.5	44

#	ARTICLE	IF	CITATIONS
146	Dissemination of KPC-2-Encoding IncX6 Plasmids Among Multiple Enterobacteriaceae Species in a Single Chinese Hospital. <i>Frontiers in Microbiology</i> , 2018, 9, 478.	1.5	26
147	Retrospective Analysis of Bacterial Cultures Sampled in German Chicken-Fattening Farms During the Years 2011–2012 Revealed Additional VIM-1 Carbapenemase-Producing <i>Escherichia coli</i> and a Serologically Rough <i>Salmonella enterica</i> Serovar Infantis. <i>Frontiers in Microbiology</i> , 2018, 9, 538.	1.5	14
148	Pentocin MQ1: A Novel, Broad-Spectrum, Pore-Forming Bacteriocin From <i>Lactobacillus pentosus</i> CS2 With Quorum Sensing Regulatory Mechanism and Biopreservative Potential. <i>Frontiers in Microbiology</i> , 2018, 9, 564.	1.5	41
149	A Polyphasic and Taxogenomic Evaluation Uncovers <i>Arcobacter cryaerophilus</i> as a Species Complex That Embraces Four Genomovars. <i>Frontiers in Microbiology</i> , 2018, 9, 805.	1.5	22
150	Diversity and Proliferation of Metallo- β -Lactamases: a Clarion Call for Clinically Effective Metallo- β -Lactamase Inhibitors. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	71
151	The diversity of uncharacterized antibiotic resistance genes can be predicted from known gene variants—but not always. <i>Microbiome</i> , 2018, 6, 125.	4.9	39
152	Comparative Genomic Analysis of Two Chilean <i>Renibacterium salmoninarum</i> Isolates and the Type Strain ATCC 33209T. <i>Genome Biology and Evolution</i> , 2018, 10, 1816-1822.	1.1	9
153	<i>Bacillus safensis</i> FO-36b and <i>Bacillus pumilus</i> SAFR-032: a whole genome comparison of two spacecraft assembly facility isolates. <i>BMC Microbiology</i> , 2018, 18, 57.	1.3	16
154	Physiological and Comparative Genomic Analysis of <i>Arthrobacter</i> sp. SRS-W-1-2016 Provides Insights on Niche Adaptation for Survival in Uraniferous Soils. <i>Genes</i> , 2018, 9, 31.	1.0	42
155	Diversity among blaKPC-containing plasmids in <i>Escherichia coli</i> and other bacterial species isolated from the same patients. <i>Scientific Reports</i> , 2018, 8, 10291.	1.6	33
156	Characterizing Phage Genomes for Therapeutic Applications. <i>Viruses</i> , 2018, 10, 188.	1.5	118
157	Reusing Treated Wastewater: Consideration of the Safety Aspects Associated with Antibiotic-Resistant Bacteria and Antibiotic Resistance Genes. <i>Water (Switzerland)</i> , 2018, 10, 244.	1.2	83
158	Multiplexed identification, quantification and genotyping of infectious agents using a semiconductor biochip. <i>Nature Biotechnology</i> , 2018, 36, 738-745.	9.4	59
159	The draft genomes and investigation of serotype distribution, antimicrobial resistance of group B <i>Streptococcus</i> strains isolated from urine in Suzhou, China. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2018, 17, 28.	1.7	15
160	Genome-Guided Characterization of <i>Ochrobactrum</i> sp. POC9 Enhancing Sewage Sludge Utilization—Biotechnological Potential and Biosafety Considerations. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 1501.	1.2	17
162	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
163	Inferring Antimicrobial Resistance from Pathogen Genomes in KEGG. <i>Methods in Molecular Biology</i> , 2018, 1807, 225-239.	0.4	10
164	DeepARG: a deep learning approach for predicting antibiotic resistance genes from metagenomic data. <i>Microbiome</i> , 2018, 6, 23.	4.9	462

#	ARTICLE	IF	CITATIONS
165	A reservoir of "historical" antibiotic resistance genes in remote pristine Antarctic soils. <i>Microbiome</i> , 2018, 6, 40.	4.9	244
166	Genomic insights into <i>Mycobacterium simiae</i> human colonization. <i>Standards in Genomic Sciences</i> , 2018, 13, 1.	1.5	18
167	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
168	Acquisition and dissemination of cephalosporin-resistant <i>E. coli</i> in migratory birds sampled at an Alaska landfill as inferred through genomic analysis. <i>Scientific Reports</i> , 2018, 8, 7361.	1.6	56
169	MetaCompare: a computational pipeline for prioritizing environmental resistome risk. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	88
170	Antimicrobial Resistance in the Environment. <i>Water Environment Research</i> , 2018, 90, 865-884.	1.3	11
171	Heterologous Production of Microbial Ribosomally Synthesized and Post-translationally Modified Peptides. <i>Frontiers in Microbiology</i> , 2018, 9, 1801.	1.5	43
172	Outbreaks of <i>Serratia marcescens</i> and <i>Serratia rubidaea</i> bacteremia in a central Kathmandu hospital following the 2015 earthquakes. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2018, 112, 467-472.	0.7	17
173	Characterization, yield optimization, scale up and biopreservative potential of fermencin SA715, a novel bacteriocin from <i>Lactobacillus fermentum</i> GA715 of goat milk origin. <i>Microbial Cell Factories</i> , 2018, 17, 125.	1.9	35
174	Understanding the impact of antibiotic therapies on the respiratory tract resistome: a novel pooled-template metagenomic sequencing strategy. <i>Multidisciplinary Respiratory Medicine</i> , 2018, 13, 30.	0.6	17
175	Genetic characterization of Shiga toxin producing <i>Escherichia coli</i> belonging to the emerging hybrid pathotype O80:H2 isolated from humans 2010"2017 in Switzerland. <i>International Journal of Medical Microbiology</i> , 2018, 308, 534-538.	1.5	30
176	Culture-independent analysis of liver abscess using nanopore sequencing. <i>PLoS ONE</i> , 2018, 13, e0190853.	1.1	22
177	Comparative genomics identifies distinct lineages of <i>S. Enteritidis</i> from Queensland, Australia. <i>PLoS ONE</i> , 2018, 13, e0191042.	1.1	29
178	Water and sanitation: an essential battlefield in the war on antimicrobial resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	104
179	Multidrug resistant pathogens respond differently to the presence of co-pathogen, commensal, probiotic and host cells. <i>Scientific Reports</i> , 2018, 8, 8656.	1.6	19
180	<i>Serratia marcescens</i> Outbreak in a Neonatal Intensive Care Unit: New Insights from Next-Generation Sequencing Applications. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	34
181	Distribution of triclosan-resistant genes in major pathogenic microorganisms revealed by metagenome and genome-wide analysis. <i>PLoS ONE</i> , 2018, 13, e0192277.	1.1	13
182	Resistome of carbapenem- and colistin-resistant <i>Klebsiella pneumoniae</i> clinical isolates. <i>PLoS ONE</i> , 2018, 13, e0198526.	1.1	53

#	ARTICLE	IF	CITATIONS
183	Microbial genomic island discovery, visualization and analysis. <i>Briefings in Bioinformatics</i> , 2019, 20, 1685-1698.	3.2	86
184	Comparative genomic analysis of <i>Myroides odoratimimus</i> isolates. <i>MicrobiologyOpen</i> , 2019, 8, e00634.	1.2	19
185	Functional annotation of the genome unravels probiotic potential of <i>Bacillus coagulans</i> HS243. <i>Genomics</i> , 2019, 111, 921-929.	1.3	69
186	Molecular Insights into Antimicrobial Resistance Traits of Commensal Human Gut Microbiota. <i>Microbial Ecology</i> , 2019, 77, 546-557.	1.4	49
187	Using Genomics to Track Global Antimicrobial Resistance. <i>Frontiers in Public Health</i> , 2019, 7, 242.	1.3	263
188	Systems biology studies in <i>Pseudomonas aeruginosa</i> PA01 to understand their role in biofilm formation and multidrug efflux pumps. <i>Microbial Pathogenesis</i> , 2019, 136, 103668.	1.3	36
189	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal <i>Salmonella enterica</i> Serovars by Using Machine Learning. <i>MSystems</i> , 2019, 4, .	1.7	21
190	Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. <i>Communications Biology</i> , 2019, 2, 294.	2.0	31
191	Whole genome sequencing revealed new molecular characteristics in multidrug resistant staphylococci recovered from high frequency touched surfaces in London. <i>Scientific Reports</i> , 2019, 9, 9637.	1.6	26
192	An integrated respiratory microbial gene catalogue to better understand the microbial aetiology of <i>Mycoplasma pneumoniae</i> pneumonia. <i>CigaScience</i> , 2019, 8, .	3.3	16
193	Multifaceted mechanisms of colistin resistance revealed by genomic analysis of multidrug-resistant <i>Klebsiella pneumoniae</i> isolates from individual patients before and after colistin treatment. <i>Journal of Infection</i> , 2019, 79, 312-321.	1.7	24
194	Assessing genetic diversity and similarity of 435 KPC-carrying plasmids. <i>Scientific Reports</i> , 2019, 9, 11223.	1.6	30
195	The Complete Genome of the Atypical Enteropathogenic <i>Escherichia coli</i> Archetype Isolate E110019 Highlights a Role for Plasmids in Dissemination of the Type III Secreted Effector EspT. <i>Infection and Immunity</i> , 2019, 87, .	1.0	6
196	Gene pool transmission of multidrug resistance among <i>Campylobacter</i> from livestock, sewage and human disease. <i>Environmental Microbiology</i> , 2019, 21, 4597-4613.	1.8	68
197	Validating the AMRFinder Tool and Resistance Gene Database by Using Antimicrobial Resistance Genotype-Phenotype Correlations in a Collection of Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	760
198	Characterization of Non-O157 <i>Escherichia coli</i> from Cattle Faecal Samples in the North-West Province of South Africa. <i>Microorganisms</i> , 2019, 7, 272.	1.6	34
199	Comparative genomics groups phages of Negativicutes and classical Firmicutes despite different Gram-staining properties. <i>Environmental Microbiology</i> , 2019, 21, 3989-4001.	1.8	8
200	Comparative Genomics and Phenotypic Investigations Into Antibiotic, Heavy Metal, and Disinfectant Susceptibilities of <i>Salmonella enterica</i> Strains Isolated in Australia. <i>Frontiers in Microbiology</i> , 2019, 10, 1620.	1.5	13

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201	Environmental and clinical antibiotic resistomes, same only different. <i>Current Opinion in Microbiology</i> , 2019, 51, 57-63.	2.3	39
202	Genome Sequence of Colistin-Resistant Bacteremic <i>Shewanella</i> algae Carrying the Beta-Lactamase Gene blaOXA-55. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2019, 2019, 1-6.	0.7	4
203	Genomic Comparison of <i>Lactobacillus helveticus</i> Strains Highlights Probiotic Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1380.	1.5	50
204	Exonuclease III-powered DNA Walking Machine for Label-free and Ultrasensitive Electrochemical Sensing of Antibiotic. <i>Sensors and Actuators B: Chemical</i> , 2019, 297, 126771.	4.0	27
205	Molecular Epidemiology of Multidrug-Resistant <i>Klebsiella pneumoniae</i> Isolates in a Brazilian Tertiary Hospital. <i>Frontiers in Microbiology</i> , 2019, 10, 1669.	1.5	20
206	A label-free electrochemical platform for the detection of antibiotics based on cascade enzymatic amplification coupled with a split G-quadruplex DNAzyme. <i>Analyst</i> , The, 2019, 144, 4995-5002.	1.7	22
207	Stimulated Growth and Innate Immunity in Brook Charr (<i>Salvelinus fontinalis</i>) Treated with a General Probiotic (Bactocell®) and Two Endogenous Probiotics That Inhibit <i>Aeromonas salmonicida</i> In Vitro. <i>Microorganisms</i> , 2019, 7, 193.	1.6	5
208	MicroScope – an integrated resource for community expertise of gene functions and comparative analysis of microbial genomic and metabolic data. <i>Briefings in Bioinformatics</i> , 2019, 20, 1071-1084.	3.2	71
209	Impact of intrapartum and postnatal antibiotics on the gut microbiome and emergence of antimicrobial resistance in infants. <i>Scientific Reports</i> , 2019, 9, 10635.	1.6	106
210	Developmental dynamics of antibiotic resistome in aerobic biofilm microbiota treating wastewater under stepwise increasing tigeicycline concentrations. <i>Environment International</i> , 2019, 131, 105008.	4.8	26
211	Insights into the antibiotic resistance dissemination in a wastewater effluent microbiome: bacteria, viruses and vesicles matter. <i>Environmental Microbiology</i> , 2019, 21, 4582-4596.	1.8	22
212	Carbapenemase-producing Enterobacteriaceae and <i>Aeromonas</i> spp. present in wastewater treatment plant effluent and nearby surface waters in the US. <i>PLoS ONE</i> , 2019, 14, e0218650.	1.1	47
213	Discovery of a Novel DNA Gyrase-Targeting Antibiotic through the Chemical Perturbation of <i>Streptomyces venezuelae</i> Sporulation. <i>Cell Chemical Biology</i> , 2019, 26, 1274-1282.e4.	2.5	18
214	Industrial wastewater treatment plant enriches antibiotic resistance genes and alters the structure of microbial communities. <i>Water Research</i> , 2019, 162, 437-445.	5.3	95
215	Unconventional Oil and Gas Energy Systems: An Unidentified Hotspot of Antimicrobial Resistance?. <i>Frontiers in Microbiology</i> , 2019, 10, 2392.	1.5	7
216	Next Generation Sequencing and Bioinformatics Methodologies for Infectious Disease Research and Public Health: Approaches, Applications, and Considerations for Development of Laboratory Capacity. <i>Journal of Infectious Diseases</i> , 2020, 221, S292-S307.	1.9	64
217	Optimizing a Whole-Genome Sequencing Data Processing Pipeline for Precision Surveillance of Health Care-Associated Infections. <i>Microorganisms</i> , 2019, 7, 388.	1.6	1
218	Antibiotic Resistance Genes in the Human-Impacted Environment: A One Health Perspective. <i>Pedosphere</i> , 2019, 29, 273-282.	2.1	100

#	ARTICLE	IF	CITATIONS
219	Staphylococcus petrasii diagnostics and its pathogenic potential enhanced by mobile genetic elements. International Journal of Medical Microbiology, 2019, 309, 151355.	1.5	2
220	Next-Generation Sequencing Approaches to Predicting Antimicrobial Susceptibility Testing Results. Advances in Molecular Pathology, 2019, 2, 99-110.	0.2	4
221	Antimicrobial resistance genotypes and phenotypes of Campylobacter jejuni isolated in Italy from humans, birds from wild and urban habitats, and poultry. PLoS ONE, 2019, 14, e0223804.	1.1	55
222	Élites chrétiennes et formes du pouvoir en Méditerranée centrale et orientale (xiii ^e -xv ^e siècles). Sous la direction de Marie-Anna Chevalier et Isabelle Ortega. French Studies, 2019, 73, 449-449.	0.0	0
223	Determinants of claim definiteness: myth of relative terms. Journal of Intellectual Property Law and Practice, 2019, 14, 796-813.	0.2	0
224	Multicenter Validation of the CamGFR Model for Estimated Glomerular Filtration Rate. JNCI Cancer Spectrum, 2019, 3, pkz068.	1.4	6
225	Non-detection of fast radio bursts from six gamma-ray burst remnants with possible magnetar engines. Monthly Notices of the Royal Astronomical Society, 2019, 489, 3643-3647.	1.6	17
226	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	6.5	60
227	MicroScope: an integrated platform for the annotation and exploration of microbial gene functions through genomic, pangenomic and metabolic comparative analysis. Nucleic Acids Research, 2020, 48, D579-D589.	6.5	166
228	CARD 2020: antibiotic resistance surveillance with the comprehensive antibiotic resistance database. Nucleic Acids Research, 2020, 48, D517-D525.	6.5	1,605
229	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. Nucleic Acids Research, 2020, 48, D606-D612.	6.5	552
230	Clinical metagenomics for infection diagnosis. , 2019, , 35-60.		1
231	Phenotypic and genotypic characterization of clinical Staphylococcus aureus isolates from Kenya. BMC Microbiology, 2019, 19, 245.	1.3	19
232	Native CRISPR-Cas-Mediated Genome Editing Enables Dissecting and Sensitizing Clinical Multidrug-Resistant P. aeruginosa. Cell Reports, 2019, 29, 1707-1717.e3.	2.9	51
233	Reductionist synthetic community approaches in root microbiome research. Current Opinion in Microbiology, 2019, 49, 97-102.	2.3	105
234	Molecular mechanism of azithromycin resistance among typhoidal Salmonella strains in Bangladesh identified through passive pediatric surveillance. PLoS Neglected Tropical Diseases, 2019, 13, e0007868.	1.3	100
235	Genome Analysis and Multiplex PCR Method for the Molecular Detection of Coresistance to Cephalosporins and Fosfomycin in Salmonella enterica Serovar Heidelberg. Journal of Food Protection, 2019, 82, 1938-1949.	0.8	11
236	mNGS in clinical microbiology laboratories: on the road to maturity. Critical Reviews in Microbiology, 2019, 45, 668-685.	2.7	172

#	ARTICLE	IF	CITATIONS
237	Comparative Study on A Novel Pathogen of European Seabass. Diversity of <i>Aeromonas veronii</i> in the Aegean Sea. <i>Microorganisms</i> , 2019, 7, 504.	1.6	13
238	Phenotypic and Genotypic Antimicrobial Resistance Traits of <i>Vibrio cholerae</i> Non-O1/Non-O139 Isolated From a Large Austrian Lake Frequently Associated With Cases of Human Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 2600.	1.5	27
239	The whole-genome sequence analysis of <i>Morchella sextelata</i> . <i>Scientific Reports</i> , 2019, 9, 15376.	1.6	18
240	Identification and characterization of OmpT-like proteases in uropathogenic <i>Escherichia coli</i> clinical isolates. <i>MicrobiologyOpen</i> , 2019, 8, e915.	1.2	22
241	Genomic Epidemiology of Major Extraintestinal Pathogenic <i>Escherichia coli</i> Lineages Causing Urinary Tract Infections in Young Women Across Canada. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz431.	0.4	30
242	Identification and Antibiotic Resistance Assessment of <i>Ensifer adhaerens</i> YX1, a Vitamin B ₁₂ -Producing Strain Used as a Food and Feed Additive. <i>Journal of Food Science</i> , 2019, 84, 2925-2931.	1.5	4
243	Alternate antimicrobial resistance genes in multidrug resistant <i>Salmonella</i> spp. isolated from retail meats in Vietnam using RNA-seq analysis. <i>Journal of Food Safety</i> , 2019, 39, e12707.	1.1	6
244	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
245	Prevalence and proliferation of antibiotic resistance genes in the subtropical mangrove wetland ecosystem of South China Sea. <i>MicrobiologyOpen</i> , 2019, 8, e871.	1.2	27
246	Machine Learning Approaches for Epidemiological Investigations of Food-Borne Disease Outbreaks. <i>Frontiers in Microbiology</i> , 2019, 10, 1722.	1.5	22
247	Antibiotic resistance and metabolic profiles as functional biomarkers that accurately predict the geographic origin of city metagenomics samples. <i>Biology Direct</i> , 2019, 14, 15.	1.9	17
248	Variation in Streptomycin Resistance Mechanisms in <i>Clavibacter michiganensis</i> . <i>Phytopathology</i> , 2019, 109, 1849-1858.	1.1	16
249	Comparative Genomic Analysis of the 2016 <i>Vibrio cholerae</i> Outbreak in South Korea. <i>Frontiers in Public Health</i> , 2019, 7, 228.	1.3	10
250	Antibiotic Resistant <i>Pseudomonas</i> Spp. Spoilers in Fresh Dairy Products: An Underestimated Risk and the Control Strategies. <i>Foods</i> , 2019, 8, 372.	1.9	61
251	Comparative genomics of <i>Aeromonas veronii</i> : Identification of a pathotype impacting aquaculture globally. <i>PLoS ONE</i> , 2019, 14, e0221018.	1.1	50
252	Chicken Meat-Associated Enterococci: Influence of Agricultural Antibiotic Use and Connection to the Clinic. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	34
253	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain BWH047, a Sequence Type 235 Multidrug-Resistant Clinical Isolate Expressing High Levels of Colistin Resistance. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
254	Using the wax moth larva <i>Galleria mellonella</i> infection model to detect emerging bacterial pathogens. <i>PeerJ</i> , 2019, 6, e6150.	0.9	24

#	ARTICLE	IF	CITATIONS
255	Persistent metagenomic signatures of early-life hospitalization and antibiotic treatment in the infant gut microbiota and resistome. <i>Nature Microbiology</i> , 2019, 4, 2285-2297.	5.9	191
256	Hospital outbreak caused by linezolid resistant <i>Enterococcus faecium</i> in Upper Austria. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 150.	1.5	13
257	Evaluation of in vitro activity of ceftazidime/avibactam and ceftolozane/tazobactam against MDR <i>Pseudomonas aeruginosa</i> isolates from Qatar. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3497-3504.	1.3	24
258	Comparative Genomic Analysis of <i>Staphylococcus haemolyticus</i> Reveals Key to Hospital Adaptation and Pathogenicity. <i>Frontiers in Microbiology</i> , 2019, 10, 2096.	1.5	33
259	Ontology based mining of pathogen-disease associations from literature. <i>Journal of Biomedical Semantics</i> , 2019, 10, 15.	0.9	7
260	Unveiling resistome profiles in the sediments of an Antarctic volcanic island. <i>Environmental Pollution</i> , 2019, 255, 113240.	3.7	15
261	Metagenome of a polluted river reveals a reservoir of metabolic and antibiotic resistance genes. <i>Environmental Microbiomes</i> , 2019, 14, 5.	2.2	44
262	In-silico Design of DNA Oligonucleotides: Challenges and Approaches. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1056-1065.	1.9	15
263	High prevalence of multidrug resistant Enterobacteriaceae among residents of long term care facilities in Amsterdam, the Netherlands. <i>PLoS ONE</i> , 2019, 14, e0222200.	1.1	22
264	Identification of genomic loci associated with genotypic and phenotypic variation among <i>Pseudomonas aeruginosa</i> clinical isolates from pneumonia. <i>Microbial Pathogenesis</i> , 2019, 136, 103702.	1.3	2
265	Horizontal Gene Transfer and Acquired Antibiotic Resistance in <i>Salmonella enterica</i> Serovar Heidelberg following <i>In Vitro</i> Incubation in Broiler Ceca. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	39
266	Genomic Insights Into Five Strains of <i>Lactobacillus plantarum</i> With Biotechnological Potential Isolated From chicha, a Traditional Maize-Based Fermented Beverage From Northwestern Argentina. <i>Frontiers in Microbiology</i> , 2019, 10, 2232.	1.5	24
267	Genomic Analysis of <i>Clostridium perfringens</i> BEC/CPile-Positive, Toxinotype D and E Strains Isolated from Healthy Children. <i>Toxins</i> , 2019, 11, 543.	1.5	11
268	Genome Mining and Comparative Pathogenomic Analysis of An Endemic Methicillin-Resistant <i>Staphylococcus Aureus</i> (MRSA) Clone, ST612-CC8-t1257-SCCmec_IVd(2B), Isolated in South Africa. <i>Pathogens</i> , 2019, 8, 166.	1.2	9
269	Whole-genome sequencing of a new sequence type (ST5352) strain of community-acquired methicillin-resistant <i>Staphylococcus aureus</i> from a hospital in Pakistan. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 19, 161-163.	0.9	4
270	Toxicity response of silkworm intestine to <i>Bacillus cereus</i> SW7-1 pathogen. <i>Science of the Total Environment</i> , 2019, 692, 1282-1290.	3.9	11
271	Occurrence of human pathogenic bacteria carrying antibiotic resistance genes revealed by metagenomic approach: A case study from an aquatic environment. <i>Journal of Environmental Sciences</i> , 2019, 80, 248-256.	3.2	31
272	Evaluation of Acquired Antibiotic Resistance in <i>Escherichia coli</i> Exposed to Long-Term Low-Shear Modeled Microgravity and Background Antibiotic Exposure. <i>MBio</i> , 2019, 10, .	1.8	46

#	ARTICLE	IF	CITATIONS
273	Molecular Characterization of Carbapenem Resistant <i>Klebsiella pneumoniae</i> and <i>Klebsiella quasipneumoniae</i> Isolated from Lebanon. <i>Scientific Reports</i> , 2019, 9, 531.	1.6	44
274	Whole-genome sequencing data-based modeling for the investigation of an outbreak of community-associated methicillin-resistant <i>Staphylococcus aureus</i> in a neonatal intensive care unit in Hong Kong. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2019, 38, 563-573.	1.3	23
275	The Quest for Novel Antimicrobial Compounds: Emerging Trends in Research, Development, and Technologies. <i>Antibiotics</i> , 2019, 8, 8.	1.5	67
276	Whole genome sequencing reveals resemblance between ESBL-producing and carbapenem resistant <i>Klebsiella pneumoniae</i> isolates from Austrian rivers and clinical isolates from hospitals. <i>Science of the Total Environment</i> , 2019, 662, 227-235.	3.9	60
277	NDM Metallo- β -Lactamases and Their Bacterial Producers in Health Care Settings. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	5.7	406
278	Diarrheal bacterial pathogens and multi-resistant enterobacteria in the Choqueyapu River in La Paz, Bolivia. <i>PLoS ONE</i> , 2019, 14, e0210735.	1.1	33
279	Uncoupled Quorum Sensing Modulates the Interplay of Virulence and Resistance in a Multidrug-Resistant Clinical <i>Pseudomonas aeruginosa</i> Isolate Belonging to the MLST550 Clonal Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	17
280	The Genetic Structures of an Extensively Drug Resistant (XDR) <i>Klebsiella pneumoniae</i> and Its Plasmids. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 446.	1.8	28
281	Virulence Characteristics and an Action Mode of Antibiotic Resistance in Multidrug-Resistant <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2019, 9, 487.	1.6	59
282	Genome analysis of <i>Salmonella enterica</i> subsp. <i>diarizonae</i> isolates from invasive human infections reveals enrichment of virulence-related functions in lineage ST1256. <i>BMC Genomics</i> , 2019, 20, 99.	1.2	24
283	Virulence and genomic features of a β -lactamase-producing CTX-M-3 and β -lactamase-producing CTX-M-14 cohabiting hypermucoviscous <i>Klebsiella pneumoniae</i> of serotype K2 and ST65. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 145-159.	1.1	13
284	Comparative genome analysis reveals niche-specific genome expansion in <i>Acinetobacter baumannii</i> strains. <i>PLoS ONE</i> , 2019, 14, e0218204.	1.1	42
285	Sludge bio-drying followed by land application could control the spread of antibiotic resistance genes. <i>Environment International</i> , 2019, 130, 104906.	4.8	26
286	PathoPhenoDB, linking human pathogens to their phenotypes in support of infectious disease research. <i>Scientific Data</i> , 2019, 6, 79.	2.4	13
287	Whole Genome Sequencing-Based Comparison of Food Isolates of <i>Cronobacter sakazakii</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1464.	1.5	28
288	NanoARG: a web service for detecting and contextualizing antimicrobial resistance genes from nanopore-derived metagenomes. <i>Microbiome</i> , 2019, 7, 88.	4.9	72
289	Deciphering extracellular antibiotic resistance genes (eARGs) in activated sludge by metagenome. <i>Water Research</i> , 2019, 161, 610-620.	5.3	97
290	Co-outbreak of multidrug resistance and a novel ST3006 <i>Klebsiella pneumoniae</i> in a neonatal intensive care unit. <i>Medicine (United States)</i> , 2019, 98, e14285.	0.4	15

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291	Genomic diversification of IncR plasmids from China. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 19, 358-364.	0.9	14
292	Nanopore metagenomics enables rapid clinical diagnosis of bacterial lower respiratory infection. <i>Nature Biotechnology</i> , 2019, 37, 783-792.	9.4	396
293	Increased genetic diversity of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) isolated from companion animals. <i>Veterinary Microbiology</i> , 2019, 235, 118-126.	0.8	27
294	Genomic and Metagenomic Approaches for Predictive Surveillance of Emerging Pathogens and Antibiotic Resistance. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 512-524.	2.3	33
295	Temperate Bacteriophages from Chronic <i>Pseudomonas aeruginosa</i> Lung Infections Show Disease-Specific Changes in Host Range and Modulate Antimicrobial Susceptibility. <i>MSystems</i> , 2019, 4, .	1.7	38
296	Host-Microbiota Interactions and Their Importance in Promoting Growth and Resistance to Opportunistic Diseases in Salmonids. , 2019, , 21-50.		3
297	Safety Evaluation of Oral Care Probiotics <i>Weissella cibaria</i> CMU and CMS1 by Phenotypic and Genotypic Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2693.	1.8	47
298	A few Ascomycota taxa dominate soil fungal communities worldwide. <i>Nature Communications</i> , 2019, 10, 2369.	5.8	341
299	Genomic analysis of human invasive <i>Salmonella enterica</i> serovar Typhimurium ST313 isolate B3589 from India. <i>Infection, Genetics and Evolution</i> , 2019, 73, 416-424.	1.0	7
300	Comparison of de-novo assembly tools for plasmid metagenome analysis. <i>Genes and Genomics</i> , 2019, 41, 1077-1083.	0.5	6
301	Comparative Genome-Scale Metabolic Modeling of Metallo-Beta-Lactamase-Producing Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 161.	1.8	33
302	Whole-Genome Shotgun Sequence of Drug-Resistant <i>Staphylococcus aureus</i> Strain SA9, Isolated from a Slaughterhouse Chicken Carcass in South Africa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
303	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
304	Microfluidics-Based Enrichment and Whole-Genome Amplification Enable Strain-Level Resolution for Airway Metagenomics. <i>MSystems</i> , 2019, 4, .	1.7	11
305	FLASH: a next-generation CRISPR diagnostic for multiplexed detection of antimicrobial resistance sequences. <i>Nucleic Acids Research</i> , 2019, 47, e83-e83.	6.5	168
306	Multiomics Assessment of Gene Expression in a Clinical Strain of CTX-M-15-Producing ST131 <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 831.	1.5	6
307	In-Depth Genomic and Phenotypic Characterization of the Antarctic Psychrotolerant Strain <i>Pseudomonas</i> sp. MPC6 Reveals Unique Metabolic Features, Plasticity, and Biotechnological Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1154.	1.5	36
308	Microbiota and Antibiotic Resistome of Lettuce Leaves and Radishes Grown in Soils Receiving Manure-Based Amendments Derived From Antibiotic-Treated Cows. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	1.8	22

#	ARTICLE	IF	CITATIONS
309	Genomic Comparison Reveals Natural Occurrence of Clinically Relevant Multidrug-Resistant Extended-Spectrum-β-Lactamase-Producing <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	29
310	Whole-genome sequencing and characterization of an antibiotic resistant <i>Neisseria meningitidis</i> B isolate from a military unit in Vietnam. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2019, 18, 16.	1.7	6
311	Whole-genome sequencing revealed independent emergence of vancomycin-resistant <i>Enterococcus faecium</i> causing sequential outbreaks over 3 years in a tertiary care hospital. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2019, 38, 1163-1170.	1.3	28
312	ARGA, a pipeline for primer evaluation on antibiotic resistance genes. <i>Environment International</i> , 2019, 128, 137-145.	4.8	14
313	Antimicrobial activity and carbohydrate metabolism in the bacterial metagenome of the soil-living invertebrate <i>Folsomia candida</i> . <i>Scientific Reports</i> , 2019, 9, 7308.	1.6	13
314	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
315	Draft Genome Sequences of <i>Macrococcus caseolyticus</i> , <i>Macrococcus canis</i> , <i>Macrococcus bohemicus</i> , and <i>Macrococcus goetzii</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
316	Comparative Genomic Analysis of <i>Lactobacillus plantarum</i> : An Overview. <i>International Journal of Genomics</i> , 2019, 2019, 1-11.	0.8	45
317	Analyses of Livestock-Associated <i>Staphylococcus aureus</i> Pan-Genomes Suggest Virulence Is Not Primary Interest in Evolution of Its Genome. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 224-236.	1.0	5
318	Draft Genome Sequence of an <i>Enterococcus faecalis</i> Strain (24FS) That Was Isolated from Healthy Infant Feces and Exhibits High Antibacterial Activity, Multiple-Antibiotic Resistance, and Multiple Virulence Factors. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
319	Genomic Features, Comparative Genomic Analysis, and Antimicrobial Susceptibility Patterns of <i>Chryseobacterium arthrosphaerae</i> Strain ED882-96 Isolated in Taiwan. <i>Genes</i> , 2019, 10, 309.	1.0	11
320	Susceptibility (re)-testing of a large collection of <i>Listeria monocytogenes</i> from foods in China from 2012 to 2015 and WGS characterization of resistant isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1786-1794.	1.3	18
321	Cystic Fibrosis Rapid Response: Translating Multi-omics Data into Clinically Relevant Information. <i>MBio</i> , 2019, 10, .	1.8	20
322	Gamma Irradiation Influences the Survival and Regrowth of Antibiotic-Resistant Bacteria and Antibiotic-Resistance Genes on Romaine Lettuce. <i>Frontiers in Microbiology</i> , 2019, 10, 710.	1.5	11
323	Plasmid detection and assembly in genomic and metagenomic data sets. <i>Genome Research</i> , 2019, 29, 961-968.	2.4	108
324	Complete Genome Sequence of a Colistin-Resistant Uropathogenic <i>Escherichia coli</i> Sequence Type 131 <i>fimH</i> 22 Strain Harboring <i>mcr-1</i> on an IncHI2 Plasmid, Isolated in Riyadh, Saudi Arabia. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
325	Genomic characterization of <i>Kerstersia gyiorum</i> SWMUKG01, an isolate from a patient with respiratory infection in China. <i>PLoS ONE</i> , 2019, 14, e0214686.	1.1	3
326	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

#	ARTICLE	IF	CITATIONS
327	Controlling intestinal colonization of high-risk haematology patients with ESBL-producing Enterobacteriaceae: a randomized, placebo-controlled, multicentre, Phase II trial (CLEAR). <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 2065-2074.	1.3	8
328	A Novel, Widespread <i>qacA</i> Allele Results in Reduced Chlorhexidine Susceptibility in <i>Staphylococcus epidermidis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	12
329	Comparison of <i>Treponema pallidum</i> genomes for the prediction of resistance genes. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	2
330	GPA: A Microbial Genetic Polymorphisms Assignments Tool in Metagenomic Analysis by Bayesian Estimation. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 106-117.	3.0	6
331	How to discover new antibiotic resistance genes?. <i>Expert Review of Molecular Diagnostics</i> , 2019, 19, 349-362.	1.5	15
332	Complex Microbiome in Brain Abscess Revealed by Whole-Genome Culture-Independent and Culture-Based Sequencing. <i>Journal of Clinical Medicine</i> , 2019, 8, 351.	1.0	6
333	Clinically Unreported Salmonellosis Outbreak Detected via Comparative Genomic Analysis of Municipal Wastewater <i>Salmonella</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	35
334	Genomic analysis of methicillin-resistant <i>Staphylococcus aureus</i> isolated from poultry and occupational farm workers in Umgungundlovu District, South Africa. <i>Science of the Total Environment</i> , 2019, 670, 704-716.	3.9	33
335	Sequencing-based methods and resources to study antimicrobial resistance. <i>Nature Reviews Genetics</i> , 2019, 20, 356-370.	7.7	263
336	Infectious Complications Are Associated With Alterations in the Gut Microbiome in Pediatric Patients With Acute Lymphoblastic Leukemia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 28.	1.8	48
337	CMY-1/MOX-family AmpC β -lactamases MOX-1, MOX-2 and MOX-9 were mobilized independently from three <i>Aeromonas</i> species. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1202-1206.	1.3	17
338	Antimicrobial-Resistant <i>Escherichia coli</i> from Environmental Waters in Northern Colorado. <i>Journal of Environmental and Public Health</i> , 2019, 2019, 1-13.	0.4	48
339	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
340	Validation of a Bioinformatics Workflow for Routine Analysis of Whole-Genome Sequencing Data and Related Challenges for Pathogen Typing in a European National Reference Center: <i>Neisseria meningitidis</i> as a Proof-of-Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 362.	1.5	51
341	In Silico Drug Repurposing for MDR Bacteria: Opportunities and Challenges. , 2019, , 781-799.		2
342	Metagenomic analysis reveals the effects of long-term antibiotic pressure on sludge anaerobic digestion and antimicrobial resistance risk. <i>Bioresource Technology</i> , 2019, 282, 179-188.	4.8	111
343	The Molecular Mechanisms Underlying Hidden Phenotypic Variation among Metallo- β -Lactamases. <i>Journal of Molecular Biology</i> , 2019, 431, 1172-1185.	2.0	18
344	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. <i>Microbiome</i> , 2019, 7, 35.	4.9	109

#	ARTICLE	IF	CITATIONS
345	The antibiotic resistance and pathogenicity of a multidrug-resistant <i>Elizabethkingia anophelis</i> isolate. <i>MicrobiologyOpen</i> , 2019, 8, e804.	1.2	23
346	Evidence for the evolution, clonal expansion and global dissemination of water treatment-resistant naturalized strains of <i>Escherichia coli</i> in wastewater. <i>Water Research</i> , 2019, 156, 208-222.	5.3	38
347	Nanopore ultra-long read sequencing technology for antimicrobial resistance detection in <i>Mannheimia haemolytica</i> . <i>Journal of Microbiological Methods</i> , 2019, 159, 138-147.	0.7	22
348	Detection of critical antibiotic resistance genes through routine microbiome surveillance. <i>PLoS ONE</i> , 2019, 14, e0213280.	1.1	26
349	Emergence of New Delhi Metallo- β -Lactamase (NDM-5) in <i>Klebsiella quasipneumoniae</i> from Neonates in a Nigerian Hospital. <i>MSphere</i> , 2019, 4, .	1.3	37
350	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
351	Identification of polysaccharide capsules among extensively drug-resistant genitourinary <i>Haemophilus parainfluenzae</i> isolates. <i>Scientific Reports</i> , 2019, 9, 4481.	1.6	16
352	Genomic analysis of multidrug-resistant clinical <i>Enterococcus faecalis</i> isolates for antimicrobial resistance genes and virulence factors from the western region of Saudi Arabia. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 55.	1.5	47
353	Continuing occurrence of vancomycin resistance determinants in Danish pig farms 20 years after removing exposure to avoparcin. <i>Veterinary Microbiology</i> , 2019, 232, 84-88.	0.8	11
354	Low-cost microarray platform to detect antibiotic resistance genes. <i>Sensing and Bio-Sensing Research</i> , 2019, 23, 100266.	2.2	5
355	Metagenomic characterization of antibiotic resistance genes in Antarctic soils. <i>Ecotoxicology and Environmental Safety</i> , 2019, 176, 300-308.	2.9	58
356	Rapid Replacement of <i>Acinetobacter baumannii</i> Strains Accompanied by Changes in Lipooligosaccharide Loci and Resistance Gene Repertoire. <i>MBio</i> , 2019, 10, .	1.8	28
357	Loss and Gain in the Evolution of the <i>Salmonella enterica</i> Serovar Gallinarum Biovar Pullorum Genome. <i>MSphere</i> , 2019, 4, .	1.3	23
358	Multicenter Study of <i>Cronobacter sakazakii</i> Infections in Humans, Europe, 2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 515-522.	2.0	47
360	Genomic surveillance links livestock production with the emergence and spread of multi-drug resistant non-typhoidal <i>Salmonella</i> in Mexico. <i>Journal of Microbiology</i> , 2019, 57, 271-280.	1.3	9
361	Characterization of <i>mecC</i> gene-carrying coagulase-negative <i>Staphylococcus</i> spp. isolated from various animals. <i>Veterinary Microbiology</i> , 2019, 230, 138-144.	0.8	38
362	Extensive drug resistant <i>Salmonella enterica</i> serovar Senftenberg carrying <i>bla_{NDM}</i> encoding plasmid p5558 (IncA/C) from India. <i>Pathogens and Global Health</i> , 2019, 113, 20-26.	1.0	8
363	Genome and Functional Characterization of Colonization Factor Antigen I- and CS6-Encoding Heat-Stable Enterotoxin-Only Enterotoxigenic <i>Escherichia coli</i> Reveals Lineage and Geographic Variation. <i>MSystems</i> , 2019, 4, .	1.7	25

#	ARTICLE	IF	CITATIONS
364	<p></p>Comparative analysis of KPC-2-encoding chimera plasmids with multi-replicon IncR:Inc_{sub>}pA1763-KPC</sub>:IncN1 or IncFII_{sub>}pHN7A8</sub>:Inc_{sub>}pA1763-KPC</sub>: IncN1</p>. Infection and Drug Resistance, 2019, Volume 12, 285-296.	1.1	30
365	SELFies and CELLfies: Whole Genome Sequencing and Annotation of Five Antibiotic Resistant Bacteria Isolated from the Surfaces of Smartphones, An Inquiry Based Laboratory Exercise in a Genomics Undergraduate Course at the Rochester Institute of Technology. Journal of Genomics, 2019, 7, 26-30.	0.6	5
366	Man-made microbial resistances in built environments. Nature Communications, 2019, 10, 968.	5.8	128
367	Complete Genome Sequences of Four Salmonella enterica Strains (Including Those of Serotypes) Tj ETQq1 1 0.784314 rgBT /Overlock Microbiology Resource Announcements, 2019, 8, .	0.3	8
368	DNA Traffic in the Environment and Antimicrobial Resistance. , 2019, , 245-271.		1
369	Oral administration of antibiotics increased the potential mobility of bacterial resistance genes in the gut of the fish <i>Piaractus mesopotamicus</i> . Microbiome, 2019, 7, 24.	4.9	98
370	Replicon-Based Typing of IncI-Complex Plasmids, and Comparative Genomics Analysis of IncI ³ /K1 Plasmids. Frontiers in Microbiology, 2019, 10, 48.	1.5	20
371	Complete Genome Sequence of the Marine Hydrocarbon Degradator <i>Alcaligenes aquatilis</i> QD168, Isolated from Crude Oil-Polluted Sediment of Quintero Bay, Central Chile. Microbiology Resource Announcements, 2019, 8, .	0.3	17
372	Metagenomic Next-Generation Sequencing in Clinical Microbiology. Indian Journal of Medical Microbiology, 2019, 37, 133-140.	0.3	12
373	Draft Genome Sequence of an <i>Acinetobacter baumannii</i> Isolate Recovered from a Horse with Conjunctivitis in Germany. Microbiology Resource Announcements, 2019, 8, .	0.3	9
374	High-Risk International Clones of Carbapenem-Nonsusceptible <i>Pseudomonas aeruginosa</i> Endemic to Indonesian Intensive Care Units: Impact of a Multifaceted Infection Control Intervention Analyzed at the Genomic Level. MBio, 2019, 10, .	1.8	21
376	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. MSystems, 2019, 4, .	1.7	36
377	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. Environmental Microbiomes, 2019, 14, 7.	2.2	69
378	Genomic analysis on broiler-associated <i>Clostridium perfringens</i> strains and exploratory caecal microbiome investigation reveals key factors linked to poultry necrotic enteritis. Animal Microbiome, 2019, 1, 12.	1.5	29
379	Capturing the Resistome: a Targeted Capture Method To Reveal Antibiotic Resistance Determinants in Metagenomes. Antimicrobial Agents and Chemotherapy, 2019, 64, .	1.4	63
380	Draft Genome Sequence and Annotation of <i>Acinetobacter junii</i> MHI21018, Isolated from Bovine Colostrum. Microbiology Resource Announcements, 2019, 8, .	0.3	2
381	PLSDB: a resource of complete bacterial plasmids. Nucleic Acids Research, 2019, 47, D195-D202.	6.5	336
382	Functional Traits Co-Occurring with Mobile Genetic Elements in the Microbiome of the Atacama Desert. Diversity, 2019, 11, 205.	0.7	5

#	ARTICLE	IF	CITATIONS
383	Draft Genome Sequences of <i>Citrobacter freundii</i> and <i>Citrobacter murlinae</i> Strains Isolated from the Feces of Preterm Infants. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
384	Whole-Genome Sequencing of <i>Mycobacterium tilburgii</i> Strain MEPHI. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
385	Characterization of the Pig Gut Microbiome and Antibiotic Resistome in Industrialized Feedlots in China. <i>MSystems</i> , 2019, 4, .	1.7	44
386	Comparative Genomics Reveals a Well-Conserved Intrinsic Resistome in the Emerging Multidrug-Resistant Pathogen <i>Cupriavidus gilardii</i> . <i>MSphere</i> , 2019, 4, .	1.3	9
387	Hypervirulent clade 2, ribotype 019/sequence type 67 <i>Clostridioides difficile</i> strain from Japan. <i>Gut Pathogens</i> , 2019, 11, 54.	1.6	7
388	In Vitro Susceptibility and Florfenicol Resistance in <i>Citrobacter</i> Isolates and Whole-Genome Analysis of Multidrug-Resistant <i>Citrobacter freundii</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-15.	0.8	6
389	Type 1, 2, and 1/2-Hybrid IncC Plasmids From China. <i>Frontiers in Microbiology</i> , 2019, 10, 2508.	1.5	15
390	<i>Acinetobacter</i> Strain KUO11TH, a Unique Organism Related to <i>Acinetobacter pittii</i> and Isolated from the Skin Mucus of Healthy Bighead Catfish and Its Efficacy Against Several Fish Pathogens. <i>Microorganisms</i> , 2019, 7, 549.	1.6	12
391	The Global Ascendency of OXA-48-Type Carbapenemases. <i>Clinical Microbiology Reviews</i> , 2019, 33, .	5.7	260
392	Genotypic diversity of <i>Streptococcus suis</i> and the <i>S. suis</i> -like bacterium <i>Streptococcus ruminantium</i> in ruminants. <i>Veterinary Research</i> , 2019, 50, 94.	1.1	13
393	Deep analysis and optimization of CARD antibiotic resistance gene discovery models. <i>BMC Genomics</i> , 2019, 20, 914.	1.2	7
394	Effects of a Four-Week High-Dosage Zinc Oxide Supplemented Diet on Commensal <i>Escherichia coli</i> of Weaned Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 2734.	1.5	20
395	Epidemiology and antimicrobial resistance of methicillin-resistant <i>Staphylococcus aureus</i> isolates colonizing pigs with different exposure to antibiotics. <i>PLoS ONE</i> , 2019, 14, e0225497.	1.1	18
396	VCGIDB: A Database and Web Resource for the Genomic Islands from <i>Vibrio cholerae</i> . <i>Pathogens</i> , 2019, 8, 261.	1.2	5
397	Intestinal microbiota domination under extreme selective pressures characterized by metagenomic read cloud sequencing and assembly. <i>BMC Bioinformatics</i> , 2019, 20, 585.	1.2	7
398	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in <i>Escherichia coli</i> of Porcine Origin in Australia. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	1.8	31
399	Comparative genomics reveals a novel genetic organization of the sad cluster in the sulfonamide-degrader <i>Candidatus Leucobacter sulfamidivorax</i> ™ strain GP. <i>BMC Genomics</i> , 2019, 20, 885.	1.2	13
400	Resistome metagenomics from plate to farm: The resistome and microbial composition during food waste feeding and composting on a Vermont poultry farm. <i>PLoS ONE</i> , 2019, 14, e0219807.	1.1	11

#	ARTICLE	IF	CITATIONS
401	First Report of Coexistence of Three Different MDR Plasmids, and That of Occurrence of IMP-Encoding Plasmid in <i>Leclercia adecarboxylata</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2468.	1.5	4
402	<i>Staphylococcus arlettae</i> Genomics: Novel Insights on Candidate Antibiotic Resistance and Virulence Genes in an Emerging Opportunistic Pathogen. <i>Microorganisms</i> , 2019, 7, 580.	1.6	10
403	Simultaneous detection of genotype and phenotype enables rapid and accurate antibiotic susceptibility determination. <i>Nature Medicine</i> , 2019, 25, 1858-1864.	15.2	85
404	Bacteriophage targeting of gut bacterium attenuates alcoholic liver disease. <i>Nature</i> , 2019, 575, 505-511.	13.7	493
405	Antibiotic Resistome Biomarkers associated to the Pelagic Sediments of the Gulfs of Kathiawar Peninsula and Arabian Sea. <i>Scientific Reports</i> , 2019, 9, 17281.	1.6	12
406	Antimicrobial Resistance, Gut Microbiota, and Health. , 2019, , 902-926.		2
407	Comparative Genomic Analysis of <i>Citrobacter</i> and Key Genes Essential for the Pathogenicity of <i>Citrobacter koseri</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2774.	1.5	32
408	Identification of Genetic Features for Attenuation of Two <i>Salmonella</i> Enteritidis Vaccine Strains and Differentiation of These From Wildtype Isolates Using Whole Genome Sequencing. <i>Frontiers in Veterinary Science</i> , 2019, 6, 447.	0.9	8
409	Omics Potential in Herbicide-Resistant Weed Management. <i>Plants</i> , 2019, 8, 607.	1.6	17
410	Genomic characterization of an emerging blaKPC-2 carrying Enterobacteriaceae clinical isolates in Thailand. <i>Scientific Reports</i> , 2019, 9, 18521.	1.6	12
411	New Genus Fibralongavirus in Siphoviridae Phages of <i>Staphylococcus pseudintermedius</i> . <i>Viruses</i> , 2019, 11, 1143.	1.5	6
412	Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. <i>Nature</i> , 2019, 574, 117-121.	13.7	617
413	<i>cfr</i> (B), <i>cfr</i> (C), and a New <i>cfr</i>-Like Gene, <i>cfr</i> (E), in <i>Clostridium difficile</i> Strains Recovered across Latin America. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 64, .	1.4	37
414	Genomic and evolutionary features of two AHPND positive <i>Vibrio parahaemolyticus</i> strains isolated from shrimp (<i>Penaeus monodon</i>) of south-west Bangladesh. <i>BMC Microbiology</i> , 2019, 19, 270.	1.3	15
415	Identifying Microbiota Signature and Functional Rules Associated With Bacterial Subtypes in Human Intestine. <i>Frontiers in Genetics</i> , 2019, 10, 1146.	1.1	1
416	Long-term impact of oral surgery with or without amoxicillin on the oral microbiome-A prospective cohort study. <i>Scientific Reports</i> , 2019, 9, 18761.	1.6	12
417	Insights on genomic diversity of <i>Vibrio</i> spp. through Pan-genome analysis. <i>Annals of Microbiology</i> , 2019, 69, 1547-1555.	1.1	4
418	Low nadir CD4+ T-cell counts predict gut dysbiosis in HIV-1 infection. <i>Mucosal Immunology</i> , 2019, 12, 232-246.	2.7	56

#	ARTICLE	IF	CITATIONS
420	Discerning strain-specific β -lactam drug resistance by clonal isolates of multi-drug resistant <i>Pseudomonas aeruginosa</i> using selected reaction monitoring. <i>International Journal of Mass Spectrometry</i> , 2019, 438, 36-43.	0.7	2
421	Inhibiting antibiotic-resistant Enterobacteriaceae by microbiota-mediated intracellular acidification. <i>Journal of Experimental Medicine</i> , 2019, 216, 84-98.	4.2	135
422	Studies on the mechanism of multidrug resistance of <i>Acinetobacter baumannii</i> by proteomic analysis of the outer membrane vesicles of the bacterium. <i>Journal of Proteins and Proteomics</i> , 2019, 10, 1-15.	1.0	14
423	ABC ATPases Involved in Protein Synthesis, Ribosome Assembly and Antibiotic Resistance: Structural and Functional Diversification across the Tree of Life. <i>Journal of Molecular Biology</i> , 2019, 431, 3568-3590.	2.0	90
424	Modelling environmental antibiotic-resistance gene abundance: A meta-analysis. <i>Science of the Total Environment</i> , 2019, 659, 335-341.	3.9	34
425	Plasmid ATLAS: plasmid visual analytics and identification in high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2019, 47, D188-D194.	6.5	34
426	Antimicrobial Resistant Genes and Organisms as Environmental Contaminants of Emerging Concern: Addressing Global Public Health Risks. , 2019, , 147-187.		9
427	Characterization of antibiotic resistance genes in the sediments of an urban river revealed by comparative metagenomics analysis. <i>Science of the Total Environment</i> , 2019, 653, 1513-1521.	3.9	45
428	Extended-Spectrum Beta-Lactamase-Producing <i>Enterobacteriaceae</i> in Dairy Farm Environments: A New Zealand Perspective. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 5-22.	0.8	25
429	Evaluation of kanamycin and neomycin resistance in <i>Lactobacillus plantarum</i> using experimental evolution and whole-genome sequencing. <i>Food Control</i> , 2019, 98, 262-267.	2.8	10
430	High-Quality Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> 268 Isolated from a Patient with a Left Ventricular Assist Device. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
431	New insights into antibiotic resistome in drinking water and management perspectives: A metagenomic based study of small-sized microbes. <i>Water Research</i> , 2019, 152, 191-201.	5.3	100
432	Molecular epidemiology of 16S rRNA methyltransferase in Brazil: RmtG in <i>Klebsiella aerogenes</i> ST93 (CC4). <i>Anais Da Academia Brasileira De Ciencias</i> , 2019, 91, e20180762.	0.3	11
433	Sequencing and Genomic Diversity Analysis of IncHI5 Plasmids. <i>Frontiers in Microbiology</i> , 2018, 9, 3318.	1.5	30
434	PER extended-spectrum β -lactamases originate from <i>Pararheinheimera</i> spp. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 158-164.	1.1	12
435	Antibiotics as both friends and foes of the human gut microbiome: The microbial community approach. <i>Drug Development Research</i> , 2019, 80, 86-97.	1.4	43
436	Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	221
437	Streptomycin resistance in <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> strains from Chile is related to an <i>rpsL</i> gene mutation. <i>Plant Pathology</i> , 2019, 68, 426-433.	1.2	11

#	ARTICLE	IF	CITATIONS
438	Fate of antibiotic resistance genes during anaerobic digestion of sewage sludge: Role of solids retention times in different configurations. <i>Bioresource Technology</i> , 2019, 274, 488-495.	4.8	50
439	ARGDIT: a validation and integration toolkit for Antimicrobial Resistance Gene Databases. <i>Bioinformatics</i> , 2019, 35, 2466-2474.	1.8	12
440	The <i>Pseudomonas aeruginosa</i> Pan-Genome Provides New Insights on Its Population Structure, Horizontal Gene Transfer, and Pathogenicity. <i>Genome Biology and Evolution</i> , 2019, 11, 109-120.	1.1	223
441	Investigation of the virulence and genomics of <i>Aeromonas salmonicida</i> strains isolated from human patients. <i>Infection, Genetics and Evolution</i> , 2019, 68, 1-9.	1.0	31
442	Comparative metagenomics of the gut microbiota in wild greylag geese (<i>Anser anser</i>) and ruddy shelducks (<i>Tadorna ferruginea</i>). <i>MicrobiologyOpen</i> , 2019, 8, e00725.	1.2	20
443	Whole-Genome Analysis of a Human <i>Enterobacter mori</i> Isolate Carrying a bla _{IMI-2} Carbapenemase in Austria. <i>Microbial Drug Resistance</i> , 2019, 25, 94-96.	0.9	8
444	Genomics of antibiotic resistance prediction in <i>Pseudomonas aeruginosa</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 5-17.	1.8	51
445	Molecular profiling of multidrug-resistant river water isolates: insights into resistance mechanism and potential inhibitors. <i>Environmental Science and Pollution Research</i> , 2020, 27, 27279-27292.	2.7	11
446	Isolation, Characterisation and Fermentation Optimisation of Bacteriocin-Producing <i>Enterococcus faecium</i> . <i>Waste and Biomass Valorization</i> , 2020, 11, 3173-3181.	1.8	16
447	Ammonia stress reduces antibiotic efflux but enriches horizontal gene transfer of antibiotic resistance genes in anaerobic digestion. <i>Bioresource Technology</i> , 2020, 295, 122191.	4.8	59
448	Late start of upper secondary education and health-compromising behaviours among Finnish adolescents—a follow-up study. <i>European Journal of Public Health</i> , 2020, 30, 457-462.	0.1	3
449	Predominantly Antibiotic-resistant Intestinal Microbiome Persists in Patients With Pouchitis Who Respond to Antibiotic Therapy. <i>Gastroenterology</i> , 2020, 158, 610-624.e13.	0.6	53
450	Biodegradation of antibiotics: The new resistance determinants “ part I. <i>New Biotechnology</i> , 2020, 54, 34-51.	2.4	97
451	Coelection for antibiotic resistance genes is induced in a soil amended with zinc. <i>Soil Use and Management</i> , 2020, 36, 328-337.	2.6	15
452	Population structure and pangenome analysis of <i>Enterobacter bugandensis</i> uncover the presence of bla _{CTX-M-55} , bla _{NDM-5} and bla _{IMI-1} , along with sophisticated iron acquisition strategies. <i>Genomics</i> , 2020, 112, 1182-1191.	1.3	14
453	Isolation and characterisation of carbapenem-resistant <i>Xanthomonas citri</i> pv. <i>mangiferaeindicae</i> -like strain gir from the faecal material of giraffes. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 137-145.	0.7	0
454	Genomic Insights into Two Colistin-Resistant <i>Klebsiella pneumoniae</i> Strains Isolated from the Stool of Preterm Neonate During the First Week of Life. <i>Microbial Drug Resistance</i> , 2020, 26, 190-203.	0.9	5
455	Applications of plant-based fermented foods and their microbes. <i>Current Opinion in Biotechnology</i> , 2020, 61, 45-52.	3.3	60

#	ARTICLE	IF	CITATIONS
456	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
457	Towards assessing the influence of sediment loading on Last Interglacial sea level. <i>Geophysical Journal International</i> , 2020, 220, 384-392.	1.0	10
458	An outbreak of ST307 extended-spectrum beta-lactamase (ESBL)-producing <i>Klebsiella pneumoniae</i> in a rehabilitation center: An unusual source and route of transmission. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, 31-36.	1.0	25
459	Characterization of antimicrobial resistance in lactobacilli and bifidobacteria used as probiotics or starter cultures based on integration of phenotypic and in silico data. <i>International Journal of Food Microbiology</i> , 2020, 314, 108388.	2.1	62
460	Hypervirulent <i>Klebsiella pneumoniae</i> - clinical and molecular perspectives. <i>Journal of Internal Medicine</i> , 2020, 287, 283-300.	2.7	291
461	Emergence of new variants of antibiotic resistance genomic islands among multidrug-resistant <i>Salmonella enterica</i> in poultry. <i>Environmental Microbiology</i> , 2020, 22, 413-432.	1.8	30
462	Draft genome sequence of a clinical <i>Acinetobacter haemolyticus</i> isolate from South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 16-17.	0.9	0
463	Pan-genome analysis of <i>Riemerella anatipestifer</i> reveals its genomic diversity and acquired antibiotic resistance associated with genomic islands. <i>Functional and Integrative Genomics</i> , 2020, 20, 307-320.	1.4	8
464	Living Trees: High-Quality Reproducible and Reusable Construction of Bacterial Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2020, 37, 563-575.	3.5	17
465	Phenotype and genomic background of <i>Arcobacter butzleri</i> strains and taxogenomic assessment of the species. <i>Food Microbiology</i> , 2020, 89, 103416.	2.1	19
466	Meta-analysis of Pandemic <i>Escherichia coli</i> ST131 Plasmidome Proves Restricted Plasmid-clade Associations. <i>Scientific Reports</i> , 2020, 10, 36.	1.6	41
467	Mobile resistome of human gut and pathogen drives anthropogenic bloom of antibiotic resistance. <i>Microbiome</i> , 2020, 8, 2.	4.9	80
468	The bacterial microbiota in florfenicol contaminated soils: The antibiotic resistome and the nitrogen cycle. <i>Environmental Pollution</i> , 2020, 259, 113901.	3.7	36
469	Detection of Antimicrobial Resistance Using Proteomics and the Comprehensive Antibiotic Resistance Database: A Case Study. <i>Proteomics - Clinical Applications</i> , 2020, 14, e1800182.	0.8	30
470	Genomic and phenotypic assessments of safety and probiotic properties of <i>Streptococcus macedonicus</i> strains of dairy origin. <i>Food Research International</i> , 2020, 130, 108931.	2.9	13
471	Detection of mobile colistin resistance gene <i>mcr-9</i> in carbapenem-resistant <i>Klebsiella pneumoniae</i> strains of human origin in Europe. <i>Journal of Infection</i> , 2020, 80, 578-606.	1.7	35
472	MinION sequencing of <i>Streptococcus suis</i> allows for functional characterization of bacteria by multilocus sequence typing and antimicrobial resistance profiling. <i>Journal of Microbiological Methods</i> , 2020, 169, 105817.	0.7	18
473	Comprehensive Understanding of the Plasmid-Mediated Colistin Resistance Gene <i>mcr-1</i> in Aquatic Environments. <i>Environmental Science & Technology</i> , 2020, 54, 1603-1613.	4.6	20

#	ARTICLE	IF	CITATIONS
474	Genomic information on <i>Stenotrophomonas maltophilia</i> ST264 isolated from a cystic fibrosis pediatric patient in Brazil. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 1125-1127.	0.8	0
475	Metagenomic analysis reveals the abundance and diversity of ARGs in children's respiratory tract microbiomes. <i>Journal of Infection</i> , 2020, 80, 232-254.	1.7	5
476	Analysis of Resistance Gene Prevalence in Whole-Genome Sequenced <i>Enterobacteriales</i> from Brazil. <i>Microbial Drug Resistance</i> , 2020, 26, 594-604.	0.9	6
477	Transmission of antimicrobial resistant non-O157 <i>Escherichia coli</i> at the interface of animal-fresh produce in sustainable farming environments. <i>International Journal of Food Microbiology</i> , 2020, 319, 108472.	2.1	15
478	Discovery of tigecycline resistance genes tet(X3) and tet(X4) in live poultry market worker gut microbiomes and the surrounded environment. <i>Science Bulletin</i> , 2020, 65, 340-342.	4.3	14
479	Cotrimoxazole Prophylaxis Increases Resistance Gene Prevalence and α -Diversity but Decreases β -Diversity in the Gut Microbiome of Human Immunodeficiency Virus-Exposed, Uninfected Infants. <i>Clinical Infectious Diseases</i> , 2020, 71, 2858-2868.	2.9	35
480	Microbiome Diagnostics. <i>Clinical Chemistry</i> , 2020, 66, 68-76.	1.5	27
481	Draft genome sequence reveals co-occurrence of multiple antimicrobial resistance and plant probiotic traits in rice root endophytic strain <i>Burkholderia</i> sp. LS-044 affiliated to <i>Burkholderia cepacia</i> complex. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 28-30.	0.9	11
482	An exploration of smokeless tobacco product nucleic acids: a combined metagenome and metatranscriptome analysis. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 751-763.	1.7	14
483	Genetic Diversity of <i>Listeria monocytogenes</i> Isolates from Invasive Listeriosis in China. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 215-227.	0.8	12
485	Prevalence and genomic characterization of Group A <i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> isolated from patients with invasive infections in Toyama prefecture, Japan. <i>Microbiology and Immunology</i> , 2020, 64, 113-122.	0.7	9
486	Shell-vial Assay in Diagnosis of Disseminated BCG Infection in an Immunodeficient Child. <i>Pediatric Infectious Disease Journal</i> , 2020, 39, 258-259.	1.1	4
487	Phenotypic and Genotypic Correlates of Penicillin Susceptibility in Nontoxigenic <i>Corynebacterium diphtheriae</i> , British Columbia, Canada, 2015-2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 97-103.	2.0	11
488	Genome Analyses and Genome-Centered Metatranscriptomics of <i>Methanothermobacter wolfeii</i> Strain SIV6, Isolated from a Thermophilic Production-Scale Biogas Fermenter. <i>Microorganisms</i> , 2020, 8, 13.	1.6	8
489	In Vitro Pharmacodynamic Analyses Help Guide the Treatment of Multidrug-Resistant <i>Enterococcus faecium</i> and Carbapenem-Resistant <i>Enterobacter cloacae</i> Bacteremia in a Liver Transplant Patient. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofz545.	0.4	5
490	Phylogeographical Analysis Reveals the Historic Origin, Emergence, and Evolutionary Dynamics of Methicillin-Resistant <i>Staphylococcus aureus</i> ST228. <i>Frontiers in Microbiology</i> , 2020, 11, 2063.	1.5	6
491	Characterization of a New Transposon, Tn6696, on a bla _{NDM} -1-Carrying Plasmid From Multidrug-Resistant <i>Enterobacter cloacae</i> ssp. <i>dissolvens</i> in China. <i>Frontiers in Microbiology</i> , 2020, 11, 525479.	1.5	9
492	<i>Lactobacillus curvatus</i> : A Candidate Probiotic with Excellent Fermentation Properties and Health Benefits. <i>Foods</i> , 2020, 9, 1366.	1.9	24

#	ARTICLE	IF	CITATIONS
493	Genome-Based Insights into the Production of Carotenoids by Antarctic Bacteria, <i>Planococcus</i> sp. ANT_H30 and <i>Rhodococcus</i> sp. ANT_H53B. <i>Molecules</i> , 2020, 25, 4357.	1.7	13
494	Genomic Analysis Reveals the Genetic Determinants Associated With Antibiotic Resistance in the Zoonotic Pathogen <i>Campylobacter</i> spp. Distributed Globally. <i>Frontiers in Microbiology</i> , 2020, 11, 513070.	1.5	14
495	Genomic Analysis of two NDM-1 <i>Providencia stuartii</i> Strains Recovered from a Single Patient. <i>Current Microbiology</i> , 2020, 77, 4029-4036.	1.0	5
498	Nanopore MinION Sequencing Reveals Possible Transfer of blaKPC ² Plasmid Across Bacterial Species in Two Healthcare Facilities. <i>Frontiers in Microbiology</i> , 2020, 11, 2007.	1.5	21
499	<i>Aliarcobacter butzleri</i> from Water Poultry: Insights into Antimicrobial Resistance, Virulence and Heavy Metal Resistance. <i>Genes</i> , 2020, 11, 1104.	1.0	9
500	Evaluation of Potential ARG Packaging by Two Environmental T7-Like Phage during Phage-Host Interaction. <i>Viruses</i> , 2020, 12, 1060.	1.5	9
501	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
502	Understanding the impact of antibiotic perturbation on the human microbiome. <i>Genome Medicine</i> , 2020, 12, 82.	3.6	148
503	Genetic and Virulence Characteristics of a Hybrid Atypical Enteropathogenic and Uropathogenic <i>Escherichia coli</i> (aEPEC/UPEC) Strain. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 492.	1.8	25
504	Hybrid assembly of multi-drug resistant, highly virulent methicillin resistant <i>Staphylococcus aureus</i> ST772-SCCmec V lineage: Maximising its potential for dissemination similar to USA300 clone. <i>Genomics</i> , 2020, 112, 5248-5253.	1.3	1
505	RBUD: A New Functional Potential Analysis Approach for Whole Microbial Genome Shotgun Sequencing. <i>Microorganisms</i> , 2020, 8, 1563.	1.6	1
506	Expression of the MexXY Aminoglycoside Efflux Pump and Presence of an Aminoglycoside-Modifying Enzyme in Clinical <i>Pseudomonas aeruginosa</i> Isolates Are Highly Correlated. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	14
507	AcGI1, a novel genomic island carrying antibiotic resistance integron In687 in multidrug resistant <i>Achromobacter xylosoxidans</i> in a teaching hospital in Thailand. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	4
508	Large-scale assessment of antimicrobial resistance marker databases for genetic phenotype prediction: a systematic review. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3099-3108.	1.3	60
509	Isolation and Characterization of Bacteriophages That Infect <i>Citrobacter rodentium</i> , a Model Pathogen for Intestinal Diseases. <i>Viruses</i> , 2020, 12, 737.	1.5	16
510	Untargeted Metagenomic Investigation of the Airway Microbiome of Cystic Fibrosis Patients with Moderate-Severe Lung Disease. <i>Microorganisms</i> , 2020, 8, 1003.	1.6	23
511	Environmental dissemination of carbapenemase-producing Enterobacteriaceae in rivers in Switzerland. <i>Environmental Pollution</i> , 2020, 265, 115081.	3.7	51
512	Complete genome sequences of <i>Streptococcus pyogenes</i> type strain reveal 100%-match between PacBio-solo and Illumina-Oxford Nanopore hybrid assemblies. <i>Scientific Reports</i> , 2020, 10, 11656.	1.6	5

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513	Two Lineages of <i>Pseudomonas aeruginosa</i> Filamentous Phages: Structural Uniformity over Integration Preferences. <i>Genome Biology and Evolution</i> , 2020, 12, 1765-1781.	1.1	22
514	PARMAP: A Pan-Genome-Based Computational Framework for Predicting Antimicrobial Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 578795.	1.5	10
515	Multidrug-Resistant <i>Proteus mirabilis</i> Strain with Cointegrate Plasmid. <i>Microorganisms</i> , 2020, 8, 1775.	1.6	13
516	DeepBL: a deep learning-based approach for <i>in silico</i> discovery of beta-lactamases. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
517	Fecal <i>Klebsiella pneumoniae</i> Carriage Is Intermittent and of High Clonal Diversity. <i>Frontiers in Microbiology</i> , 2020, 11, 581081.	1.5	9
518	<i>Aeromonas hydrophila</i> RIT668 and <i>Citrobacter portucalensis</i> RIT669—Potential Zoonotic Pathogens Isolated from Spotted Turtles. <i>Microorganisms</i> , 2020, 8, 1805.	1.6	3
519	Genotyping and Antibiotic Resistance Traits in <i>Campylobacter jejuni</i> and <i>coli</i> From Pigs and Wild Boars in Italy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 592512.	1.8	18
520	The Lung Microbiome of Three Young Brazilian Patients With Cystic Fibrosis Colonized by Fungi. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 598938.	1.8	8
521	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020, 11, 563975.	1.1	12
522	Genome- and Proteome-Wide Analysis of Lysine Acetylation in <i>Vibrio vulnificus</i> Vv180806 Reveals Its Regulatory Roles in Virulence and Antibiotic Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 591287.	1.5	11
523	Removal of antibiotic resistance genes in pig manure composting influenced by inoculation of compound microbial agents. <i>Bioresource Technology</i> , 2020, 317, 123966.	4.8	33
524	Concentration and chemical form of dietary zinc shape the porcine colon microbiome, its functional capacity and antibiotic resistance gene repertoire. <i>ISME Journal</i> , 2020, 14, 2783-2793.	4.4	37
525	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. <i>Chinese Medical Journal</i> , 2020, 133, 1844-1855.	0.9	55
526	Investigating the Meat Pathway as a Source of Human Nontyphoidal <i>Salmonella</i> Bloodstream Infections and Diarrhea in East Africa. <i>Clinical Infectious Diseases</i> , 2021, 73, e1570-e1578.	2.9	23
527	Characterization of a SPM-1 metallo-beta-lactamase-producing <i>Pseudomonas aeruginosa</i> by comparative genomics and phenotypic analysis. <i>Scientific Reports</i> , 2020, 10, 13192.	1.6	9
528	Complete Genome Sequence of <i>Ralstonia</i> Phage Remenis, a Member of Putative New Genus within the Siphoviridae. <i>American Journal of Potato Research</i> , 2020, 97, 447-449.	0.5	1
529	Standardized bacteriophage purification for personalized phage therapy. <i>Nature Protocols</i> , 2020, 15, 2867-2890.	5.5	109
530	Targeted domain assembly for fast functional profiling of metagenomic datasets with S3A. <i>Bioinformatics</i> , 2020, 36, 3975-3981.	1.8	2

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531	Metatranscriptomic Analysis Reveals Active Bacterial Communities in Diabetic Foot Infections. <i>Frontiers in Microbiology</i> , 2020, 11, 1688.	1.5	18
532	Phenotypic and WGS-derived antimicrobial resistance profiles of clinical and non-clinical <i>Acinetobacter baumannii</i> isolates from Germany and Vietnam. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106127.	1.1	16
533	Source tracking of antibiotic resistance genes in the environment “ Challenges, progress, and prospects. <i>Water Research</i> , 2020, 185, 116127.	5.3	82
534	Microbiome and Metagenome Analyses of a Closed Habitat during Human Occupation. <i>MSystems</i> , 2020, 5, .	1.7	4
535	The incidence of antibiotic resistance within and beyond the agricultural ecosystem: A concern for public health. <i>MicrobiologyOpen</i> , 2020, 9, e1035.	1.2	108
536	Expression of a Shiga-Like Toxin during Plastic Colonization by Two Multidrug-Resistant Bacteria, <i>Aeromonas hydrophila</i> RIT668 and <i>Citrobacter freundii</i> RIT669, Isolated from Endangered Turtles (<i>Clemmys guttata</i>). <i>Microorganisms</i> , 2020, 8, 1172.	1.6	14
537	Enterococci from Wild Magellanic Penguins (<i>Spheniscus magellanicus</i>) as an Indicator of Marine Ecosystem Health and Human Impact. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	5
538	Metagenomics revealing molecular profiling of community structure and metabolic pathways in natural hot springs of the Sikkim Himalaya. <i>BMC Microbiology</i> , 2020, 20, 246.	1.3	32
539	A new plasmid carrying mphA causes prevalence of azithromycin resistance in enterotoxigenic <i>Escherichia coli</i> serogroup O6. <i>BMC Microbiology</i> , 2020, 20, 247.	1.3	22
540	Comparative Genomic Analysis Reveals Genetic Mechanisms of the Variety of Pathogenicity, Antibiotic Resistance, and Environmental Adaptation of <i>Providencia</i> Genus. <i>Frontiers in Microbiology</i> , 2020, 11, 572642.	1.5	24
541	Colonization of a hand washing sink in a veterinary hospital by an <i>Enterobacter hormaechei</i> strain carrying multiple resistances to high importance antimicrobials. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 163.	1.5	13
542	Mechanism of the Potential Therapeutic Candidate <i>Bacillus subtilis</i> BSXE-1601 Against Shrimp Pathogenic <i>Vibrios</i> and Multifunctional Metabolites Biosynthetic Capability of the Strain as Predicted by Genome Analysis. <i>Frontiers in Microbiology</i> , 2020, 11, 581802.	1.5	6
543	A pilot RNA-seq study in 40 pietrain ejaculates to characterize the porcine sperm microbiome. <i>Theriogenology</i> , 2020, 157, 525-533.	0.9	19
544	Global Epidemiology and Evolutionary History of <i>Staphylococcus aureus</i> ST45. <i>Journal of Clinical Microbiology</i> , 2020, 59, .	1.8	14
545	Impact of investigational microbiota therapeutic RBX2660 on the gut microbiome and resistome revealed by a placebo-controlled clinical trial. <i>Microbiome</i> , 2020, 8, 125.	4.9	41
546	Widespread transfer of mobile antibiotic resistance genes within individual gut microbiomes revealed through bacterial Hi-C. <i>Nature Communications</i> , 2020, 11, 4379.	5.8	116
547	Whole-genome sequence of multi-drug resistant <i>Pseudomonas aeruginosa</i> strains UY1PSABAL and UY1PSABAL2 isolated from human broncho-alveolar lavage, Yaounda, Cameroon. <i>PLoS ONE</i> , 2020, 15, e0238390.	1.1	24
548	<i>Campylobacter jejuni</i> from Canine and Bovine Cases of Campylobacteriosis Express High Antimicrobial Resistance Rates against (Fluoro)quinolones and Tetracyclines. <i>Pathogens</i> , 2020, 9, 691.	1.2	5

#	ARTICLE	IF	CITATIONS
549	A Nosocomial Respiratory Infection Outbreak of Carbapenem-Resistant <i>Escherichia coli</i> ST131 With Multiple Transmissible blaKPC ² Carrying Plasmids. <i>Frontiers in Microbiology</i> , 2020, 11, 2068.	1.5	18
550	Hybrid Harris hawks optimization with cuckoo search for drug design and discovery in chemoinformatics. <i>Scientific Reports</i> , 2020, 10, 14439.	1.6	73
551	Is Long-Term Heavy Metal Exposure Driving Carriage of Antibiotic Resistance in Environmental Opportunistic Pathogens: A Comprehensive Phenomic and Genomic Assessment Using <i>Serratia</i> sp. SRS-8-S-2018. <i>Frontiers in Microbiology</i> , 2020, 11, 1923.	1.5	4
552	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
553	STing: accurate and ultrafast genomic profiling with exact sequence matches. <i>Nucleic Acids Research</i> , 2020, 48, 7681-7689.	6.5	5
554	Analytical Performance Validation of Next-Generation Sequencing Based Clinical Microbiology Assays Using a K-mer Analysis Workflow. <i>Frontiers in Microbiology</i> , 2020, 11, 1883.	1.5	12
555	Characterizing Phage-Host Interactions in a Simplified Human Intestinal Barrier Model. <i>Microorganisms</i> , 2020, 8, 1374.	1.6	12
556	Genomic Prediction of Antimicrobial Resistance: Ready or Not, Here It Comes!. <i>Clinical Chemistry</i> , 2020, 66, 1278-1289.	1.5	25
557	Activity of Aztreonam in Combination with Avibactam, Clavulanate, Relebactam, and Vaborbactam against Multidrug-Resistant <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	21
558	Genome-Assisted Characterization of <i>Lactobacillus fermentum</i> , <i>Weissella cibaria</i> , and <i>Weissella confusa</i> Strains Isolated from Sorghum as Starters for Sourdough Fermentation. <i>Microorganisms</i> , 2020, 8, 1388.	1.6	32
559	Horizontal Gene Transfer Clarifies Taxonomic Confusion and Promotes the Genetic Diversity and Pathogenicity of <i>Plesiomonas shigelloides</i> . <i>MSystems</i> , 2020, 5, .	1.7	18
560	MAIRA- real-time taxonomic and functional analysis of long reads on a laptop. <i>BMC Bioinformatics</i> , 2020, 21, 390.	1.2	2
561	Antimicrobial Resistance and Virulence-Associated Markers in <i>Campylobacter</i> Strains From Diarrheic and Non-diarrheic Humans in Poland. <i>Frontiers in Microbiology</i> , 2020, 11, 1799.	1.5	23
562	Phylogenetic Characterization Reveals Prevalent <i>Shigella flexneri</i> ST100 Clone in Beijing, China, 2005 to 2018. <i>MSphere</i> , 2020, 5, .	1.3	1
563	Increase of vancomycin-resistant <i>Enterococcus faecium</i> strain type ST117 CT71 at CharitÄ© - UniversitÄtsmedizin Berlin, 2008 to 2018. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 109.	1.5	21
564	The Clinical and Molecular Epidemiology of Noncarbapenemase-Producing Carbapenem-Resistant Enterobacteriaceae: A Case-Case-Control Matched Analysis. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa299.	0.4	20
565	Gut microbiome of endangered <i>Tor putitora</i> (Ham.) as a reservoir of antibiotic resistance genes and pathogens associated with fish health. <i>BMC Microbiology</i> , 2020, 20, 249.	1.3	10
566	Human Movement and Transmission of Antimicrobial-Resistant Bacteria. <i>Handbook of Environmental Chemistry</i> , 2020, , 311-344.	0.2	2

#	ARTICLE	IF	CITATIONS
567	Draft genome sequence of multi-resistant <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Rissen strain 19CS0416 isolated from Vietnam reveals <i>mcr-1</i> plasmid mediated resistance to colistin already in 2013. <i>Journal of Genomics</i> , 2020, 8, 76-79.	0.6	4
568	Antibiotic Resistance in the Environment. <i>Handbook of Environmental Chemistry</i> , 2020, , .	0.2	5
569	A Clinical Extensively-Drug Resistant (XDR) <i>Escherichia coli</i> and Role of Its β -Lactamase Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 590357.	1.5	8
570	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
571	Raw Cow Milk Bacterial Consortium as Bioindicator of Circulating Anti-Microbial Resistance (AMR). <i>Animals</i> , 2020, 10, 2378.	1.0	11
572	Comparative Pathogenomics of <i>Aeromonas veronii</i> from Pigs in South Africa: Dominance of the Novel ST657 Clone. <i>Microorganisms</i> , 2020, 8, 2008.	1.6	6
573	Completing the Picture—Capturing the Resistome in Antibiotic Clinical Trials. <i>Clinical Infectious Diseases</i> , 2021, 72, e1122-e1129.	2.9	2
574	Characterization of an IncR Plasmid with Two Copies of ISCR-Linked <i>qnrB6</i> from ST968 <i>Klebsiella pneumoniae</i> . <i>International Journal of Genomics</i> , 2020, 2020, 1-8.	0.8	4
575	Which Current and Novel Diagnostic Avenues for Bacterial Respiratory Diseases?. <i>Frontiers in Microbiology</i> , 2020, 11, 616971.	1.5	10
576	Evidence for the Dissemination to Humans of Methicillin-Resistant <i>Staphylococcus aureus</i> ST398 through the Pork Production Chain: A Study in a Portuguese Slaughterhouse. <i>Microorganisms</i> , 2020, 8, 1892.	1.6	18
577	Assessment of Safety and Probiotic Traits of <i>Enterococcus durans</i> OSY-EGY, Isolated From Egyptian Artisanal Cheese, Using Comparative Genomics and Phenotypic Analyses. <i>Frontiers in Microbiology</i> , 2020, 11, 608314.	1.5	25
578	Multidrug-resistant enterobacteriaceae in coastal water: an emerging threat. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 169.	1.5	16
579	Comparative Evolutionary Patterns of <i>Burkholderia cenocepacia</i> and <i>B. multivorans</i> During Chronic Co-infection of a Cystic Fibrosis Patient Lung. <i>Frontiers in Microbiology</i> , 2020, 11, 574626.	1.5	7
580	Efflux Pump-Driven Antibiotic and Biocide Cross-Resistance in <i>Pseudomonas aeruginosa</i> Isolated from Different Ecological Niches: A Case Study in the Development of Multidrug Resistance in Environmental Hotspots. <i>Microorganisms</i> , 2020, 8, 1647.	1.6	52
581	Comparative Genomics of Pathogenic <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> Strains from Chile Reveals Potential Virulence Features for Tomato Plants. <i>Microorganisms</i> , 2020, 8, 1679.	1.6	14
582	Genetic factors related to the widespread dissemination of ST11 extensively drug-resistant carbapenemase-producing <i>Klebsiella pneumoniae</i> strains within hospital. <i>Chinese Medical Journal</i> , 2020, 133, 2573-2585.	0.9	4
583	Identification and Elimination of the Clinically Relevant Multi-Resistant Environmental Bacteria <i>Ralstonia insidiosa</i> in Primary Cell Culture. <i>Microorganisms</i> , 2020, 8, 1599.	1.6	6
584	Comparative Genomic Analysis Provides Insights into the Phylogeny, Resistome, Virulome, and Host Adaptation in the Genus <i>Ewingella</i> . <i>Pathogens</i> , 2020, 9, 330.	1.2	7

#	ARTICLE	IF	CITATIONS
585	Factors associated with elevated levels of antibiotic resistance genes in sewer sediments and wastewater. <i>Environmental Science: Water Research and Technology</i> , 2020, 6, 1697-1710.	1.2	15
586	Predatory Organisms with Untapped Biosynthetic Potential: Descriptions of Novel <i>Corallococcus</i> Species <i>C. aberystwythensis</i> sp. nov., <i>C. carmarthensis</i> sp. nov., <i>C. exercitus</i> sp. nov., <i>C. interemptor</i> sp. nov., <i>C. llansteffanensis</i> sp. nov., <i>C. praedator</i> sp. nov., <i>C. sicarius</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	52
587	Complete Genome Sequence of Collection Strain <i>Acinetobacter baumannii</i> ATCC BAA-1790, Used as a Model To Study the Antibiotic Resistance Reversion Induced by Iodine-Containing Complexes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
588	Next-Generation Sequencing and MALDI Mass Spectrometry in the Study of Multiresistant Processed Meat Vancomycin-Resistant Enterococci (VRE). <i>Biology</i> , 2020, 9, 89.	1.3	13
589	The Role of European Starlings (<i>Sturnus vulgaris</i>) in the Dissemination of Multidrug-Resistant <i>Escherichia coli</i> among Concentrated Animal Feeding Operations. <i>Scientific Reports</i> , 2020, 10, 8093.	1.6	8
590	Ventricidin A, A Membrane-active Natural Product Inhibitor of ATP synthase Potentiates Aminoglycoside Antibiotics. <i>Scientific Reports</i> , 2020, 10, 8134.	1.6	35
591	Metagenomic Diagnosis for a Culture-Negative Sample From a Patient With Severe Pneumonia by Nanopore and Next-Generation Sequencing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 182.	1.8	17
592	Reused poultry litter microbiome with competitive exclusion potential against <i>Salmonella</i> Heidelberg. <i>Journal of Environmental Quality</i> , 2020, 49, 869-881.	1.0	39
593	Rapid identification of pathogens, antibiotic resistance genes and plasmids in blood cultures by nanopore sequencing. <i>Scientific Reports</i> , 2020, 10, 7622.	1.6	66
594	Global ocean resistome revealed: Exploring antibiotic resistance gene abundance and distribution in TARA Oceans samples. <i>GigaScience</i> , 2020, 9, .	3.3	60
595	Plasmids of novel incompatibility group IncpRBL16 from <i>Pseudomonas</i> species. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2093-2100.	1.3	19
596	Antimicrobial resistance genes in raw milk for human consumption. <i>Scientific Reports</i> , 2020, 10, 7464.	1.6	53
597	Freshwater viral metagenome reveals novel and functional phage-borne antibiotic resistance genes. <i>Microbiome</i> , 2020, 8, 75.	4.9	118
598	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020, 11, 2719.	5.8	62
599	Genome sequence analysis of multidrug-resistant <i>Mycobacterium tuberculosis</i> from Malaysia. <i>Scientific Data</i> , 2020, 7, 135.	2.4	4
600	Genome Dynamics of <i>Vibrio cholerae</i> Isolates Linked to Seasonal Outbreaks of Cholera in Dhaka, Bangladesh. <i>MBio</i> , 2020, 11, .	1.8	39
601	Prophage-Mediated Disruption of Genetic Competence in <i>Staphylococcus pseudintermedius</i> . <i>MSystems</i> , 2020, 5, .	1.7	24
602	Draft Genome Sequence of a <i>Mycobacterium porcinum</i> Strain Isolated from a Pet Cat with Atypical <i>Mycobacterial Panniculitis</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1

#	ARTICLE	IF	CITATIONS
603	Isolation of a novel species in the genus <i>Cupriavidus</i> from a patient with sepsis using whole genome sequencing. <i>PLoS ONE</i> , 2020, 15, e0232850.	1.1	5
604	Whole genome sequencing and antibiotic diffusion assays, provide new insight on drug resistance in the genus <i>Pedobacter</i> . <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	5
605	Dental Calculus as a Tool to Study the Evolution of the Mammalian Oral Microbiome. <i>Molecular Biology and Evolution</i> , 2020, 37, 3003-3022.	3.5	28
606	Case Report: Successful Rescue Therapy of Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Osteomyelitis With Cefiderocol. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa150.	0.4	32
607	Phenotypic and genotypic characterization of non-typhoidal <i>Salmonella</i> isolated from a Brazilian pork production chain. <i>Food Research International</i> , 2020, 137, 109406.	2.9	16
608	Identification of a mobilizable, multidrug-resistant genomic island in <i>Myroides odoratimimus</i> isolated from Tibetan pasture. <i>Science of the Total Environment</i> , 2020, 723, 137970.	3.9	10
609	A systematic strategy for the investigation of vaccines and drugs targeting bacteria. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1525-1538.	1.9	13
610	First report of a clinical multidrug-resistant <i>Pseudomonas aeruginosa</i> ST532 isolate harbouring a ciprofloxacin-modifying enzyme (CrpP) in South Africa. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 145-146.	0.9	6
611	Characterization of water treatment-resistant and multidrug-resistant urinary pathogenic <i>Escherichia coli</i> in treated wastewater. <i>Water Research</i> , 2020, 182, 115827.	5.3	31
612	<i>Vibrios</i> from the Norwegian marine environment: Characterization of associated antibiotic resistance and virulence genes. <i>MicrobiologyOpen</i> , 2020, 9, e1093.	1.2	28
613	Genetic dominance governs the evolution and spread of mobile genetic elements in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15755-15762.	3.3	41
614	Live Biotherapeutic Products, A Road Map for Safety Assessment. <i>Frontiers in Medicine</i> , 2020, 7, 237.	1.2	48
615	Comparative genomics shows niche-specific variations of <i>Lactobacillus plantarum</i> strains isolated from human, <i>Drosophila melanogaster</i> , vegetable and dairy sources. <i>Food Bioscience</i> , 2020, 35, 100581.	2.0	27
616	Origin of OXA-23 Variant OXA-239 from a Recently Emerged Lineage of <i>Acinetobacter baumannii</i> International Clone V. <i>MSphere</i> , 2020, 5, .	1.3	50
617	Physiological function analysis of <i>Lactobacillus plantarum</i> Y44 based on genotypic and phenotypic characteristics. <i>Journal of Dairy Science</i> , 2020, 103, 5916-5930.	1.4	23
618	Interest of bacterial pangenome analyses in clinical microbiology. <i>Microbial Pathogenesis</i> , 2020, 149, 104275.	1.3	12
619	A single <i>Proteus mirabilis</i> lineage from human and animal sources: a hidden reservoir of OXA-23 or OXA-58 carbapenemases in Enterobacterales. <i>Scientific Reports</i> , 2020, 10, 9160.	1.6	17
620	Rapid detection and quantification of plasmid-mediated colistin resistance genes (<i>mcr</i> to <i>Tj ETQq1</i>) in <i>Escherichia coli</i> O157:H7. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 129, 1523-1529.	1.4	14

#	ARTICLE	IF	CITATIONS
621	Comparative Genome Analysis of a Pathogenic <i>Erysipelothrix rhusiopathiae</i> Isolate WH13013 from Pig Reveals Potential Genes Involve in Bacterial Adaptions and Pathogenesis. <i>Veterinary Sciences</i> , 2020, 7, 74.	0.6	4
622	Chromosome Architecture and Gene Content of the Emergent Pathogen <i>Acinetobacter haemolyticus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 926.	1.5	4
623	Characterization of Extremely Drug-Resistant and Hypervirulent <i>Acinetobacter baumannii</i> ABO30. <i>Antibiotics</i> , 2020, 9, 328.	1.5	11
624	Use of artificial intelligence in infectious diseases. , 2020, , 415-438.		78
625	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	5.8	133
626	A Novel, Integron-Regulated, Class C β -Lactamase. <i>Antibiotics</i> , 2020, 9, 123.	1.5	11
627	Antibiotic resistance gene sharing networks and the effect of dietary nutritional content on the canine and feline gut resistome. <i>Animal Microbiome</i> , 2020, 2, 4.	1.5	17
628	ASA3P: An automatic and scalable pipeline for the assembly, annotation and higher-level analysis of closely related bacterial isolates. <i>PLoS Computational Biology</i> , 2020, 16, e1007134.	1.5	59
629	Antibiotic Resistance in Municipal Wastewater: A Special Focus on Hospital Effluents. <i>Handbook of Environmental Chemistry</i> , 2020, , 123-146.	0.2	1
630	Comparative Genomic Analysis of a Multidrug-Resistant <i>Campylobacter jejuni</i> Strain YH002 Isolated from Retail Beef Liver. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 576-584.	0.8	14
631	The microbiome and resistome of chimpanzees, gorillas, and humans across host lifestyle and geography. <i>ISME Journal</i> , 2020, 14, 1584-1599.	4.4	78
632	Phylogeography and Genetic Diversity of <i>Francisella tularensis</i> subsp. <i>holarctica</i> in France (1947â€”2018). <i>Frontiers in Microbiology</i> , 2020, 11, 287.	1.5	17
633	Relational dynamics obtained through simulation studies of thioredoxin reductase: From a multi-drug resistant <i>Entamoeba histolytica</i> . <i>Journal of Molecular Liquids</i> , 2020, 307, 112939.	2.3	4
634	Integrated metagenomic and metatranscriptomic profiling reveals differentially expressed resistomes in human, chicken, and pig gut microbiomes. <i>Environment International</i> , 2020, 138, 105649.	4.8	51
635	Antimicrobial-resistant microorganisms and their genetic determinants in stormwater: A systematic review. <i>Current Opinion in Environmental Science and Health</i> , 2020, 16, 101-112.	2.1	18
636	A megaplasmid family driving dissemination of multidrug resistance in <i>Pseudomonas</i> . <i>Nature Communications</i> , 2020, 11, 1370.	5.8	90
637	Metagenomic analysis reveals the microbiome and resistome in migratory birds. <i>Microbiome</i> , 2020, 8, 26.	4.9	109
638	Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens. <i>PLoS Computational Biology</i> , 2020, 16, e1007608.	1.5	49

#	ARTICLE	IF	CITATIONS
639	Genomic characterisation of <i>Salmonella enterica</i> serovar Wangata isolates obtained from different sources reveals low genomic diversity. <i>PLoS ONE</i> , 2020, 15, e0229697.	1.1	2
640	Novel Bacteriophages Capable of Disrupting Biofilms From Clinical Strains of <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 194.	1.5	22
641	Whole genome sequencing provides genomic insights into three <i>Morganella morganii</i> strains isolated from bovine rectal swabs in Dhaka, Bangladesh. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	6
642	Longitudinal survey of microbiome associated with particulate matter in a megacity. <i>Genome Biology</i> , 2020, 21, 55.	3.8	59
643	Investigation of a Salmonellosis Outbreak Caused by Multidrug Resistant <i>Salmonella</i> Typhimurium in China. <i>Frontiers in Microbiology</i> , 2020, 11, 801.	1.5	39
644	Isolation and Characterization of <i>Pectobacterium</i> Phage vB_PatM_CB7: New Insights into the Genus <i>Certevirus</i> . <i>Antibiotics</i> , 2020, 9, 352.	1.5	21
645	Constructing knowledge graphs and their biomedical applications. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1414-1428.	1.9	132
646	First Report on the Plasmidome From a High-Altitude Lake of the Andean Puna. <i>Frontiers in Microbiology</i> , 2020, 11, 1343.	1.5	17
647	Detection of S83V GyrA mutation in quinolone-resistant <i>Shewanella</i> algae using comparative genomics. <i>Journal of Microbiology, Immunology and Infection</i> , 2021, 54, 658-664.	1.5	6
648	Revealing antimicrobial resistance in stormwater with MinION. <i>Chemosphere</i> , 2020, 258, 127392.	4.2	15
649	Genomic Analysis and Antimicrobial Resistance of <i>Aliarcobacter cryaerophilus</i> Strains From German Water Poultry. <i>Frontiers in Microbiology</i> , 2020, 11, 1549.	1.5	10
650	Safety Assessment of a Nham Starter Culture <i>Lactobacillus plantarum</i> BCC9546 via Whole-genome Analysis. <i>Scientific Reports</i> , 2020, 10, 10241.	1.6	53
651	Emergence of vancomycin- and teicoplanin-resistant <i>Enterococcus faecium</i> via vanD5-harboring large genomic island. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2411-2415.	1.3	8
652	Evaluation of experimental protocols for shotgun whole-genome metagenomic discovery of antibiotic resistance genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	2
653	Genomic Analysis of Bovine <i>Staphylococcus aureus</i> Isolates from Milk To Elucidate Diversity and Determine the Distributions of Antimicrobial and Virulence Genes and Their Association with Mastitis. <i>MSystems</i> , 2020, 5, .	1.7	35
654	Fate and toxicity of pharmaceuticals in water environment: An insight on their occurrence in South Asia. <i>Journal of Environmental Management</i> , 2020, 271, 111030.	3.8	105
655	PARGT: a software tool for predicting antimicrobial resistance in bacteria. <i>Scientific Reports</i> , 2020, 10, 11033.	1.6	28
656	Comparative genomic analyses of <i>Lactobacillus rhamnosus</i> isolated from Chinese subjects. <i>Food Bioscience</i> , 2020, 36, 100659.	2.0	13

#	ARTICLE	IF	CITATIONS
657	Phylogeographical Analyses and Antibiotic Resistance Genes of <i>Acinetobacter johnsonii</i> Highlight Its Clinical Relevance. <i>MSphere</i> , 2020, 5, .	1.3	13
658	Genomic characterization of the most barotolerant <i>Listeria monocytogenes</i> RO15 strain compared to reference strains used to evaluate food high pressure processing. <i>BMC Genomics</i> , 2020, 21, 455.	1.2	14
659	Comparative genomics of multidrug-resistant <i>Enterococcus</i> spp. isolated from wastewater treatment plants. <i>BMC Microbiology</i> , 2020, 20, 20.	1.3	31
660	sraX: A Novel Comprehensive Resistome Analysis Tool. <i>Frontiers in Microbiology</i> , 2020, 11, 52.	1.5	15
661	Complete genome sequence and genome-scale metabolic modelling of <i>Acinetobacter baumannii</i> type strain ATCC 19606. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151412.	1.5	11
662	Acquisition of Plasmid with Carbapenem-Resistance Gene <i>bla</i> _{KPC2} in Hypervirulent <i>Klebsiella pneumoniae</i> , Singapore. <i>Emerging Infectious Diseases</i> , 2020, 26, 549-559.	2.0	39
663	Novel Cassette Assay To Quantify the Outer Membrane Permeability of Five β -Lactams Simultaneously in Carbapenem-Resistant <i>Klebsiella pneumoniae</i> and <i>Enterobacter cloacae</i> . <i>MBio</i> , 2020, 11, .	1.8	17
664	Resistome in Lake Bolonha, Brazilian Amazon: Identification of Genes Related to Resistance to Broad-Spectrum Antibiotics. <i>Frontiers in Microbiology</i> , 2020, 11, 67.	1.5	19
665	<i>Escherichia coli</i> ST302: Genomic Analysis of Virulence Potential and Antimicrobial Resistance Mediated by Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2020, 10, 3098.	1.5	14
666	Contents, Construction Methods, Data Resources, and Functions Comparative Analysis of Bacteria Databases. <i>International Journal of Biological Sciences</i> , 2020, 16, 838-848.	2.6	1
667	Exploring the resistome, virulome and microbiome of drinking water in environmental and clinical settings. <i>Water Research</i> , 2020, 174, 115630.	5.3	44
668	Multiomics Substrates of Resistance to Emerging Pathogens? Transcriptome and Proteome Profile of a Vancomycin-Resistant <i>Enterococcus faecalis</i> Clinical Strain. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 81-95.	1.0	3
669	Typing methods based on whole genome sequencing data. <i>One Health Outlook</i> , 2020, 2, 3.	1.4	90
670	Comparative genetic and physiological characterisation of <i>Pectinatus</i> species reveals shared tolerance to beer-associated stressors but halotolerance specific to pickle-associated strains. <i>Food Microbiology</i> , 2020, 90, 103462.	2.1	6
671	Whole-genome analysis of vancomycin-resistant <i>Enterococcus faecium</i> causing nosocomial outbreaks suggests the occurrence of few endemic clonal lineages in Bavaria, Germany. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1398-1404.	1.3	26
672	Phenotypic traits of <i>Burkholderia</i> spp. associated with ecological adaptation and plant-host interaction. <i>Microbiological Research</i> , 2020, 236, 126451.	2.5	7
673	Rapid inference of antibiotic resistance and susceptibility by genomic neighbour typing. <i>Nature Microbiology</i> , 2020, 5, 455-464.	5.9	74
674	Prevalence, Population Diversity and Antimicrobial Resistance of <i>Campylobacter coli</i> Isolated in Italian Swine at Slaughterhouse. <i>Microorganisms</i> , 2020, 8, 222.	1.6	20

#	ARTICLE	IF	CITATIONS
675	Prevalence of extended-spectrum β -lactamases in the local farm environment and livestock: challenges to mitigate antimicrobial resistance. <i>Critical Reviews in Microbiology</i> , 2020, 46, 1-14.	2.7	52
676	Characterization and whole genome sequencing of a novel strain of <i>Bergeyella cardium</i> related to infective endocarditis. <i>BMC Microbiology</i> , 2020, 20, 32.	1.3	2
677	The profile of antibiotic resistance genes in pig manure composting shaped by composting stage: Mesophilic-thermophilic and cooling-maturation stages. <i>Chemosphere</i> , 2020, 250, 126181.	4.2	65
678	Comparative genomic analysis reveals an α -pan-genome of African swine fever virus. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1553-1562.	1.3	22
679	PRAP: Pan Resistome analysis pipeline. <i>BMC Bioinformatics</i> , 2020, 21, 20.	1.2	11
680	Mobilizable antibiotic resistance genes are present in dust microbial communities. <i>PLoS Pathogens</i> , 2020, 16, e1008211.	2.1	25
681	Genomic Analysis of Carbapenemase-Producing Extensively Drug-Resistant <i>Klebsiella pneumoniae</i> Isolates Reveals the Horizontal Spread of p18-43_01 Plasmid Encoding bla _{NDM-1} in South Africa. <i>Microorganisms</i> , 2020, 8, 137.	1.6	25
682	A broad-spectrum phage controls multidrug-resistant <i>Salmonella</i> in liquid eggs. <i>Food Research International</i> , 2020, 132, 109011.	2.9	45
683	Systematic review of human gut resistome studies revealed variable definitions and approaches. <i>Gut Microbes</i> , 2020, 12, 1700755.	4.3	15
684	Host-Specific Evolutionary and Transmission Dynamics Shape the Functional Diversification of <i>Staphylococcus epidermidis</i> in Human Skin. <i>Cell</i> , 2020, 180, 454-470.e18.	13.5	102
685	Culture-enriched metagenomic sequencing enables in-depth profiling of the cystic fibrosis lung microbiota. <i>Nature Microbiology</i> , 2020, 5, 379-390.	5.9	57
686	The Wild Mouse (<i>Micromys minutus</i>): Reservoir of a Novel <i>Campylobacter jejuni</i> Strain. <i>Frontiers in Microbiology</i> , 2019, 10, 3066.	1.5	6
687	Network-Based Metabolism-Centered Screening of Potential Drug Targets in <i>Klebsiella pneumoniae</i> at Genome Scale. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 447.	1.8	31
688	Transcriptome Analysis Reveals the Resistance Mechanism of <i>Pseudomonas aeruginosa</i> to Tachyplesin I. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 155-169.	1.1	5
689	Hybrid Genome Assembly and Annotation of a Pandrug-Resistant <i>Klebsiella pneumoniae</i> Strain Using Nanopore and Illumina Sequencing. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 199-206.	1.1	26
690	Pathogenomic Analysis of a Novel Extensively Drug-Resistant <i>Citrobacter freundii</i> Isolate Carrying a bla _{NDM-1} Carbapenemase in South Africa. <i>Pathogens</i> , 2020, 9, 89.	1.2	10
691	Co-existence of the oxazolidinone resistance genes cfr and oprA on two transferable multi-resistance plasmids in one <i>Enterococcus faecalis</i> isolate from swine. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 105993.	1.1	20
692	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

#	ARTICLE	IF	CITATIONS
693	Abundance of Colistin-Resistant, OXA-23- and ArmA-Producing <i>Acinetobacter baumannii</i> Belonging to International Clone 2 in Greece. <i>Frontiers in Microbiology</i> , 2020, 11, 668.	1.5	29
694	Whole-Genome Sequences of Two NDM-1-Producing <i>Pseudomonas aeruginosa</i> Strains Isolated in a Clinical Setting in Albania in 2018. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
695	Platforms for elucidating antibiotic resistance in single genomes and complex metagenomes. <i>Environment International</i> , 2020, 138, 105667.	4.8	48
696	Tracking resistomes, virulence genes, and bacterial pathogens in long-term manure-amended greenhouse soils. <i>Journal of Hazardous Materials</i> , 2020, 396, 122618.	6.5	55
697	Evolutions of antibiotic resistance genes (ARGs), class 1 integron-integrase (<i>intI1</i>) and potential hosts of ARGs during sludge anaerobic digestion with the iron nanoparticles addition. <i>Science of the Total Environment</i> , 2020, 724, 138248.	3.9	68
698	Microbiome structure and function in rhizosphere of Jerusalem artichoke grown in saline land. <i>Science of the Total Environment</i> , 2020, 724, 138259.	3.9	44
699	Rhizosphere Microbiome Assembly and Its Impact on Plant Growth. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 5024-5038.	2.4	238
700	Milk microbial composition of Brazilian dairy cows entering the dry period and genomic comparison between <i>Staphylococcus aureus</i> strains susceptible to the bacteriophage ν B_SauM-UFV_DC4. <i>Scientific Reports</i> , 2020, 10, 5520.	1.6	4
701	Vertical Transmission of Gut Microbiome and Antimicrobial Resistance Genes in Infants Exposed to Antibiotics at Birth. <i>Journal of Infectious Diseases</i> , 2021, 224, 1236-1246.	1.9	41
702	Long-Term Compassionate Use of Cefiderocol To Treat Chronic Osteomyelitis Caused by Extensively Drug-Resistant <i>Pseudomonas aeruginosa</i> and Extended-Spectrum- β -Lactamase-Producing <i>Klebsiella pneumoniae</i> in a Pediatric Patient. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	44
703	Activity of Imipenem-Relebactam and Meropenem-Vaborbactam against Carbapenem-Resistant, SME-Producing <i>Serratia marcescens</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	12
704	Draft Genome Sequence of a <i>Pseudomonas aeruginosa</i> Sequence Type 3351 Strain Exhibiting High-Level Resistance to Polymyxins in a Pediatric Patient with Cystic Fibrosis in Mexico. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
705	Dairy Products and Dairy-Processing Environments as a Reservoir of Antibiotic Resistance and Quorum-Quenching Determinants as Revealed through Functional Metagenomics. <i>MSystems</i> , 2020, 5, .	1.7	18
706	Confronting Tigecycline-Resistant <i>Acinetobacter baumannii</i> via Immunization Against Conserved Resistance Determinants. <i>Frontiers in Microbiology</i> , 2020, 11, 536.	1.5	7
707	Resistome, Mobilome and Virulome Analysis of <i>Shewanella</i> algae and <i>Vibrio</i> spp. Strains Isolated in Italian Aquaculture Centers. <i>Microorganisms</i> , 2020, 8, 572.	1.6	27
708	Molecular Characterization and Antimicrobial Susceptibility of <i>C. jejuni</i> Isolates from Italian Wild Bird Populations. <i>Pathogens</i> , 2020, 9, 304.	1.2	18
709	<p>Genomic Epidemiology of an Outbreak of <i>Klebsiella pneumoniae</i> ST471 Producing Extended-Spectrum β -Lactamases in a Neonatal Intensive Care Unit</p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1081-1090.	1.1	7
710	Exploring the success of Brazilian endemic clone <i>Pseudomonas aeruginosa</i> ST277 and its association with the CRISPR-Cas system type I-C. <i>BMC Genomics</i> , 2020, 21, 255.	1.2	15

#	ARTICLE	IF	CITATIONS
711	Metagenome sequencing to unveil the resistome in a deep subtropical lake on the Yunnan-Guizhou Plateau, China. <i>Environmental Pollution</i> , 2020, 263, 114470.	3.7	47
712	Draft Genome Sequence of an <i>Escherichia coli</i> Strain Harboring bla CTX-M-115 , bla CMY-2 , Aminoglycoside, Tetracycline, and Sulfonamide Resistance Genes, Isolated from a Costa Rican Wastewater Treatment Plant. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
713	Detection of Antimicrobial Resistance Genes Associated with Carbapenem Resistance from the Whole-Genome Sequence of <i>Acinetobacter baumannii</i> Isolates from Malaysia. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2020, 2020, 1-9.	0.7	21
714	Whole genome analysis of multidrug-resistant <i>Citrobacter freundii</i> B9-C2 isolated from preterm neonate's stool in the first week. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 21, 246-251.	0.9	8
715	Nutrients influence the dynamics of <i>Klebsiella pneumoniae</i> carbapenemase producing enterobacteriales in transplanted hospital sinks. <i>Water Research</i> , 2020, 176, 115707.	5.3	17
716	Metagenomics Reveals a Core Macrolide Resistome Related to Microbiota in Chronic Respiratory Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 433-447.	2.5	58
717	Genomic Characterization of Antimicrobial Resistance, Virulence, and Phylogeny of the Genus <i>Ochrobactrum</i> . <i>Antibiotics</i> , 2020, 9, 177.	1.5	11
718	Genomic analysis of <i>Chromobacterium haemolyticum</i> : insights into the species resistome, virulence determinants and genome plasticity. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1001-1012.	1.0	7
719	Reverse vaccinology and drug target identification through pan-genomics. , 2020, , 317-333.		5
720	Impact of short-term storage on the quantity of extended-spectrum beta-lactamase-producing <i>Escherichia coli</i> in broiler litter under practical conditions. <i>Poultry Science</i> , 2020, 99, 2125-2135.	1.5	17
721	Genomic characterization of 16S rRNA methyltransferase-producing <i>Escherichia coli</i> isolates from the Parisian area, France. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1726-1735.	1.3	13
722	Draft Genome Sequence of <i>Clostridium perfringens</i> Strain TAMU, Which Causes Necrotic Enteritis in Broiler Chickens. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
723	Genomic characterization of an emerging Enterobacteriaceae species: the first case of co-infection with a typical pathogen in a human patient. <i>BMC Genomics</i> , 2020, 21, 297.	1.2	3
724	Determining Hosts of Antibiotic Resistance Genes: A Review of Methodological Advances. <i>Environmental Science and Technology Letters</i> , 2020, 7, 282-291.	3.9	85
725	Gene interaction network approach to elucidate the multidrug resistance mechanisms in the pathogenic bacterial strain <i>Proteus mirabilis</i> . <i>Journal of Cellular Physiology</i> , 2021, 236, 468-479.	2.0	24
726	Antibiotic resistome in the livestock and aquaculture industries: Status and solutions. <i>Critical Reviews in Environmental Science and Technology</i> , 2021, 51, 2159-2196.	6.6	109
727	Applying Genomics to Track Antimicrobial Resistance in the Food Chain. , 2021, , 188-211.		3
728	Pandrug-resistant <i>Pseudomonas</i> sp. expresses New Delhi metallo- β -lactamase-1 and consumes ampicillin as sole carbon source. <i>Clinical Microbiology and Infection</i> , 2021, 27, 472.e1-472.e5.	2.8	4

#	ARTICLE	IF	CITATIONS
729	IS <i>26</i> -mediated amplification of <i>bla</i> OXA-1 and <i>bla</i> CTX-M-15 with concurrent outer membrane porin disruption associated with <i>de novo</i> carbapenem resistance in a recurrent bacteraemia cohort. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 385-395.	1.3	29
730	First report of a livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> ST126 harbouring the <i>mecC</i> variant in Brazil. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 1019-1025.	1.3	6
731	A newly isolated <i>E. thailandicus</i> strain d5B with exclusively antimicrobial activity against <i>C. difficile</i> might be a novel therapy for controlling CDI. <i>Genomics</i> , 2021, 113, 475-483.	1.3	9
732	A review of artificial intelligence applications for antimicrobial resistance. <i>Biosafety and Health</i> , 2021, 3, 22-31.	1.2	65
733	Activity of aztreonam in combination with ceftazidime-avibactam against serine- and metallo- β -lactamase-producing <i>Pseudomonas aeruginosa</i> . <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 99, 115227.	0.8	28
734	Characterization of <i>Bacillus cereus</i> Group Isolates From Human Bacteremia by Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 599524.	1.5	35
735	Comparative Genomics of Atypical Enteropathogenic <i>Escherichia coli</i> from Kittens and Children Identifies Bacterial Factors Associated with Virulence in Kittens. <i>Infection and Immunity</i> , 2021, 89, .	1.0	4
736	Taking the next-gen step: Comprehensive antimicrobial resistance detection from <i>Burkholderia pseudomallei</i> . <i>EBioMedicine</i> , 2021, 63, 103152.	2.7	18
737	PCR identification of <i>Salmonella</i> serovars for the E serogroup based on novel specific targets obtained by pan-genome analysis. <i>LWT - Food Science and Technology</i> , 2021, 145, 110535.	2.5	7
738	Prevalence of multi-resistant plasmids in hospital inhalable particulate matter (PM) and its impact on horizontal gene transfer. <i>Environmental Pollution</i> , 2021, 270, 116296.	3.7	18
739	The <i>Roseobacter</i> -Group Bacterium <i>Phaeobacter</i> as a Safe Probiotic Solution for Aquaculture. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0258120.	1.4	22
740	The Shared Resistome of Human and Pig Microbiota Is Mobilized by Distinct Genetic Elements. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	5
741	Safety demonstration of a microbial species for use in the food chain: <i>Weissella confusa</i> . <i>International Journal of Food Microbiology</i> , 2021, 339, 109028.	2.1	17
742	Characterization and Genomic Analysis of <i>Escherichia coli</i> O157:H7 Bacteriophage FEC14, a New Member of Genus Kuttervirus. <i>Current Microbiology</i> , 2021, 78, 159-166.	1.0	12
743	Foam shares antibiotic resistomes and bacterial pathogens with activated sludge in wastewater treatment plants. <i>Journal of Hazardous Materials</i> , 2021, 408, 124855.	6.5	25
744	Fecal Microbiota Transplant in Cirrhosis Reduces Gut Microbial Antibiotic Resistance Genes: Analysis of Two Trials. <i>Hepatology Communications</i> , 2021, 5, 258-271.	2.0	41
745	gcType: a high-quality type strain genome database for microbial phylogenetic and functional research. <i>Nucleic Acids Research</i> , 2021, 49, D694-D705.	6.5	53
746	Characterization of putative circular plasmids in sponge-associated bacterial communities using a selective multiply-primed rolling circle amplification. <i>Molecular Ecology Resources</i> , 2021, 21, 110-121.	2.2	6

#	ARTICLE	IF	CITATIONS
747	Sediment Plasmidome of the Gulfs of Kathiawar Peninsula and Arabian Sea: Insights Gained from Metagenomics Data. <i>Microbial Ecology</i> , 2021, 81, 540-548.	1.4	4
748	Genome Sequence and Adaptation Analysis of the Human and Rice Pathogenic Strain <i>Burkholderia glumae</i> AU6208. <i>Pathogens</i> , 2021, 10, 87.	1.2	5
749	OUP accepted manuscript. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab147.	0.9	4
750	Genomic and Functional Characterization of <i>Enterococcus faecalis</i> Isolates Recovered From the International Space Station and Their Potential for Pathogenicity. <i>Frontiers in Microbiology</i> , 2020, 11, 515319.	1.5	10
751	WGS for Bacterial Identification and Susceptibility Testing in the Clinical Lab. , 2021, , 25-44.		1
752	Plasmids shape the diverse accessory resistomes of <i>Escherichia coli</i> ST131. <i>Access Microbiology</i> , 2021, 3, acmi000179.	0.2	10
753	AMR-Diag: Neural network based genotype-to-phenotype prediction of resistance towards β -lactams in <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1896-1906.	1.9	38
754	A framework for identifying the recent origins of mobile antibiotic resistance genes. <i>Communications Biology</i> , 2021, 4, 8.	2.0	73
755	Dissemination mechanisms of NDM genes in hospitalized patients. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab032.	0.9	6
756	Niche-Specific Adaptive Evolution of <i>Lactobacillus plantarum</i> Strains Isolated From Human Feces and Paocai. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 615876.	1.8	10
757	Integrative Analysis of Whole Genome Sequencing and Phenotypic Resistance Toward Prediction of Trimethoprim-Sulfamethoxazole Resistance in <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 607842.	1.5	18
758	Unearthing Antibiotic Resistance Associated with Disturbance-Induced Permafrost Thaw in Interior Alaska. <i>Microorganisms</i> , 2021, 9, 116.	1.6	15
759	Metagenomic Approaches to Analyze Antimicrobial Resistance: An Overview. <i>Frontiers in Genetics</i> , 2020, 11, 575592.	1.1	41
760	Genome Sequence of <i>Bifidobacterium breve</i> INIA P734 (CECT 8178), a Strain Isolated from Human Breast Milk. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
761	Antimicrobial Resistance of Non-O157 Shiga Toxin-Producing <i>Escherichia coli</i> Isolated from Humans and Domestic Animals. <i>Antibiotics</i> , 2021, 10, 74.	1.5	15
762	The microbiome of deep-sea fish reveals new microbial species and a sparsity of antibiotic resistance genes. <i>Gut Microbes</i> , 2021, 13, 1-13.	4.3	19
763	Whole Genome Analysis of Environmental <i>Pseudomonas mendocina</i> Strains: Virulence Mechanisms and Phylogeny. <i>Genes</i> , 2021, 12, 115.	1.0	3
765	The genomic characterisation and comparison of <i>Bacillus cereus</i> strains isolated from indoor air. <i>Gut Pathogens</i> , 2021, 13, 6.	1.6	9

#	ARTICLE	IF	CITATIONS
766	BlastFrost: fast querying of 100,000s of bacterial genomes in Bifrost graphs. <i>Genome Biology</i> , 2021, 22, 30.	3.8	15
767	Drug Design and Discovery: Theory, Applications, Open Issues and Challenges. <i>Studies in Computational Intelligence</i> , 2021, , 337-358.	0.7	0
768	Functional Metagenomics for Identification of Antibiotic Resistance Genes (ARGs). <i>Methods in Molecular Biology</i> , 2021, 2242, 173-183.	0.4	2
769	Characterization of the gut DNA and RNA Viromes in a Cohort of Chinese Residents and Visiting Pakistanis. <i>Virus Evolution</i> , 2021, 7, veab022.	2.2	21
770	The Human Gut Microbiota in all its States: From Disturbance to Resilience. , 2022, , 161-178.		4
771	Critical evaluation of short, long, and hybrid assembly for contextual analysis of antibiotic resistance genes in complex environmental metagenomes. <i>Scientific Reports</i> , 2021, 11, 3753.	1.6	53
772	Expanded catalog of microbial genes and metagenome-assembled genomes from the pig gut microbiome. <i>Nature Communications</i> , 2021, 12, 1106.	5.8	116
773	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, 2018â€“2019. <i>PLoS ONE</i> , 2021, 16, e0246571.	1.1	34
775	Comparative genomic analyses of Inc pA1763â€“KPC plasmids. <i>Journal of Basic Microbiology</i> , 2021, 61, 219-229.	1.8	3
777	Approaches for characterizing and tracking hospital-associated multidrug-resistant bacteria. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2585-2606.	2.4	21
778	Emergence of nosocomial associated opportunistic pathogens in the gut microbiome after antibiotic treatment. <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 36.	1.5	18
779	Characterization of the human skin resistome and identification of two microbiota cutotypes. <i>Microbiome</i> , 2021, 9, 47.	4.9	42
780	Genomic analysis of the diversity, antimicrobial resistance and virulence potential of clinical <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> strains from Chile. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009207.	1.3	23
781	A <i>Sarcina</i> bacterium linked to lethal disease in sanctuary chimpanzees in Sierra Leone. <i>Nature Communications</i> , 2021, 12, 763.	5.8	17
783	HMD-ARG: hierarchical multi-task deep learning for annotating antibiotic resistance genes. <i>Microbiome</i> , 2021, 9, 40.	4.9	48
784	Genomic and clinical characterisation of multidrug-resistant carbapenemase-producing ST231 and ST16 <i>Klebsiella pneumoniae</i> isolates colonising patients at Siriraj hospital, Bangkok, Thailand from 2015 to 2017. <i>BMC Infectious Diseases</i> , 2021, 21, 142.	1.3	18
785	Unraveling the emergence and population diversity of <i>Listeria monocytogenes</i> in a newly built meat facility through whole genome sequencing. <i>International Journal of Food Microbiology</i> , 2021, 340, 109043.	2.1	28
786	Characterization of multidrug-resistant <i>Acinetobacter baumannii</i> strain ATCC BAA1605 using whole-genome sequencing. <i>BMC Research Notes</i> , 2021, 14, 83.	0.6	8

#	ARTICLE	IF	CITATIONS
787	Differences in the gut microbiomes of dogs and wolves: roles of antibiotics and starch. BMC Veterinary Research, 2021, 17, 112.	0.7	9
788	Genomic insights into evolution of pathogenicity and resistance of multidrug-resistant <i>Raoultella ornithinolytica</i> WM1. Annals of the New York Academy of Sciences, 2021, 1497, 74-90.	1.8	7
789	Resistance Determinants and Their Genetic Context in Enterobacteria from a Longitudinal Study of Pigs Reared under Various Husbandry Conditions. Applied and Environmental Microbiology, 2021, 87, .	1.4	14
790	Comparative genomics of ST5 and ST30 methicillin-resistant <i>Staphylococcus aureus</i> sequential isolates recovered from paediatric patients with cystic fibrosis. Microbial Genomics, 2021, 7, .	1.0	5
792	Detection of blaOXA-1, blaTEM-1, and Virulence Factors in <i>E. coli</i> Isolated From Seals. Frontiers in Veterinary Science, 2021, 8, 583759.	0.9	8
793	Validation strategy of a bioinformatics whole genome sequencing workflow for Shiga toxin-producing <i>Escherichia coli</i> using a reference collection extensively characterized with conventional methods. Microbial Genomics, 2021, 7, .	1.0	20
794	Genomic Insights Into the Pathogenicity of a Novel Biofilm-Forming <i>Enterococcus</i> sp. Bacteria (<i>Enterococcus lacertideformus</i>) Identified in Reptiles. Frontiers in Microbiology, 2021, 12, 635208.	1.5	6
795	Comprehensive Pathogen Identification, Antibiotic Resistance, and Virulence Genes Prediction Directly From Simulated Blood Samples and Positive Blood Cultures by Nanopore Metagenomic Sequencing. Frontiers in Genetics, 2021, 12, 620009.	1.1	16
796	Hidden Markov Model: a shortest unique representative approach to detect the protein toxins, virulence factors and antibiotic resistance genes. BMC Research Notes, 2021, 14, 122.	0.6	4
797	Outcome of Different Sequencing and Assembly Approaches on the Detection of Plasmids and Localization of Antimicrobial Resistance Genes in Commensal <i>Escherichia coli</i> . Microorganisms, 2021, 9, 598.	1.6	36
798	Bacterial cyclic diguanylate signaling networks sense temperature. Nature Communications, 2021, 12, 1986.	5.8	35
799	Multidrug Resistance Dissemination in <i>Escherichia coli</i> Isolated from Wild Animals: Bacterial Clones and Plasmid Complicity. Microbiology Research, 2021, 12, 123-137.	0.8	4
800	Comprehensive in silico survey of the Mycolicibacterium mobilome reveals an as yet underexplored diversity. Microbial Genomics, 2021, 7, .	1.0	11
801	Novel Chromosome-Borne Accessory Genetic Elements Carrying Multiple Antibiotic Resistance Genes in <i>Pseudomonas aeruginosa</i> . Frontiers in Cellular and Infection Microbiology, 2021, 11, 638087.	1.8	15
802	A Degeneration Gradient of Poplar Trees Contributes to the Taxonomic, Functional, and Resistome Diversity of Bacterial Communities in Rhizosphere Soils. International Journal of Molecular Sciences, 2021, 22, 3438.	1.8	10
803	The extent of carbapenemase-encoding genes in public genome sequences. PeerJ, 2021, 9, e11000.	0.9	0
804	Draft Genome Sequence of a <i>Burkholderia cepacia</i> Complex Strain Isolated from a Human Intra-abdominal Abscess. Microbiology Resource Announcements, 2021, 10, .	0.3	1
805	Removal of antibiotic resistance genes from swine wastewater by membrane filtration treatment. Ecotoxicology and Environmental Safety, 2021, 210, 111885.	2.9	77

#	ARTICLE	IF	CITATIONS
806	Genomic Epidemiology of CC30 Methicillin-Resistant <i>Staphylococcus aureus</i> Strains from Argentina Reveals Four Major Clades with Distinctive Genetic Features. <i>MSphere</i> , 2021, 6, .	1.3	11
807	Surveillance of antimicrobial resistance in low- and middle-income countries: a scattered picture. <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 63.	1.5	137
808	Metagenomic analysis reveals the fate of antibiotic resistance genes in two-stage and one-stage anaerobic digestion of waste activated sludge. <i>Journal of Hazardous Materials</i> , 2021, 406, 124595.	6.5	42
809	Global Landscape of <i>Clostridioides Difficile</i> Phylogeography, Antibiotic Susceptibility, and Toxin Polymorphisms by Post-Hoc Whole-Genome Sequencing from the MODIFY I/II Studies. <i>Infectious Diseases and Therapy</i> , 2021, 10, 853-870.	1.8	17
810	Lytic Bacteriophage EFA1 Modulates HCT116 Colon Cancer Cell Growth and Upregulates ROS Production in an <i>Enterococcus faecalis</i> Co-culture System. <i>Frontiers in Microbiology</i> , 2021, 12, 650849.	1.5	16
811	Nitric oxide (NO) elicits aminoglycoside tolerance in <i>Escherichia coli</i> but antibiotic resistance gene carriage and NO sensitivity have not co-evolved. <i>Archives of Microbiology</i> , 2021, 203, 2541-2550.	1.0	7
812	Transmission of Similar <i>Mcr-1</i> Carrying Plasmids among Different <i>Escherichia coli</i> Lineages Isolated from Livestock and the Farmer. <i>Antibiotics</i> , 2021, 10, 313.	1.5	24
813	Antibiotic prophylaxis and the gastrointestinal resistome in paediatric patients with acute lymphoblastic leukaemia: a cohort study with metagenomic sequencing analysis. <i>Lancet Microbe</i> , The, 2021, 2, e159-e167.	3.4	10
814	The coexistence of monopartite integrative and conjugative elements in the genomes of <i>Acidobacteria</i> . <i>Gene</i> , 2021, 777, 145476.	1.0	16
815	Combined effects of composting and antibiotic administration on cattle manure-borne antibiotic resistance genes. <i>Microbiome</i> , 2021, 9, 81.	4.9	36
816	Mining and evaluating novel serovar-specific <i>Salmonella</i> C1 serogroup genes by polymerase chain reaction analysis. <i>LWT - Food Science and Technology</i> , 2021, 141, 110821.	2.5	5
817	Possible Prosthetic Valve Endocarditis by <i>Pandoraea pnomenus</i> and Specific Virulence Mechanisms. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 1319-1324.	1.1	4
818	The safety and potential probiotic properties analysis of <i>Streptococcus alactolyticus</i> strain FGM isolated from the chicken cecum. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	9
819	Genomic Characterization of <i>Salmonella typhimurium</i> DT104 Strains Associated with Cattle and Beef Products. <i>Pathogens</i> , 2021, 10, 529.	1.2	7
820	Characterization of <i>Proteus vulgaris</i> Strain P3M, a Foodborne Multidrug-Resistant Bacterium Isolated from <i>Penaeus vannamei</i> in China. <i>Microbial Drug Resistance</i> , 2021, 27, 1360-1370.	0.9	3
821	Multidrug-Resistant (MDR) <i>Klebsiella variicola</i> Strains Isolated in a Brazilian Hospital Belong to New Clones. <i>Frontiers in Microbiology</i> , 2021, 12, 604031.	1.5	9
822	Stereoselective Bacterial Metabolism of Antibiotics in Environmental Bacteria – A Novel Biochemical Workflow. <i>Frontiers in Microbiology</i> , 2021, 12, 562157.	1.5	4
823	Cross-comparison of methods for quantifying antibiotic resistance in agricultural soils amended with dairy manure and compost. <i>Science of the Total Environment</i> , 2021, 766, 144321.	3.9	16

#	ARTICLE	IF	CITATIONS
824	Increased expression of antibiotic-resistance genes in biofilm communities upon exposure to cetyltrimethylammonium bromide (CTAB) and other stress conditions. <i>Science of the Total Environment</i> , 2021, 765, 144264.	3.9	19
825	Genome Characterization of <i>Lactiplantibacillus plantarum</i> Strain UTNGt2 Originated from <i>Theobroma grandiflorum</i> (White Cacao) of Ecuadorian Amazon: Antimicrobial Peptides from Safety to Potential Applications. <i>Antibiotics</i> , 2021, 10, 383.	1.5	22
827	Complete genome sequence of the <i>Pseudomonas oleovorans</i> strain ODT-83 isolated from oyster. <i>Archives of Microbiology</i> , 2021, 203, 3117-3124.	1.0	2
828	Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic <i>Escherichia coli</i> (EPEC) circulating in modern time. <i>Scientific Reports</i> , 2021, 11, 9256.	1.6	12
830	High-Level Aminoglycoside Resistance in Human Clinical <i>Klebsiella pneumoniae</i> Complex Isolates and Characteristics of <i>armA</i> -Carrying <i>InchI5</i> Plasmids. <i>Frontiers in Microbiology</i> , 2021, 12, 636396.	1.5	8
831	Clin-mNGS: Automated Pipeline for Pathogen Detection from Clinical Metagenomic Data. <i>Current Bioinformatics</i> , 2021, 16, 306-314.	0.7	1
833	Five-year microevolution of a multidrug-resistant <i>Mycobacterium tuberculosis</i> strain within a patient with inadequate compliance to treatment. <i>BMC Infectious Diseases</i> , 2021, 21, 394.	1.3	3
834	Forecasting the dissemination of antibiotic resistance genes across bacterial genomes. <i>Nature Communications</i> , 2021, 12, 2435.	5.8	111
836	Genomic description and characterization of <i>Nigeribacterium massiliense</i> gen. nov., sp. nov., isolated from the human gut. <i>Microbes and Infection</i> , 2021, 23, 104842.	1.0	0
837	Artificial intelligence as a fundamental tool in management of infectious diseases and its current implementation in COVID-19 pandemic. <i>Environmental Science and Pollution Research</i> , 2021, 28, 40515-40532.	2.7	15
838	Evaluation of Metagenomic-Enabled Antibiotic Resistance Surveillance at a Conventional Wastewater Treatment Plant. <i>Frontiers in Microbiology</i> , 2021, 12, 657954.	1.5	46
839	Characterization of the public transit air microbiome and resistome reveals geographical specificity. <i>Microbiome</i> , 2021, 9, 112.	4.9	26
840	Metagenomics Analysis Reveals the Microbial Communities, Antimicrobial Resistance Gene Diversity and Potential Pathogen Transmission Risk of Two Different Landfills in China. <i>Diversity</i> , 2021, 13, 230.	0.7	9
841	Whole genome sequence analysis of multi drug resistant community associated methicillin resistant <i>Staphylococcus aureus</i> from food fish: detection of clonal lineage ST 28 and its antimicrobial resistance and virulence genes. <i>PeerJ</i> , 2021, 9, e11224.	0.9	3
842	ProkEvo: an automated, reproducible, and scalable framework for high-throughput bacterial population genomics analyses. <i>PeerJ</i> , 2021, 9, e11376.	0.9	4
843	MyCLADE: a multi-source domain annotation server for sequence functional exploration. <i>Nucleic Acids Research</i> , 2021, 49, W452-W458.	6.5	2
844	Molecular Epidemiology of Third-Generation-Cephalosporin-Resistant <i>Enterobacteriaceae</i> in Southeast Queensland, Australia. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	9
846	A Machine Learning Bioinformatics Method to Predict Biological Activity from Biosynthetic Gene Clusters. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2560-2571.	2.5	38

#	ARTICLE	IF	CITATIONS
847	Metagenomic analysis reveals the shared and distinct features of the soil resistome across tundra, temperate prairie, and tropical ecosystems. <i>Microbiome</i> , 2021, 9, 108.	4.9	60
848	<i>Salmonella enterica</i> Subsp. <i>houtenae</i> Associated with an Abscess in Young Roe Deer (<i>Capreolus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11	1.2	3
849	WGS-Based Analysis of Carbapenem-Resistant <i>Acinetobacter baumannii</i> in Vietnam and Molecular Characterization of Antimicrobial Determinants and MLST in Southeast Asia. <i>Antibiotics</i> , 2021, 10, 563.	1.5	14
850	<i>Salmonella</i> Derby: A Comparative Genomic Analysis of Strains From Germany. <i>Frontiers in Microbiology</i> , 2021, 12, 591929.	1.5	5
851	Widespread distribution of prophages signaling the potential for adaptability and pathogenicity evolution of <i>Ralstonia solanacearum</i> species complex. <i>Genomics</i> , 2021, 113, 992-1000.	1.3	11
852	Long-read metagenomics retrieves complete single-contig bacterial genomes from canine feces. <i>BMC Genomics</i> , 2021, 22, 330.	1.2	41
853	Variation of Metagenome From Feedstock to Digestate in Full-Scale Biogas Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 660225.	1.5	7
854	Fatal exudative dermatitis in island populations of red squirrels (<i>Sciurus vulgaris</i>): spillover of a virulent <i>Staphylococcus aureus</i> clone (ST49) from reservoir hosts. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
855	Complete Genome Sequences of <i>Francisella marina</i> Strains E95-16 and E103-15, Isolated from Maricultured Spotted Rose Snapper (<i>Lutjanus guttatus</i>) on the Pacific Coast of Central America. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
856	Phenotypic and genomic characterization of a <i>Vibrio parahaemolyticus</i> strain causing disease in <i>Penaeus vannamei</i> provides insights into its niche adaptation and pathogenic mechanism. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
858	Gut microbiota in healthy and unhealthy long-living people. <i>Gene</i> , 2021, 779, 145510.	1.0	17
859	<i>Ornithobacterium rhinotracheale</i> : MALDI-TOF MS and Whole Genome Sequencing Confirm That Serotypes K, L and M Deviate from Well-Known Reference Strains and Numerous Field Isolates. <i>Microorganisms</i> , 2021, 9, 1006.	1.6	7
860	Comparative genome analysis of multidrug-resistant <i>Pseudomonas aeruginosa</i> JNQH-PA57, a clinically isolated mucoid strain with comprehensive carbapenem resistance mechanisms. <i>BMC Microbiology</i> , 2021, 21, 133.	1.3	10
861	Diversity of Plasmids and Genes Encoding Resistance to Extended-Spectrum β -Lactamase in <i>Escherichia coli</i> from Different Animal Sources. <i>Microorganisms</i> , 2021, 9, 1057.	1.6	5
862	Successful treatment of infective endocarditis due to pandrug-resistant <i>Klebsiella pneumoniae</i> with ceftazidime-avibactam and aztreonam. <i>Scientific Reports</i> , 2021, 11, 9684.	1.6	20
863	Characterization and description of <i>Faecalibacterium butyricigenerans</i> sp. nov. and <i>F. longum</i> sp. nov., isolated from human faeces. <i>Scientific Reports</i> , 2021, 11, 11340.	1.6	42
864	Prevalence of Antibiotic Resistance Genes in Pharmaceutical Wastewaters. <i>Water (Switzerland)</i> , 2021, 13, 1731.	1.2	3
865	<i>Sphingobacterium rhinopithecii</i> sp. Nov., isolated from the faeces of <i>Rhinopithecus bieti</i> in China. <i>Archives of Microbiology</i> , 2021, 203, 4629-4634.	1.0	8

#	ARTICLE	IF	CITATIONS
866	Genomic Analysis of <i>Delftia tsuruhatensis</i> Strain TR1180 Isolated From A Patient From China With In4-Like Integron-Associated Antimicrobial Resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 663933.	1.8	12
867	Identification of <i>floR</i> Variants Associated With a Novel Tn4371-Like Integrative and Conjugative Element in Clinical <i>Pseudomonas aeruginosa</i> Isolates. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 685068.	1.8	5
868	The occurrence of antibiotic resistance genes in the microbiota of yak, beef and dairy cattle characterized by a metagenomic approach. <i>Journal of Antibiotics</i> , 2021, 74, 508-518.	1.0	11
869	Profiling the Virulence and Antibiotic Resistance Genes of <i>Cronobacter sakazakii</i> Strains Isolated From Powdered and Dairy Formulas by Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 694922.	1.5	18
870	Role of anaerobic sludge digestion in handling antibiotic resistant bacteria and antibiotic resistance genes – A review. <i>Bioresource Technology</i> , 2021, 330, 124970.	4.8	51
871	Next-Generation Sequencing for Whole-Genome Characterization of <i>Weissella cibaria</i> UTNGt21O Strain Originated From Wild <i>Solanum quitoense</i> Lam. <i>Fruits: An Atlas of Metabolites With Biotechnological Significance</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 675002.	1.5	11
872	High-throughput sequencing reveals genetic determinants associated with antibiotic resistance in <i>Campylobacter</i> spp. from farm-to-fork. <i>PLoS ONE</i> , 2021, 16, e0253797.	1.1	17
873	On-Farm Anaerobic Digestion of Dairy Manure Reduces the Abundance of Antibiotic Resistance-Associated Gene Targets and the Potential for Plasmid Transfer. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0298020.	1.4	21
874	Molecular characterization of antimicrobial resistance in <i>Klebsiella pneumoniae</i> isolated from Brazilian dairy herds. <i>Journal of Dairy Science</i> , 2021, 104, 7210-7224.	1.4	8
875	Genome Mining for Antimicrobial Compounds in Wild Marine Animals-Associated Enterococci. <i>Marine Drugs</i> , 2021, 19, 328.	2.2	11
876	Population-level faecal metagenomic profiling as a tool to predict antimicrobial resistance in Enterobacterales isolates causing invasive infections: An exploratory study across Cambodia, Kenya, and the UK. <i>EClinicalMedicine</i> , 2021, 36, 100910.	3.2	10
877	Regional sequencing collaboration reveals persistence of the T12 <i>Vibrio cholerae</i> O1 lineage in West Africa. <i>ELife</i> , 2021, 10, .	2.8	6
879	Antibiotic Susceptibility, Virulome, and Clinical Outcomes in European Infants with Bloodstream Infections Caused by Enterobacterales. <i>Antibiotics</i> , 2021, 10, 706.	1.5	7
880	Gene-Gene Interactions Dictate Ciprofloxacin Resistance in <i>Pseudomonas aeruginosa</i> and Facilitate Prediction of Resistance Phenotype from Genome Sequence Data. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0269620.	1.4	16
882	Isolation and Characterization of a Novel <i>Salmonella</i> Phage vB_SalP_TR2. <i>Frontiers in Microbiology</i> , 2021, 12, 664810.	1.5	35
883	Draft genome sequence and potential identification of a biosurfactant from <i>Brevibacterium casei</i> strain LS14 an isolate from fresh water Loktak Lake. <i>3 Biotech</i> , 2021, 11, 326.	1.1	3
884	A deep-sea bacterium related to coastal marine pathogens. <i>Environmental Microbiology</i> , 2021, 23, 5349-5363.	1.8	4
885	The infant gut resistome associates with <i>E. coli</i> , environmental exposures, gut microbiome maturity, and asthma-associated bacterial composition. <i>Cell Host and Microbe</i> , 2021, 29, 975-987.e4.	5.1	64

#	ARTICLE	IF	CITATIONS
886	Distribution of antibiotic resistance genes and their association with bacteria and viruses in decentralized sewage treatment facilities. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 35.	3.3	18
888	Recovery of human gut microbiota genomes with third-generation sequencing. <i>Cell Death and Disease</i> , 2021, 12, 569.	2.7	10
889	ARG-SHINE: improve antibiotic resistance class prediction by integrating sequence homology, functional information and deep convolutional neural network. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab066.	1.5	6
890	Genome analysis to decipher syntrophy in the bacterial consortium "SCP"™ for azo dye degradation. <i>BMC Microbiology</i> , 2021, 21, 177.	1.3	12
891	Chromosomal Integration of Huge and Complex bla _{NDM} -Carrying Genetic Elements in Enterobacteriaceae. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 690799.	1.8	12
892	Molecular Characterization and Survive Abilities of Salmonella Heidelberg Strains of Poultry Origin in Brazil. <i>Frontiers in Microbiology</i> , 2021, 12, 674147.	1.5	14
893	Identification of pathogen(s) in infectious diseases using shotgun metagenomic sequencing and conventional culture: a comparative study. <i>PeerJ</i> , 2021, 9, e11699.	0.9	2
895	Acquisition of antibiotic resistance genes on human skin after swimming in the ocean. <i>Environmental Research</i> , 2021, 197, 110978.	3.7	9
896	Whole Genome Analysis of Three Multi-Drug Resistant <i>Listeria innocua</i> and Genomic Insights Into Their Relatedness With Resistant <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 694361.	1.5	2
898	Draft Genome Sequence of <i>Serratia rubidaea</i> , a Potential Opportunistic Pathogen Isolated from Food in Italy. <i>Microbiology Resource Announcements</i> , 2021, 10, e0070721.	0.3	2
899	WGS based analysis of acquired antimicrobial resistance in human and non-human <i>Acinetobacter baumannii</i> isolates from a German perspective. <i>BMC Microbiology</i> , 2021, 21, 210.	1.3	12
900	Successful Dissemination of Plasmid-Mediated Extended-Spectrum β -Lactamases in Enterobacterales over Humans to Wild Fauna. <i>Microorganisms</i> , 2021, 9, 1471.	1.6	2
901	Integrated Phenotypicâ€“Genotypic Analysis of <i>Lactobacillus sakei</i> from Different Niches. <i>Foods</i> , 2021, 10, 1717.	1.9	10
902	The Potential Role of Clinical Metagenomics in Infectious Diseases: Therapeutic Perspectives. <i>Drugs</i> , 2021, 81, 1453-1466.	4.9	18
903	Safety assessment of <i>Streptococcus salivarius</i> DB-B5 as a probiotic candidate for oral health. <i>Food and Chemical Toxicology</i> , 2021, 153, 112277.	1.8	7
906	<i>Arenibaculum pallidiluteum</i> gen. nov., sp. nov., a novel bacterium in the family Azospirillaceae, isolated from desert soil, and reclassification of <i>Skermanella xinjiangensis</i> to a new genus <i>Deserticella</i> as <i>Deserticella xinjiangensis</i> comb. nov., and transfer of the genera <i>Indioceanicola</i> and <i>Oleisolibacter</i> from the family Rhodospirillaceae to the family Azospirillaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	22
907	Integrated Metagenomic Assessment of Multiple Pre-harvest Control Points on Lettuce Resistomes at Field-Scale. <i>Frontiers in Microbiology</i> , 2021, 12, 683410.	1.5	5
908	Tracking the transition to agriculture in Southern Europe through ancient DNA analysis of dental calculus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	29

#	ARTICLE	IF	CITATIONS
909	Characterisation of <i>Listeria monocytogenes</i> food-associated isolates to assess environmental fitness and virulence potential. <i>International Journal of Food Microbiology</i> , 2021, 350, 109247.	2.1	18
910	Genomic epidemiology of group B streptococci spanning 10 years in an Irish maternity hospital, 2008–2017. <i>Journal of Infection</i> , 2021, 83, 37-45.	1.7	4
911	Characterization of Carbapenem-Resistant <i>Acinetobacter baumannii</i> Isolates from Clinical Specimens. <i>Microbiology Resource Announcements</i> , 2021, 10, e0057121.	0.3	1
912	Whole Genome-Based Characterization of <i>Listeria monocytogenes</i> Isolates Recovered From the Food Chain in South Africa. <i>Frontiers in Microbiology</i> , 2021, 12, 669287.	1.5	19
913	In Silico Analysis of Potential Outer Membrane Beta-Barrel Proteins in <i>Aeromonas hydrophila</i> Pangenome. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, , 1-9.	0.9	1
914	The dissemination of antimicrobial resistance determinants in surface water sources in Lebanon. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	5
915	The oral microbiota of wild bears in Sweden reflects the history of antibiotic use by humans. <i>Current Biology</i> , 2021, 31, 4650-4658.e6.	1.8	15
917	Recent advances in understanding and combatting <i>Neisseria gonorrhoeae</i> : a genomic perspective. <i>Faculty Reviews</i> , 2021, 10, 65.	1.7	4
918	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
919	Short-term cold stress can reduce the abundance of antibiotic resistance genes in the cecum and feces in a pig model. <i>Journal of Hazardous Materials</i> , 2021, 416, 125868.	6.5	21
921	Comparative evaluation of Assays for Broad Detection of Molecular Resistance Mechanisms in Enterobacterales Isolates. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0103321.	1.8	2
922	Phylum barrier and <i>Escherichia coli</i> intra-species phylogeny drive the acquisition of antibiotic-resistance genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
925	Antimicrobial resistance in <i>Bacillus</i> -based biopesticide products. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	5
926	Genomic Characterization of Multidrug-Resistant <i>Salmonella</i> Serovars Derby and Rissen From the Pig Value Chain in Vietnam. <i>Frontiers in Veterinary Science</i> , 2021, 8, 705044.	0.9	7
927	Characterization and Application of a Lytic Phage D10 against Multidrug-Resistant <i>Salmonella</i> . <i>Viruses</i> , 2021, 13, 1626.	1.5	7
928	Diversity in the composition of the accessory genome of Mexican <i>Pseudomonas aeruginosa</i> strains. <i>Genes and Genomics</i> , 2021, , 1.	0.5	0
929	Metagenomics-Based Analysis of the Age-Related Cumulative Effect of Antibiotic Resistance Genes in Gut Microbiota. <i>Antibiotics</i> , 2021, 10, 1006.	1.5	12
930	More diversified antibiotic resistance genes in chickens and workers of the live poultry markets. <i>Environment International</i> , 2021, 153, 106534.	4.8	41

#	ARTICLE	IF	CITATIONS
931	The survival and removal mechanism of <i>Sphingobacterium changzhouense</i> TC931 under tetracycline stress and its™ ecological safety after application. <i>Bioresource Technology</i> , 2021, 333, 125067.	4.8	31
932	Identification of an mcr-9-Carrying <i>Salmonella enterica</i> Serotype Heidelberg Strain Isolated from Blood. <i>Microbiology Resource Announcements</i> , 2021, 10, e0067621.	0.3	1
933	Antimicrobial susceptibilities and comparative whole genome analysis of two isolates of the probiotic bacterium <i>Lactiplantibacillus plantarum</i> , strain ATCC 202195. <i>Scientific Reports</i> , 2021, 11, 15893.	1.6	6
936	Comparison between genome sequences of Chilean <i>Tenacibaculum dicentrarchi</i> isolated from red conger eel (<i>Genypterus chilensis</i>) and Atlantic salmon (<i>Salmo salar</i>) focusing on bacterial virulence determinants. <i>Journal of Fish Diseases</i> , 2021, 44, 1843-1860.	0.9	11
937	Functional meta-omics provide critical insights into long- and short-read assemblies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
938	Genome Resource of <i>Ancylobacter pratisalsi</i> E130 ^T : A Novel Plant-Growth-Promoting Bacterium Isolated from the Rhizosphere. <i>Phytopathology</i> , 2022, 112, 729-731.	1.1	5
939	Dynamic Colonization of Microbes and Their Functions after Fecal Microbiota Transplantation for Inflammatory Bowel Disease. <i>MBio</i> , 2021, 12, e0097521.	1.8	26
940	Antibiotic Resistance Characterization of Bacteria Isolated from Traditional Chinese Paocai. <i>Current Microbiology</i> , 2021, 78, 3853-3862.	1.0	0
941	Impact of Antibiotic Resistance Genes in Gut Microbiome of Patients With Cirrhosis. <i>Gastroenterology</i> , 2021, 161, 508-521.e7.	0.6	33
942	Comparative genomics reveals environmental adaptation differences between <i>Cronobacter</i> species. <i>Food Research International</i> , 2021, 147, 110541.	2.9	3
943	Dynamics of the fecal microbiome and antimicrobial resistome in commercial piglets during the weaning period. <i>Scientific Reports</i> , 2021, 11, 18091.	1.6	5
944	Genomic Analysis of Heterogeneous Vancomycin-Intermediate <i>Staphylococcus aureus</i> Strains from Different Clonal Lineages in South Korea. <i>Microbial Drug Resistance</i> , 2021, 27, 1271-1281.	0.9	3
945	Insight Into Whole Genome of <i>Aeromonas veronii</i> Isolated From Freshwater Fish by Resistome Analysis Reveal Extensively Antibiotic Resistant Traits. <i>Frontiers in Microbiology</i> , 2021, 12, 733668.	1.5	13
946	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal <i>Methanobrevibacter</i> . <i>Microbiome</i> , 2021, 9, 197.	4.9	18
947	Genomic analysis revealed conserved acid tolerance mechanisms from native microorganisms in fermented feed. <i>Journal of Applied Microbiology</i> , 2022, 132, 1152-1165.	1.4	2
948	Genomic analysis of carbapenem-resistant <i>Pseudomonas aeruginosa</i> ST143 clone showing susceptibility to broad-spectrum cephalosporins. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 26, 177-179.	0.9	1
949	Emergence and genomics of OXA-232-producing <i>Klebsiella pneumoniae</i> in a hospital in Yancheng, China. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 26, 194-198.	0.9	9
950	Genomic Stability and Genetic Defense Systems in <i>Dolosigranulum pigrum</i> , a Candidate Beneficial Bacterium from the Human Microbiome. <i>MSystems</i> , 2021, 6, e0042521.	1.7	11

#	ARTICLE	IF	CITATIONS
951	Whole genome sequencing and comparative genomics analysis of <i>Pectobacterium carotovorum</i> identifies key pathogenic genes. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107114.	1.2	7
952	Complete Genome Sequence of the Newly Developed <i>Lactobacillus acidophilus</i> Strain With Improved Thermal Adaptability. <i>Frontiers in Microbiology</i> , 2021, 12, 697351.	1.5	5
953	Structural, functional, resistome and pathogenicity profiling of the Cooum river. <i>Microbial Pathogenesis</i> , 2021, 158, 105048.	1.3	8
954	Antibiotic resistance genes in layer farms and their correlation with environmental samples. <i>Poultry Science</i> , 2021, 100, 101485.	1.5	21
955	Natural Horizontal Gene Transfer of Antimicrobial Resistance Genes in <i>Campylobacter</i> spp. From Turkeys and Swine. <i>Frontiers in Microbiology</i> , 2021, 12, 732969.	1.5	11
956	Accuracy of Broad-Panel PCR-Based Bacterial Identification for Blood Cultures in a Pediatric Oncology Population. <i>Microbiology Spectrum</i> , 2021, 9, e0022121.	1.2	5
958	Comparative Genome Analysis of <i>Bacillus amyloliquefaciens</i> Focusing on Phylogenomics, Functional Traits, and Prevalence of Antimicrobial and Virulence Genes. <i>Frontiers in Genetics</i> , 2021, 12, 724217.	1.1	4
959	The Human Gut Resistome up to Extreme Longevity. <i>MSphere</i> , 2021, 6, e0069121.	1.3	12
960	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
961	Large-scale genomic analysis of antimicrobial resistance in the zoonotic pathogen <i>Streptococcus suis</i> . <i>BMC Biology</i> , 2021, 19, 191.	1.7	26
962	Seasonality and Geography Have a Greater Influence than the Use of Chlorine-Based Cleaning Agents on the Microbiota of Bulk Tank Raw Milk. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0108121.	1.4	8
963	Genomic Features Associated with the Degree of Phenotypic Resistance to Carbapenems in Carbapenem-Resistant <i>Klebsiella pneumoniae</i> . <i>MSystems</i> , 2021, 6, e0019421.	1.7	26
964	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
965	Whole-genome analysis uncovers loss of <i>bla_Z</i> associated with carriage isolates belonging to methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) clone ST5-VI in Cape Verde. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 26, 77-83.	0.9	2
966	Viability-Resolved Metagenomics Reveals Antagonistic Colonization Dynamics of <i>Staphylococcus epidermidis</i> Strains on Preterm Infant Skin. <i>MSphere</i> , 2021, 6, e0053821.	1.3	5
967	Genetic Analysis of <i>mcr-1</i> -Carrying Plasmids From Gram-Negative Bacteria in a Dutch Tertiary Care Hospital: Evidence for Inpatient and Interspecies Transmission Events. <i>Frontiers in Microbiology</i> , 2021, 12, 727435.	1.5	7
968	VicPred: A <i>Vibrio cholerae</i> Genotype Prediction Tool. <i>Frontiers in Microbiology</i> , 2021, 12, 691895.	1.5	12
969	Phenotypic features and analysis of genes supporting probiotic action unravel underlying perspectives of <i>Bacillus velezensis</i> VTX9 as a potential feed additive for swine. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	8

#	ARTICLE	IF	CITATIONS
970	Co-occurrence of antimicrobial and metal resistance genes in pig feces and agricultural fields fertilized with slurry. <i>Science of the Total Environment</i> , 2021, 792, 148259.	3.9	21
971	Metagenomic Analysis Identifies Sex-Related Cecal Microbial Gene Functions and Bacterial Taxa in the Quail. <i>Frontiers in Veterinary Science</i> , 2021, 8, 693755.	0.9	2
972	Whole Genome Sequencing of Extended-Spectrum- and AmpC- β -Lactamase-Positive Enterobacterales Isolated From Spinach Production in Gauteng Province, South Africa. <i>Frontiers in Microbiology</i> , 2021, 12, 734649.	1.5	6
973	Swine as reservoirs of zoonotic borderline oxacillin-resistant <i>Staphylococcus aureus</i> ST398. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2021, 79, 101697.	0.7	7
974	Molecular characterization and antimicrobial susceptibility testing of clinical and non-clinical <i>Brucella melitensis</i> and <i>Brucella abortus</i> isolates from Egypt. <i>One Health</i> , 2021, 13, 100255.	1.5	27
975	Genomics landscape of 185 <i>Streptococcus thermophilus</i> and identification of fermentation biomarkers. <i>Food Research International</i> , 2021, 150, 110711.	2.9	8
976	A multi-omics study on quantifying antimicrobial resistance in European freshwater lakes. <i>Environment International</i> , 2021, 157, 106821.	4.8	9
977	The role of iron-based nanoparticles (Fe-NPs) on methanogenesis in anaerobic digestion (AD) performance. <i>Environmental Research</i> , 2022, 204, 112043.	3.7	25
978	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. <i>Environment International</i> , 2022, 158, 106899.	4.8	40
979	Long-term spatiotemporal variation of antimicrobial resistance genes within the <i>Serratia marcescens</i> population and transmission of <i>S. marcescens</i> revealed by public whole-genome datasets. <i>Journal of Hazardous Materials</i> , 2022, 423, 127220.	6.5	7
980	Toothbrush microbiomes feature a meeting ground for human oral and environmental microbiota. <i>Microbiome</i> , 2021, 9, 32.	4.9	9
981	ResiDB: An automated database manager for sequence data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 847-851.	1.9	1
982	Metagenomic Analyses Expand Bacterial and Functional Profiling Biomarkers for Colorectal Cancer in a Hainan Cohort, China. <i>Current Microbiology</i> , 2021, 78, 705-712.	1.0	13
983	MGATMDA: Predicting microbe-disease associations via multi-component graph attention network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	15
985	Metagenomic Sequencing Revealed the Potential Pathogenic Threats of Banknotes. <i>ACS Omega</i> , 2021, 6, 3499-3507.	1.6	4
986	Application of a Novel Lytic Podoviridae Phage Pu20 for Biological Control of Drug-Resistant <i>Salmonella</i> in Liquid Eggs. <i>Pathogens</i> , 2021, 10, 34.	1.2	17
987	<i>Acinetobacter lanii</i> sp. nov., <i>Acinetobacter shaoyimingii</i> sp. nov. and <i>Acinetobacter wanghuae</i> sp. nov., isolated from faeces of Equus kiang. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	21
988	Physiological and genomic characterization of an exopolysaccharide-producing <i>Weissella cibaria</i> CH2 from cheese of the western Himalayas. <i>Food Bioscience</i> , 2020, 35, 100570.	2.0	10

#	ARTICLE	IF	CITATIONS
989	MicroPhenoDB Associates Metagenomic Data with Pathogenic Microbes, Microbial Core Genes, and Human Disease Phenotypes. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 760-772.	3.0	19
990	Co-occurrence of aminoglycoside and β -lactam resistance mechanisms in aminoglycoside-non-susceptible <i>Escherichia coli</i> isolated in the Zurich area, Switzerland. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106019.	1.1	25
991	Low prevalence of combined linezolid- and vancomycin-resistant <i>Enterococcus faecium</i> from hospital admission screening in an endemic region in Germany. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 646-650.	0.9	12
992	The impact of manure and soil texture on antimicrobial resistance gene levels in farmlands and adjacent ditches. <i>Science of the Total Environment</i> , 2020, 737, 139563.	3.9	31
993	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	9.4	402
994	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159.	9.4	123
995	A Common Practice of Widespread Antimicrobial Use in Horse Production Promotes Multi-Drug Resistance. <i>Scientific Reports</i> , 2020, 10, 911.	1.6	30
996	Detection of <i>mcr-1</i> -Carrying <i>Escherichia coli</i> Causing Bloodstream Infection in a New York City Hospital: Avian Origins, Human Concerns?. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx115.	0.4	20
997	Application of whole genome sequencing to query a potential outbreak of <i>Elizabethkingia anophelis</i> in Ontario, Canada. <i>Access Microbiology</i> , 2019, 1, e000017.	0.2	7
998	<i>Acidipropionibacterium virtanenii</i> sp. nov., isolated from malted barley. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3175-3183.	0.8	9
999	<i>Salinibaculum litoreum</i> gen. nov., sp. nov., isolated from salted brown alga <i>Laminaria</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2879-2887.	0.8	13
1000	<i>Staphylococcus borealis</i> sp. nov., isolated from human skin and blood. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6067-6078.	0.8	23
1001	Insights into the genome diversity and virulence of two clinical isolates of <i>Burkholderia cenocepacia</i> . <i>Journal of Medical Microbiology</i> , 2018, 67, 1157-1167.	0.7	4
1002	An identification protocol for ESBL-producing Gram-negative bacteria bloodstream infections using a MiniON nanopore sequencer. <i>Journal of Medical Microbiology</i> , 2019, 68, 1219-1226.	0.7	22
1003	Pneumococcal vaccine impacts on the population genomics of non-typeable <i>Haemophilus influenzae</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	12
1004	Phylogenomic analysis of gastroenteritis-associated <i>Clostridium perfringens</i> in England and Wales over a 7-year period indicates distribution of clonal toxigenic strains in multiple outbreaks and extensive involvement of enterotoxin-encoding (CPE) plasmids. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
1005	Complete hybrid genome assembly of clinical multidrug-resistant <i>Bacteroides fragilis</i> isolates enables comprehensive identification of antimicrobial-resistance genes and plasmids. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
1006	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. <i>Microbial Genomics</i> , 2020, 6, .	1.0	69

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1007	Benchmarking bacterial genome-wide association study methods using simulated genomes and phenotypes. <i>Microbial Genomics</i> , 2020, 6, .	1.0	38
1008	Transposable elements contribute to the genome plasticity of <i>Ralstonia solanacearum</i> species complex. <i>Microbial Genomics</i> , 2020, 6, .	1.0	13
1009	Preterm infants harbour diverse <i>Klebsiella</i> populations, including atypical species that encode and produce an array of antimicrobial resistance- and virulence-associated factors. <i>Microbial Genomics</i> , 2020, 6, .	1.0	35
1010	Phylogenetic and genomic analysis reveals high genomic openness and genetic diversity of <i>Clostridium perfringens</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	20
1011	Comprehensive genome analyses of <i>Sellimonas intestinalis</i> , a potential biomarker of homeostasis gut recovery. <i>Microbial Genomics</i> , 2020, 6, .	1.0	28
1050	Draft Genome Sequence of <i>Raoultella ornithinolytica</i> P079F W, Isolated from the Feces of a Preterm Infant. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1051	Genome Sequence of <i>Oxalobacter formigenes</i> Strain SSYG-15. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
1052	Applying clinical metagenomics for the detection and characterisation of respiratory infections. , 2019, , 35-49.		3
1053	Predicting antimicrobial resistance in <i>Pseudomonas aeruginosa</i> with machine learning-enabled molecular diagnostics. <i>EMBO Molecular Medicine</i> , 2020, 12, e10264.	3.3	111
1054	MOLECULAR CHARACTERIZATION OF FECAL <i>ESCHERICHIA COLI</i> ISOLATED FROM ZOO ANIMALS. <i>Journal of Zoo and Wildlife Medicine</i> , 2020, 50, 813.	0.3	3
1056	Antimicrobial Agents and Urinary Tract Infections. <i>Current Pharmaceutical Design</i> , 2019, 25, 1409-1423.	0.9	46
1057	Diverse Distribution of Resistomes in the Human and Environmental Microbiomes. <i>Current Genomics</i> , 2018, 19, 701-711.	0.7	10
1058	Brief Protocol for EDGE Bioinformatics: Analyzing Microbial and Metagenomic NGS Data. <i>Bio-protocol</i> , 2017, 7, e2622.	0.2	8
1059	<i>Campylobacter</i> species prevalence, characterisation of antimicrobial resistance and analysis of whole-genome sequence of isolates from livestock and humans, Latvia, 2008 to 2016. <i>Eurosurveillance</i> , 2019, 24, .	3.9	29
1060	Urban brown rats (<i>Rattus norvegicus</i>) as possible source of multidrug-resistant Enterobacteriaceae and methicillin-resistant <i>Staphylococcus</i> spp., Vienna, Austria, 2016 and 2017. <i>Eurosurveillance</i> , 2019, 24, .	3.9	29
1061	Two multi-fragment recombination events resulted in the β -lactam-resistant serotype 11A-ST6521 related to Spain9V-ST156 pneumococcal clone spreading in south-western Europe, 2008 to 2016. <i>Eurosurveillance</i> , 2020, 25, .	3.9	12
1062	Emergence of carbapenem-resistant ST131 <i>Escherichia coli</i> carrying blaOXA-244 in Germany, 2019 to 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	11
1063	Relating next-generation sequencing and bioinformatics concepts to routine microbiological testing. <i>Electronic Journal of General Medicine</i> , 2019, 16, em136.	0.3	4

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1064	mcr-Colistin Resistance Genes Mobilized by IncX4, IncHI2, and IncI2 Plasmids in Escherichia coli of Pigs and White Stork in Spain. <i>Frontiers in Microbiology</i> , 2019, 10, 3072.	1.5	57
1065	NGS-Based <i>S. aureus</i> Typing and Outbreak Analysis in Clinical Microbiology Laboratories: Lessons Learned From a Swiss-Wide Proficiency Test. <i>Frontiers in Microbiology</i> , 2020, 11, 591093.	1.5	9
1066	Combining Standard Molecular Typing and Whole Genome Sequencing to Investigate <i>Pseudomonas aeruginosa</i> Epidemiology in Intensive Care Units. <i>Frontiers in Public Health</i> , 2020, 8, 3.	1.3	28
1067	Molecular Characterization of <i>Cronobacter sakazakii</i> Strains Isolated from Powdered Milk. <i>Foods</i> , 2021, 10, 20.	1.9	16
1068	Phenotypic and Genotypic Traits of Vancomycin-Resistant Enterococci from Healthy Food-Producing Animals. <i>Microorganisms</i> , 2020, 8, 261.	1.6	15
1069	Mumame: a software tool for quantifying gene-specific point-mutations in shotgun metagenomic data. <i>Metabarcoding and Metagenomics</i> , 0, 3, .	0.0	2
1070	Antibiotic Susceptibility Profiles of <i>Pediococcus pentosaceus</i> from Various Origins and Their Implications for the Safety Assessment of Strains with Food-Technology Applications. <i>Journal of Food Protection</i> , 2021, 84, 1160-1168.	0.8	12
1071	Systematic detection of horizontal gene transfer across genera among multidrug-resistant bacteria in a single hospital. <i>ELife</i> , 2020, 9, .	2.8	85
1072	Comprehensive exploration of the translocation, stability and substrate recognition requirements in VIM-2 lactamase. <i>ELife</i> , 2020, 9, .	2.8	26
1073	Genome sequencing and analysis of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Stanley UPM 517: Insights on its virulence-associated elements and their potentials as vaccine candidates. <i>PeerJ</i> , 2019, 7, e6948.	0.9	1
1074	Whole-Genome Sequencing, Phylogenetic and Genomic Analysis of <i>Lactiplantibacillus pentosus</i> L33, a Potential Probiotic Strain Isolated From Fermented Sausages. <i>Frontiers in Microbiology</i> , 2021, 12, 746659.	1.5	24
1075	Genomic Characterisation of <i>Campylobacter jejuni</i> Isolates Recovered During Commercial Broiler Production. <i>Frontiers in Microbiology</i> , 2021, 12, 716182.	1.5	4
1076	<i>Flavobacterium flabelliforme</i> sp. nov. and <i>Flavobacterium geliluteum</i> sp. nov., Two Multidrug-Resistant Psychrotrophic Species Isolated From Antarctica. <i>Frontiers in Microbiology</i> , 2021, 12, 729977.	1.5	7
1077	Evolution of trimethoprim/sulfamethoxazole resistance in <i>Shewanella</i> algae from the perspective of comparative genomics and global phylogenetic analysis. <i>Journal of Microbiology, Immunology and Infection</i> , 2022, 55, 1195-1202.	1.5	5
1078	Characterization of IncHI1B Plasmids Encoding Efflux Pump TmexCD2-ToprJ2 in Carbapenem-Resistant <i>Klebsiella variicola</i> , <i>Klebsiella quasipneumoniae</i> , and <i>Klebsiella michiganensis</i> Strains. <i>Frontiers in Microbiology</i> , 2021, 12, 759208.	1.5	13
1079	Graph-Based Approaches Significantly Improve the Recovery of Antibiotic Resistance Genes From Complex Metagenomic Datasets. <i>Frontiers in Microbiology</i> , 2021, 12, 714836.	1.5	7
1080	Monitoring the Microevolution of <i>Salmonella enterica</i> in Healthy Dairy Cattle Populations at the Individual Farm Level Using Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 763669.	1.5	10
1081	Mobile Antimicrobial Resistance Genes in Probiotics. <i>Antibiotics</i> , 2021, 10, 1287.	1.5	22

#	ARTICLE	IF	CITATIONS
1083	Characterization of blaKPC-2-Carrying Plasmid pR31-KPC from a Pseudomonas aeruginosa Strain Isolated in China. <i>Antibiotics</i> , 2021, 10, 1234.	1.5	6
1085	NastyBugs: A simple method for extracting antimicrobial resistance information from metagenomes. <i>F1000Research</i> , 0, 6, 1971.	0.8	0
1087	The gut microbiota resistome provides development of drug resistance in causative agents of human infectious diseases. <i>Nauchno-prakticheskii Zhurnal "Patogeneza"</i> , 2017, , 20-32.	0.2	2
1098	Exploring Foodborne Pathogen Ecology and Antimicrobial Resistance in the Light of Shotgun Metagenomics. <i>Methods in Molecular Biology</i> , 2019, 1918, 229-245.	0.4	7
1107	A review of information resources on antimicrobial resistance genes. <i>Kazan Medical Journal</i> , 2019, 100, 457-463.	0.1	1
1108	Austria-wide survey on resistant, potentially pathogenic bacteria at Austrian bathing sites, 2017. <i>Bodenkultur</i> , 2019, 70, 81-88.	0.1	0
1115	Methionine Sulfoxide Reductase Enzymes: A Possible Virulence Factor for the Management of Antibiotic Resistance Crisis in the Climate Change Era. <i>International Journal of Environment and Climate Change</i> , 0, , 443-446.	0.0	0
1116	Complete Genome Sequence of Hydrocarbon-Degrading Halotolerant <i>Acinetobacter radioresistens</i> DD78, Isolated from the Aconcagua River Mouth in Central Chile. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
1118	Draft Genome Sequences of Three Novel <i>Acinetobacter</i> Isolates from an Irish Commercial Pig Farm. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
1124	Complete Genome Sequence of a <i>Staphylococcus aureus</i> Isolate from a Nasopharyngeal Swab from a Mine Worker in South Africa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
1125	Lumen and mucosa-associated <i>Lactobacillus rhamnosus</i> from the intestinal tract of organ donors. <i>Gut Microbiome</i> , 2020, 1, .	0.8	1
1126	Wider Context of Antimicrobial Resistance, Including Molecular Biology Perspective and Implications for Clinical Practice. , 2020, , 233-279.		1
1129	Whole genome sequence and comparative genome analyses of multi-resistant <i>Staphylococcus warneri</i> GDO1 isolated from a diseased pig in China. <i>PLoS ONE</i> , 2020, 15, e0233363.	1.1	4
1130	Genomic characterization of Inc _{pA1763-KPC} : IncFII _{K7} type plasmids p13294-KPC and pA1966-NR from <i>Klebsiella pneumoniae</i> . <i>Future Microbiology</i> , 2020, 15, 713-721.	1.0	0
1135	Genomic Determinants of Pathogenicity and Antimicrobial Resistance for 60 Global <i>Listeria monocytogenes</i> Isolates Responsible for Invasive Infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 718840.	1.8	22
1136	Cultivation and Genomic Characterization of the Bile Bacterial Species From Cholecystitis Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 739621.	1.5	5
1141	Metagenomic assembly deciphered the type-dependent effects of surfactants on the fates of antibiotics resistance genes during sludge fermentation and the underlying mechanisms. <i>Science of the Total Environment</i> , 2022, 807, 150822.	3.9	11
1144	Prevalence and Molecular Characteristics of Extended-Spectrum and AmpC β -Lactamase Producing <i>Escherichia coli</i> in Grazing Beef Cattle. <i>Frontiers in Microbiology</i> , 2019, 10, 3076.	1.5	7

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1145	A Comprehensive Analysis of the Global Human Gut Archaeome from a Thousand Genome Catalogue. SSRN Electronic Journal, 0, , .	0.4	0
1148	Assessment of the plasmidome of an extremophilic microbial community from the Diamante Lake, Argentina. Scientific Reports, 2021, 11, 21459.	1.6	2
1149	Laniakea@ReCaS: exploring the potential of customisable Galaxy on-demand instances as a cloud-based service. BMC Bioinformatics, 2021, 22, 544.	1.2	4
1154	Predictive comparative antibiotic resistance (AMR) profiles of rhizobacteria genes using CARD: a bioinformatics approach. Highlights in BioScience, 0, , .	0.0	1
1155	Isolation and sequence-based characterization of a koala symbiont: <i>Lonepinella koalarum</i> . PeerJ, 2020, 8, e10177.	0.9	5
1158	A glimpse of antimicrobial resistance gene diversity in kefir and yoghurt. Scientific Reports, 2020, 10, 22458.	1.6	27
1161	Genome Sequence of Eubacterium callanderi AMC0717, Isolated from the Colonic Mucosa of an 11-Year-Old Organ Donor. Microbiology Resource Announcements, 2020, 9, .	0.3	0
1162	Investigating hospital Mycobacterium chelonae infection using whole genome sequencing and hybrid assembly. PLoS ONE, 2020, 15, e0236533.	1.1	5
1163	CDRgator: An Integrative Navigator of Cancer Drug Resistance Gene Signatures. Molecules and Cells, 2019, 42, 237-244.	1.0	2
1164	Genomic analysis of antibiotic-resistant Enterococcus spp. reveals novel enterococci strains and the spread of plasmid-borne Tet(M), Tet(L) and Erm(B) genes from chicken litter to agricultural soil in South Africa. Journal of Environmental Management, 2022, 302, 114101.	3.8	12
1165	Molecular Surveillance of Carbapenem-Resistant Gram-Negative Bacteria in Liver Transplant Candidates. Frontiers in Microbiology, 2021, 12, 791574.	1.5	4
1166	Genetic Characterization of Staphylococcus aureus From Subclinical Mastitis Cases in Dairy Cows in Rwanda. Frontiers in Veterinary Science, 2021, 8, 751229.	0.9	7
1167	PangenomeNet: a pan-genome-based network reveals functional modules on antimicrobial resistome for Escherichia coli strains. BMC Bioinformatics, 2021, 22, 548.	1.2	7
1168	Evolutionary Divergence of the Novel Staphylococcal Species Staphylococcus argenteus. Frontiers in Microbiology, 2021, 12, 769642.	1.5	4
1169	The highly diverse Antarctic Peninsula soil microbiota as a source of novel resistance genes. Science of the Total Environment, 2022, 810, 152003.	3.9	18
1170	The Genetic Relatedness and Antimicrobial Resistance Patterns of Mastitis-Causing Staphylococcus aureus Strains Isolated from New Zealand Dairy Cattle. Veterinary Sciences, 2021, 8, 287.	0.6	5
1171	Whole genome sequencing and <i>de novo</i> assembly of <i>Staphylococcus pseudintermedius</i> : a pangenome approach to unravelling pathogenesis of canine pyoderma. Veterinary Dermatology, 2021, 32, 654-663.	0.4	7
1172	A Severe Gastroenteritis Outbreak of Salmonella enterica Serovar Enteritidis Linked to Contaminated Egg Fried Rice, China, 2021. Frontiers in Microbiology, 2021, 12, 779749.	1.5	7

#	ARTICLE	IF	CITATIONS
1173	Prediction and Analysis in silico of Genomic Islands in <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 769380.	1.5	2
1174	Invasive atypical non-typhoidal <i>Salmonella</i> serovars in The Gambia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
1175	A review of the resistome within the digestive tract of livestock. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 121.	2.1	17
1176	Antibiotics, antibiotic resistance genes and microbial community in grouper mariculture. <i>Science of the Total Environment</i> , 2022, 808, 152042.	3.9	26
1177	Genetic and Phenotypic Diversity of <i>Morganella morganii</i> Isolated From Cheese. <i>Frontiers in Microbiology</i> , 2021, 12, 738492.	1.5	8
1178	Virulence Genotype and Phenotype of Multiple Antimicrobial-Resistant <i>Escherichia coli</i> Isolates from Broilers Assessed from a "One-Health" Perspective. <i>Journal of Food Protection</i> , 2022, 85, 336-354.	0.8	7
1180	Genomic Insights into the Adaptability of the Spoilage Bacterium <i>Lactobacillus acetotolerans</i> CN247 to the Beer Microenvironment. <i>Journal of the American Society of Brewing Chemists</i> , 2023, 81, 171-180.	0.8	1
1181	Clinical outcomes, molecular epidemiology and resistance mechanisms of multidrug-resistant <i>Pseudomonas aeruginosa</i> isolated from bloodstream infections from Qatar. <i>Annals of Medicine</i> , 2021, 53, 2345-2353.	1.5	2
1182	OUP accepted manuscript. Database: the <i>Journal of Biological Databases and Curation</i> , 2022, , .	1.4	1
1183	Emergence of ST39 carbapenem-resistant <i>Klebsiella pneumoniae</i> producing VIM-1 and KPC-2. <i>Microbial Pathogenesis</i> , 2022, 162, 105373.	1.3	6
1184	Comparative genomics and antibiotic resistance of <i>Yersinia enterocolitica</i> obtained from a pork production chain and human clinical cases in Brazil. <i>Food Research International</i> , 2022, 152, 110917.	2.9	4
1185	Revealing antimicrobial resistance profile of the novel probiotic candidate <i>Faecalibacterium prausnitzii</i> DSM 17677. <i>International Journal of Food Microbiology</i> , 2022, 363, 109501.	2.1	8
1186	Metagenomic features of traditional fermented milk products. <i>LWT - Food Science and Technology</i> , 2022, 155, 112945.	2.5	24
1187	Metagenomics combined with comprehensive validation as a public health risk assessment tool for urban and agricultural run-off. <i>Water Research</i> , 2022, 209, 117941.	5.3	9
1188	Cropping system exerts stronger influence on antibiotic resistance gene assemblages in greenhouse soils than reclaimed wastewater irrigation. <i>Journal of Hazardous Materials</i> , 2022, 425, 128046.	6.5	12
1189	Alterations of fecal antibiotic resistome in COVID-19 patients after empirical antibiotic exposure. <i>International Journal of Hygiene and Environmental Health</i> , 2022, 240, 113882.	2.1	21
1190	The First Report of the <i>bla</i> _{IMP-10} Gene and Complete Sequence of the IMP-10-Encoding Plasmid p12NE515 from <i>Pseudomonas Aeruginosa</i> in China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1191	Microplastics Exhibit Accumulation and Horizontal Transfer of Antibiotic Resistance Genes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
1192	Nosocomial Outbreak of Carbapenemase-Producing <i>Proteus mirabilis</i> With Two Novel Salmonella Genomic Island 1 Variants Carrying Different bla _{NDM} -1 Gene Copies in China. <i>Frontiers in Microbiology</i> , 2021, 12, 800938.	1.5	5
1193	Close genetic linkage between human and companion animal extraintestinal pathogenic <i>Escherichia coli</i> ST127. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100106.	1.4	9
1194	A Polyvalent Broad-Spectrum <i>Escherichia</i> Phage Tequatrovirus EP01 Capable of Controlling Salmonella and <i>Escherichia coli</i> Contamination in Foods. <i>Viruses</i> , 2022, 14, 286.	1.5	11
1195	Effects of activated sludge and UV disinfection processes on the bacterial community and antibiotic resistance profile in a municipal wastewater treatment plant. <i>Environmental Science and Pollution Research</i> , 2022, 29, 36088-36099.	2.7	4
1197	<i>Sphingomonas arenae</i> sp. nov., isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	11
1198	Genomic Analysis and Antimicrobial Resistance of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> in Peru. <i>Frontiers in Microbiology</i> , 2021, 12, 802404.	1.5	18
1199	Characterization of the genome and serine protease of a novel <i>Bacillus subtilis</i> isolate. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 281-295.	0.7	2
1200	A framework for standardized qPCR-targets and protocols for quantifying antibiotic resistance in surface water, recycled water and wastewater. <i>Critical Reviews in Environmental Science and Technology</i> , 2022, 52, 4395-4419.	6.6	27
1201	New Sequence Types and Antimicrobial Drug-Resistant Strains of <i>Streptococcus suis</i> in Diseased Pigs, Italy, 2017-2019. <i>Emerging Infectious Diseases</i> , 2022, 28, 139-147.	2.0	12
1202	Large-scale WGS of carbapenem-resistant <i>Acinetobacter baumannii</i> isolates reveals patterns of dissemination of ST clades associated with antibiotic resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 934-943.	1.3	5
1203	Hybrid, ultra-deep metagenomic sequencing enables genomic and functional characterization of low-abundance species in the human gut microbiome. <i>Gut Microbes</i> , 2022, 14, 2021790.	4.3	27
1204	<i>Advenella mandrilli</i> sp. nov., a bacterium isolated from the faeces of <i>Mandrillus sphinx</i> . <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 271-280.	0.7	6
1205	Genome Sequence and Assessment of Safety and Potential Probiotic Traits of <i>Lactobacillus johnsonii</i> CNCM I-4884. <i>Microorganisms</i> , 2022, 10, 273.	1.6	8
1206	WHOLE GENOME SEQUENCING OF ANTIBIOTIC RESISTANT GENES IN ISOLATES FROM SURFACES IN A SCIENCE LABORATORY. <i>Turkish Journal of Pharmaceutical Sciences</i> , 2022, .	0.6	0
1208	Metagenomic Analysis of Bacterial Communities and Antibiotic Resistance Genes in <i>Penaeus monodon</i> Biofloc-Based Aquaculture Environments. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	6
1209	Draft Genome Sequences of <i>Lactocaseibacillus rhamnosus</i> cek-R1, <i>Lactocaseibacillus paracasei</i> cek-R2, and <i>Lentilactobacillus otakiensis</i> cek-R3, Isolated from a Beetroot Product. <i>Microbiology Resource Announcements</i> , 2022, 11, e0092121.	0.3	1
1211	Genome Characterization and Probiotic Potential of <i>Corynebacterium amycolatum</i> Human Vaginal Isolates. <i>Microorganisms</i> , 2022, 10, 249.	1.6	11
1212	Bacteroidales species in the human gut are a reservoir of antibiotic resistance genes regulated by invertible promoters. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 1.	2.9	22

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1213	Genetic and genomic characterization of multidrug resistant <i>Bacillus subtilis</i> M3 isolated from an activated sludge reactor treating wastewater. <i>Biologia (Poland)</i> , 2022, 77, 1151-1160.	0.8	0
1214	Association of blaVIM-2, blaPDC-35, blaOXA-10, blaOXA-488 and blaVEB-9 β -Lactamase Genes with Resistance to Ceftazidime, Avibactam and Ceftolozane-Tazobactam in Multidrug-Resistant <i>Pseudomonas aeruginosa</i> . <i>Antibiotics</i> , 2022, 11, 130.	1.5	7
1215	Comparative Genomics of Typical and Atypical <i>Aeromonas salmonicida</i> Complete Genomes Revealed New Insights into Pathogenesis Evolution. <i>Microorganisms</i> , 2022, 10, 189.	1.6	15
1216	Sal-type ABC-F proteins: intrinsic and common mediators of pleuromutilin resistance by target protection in staphylococci. <i>Nucleic Acids Research</i> , 2022, 50, 2128-2142.	6.5	16
1217	Changes in the skin microbiome associated with squamous cell carcinoma in transplant recipients. <i>ISME Communications</i> , 2022, 2, .	1.7	6
1218	Response behavior of antibiotic resistance genes to zinc oxide nanoparticles in cattle manure thermophilic anaerobic digestion process: A metagenomic analysis. <i>Bioresource Technology</i> , 2022, 347, 126709.	4.8	11
1219	The antagonistic interactions between a polyvalent phage SaP7 and β -lactam antibiotics on combined therapies. <i>Veterinary Microbiology</i> , 2022, 266, 109332.	0.8	5
1220	The first report of the blaIMP-10 gene and complete sequence of the IMP-10-encoding plasmid p12NE515 from <i>Pseudomonas aeruginosa</i> in China. <i>Acta Tropica</i> , 2022, 228, 106326.	0.9	3
1221	Novel multiplex PCR assays for rapid identification of <i>Salmonella</i> serogroups B, C1, C2, D, E, <i>S. enteritidis</i> , and <i>S. typhimurium</i> . <i>Analytical Methods</i> , 2022, 14, 1445-1453.	1.3	4
1222	<i>Pedobacter aquae</i> sp. nov., a multi-drug resistant bacterium isolated from fresh water. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 445-457.	0.7	2
1223	Exploration of Diverse Secondary Metabolites From <i>Streptomyces</i> sp. YINM00001, Using Genome Mining and One Strain Many Compounds Approach. <i>Frontiers in Microbiology</i> , 2022, 13, 831174.	1.5	10
1224	PhageLeads: Rapid Assessment of Phage Therapeutic Suitability Using an Ensemble Machine Learning Approach. <i>Viruses</i> , 2022, 14, 342.	1.5	31
1225	Exploration of the molecular mechanisms underlying the antibiotic resistance of <i>Helicobacter pylori</i> : A whole-genome sequencing-based study in Southern China. <i>Helicobacter</i> , 2022, 27, e12879.	1.6	7
1226	Accessory Genome Dynamics of Local and Global <i>Staphylococcus pseudintermedius</i> Populations. <i>Frontiers in Microbiology</i> , 2022, 13, 798175.	1.5	7
1227	Characterization of a Multidrug-Resistant <i>Salmonella</i> Enteritidis Clinical Strain Carrying a Novel Hybrid Plasmid. <i>Foodborne Pathogens and Disease</i> , 2022, , .	0.8	0
1228	Complete Genome Sequencing and Comparative Analysis of the Clinically-Derived <i>Apiotrichum mycotoxinivorans</i> Strain GMU1709. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 834015.	1.8	3
1229	<i>Shingobacterium bovistauri</i> sp. nov., Isolated from the Faeces of <i>Bos Taurus</i> . <i>Current Microbiology</i> , 2022, 79, 92.	1.0	6
1230	Whole-Genome Sequences of <i>Vibrio</i> Species from Warm-Water Shrimps Imported into Canada: Detection of Genetic Elements Associated with Antimicrobial Resistance and Potential Mobilizing Capacities. <i>Microbiology Resource Announcements</i> , 2022, , e0101421.	0.3	1

#	ARTICLE	IF	CITATIONS
1231	Context-aware genomic surveillance reveals hidden transmission of a carbapenemase-producing <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
1232	A catalogue of 1,167 genomes from the human gut archaeome. <i>Nature Microbiology</i> , 2022, 7, 48-61.	5.9	72
1233	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	85
1234	Antimicrobial Susceptibility of <i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i> from Milk Products and Other Habitats. <i>Foods</i> , 2021, 10, 3145.	1.9	5
1235	Comparative Genomics of Clinical and Environmental Isolates of <i>Vibrio</i> spp. of Colombia: Implications of Traits Associated with Virulence and Resistance. <i>Pathogens</i> , 2021, 10, 1605.	1.2	8
1236	Occurrence and Distribution of Antibiotic Resistance Genes in Municipal Wastewater Treatment Plants with D-Type Filters. <i>Water (Switzerland)</i> , 2021, 13, 3398.	1.2	2
1237	Comparison of genomes for the prediction of resistance genes. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	1
1238	Metagenomic Prediction of Antimicrobial Resistance in Critically Ill Patients with Lower Respiratory Tract Infections. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
1239	Solar Photo-Fenton Mediated by Alternative Oxidants for Mwwtp Effluent Quality Improvement: Impact on Microbial Community, Priority Pathogens and Removal of Antibiotic-Resistant Genes. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
1240	Profile and Actual Transmissibility of Carbapenem Resistance Genes: Intracellular and Extracellular DNA in Hospital Wastewater. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
1241	Antimicrobial Resistance in Rivers: A Review of the Genes Detected and New Challenges. <i>Environmental Toxicology and Chemistry</i> , 2022, 41, 687-714.	2.2	39
1242	<i>Shewanella jiangmenensis</i> sp. nov., isolated from aquaculture water. <i>Archives of Microbiology</i> , 2022, 204, 198.	1.0	7
1243	Coexistence of antibiotic resistance genes, fecal bacteria, and potential pathogens in anthropogenically impacted water. <i>Environmental Science and Pollution Research</i> , 2022, 29, 46977-46990.	2.7	6
1244	Host ecology regulates interspecies recombination in bacteria of the genus <i>Campylobacter</i> . <i>ELife</i> , 2022, 11, .	2.8	17
1245	<i>Paraphocaecicola brunensis</i> gen. nov., sp. nov., Carrying Two Variants of <i>nimB</i> Resistance Gene from <i>Bacteroides fragilis</i> , and <i>Caecibacteroides pullorum</i> gen. nov., sp. nov., Two Novel Genera Isolated from Chicken Caeca. <i>Microbiology Spectrum</i> , 2022, 10, e0195421.	1.2	2
1246	Application of Psychrotolerant Antarctic Bacteria and Their Metabolites as Efficient Plant Growth Promoting Agents. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 772891.	2.0	15
1247	Gut Microbiome Characteristics in feral and domesticated horses from different geographic locations. <i>Communications Biology</i> , 2022, 5, 172.	2.0	20
1248	Genome Informatics and Machine Learning-Based Identification of Antimicrobial Resistance-Encoding Features and Virulence Attributes in <i>Escherichia coli</i> Genomes Representing Globally Prevalent Lineages, Including High-Risk Clonal Complexes. <i>MBio</i> , 2022, 13, e0379621.	1.8	4

#	ARTICLE	IF	CITATIONS
1249	Genomic Characteristics and Pan-Genome Analysis of <i>Rhodococcus equi</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 807610.	1.8	6
1250	Multidrug-resistant <i>Mycolicibacterium fortuitum</i> infection in a companion cat (<i>Felis silvestris catus</i>) in Brazil. <i>Access Microbiology</i> , 2022, 4, 000317.	0.2	2
1251	Virulence and Antibiotic Resistance Genes in <i>Listeria monocytogenes</i> Strains Isolated From Ready-to-Eat Foods in Chile. <i>Frontiers in Microbiology</i> , 2021, 12, 796040.	1.5	17
1252	Genetic Characterization of Antibiotic Resistant Enterobacteriaceae Isolates From Bovine Animals and the Environment in Nigeria. <i>Frontiers in Microbiology</i> , 2022, 13, 793541.	1.5	3
1253	A Comparative Genomic and Safety Assessment of Six <i>Lactiplantibacillus plantarum</i> subsp. <i>argentoratensis</i> Strains Isolated from Spontaneously Fermented Greek Wheat Sourdoughs for Potential Biotechnological Application. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2487.	1.8	13
1255	Review and Comparison of Antimicrobial Resistance Gene Databases. <i>Antibiotics</i> , 2022, 11, 339.	1.5	28
1256	Extensive metagenomic analysis of the porcine gut resistome to identify indicators reflecting antimicrobial resistance. <i>Microbiome</i> , 2022, 10, 39.	4.9	19
1257	PHISDetector: A Tool to Detect Diverse <i>In Silico</i> Phage-Host Interaction Signals for Virome Studies. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 508-523.	3.0	20
1258	Intestinal Exposure to Ceftiofur and Cefquinome after Intramuscular Treatment and the Impact of Ceftiofur on the Pig Fecal Microbiome and Resistome. <i>Antibiotics</i> , 2022, 11, 342.	1.5	3
1259	Assessment of global health risk of antibiotic resistance genes. <i>Nature Communications</i> , 2022, 13, 1553.	5.8	193
1260	Identification and Characterization of vB_PreP_EPr2, a Lytic Bacteriophage of Pan-Drug Resistant <i>Providencia rettgeri</i> . <i>Viruses</i> , 2022, 14, 708.	1.5	5
1261	Novel canine high-quality metagenome-assembled genomes, prophages and host-associated plasmids provided by long-read metagenomics together with Hi-C proximity ligation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
1262	IncFIB-4.1 and IncFIB-4.2 Single-Replicon Plasmids: Small Backbones with Large Accessory Regions. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1191-1203.	1.1	2
1263	Inhalable MOF-Derived Nanoparticles for Sonodynamic Therapy of Bacterial Pneumonia. <i>Advanced Functional Materials</i> , 2022, 32, .	7.8	31
1264	WGS-Based Phenotyping and Molecular Characterization of the Resistome, Virulome and Plasmid Replicons in <i>Klebsiella pneumoniae</i> Isolates from Powdered Milk Produced in Germany. <i>Microorganisms</i> , 2022, 10, 564.	1.6	3
1265	Shared antibiotic resistance and virulence genes in <i>Staphylococcus aureus</i> from diverse animal hosts. <i>Scientific Reports</i> , 2022, 12, 4413.	1.6	23
1266	Virulence Determinants in <i>Staphylococcus aureus</i> Clones Causing Osteomyelitis in Italy. <i>Frontiers in Microbiology</i> , 2022, 13, 846167.	1.5	5
1267	The genomic basis of the <i>Streptococcus thermophilus</i> health-promoting properties. <i>BMC Genomics</i> , 2022, 23, 210.	1.2	18

#	ARTICLE	IF	CITATIONS
1268	IntegronFinder 2.0: Identification and Analysis of Integrons across Bacteria, with a Focus on Antibiotic Resistance in Klebsiella. <i>Microorganisms</i> , 2022, 10, 700.	1.6	61
1270	Clinical Perspective of Antimicrobial Resistance in Bacteria. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 735-746.	1.1	49
1271	Determination of Antiviral Mechanism of Centenarian Gut-Derived <i>Limosilactobacillus fermentum</i> Against Norovirus. <i>Frontiers in Nutrition</i> , 2022, 9, 812623.	1.6	4
1272	Methods for the targeted sequencing and analysis of integrons and their gene cassettes from complex microbial communities. <i>Microbial Genomics</i> , 2022, 8, .	1.0	9
1273	Bacteriocin Producing <i>Streptococcus agalactiae</i> Strains Isolated from Bovine Mastitis in Brazil. <i>Microorganisms</i> , 2022, 10, 588.	1.6	7
1274	The Human Health Implications of Antibiotic Resistance in Environmental Isolates from Two Nebraska Watersheds. <i>Microbiology Spectrum</i> , 2022, 10, e0208221.	1.2	4
1275	Genomic heterogeneity underlies multidrug resistance in <i>Pseudomonas aeruginosa</i> : A population-level analysis beyond susceptibility testing. <i>PLoS ONE</i> , 2022, 17, e0265129.	1.1	13
1277	Genomic analysis of virulence factors and antimicrobial resistance of group B <i>Streptococcus</i> isolated from pregnant women in northeastern Mexico. <i>PLoS ONE</i> , 2022, 17, e0264273.	1.1	2
1278	Analysis of Antimicrobial Resistance in Non-typhoidal <i>Salmonella</i> Collected From Pork Retail Outlets and Slaughterhouses in Vietnam Using Whole Genome Sequencing. <i>Frontiers in Veterinary Science</i> , 2022, 9, 816279.	0.9	7
1279	Antimicrobial resistance determinants in silage. <i>Scientific Reports</i> , 2022, 12, 5243.	1.6	2
1280	VIM-encoding IncpSTY plasmids and chromosome-borne integrative and mobilizable elements (IMEs) and integrative and conjugative elements (ICEs) in <i>Pseudomonas</i> . <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2022, 21, 10.	1.7	5
1281	The First Whole Genome Sequence Discovery of the Devastating Fungus <i>Arthrinium rasikravindrae</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 255.	1.5	2
1282	Harnessing <i>Paenarthrobacter ureafaciens</i> YL1 and <i>Pseudomonas koreensis</i> YL2 Interactions to Improve Degradation of Sulfamethoxazole. <i>Microorganisms</i> , 2022, 10, 648.	1.6	10
1283	Strain-level characterization of broad host range mobile genetic elements transferring antibiotic resistance from the human microbiome. <i>Nature Communications</i> , 2022, 13, 1445.	5.8	52
1284	Whole-genome sequencing for the characterization of resistance mechanisms and epidemiology of colistin-resistant <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2022, 17, e0264335.	1.1	6
1285	Metagenomic Approaches Reveal Strain Profiling and Genotyping of <i>Klebsiella pneumoniae</i> from Hospitalized Patients in China. <i>Microbiology Spectrum</i> , 2022, , e0219021.	1.2	2
1286	Impacts of farmland application of antibiotic-contaminated manures on the occurrence of antibiotic residues and antibiotic resistance genes in soil: A meta-analysis study. <i>Chemosphere</i> , 2022, 300, 134529.	4.2	63
1287	Deciphering antibiotic resistance genes and microbial community of anammox consortia under sulfadiazine and chlortetracycline stress. <i>Ecotoxicology and Environmental Safety</i> , 2022, 234, 113343.	2.9	10

#	ARTICLE	IF	CITATIONS
1288	Bioprospecting of Ribosomally Synthesized and Post-translationally Modified Peptides Through Genome Characterization of a Novel Probiotic <i>Lactiplantibacillus plantarum</i> UTNGt21A Strain: A Promising Natural Antimicrobials Factory. <i>Frontiers in Microbiology</i> , 2022, 13, 868025.	1.5	3
1289	Co-expression Mechanism Analysis of Different Tachyplesin Resistant Strains in <i>Pseudomonas aeruginosa</i> Based on Transcriptome Sequencing. <i>Frontiers in Microbiology</i> , 2022, 13, 871290.	1.5	1
1290	Safety Assessment of <i>Lactiplantibacillus plantarum</i> TWK10 Based on Whole-Genome Sequencing, Phenotypic, and Oral Toxicity Analysis. <i>Microorganisms</i> , 2022, 10, 784.	1.6	9
1291	<i>Pseudomonas tumuqii</i> sp. nov., isolated from greenhouse soil. <i>Archives of Microbiology</i> , 2022, 204, 249.	1.0	1
1292	Metagenomics highlights the impact of climate and human activities on antibiotic resistance genes in China's estuaries. <i>Environmental Pollution</i> , 2022, 301, 119015.	3.7	20
1293	A longitudinal study of dominant <i>E. coli</i> lineages and antimicrobial resistance in the gut of children living in an upper middle-income country. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 136-140.	0.9	3
1294	Metabolic hazards of pharmaceuticals and personal care products (PPCPs) in sewers. <i>Journal of Hazardous Materials</i> , 2022, 432, 128539.	6.5	17
1295	Profiling of emerging pathogens, antibiotic resistance genes and mobile genetic elements in different biological wastewater treatment plants. <i>Journal of Environmental Chemical Engineering</i> , 2022, 10, 107596.	3.3	14
1296	Short- and long-read metagenomics insight into the genetic contexts and hosts of mobile antibiotic resistome in Chinese swine farms. <i>Science of the Total Environment</i> , 2022, 827, 154352.	3.9	8
1297	Exploring the resistome, virulome, mobilome and microbiome along pork production chain using metagenomics. <i>International Journal of Food Microbiology</i> , 2022, 371, 109674.	2.1	4
1298	Aztreonam in combination with imipenem-relebactam against clinical and isogenic strains of serine and metallo- β -lactamase-producing enterobacterales. <i>Diagnostic Microbiology and Infectious Disease</i> , 2022, 103, 115674.	0.8	8
1299	Impact of nitrate addition on the resistome and mobilome from a full-scale sewer. <i>Chemical Engineering Journal</i> , 2022, 439, 135653.	6.6	3
1300	Solar photo-Fenton mediated by alternative oxidants for MWWTP effluent quality improvement: Impact on microbial community, priority pathogens and removal of antibiotic-resistant genes. <i>Chemical Engineering Journal</i> , 2022, 441, 136060.	6.6	10
1301	Phenotypic and genetic analyses of two <i>Campylobacter fetus</i> isolates from a patient with relapsed prosthetic valve endocarditis. <i>Pathogens and Disease</i> , 2022, 79, .	0.8	3
1302	Identification of Carbapenemase within Class 1 Integron Structure in Intrinsically Colistin-resistant Enterobacteriaceae. <i>Journal of Medical Microbiology and Infectious Diseases</i> , 2021, 9, 203-209.	0.1	0
1303	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	5.9	32
1304	Genomic diversity of antimicrobial resistance in non-typhoidal <i>Salmonella</i> in Victoria, Australia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
1305	Dynamic changes in antibiotic resistance genes and gut microbiota after <i>Helicobacter pylori</i> eradication therapies. <i>Helicobacter</i> , 2022, 27, e12871.	1.6	8

#	ARTICLE	IF	CITATIONS
1307	The Formation of Antibiotic Resistance Genes in Bacterial Communities During Garlic Powder Processing. <i>Frontiers in Nutrition</i> , 2021, 8, 800932.	1.6	1
1308	Isolation and Sequencing of the First Case of Symptomatic MDR <i>Salmonella enterica</i> Subsp. <i>Enterica</i> ST40 in Human in Italy, July 2020. <i>Microbial Drug Resistance</i> , 2021, , .	0.9	1
1310	Worldwide distribution and environmental origin of the Adelaide imipenemase (AIM-1), a potent carbapenemase in <i>Pseudomonas aeruginosa</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	3
1311	Microbiome Compositions and Resistome Levels after Antibiotic Treatment of Critically Ill Patients: An Observational Cohort Study. <i>Microorganisms</i> , 2021, 9, 2542.	1.6	4
1313	Metagenomic and metabolomic remodeling in nonagenarians and centenarians and its association with genetic and socioeconomic factors. <i>Nature Aging</i> , 2022, 2, 438-452.	5.3	17
1314	Environmental factors shaping the gut microbiome in a Dutch population. <i>Nature</i> , 2022, 604, 732-739.	13.7	239
1315	MVGCNMDA: Multi-view Graph Augmentation Convolutional Network for Uncovering Disease-Related Microbes. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 669-682.	2.2	9
1316	Two Novel Lytic Bacteriophages Infecting <i>Enterococcus</i> spp. Are Promising Candidates for Targeted Antibacterial Therapy. <i>Viruses</i> , 2022, 14, 831.	1.5	7
1317	Acquisition of Daptomycin Resistance by <i>Enterococcus faecium</i> Confers Collateral Sensitivity to Glycopeptides. <i>Frontiers in Microbiology</i> , 2022, 13, 815600.	1.5	6
1598	Molecular epidemiology of antimicrobial-resistant <i>Pseudomonas aeruginosa</i> in a veterinary teaching hospital environment. <i>Veterinary Research Communications</i> , 2023, 47, 73-86.	0.6	6
1599	Metagenomic tracking of antibiotic resistance genes through a pre-harvest vegetable production system: an integrated lab, microcosm and greenhouse scale analysis. <i>Environmental Microbiology</i> , 2022, 24, 3705-3721.	1.8	6
1601	Knowledge integration and decision support for accelerated discovery of antibiotic resistance genes. <i>Nature Communications</i> , 2022, 13, 2360.	5.8	5
1602	Metagenomic investigation of the seasonal distribution of bacterial community and antibiotic-resistant genes in Day River Downstream, Ninh Binh, Vietnam. <i>Applied Biological Chemistry</i> , 2022, 65, .	0.7	5
1603	Detection of Antimicrobial Resistance, Pathogenicity, and Virulence Potentials of Non-Typhoidal <i>Salmonella</i> Isolates at the Yaounde Abattoir Using Whole-Genome Sequencing Technique. <i>Pathogens</i> , 2022, 11, 502.	1.2	7
1604	Draft Genome Sequence of <i>Corynebacterium sanguinis</i> Strain Marseille-P8776. <i>Microbiology Resource Announcements</i> , 2022, 11, e0000822.	0.3	0
1605	Persisting uropathogenic <i>Escherichia coli</i> lineages show signatures of niche-specific within-host adaptation mediated by mobile genetic elements. <i>Cell Host and Microbe</i> , 2022, 30, 1034-1047.e6.	5.1	13
1606	Whole-genome sequencing analysis of a rare <i>Salmonella diarizonae</i> clinical strain carrying multiple plasmids and novel gene cassettes. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 339-342.	0.9	2
1607	Functional annotation and complete genome analysis confirm the probiotic characteristics of <i>Bacillus</i> species isolated from the gut of Nile tilapia. <i>LWT - Food Science and Technology</i> , 2022, 163, 113541.	2.5	3

#	ARTICLE	IF	CITATIONS
1608	Colistin Resistance and Molecular Characterization of the Genomes of <i>mcr-1</i> -Positive <i>Escherichia coli</i> Clinical Isolates. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	1.8	0
1609	Genomic and biological characteristics of a newly isolated lytic bacteriophage PZJ0206 infecting the <i>Enterobacter cloacae</i> . <i>Virus Research</i> , 2022, 316, 198800.	1.1	1
1610	Inferring antibiotic susceptibility from metagenomic data: dream or reality?. <i>Clinical Microbiology and Infection</i> , 2022, 28, 1225-1229.	2.8	3
1611	A Resistome Roadmap: From the Human Body to Pristine Environments. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	6
1612	Revealing the microbial heritage of traditional Brazilian cheeses through metagenomics. <i>Food Research International</i> , 2022, 157, 111265.	2.9	12
1613	Xenobiotic pollution affects transcription of antibiotic resistance and virulence factors in aquatic microcosms. <i>Environmental Pollution</i> , 2022, 306, 119396.	3.7	11
1614	Diversity and distribution of Type VI Secretion System gene clusters in bacterial plasmids. <i>Scientific Reports</i> , 2022, 12, 8249.	1.6	10
1615	Rapid Detection of Bacterial Pathogens and Antimicrobial Resistance Genes in Clinical Urine Samples With Urinary Tract Infection by Metagenomic Nanopore Sequencing. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	18
1616	<i>Oceanisphaera pacifica</i> sp. nov., isolated from the intestine of <i>Trichiurus japonicus</i> . <i>Archives of Microbiology</i> , 2022, 204, 338.	1.0	1
1617	AMR-meta: a <i>k</i> -mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. <i>GigaScience</i> , 2022, 11, .	3.3	8
1618	Enabling genomic island prediction and comparison in multiple genomes to investigate bacterial evolution and outbreaks. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
1619	Health-Promoting Nature of <i>Lactococcus lactis</i> IBB109 and <i>Lactococcus lactis</i> IBB417 Strains Exhibiting Proliferation Inhibition and Stimulation of Interleukin-18 Expression in Colorectal Cancer Cells. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	13
1620	Comparative pan-genomic analysis of 51 <i>Renibacterium salmoninarum</i> indicates heterogeneity in the principal virulence factor, the 57 kDa <i>D</i> protein. <i>Journal of Fish Diseases</i> , 0, .	0.9	1
1621	The Lysine Acetylation Modification in the Porin Aha1 of <i>Aeromonas hydrophila</i> Regulates the Uptake of Multidrug Antibiotics. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100248.	2.5	8
1622	Wild Birds-The Sentinel of Antibiotic Resistance for Urban River: Study on Egrets and Jinjiang River in Chengdu, China. <i>SSRN Electronic Journal</i> , 0, .	0.4	0
1623	ROcker Models for Reliable Detection and Typing of Short-Read Sequences Carrying $\hat{2}$ -Lactamase Genes. <i>MSystems</i> , 2022, 7, .	1.7	1
1624	Gelatinase-Responsive Photothermal Nanotherapy Based on Au Nanostars Functionalized with Antimicrobial Peptides for Treating <i>Staphylococcus aureus</i> Infections. <i>ACS Applied Nano Materials</i> , 2022, 5, 8324-8333.	2.4	5
1625	Complete Genome Analysis of Highly Pathogenic Non-O1/O139 <i>Vibrio cholerae</i> Isolated From <i>Macrobrachium rosenbergii</i> Reveals Pathogenicity and Antibiotic Resistance-Related Genes. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	5

#	ARTICLE	IF	CITATIONS
1626	Transcriptomics and metagenomics of common cutworm (<i>Spodoptera litura</i>) and fall armyworm (<i>Spodoptera frugiperda</i>) demonstrate differences in detoxification and development. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
1628	Deciphering environmental resistome and mobilome risks on the stone monument: A reservoir of antimicrobial resistance genes. <i>Science of the Total Environment</i> , 2022, 838, 156443.	3.9	8
1629	The effect of 100% single-occupancy rooms on acquisition of extended-spectrum beta-lactamase-producing Enterobacterales and intra-hospital patient transfers: a prospective before-and-after study. <i>Antimicrobial Resistance and Infection Control</i> , 2022, 11, .	1.5	6
1630	Comparative in silico characterization of <i>Klebsiella pneumoniae</i> hypervirulent plasmids and their antimicrobial resistance genes. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2022, 21, .	1.7	10
1631	Activity of Omadacycline Alone and in Combination against Carbapenem-Nonsusceptible <i>Acinetobacter baumannii</i> with Varying Minocycline Susceptibility. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
1632	Genomic Characterization of <i>Cronobacter</i> spp. and <i>Salmonella</i> spp. Strains Isolated From Powdered Infant Formula in Chile. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	7
1633	Prevalence and microbiological and genetic characteristics of multidrug-resistant <i>Pseudomonas aeruginosa</i> over three years in Qatar. <i>Antimicrobial Stewardship & Healthcare Epidemiology</i> , 2022, 2, .	0.2	6
1634	Cultured Bacteria Provide Insight into the Functional Potential of the Coral-Associated Microbiome. <i>MSystems</i> , 2022, 7, .	1.7	14
1636	Antimicrobial Resistance Monitoring of Water Environments: A Framework for Standardized Methods and Quality Control. <i>Environmental Science & Technology</i> , 2022, 56, 9149-9160.	4.6	80
1637	Whole-genome sequencing analysis of Shiga toxin-producing <i>Escherichia coli</i> O22:H8 isolated from cattle prediction pathogenesis and colonization factors and position in STEC universe phylogeny. <i>Journal of Microbiology</i> , 0, , .	1.3	4
1638	Genomic and Temporal Trends in Canine ExPEC Reflect Those of Human ExPEC. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11
1639	The migration and residual regularity of doxycycline and antibiotic resistance genes at different depths of sandy loam with the influence of an oversized microplastic contamination layer. <i>Chemical Engineering Journal</i> , 2022, 450, 137449.	6.6	5
1640	Isolation, identification, virulence potential and genomic features of <i>Tenacibaculum piscium</i> isolates recovered from Chilean salmonids. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	5
1641	New Mutations in <i>cls</i> Lead to Daptomycin Resistance in a Clinical Vancomycin- and Daptomycin-Resistant <i>Enterococcus faecium</i> Strain. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1642	First Report of the Colistin Resistance Gene <i>mcr-10.1</i> Carried by Inc _{pA1763-KPC} Plasmid pSL12517-mcr10.1 in <i>Enterobacter cloacae</i> in Sierra Leone. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
1643	Genome analysis uncovers the prolific antagonistic and plant growth-promoting potential of endophyte <i>Bacillus velezensis</i> K1. <i>Gene</i> , 2022, 836, 146671.	1.0	15
1644	Antibiotic Resistance Genes Distribution and Relevant Risk Assessment in Karst Caves-Taking Guizhou Shuanghe Cave as an Example. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1645	A genome and gene catalog of glacier microbiomes. <i>Nature Biotechnology</i> , 2022, 40, 1341-1348.	9.4	50

#	ARTICLE	IF	CITATIONS
1646	Demonstrating a Comprehensive Wastewater-Based Surveillance Approach That Differentiates Globally Sourced Resistomes. <i>Environmental Science & Technology</i> , 2022, 56, 14982-14993.	4.6	27
1647	Multiresistant Enterobacteriaceae in yellow-legged gull chicks in their first weeks of life. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
1650	Identification and Characterization of a Novel Species of Genus <i>Akkermansia</i> with Metabolic Health Effects in a Diet-Induced Obesity Mouse Model. <i>Cells</i> , 2022, 11, 2084.	1.8	5
1651	Comparative analysis of multiplexed PCR and short- and long-read whole genome sequencing to investigate a large <i>Klebsiella pneumoniae</i> outbreak in New York State. <i>Diagnostic Microbiology and Infectious Disease</i> , 2022, , 115765.	0.8	0
1652	Phenotypic and genomic characterization of pathogenic <i>Providencia rettgeri</i> from kuruma shrimp <i>Marsupenaeus japonicus</i> . <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	3
1653	An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species. <i>Nature Communications</i> , 2022, 13, .	5.8	31
1654	Metagenomic prediction of antimicrobial resistance in critically ill patients with lower respiratory tract infections. <i>Genome Medicine</i> , 2022, 14, .	3.6	25
1655	<i>Bacillus licheniformis</i> MCC 2514 genome sequencing and functional annotation for providing genetic evidence for probiotic gut adhesion properties and its applicability as a bio-preservative agent. <i>Gene</i> , 2022, 840, 146744.	1.0	6
1656	Differential survival of potentially pathogenic, septicemia- and meningitis-causing <i>E. coli</i> across the wastewater treatment train. <i>Npj Clean Water</i> , 2022, 5, .	3.1	1
1659	Insights into the Antimicrobial Resistance Profile of a Next Generation Probiotic <i>Akkermansia muciniphila</i> DSM 22959. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 9152.	1.2	7
1660	A <i>bla</i> _{SIM-1} and <i>mcr</i> -9.2 harboring <i>Klebsiella michiganensis</i> strain reported and genomic characteristics of <i>Klebsiella michiganensis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
1661	Review of <i>Escherichia coli</i> O157:H7 Prevalence, Pathogenicity, Heavy Metal and Antimicrobial Resistance, African Perspective. <i>Infection and Drug Resistance</i> , 0, Volume 15, 4645-4673.	1.1	23
1662	<i>Acinetobacter baumannii</i> complex, national laboratory-based surveillance in South Africa, 2017 to 2019. <i>PLoS ONE</i> , 2022, 17, e0271355.	1.1	7
1663	Antibiotic resistance genes of public health importance in livestock and humans in an informal urban community in Nepal. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
1664	Comparative Genomic Analysis of Antimicrobial-Resistant <i>Escherichia coli</i> from South American Camelids in Central Germany. <i>Microorganisms</i> , 2022, 10, 1697.	1.6	3
1665	Systematic profiling of the chicken gut microbiome reveals dietary supplementation with antibiotics alters expression of multiple microbial pathways with minimal impact on community structure. <i>Microbiome</i> , 2022, 10, .	4.9	12
1666	Occurrence and dissemination of antibiotic resistance genes in mine soil ecosystems. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 6289-6299.	1.7	6
1667	Evolutionary and genomic insights into the long-term colonization of <i>Shigella flexneri</i> in animals. <i>Emerging Microbes and Infections</i> , 2022, 11, 2069-2079.	3.0	1

#	ARTICLE	IF	CITATIONS
1668	Genomic characterization of <i>Salmonella enterica</i> serovar Kentucky and London recovered from food and human salmonellosis in Zhejiang Province, China (2016–2021). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
1669	Identification and whole-genome sequencing analysis of <i>Vibrio vulnificus</i> strains causing pearl gentian grouper disease in China. <i>BMC Microbiology</i> , 2022, 22, .	1.3	4
1670	The New Precision Stewards?. <i>Journal of Personalized Medicine</i> , 2022, 12, 1308.	1.1	2
1671	Soil antibiotic abatement associates with the manipulation of soil microbiome via long-term fertilizer application. <i>Journal of Hazardous Materials</i> , 2022, 439, 129704.	6.5	11
1672	Assessing the genomic composition, putative ecological relevance and biotechnological potential of plasmids from sponge bacterial symbionts. <i>Microbiological Research</i> , 2022, 265, 127183.	2.5	1
1673	Comparative analysis of two next-generation sequencing platforms for analysis of antimicrobial resistance genes. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 31, 167-174.	0.9	1
1674	A proposed framework for the identification of indicator genes for monitoring antibiotic resistance in wastewater: Insights from metagenomic sequencing. <i>Science of the Total Environment</i> , 2023, 854, 158698.	3.9	6
1675	Wild Birds-The Sentinel of Antibiotic Resistance for Urban River: Study on Egrets and Jinjiang River in Chengdu, China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1676	New-Age Genomic Measures for Uncovering Plant-Microbiome Interactions: Tools, Pipelines and Guidance Map for Genomic Data Mining. , 2022, , 207-232.		0
1677	In Silico Analysis and PCR Characterization of non-Tn4401 Transposable Elements in <i>Pseudomonas aeruginosa</i> . , 0, , .		0
1678	WGS-Based Lineage and Antimicrobial Resistance Pattern of <i>Salmonella</i> Typhimurium Isolated during 2000–2017 in Peru. <i>Antibiotics</i> , 2022, 11, 1170.	1.5	7
1680	Genomic Evolution of ST11 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> from 2011 to 2020 Based on Data from the Pathosystems Resource Integration Center. <i>Genes</i> , 2022, 13, 1624.	1.0	0
1681	Emerging of Multidrug-Resistant <i>Cronobacter sakazakii</i> Isolated from Infant Supplementary Food in China. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11
1682	Comparative genome analysis unravels pathogenicity of <i>Xanthomonas albilineans</i> causing sugarcane leaf scald disease. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
1683	A Comprehensive Metagenomic Analysis Framework Revealing Microbiome Profile and Potential for Hydrocarbon Degradation and Carbohydrate Metabolism in a Himalayan Artificial Lake. <i>Sustainability</i> , 2022, 14, 11455.	1.6	2
1684	The effect of “Fishery-PV Integration” on <i>Penaeus monodon</i> culture and research on the micro-ecological environment. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
1685	Lactic acid bacteria and bifidobacteria deliberately introduced into the agro-food chain do not significantly increase the antimicrobial resistance gene pool. <i>Gut Microbes</i> , 2022, 14, .	4.3	6
1686	Genomic characterization of two metagenome-assembled genomes of <i>Tropheryma whippelii</i> from China. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2

#	ARTICLE	IF	CITATIONS
1687	Codiversification of gut microbiota with humans. <i>Science</i> , 2022, 377, 1328-1332.	6.0	67
1688	Antibiotic and metal resistance of <i>Stenotrophomonas maltophilia</i> isolates from Eboling permafrost of the Tibetan Plateau. <i>Environmental Science and Pollution Research</i> , 2023, 30, 11798-11810.	2.7	3
1690	Clinically relevant pathogens on surfaces display differences in survival and transcriptomic response in relation to probiotic and traditional cleaning strategies. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	3
1691	Advantages and challenges of metagenomic sequencing for the diagnosis of pulmonary infectious diseases. <i>Clinical Respiratory Journal</i> , 2022, 16, 646-656.	0.6	14
1692	Antimicrobial Activity of Ceftolozane-Tazobactam, Ceftazidime-Avibactam, and Cefiderocol against Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Recovered at a German University Hospital. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	10
1693	Metabolomics and gene-metabolite networks reveal the potential of <i>Leuconostoc</i> and <i>Weissella</i> strains as starter cultures in the manufacturing of bread without baker's yeast. <i>Food Research International</i> , 2022, 162, 112023.	2.9	2
1694	Molecular Epidemiology of <i>Staphylococcus aureus</i> in China Reveals the Key Gene Features Involved in Epidemic Transmission and Adaptive Evolution. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
1695	Function-based classification of hazardous biological sequences: Demonstration of a new paradigm for biohazard assessments. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	3
1696	Early life dynamics of ARG and MGE associated with intestinal virome in neonatal piglets. <i>Veterinary Microbiology</i> , 2022, 274, 109575.	0.8	3
1697	Considerations for determining safety of probiotics: A USP perspective. <i>Regulatory Toxicology and Pharmacology</i> , 2022, 136, 105266.	1.3	15
1698	Canine Saliva as a Possible Source of Antimicrobial Resistance Genes. <i>Antibiotics</i> , 2022, 11, 1490.	1.5	4
1699	<i>Dongia deserti</i> sp. nov., Isolated from the Gurbantunggut Desert Soil. <i>Current Microbiology</i> , 2022, 79, .	1.0	3
1700	Putative Pathogenic Genes of <i>Leptospira interrogans</i> and <i>Leptospira weilii</i> Isolated from Patients with Acute Febrile Illness. <i>Tropical Medicine and Infectious Disease</i> , 2022, 7, 284.	0.9	1
1701	Wild birds-the sentinel of antibiotic resistance for urban river: Study on egrets and Jinjiang river in Chengdu, China. <i>Environmental Research</i> , 2023, 216, 114566.	3.7	2
1702	Whole genome sequencing and characteristics of extended-spectrum beta-lactamase producing <i>Escherichia coli</i> isolated from poultry farms in Banaskantha, India. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
1703	<i>Pseudomonas</i> sp., Strain L5B5: A Genomic and Transcriptomic Insight into an Airborne Mine Bacterium. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 10854.	1.3	0
1704	CARD 2023: expanded curation, support for machine learning, and resistome prediction at the Comprehensive Antibiotic Resistance Database. <i>Nucleic Acids Research</i> , 2023, 51, D690-D699.	6.5	213
1705	<i>Photorhabdus antumapuensis</i> sp. nov., a novel symbiotic bacterial species associated with <i>Heterorhabditis atacamensis</i> entomopathogenic nematodes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	2

#	ARTICLE	IF	CITATIONS
1706	Comparative Genomic Analysis of <i>Fusobacterium necrophorum</i> Provides Insights into Conserved Virulence Genes. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
1707	Phenotypic and genomic assessment of the potential threat of human spaceflight-relevant <i>Staphylococcus capitis</i> isolates under stress conditions. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1708	Bacterial Community and Antibiotic Resistance Gene Profiles of Fish Gut Contents and Their Aquaculture Environment in Tianjin, China. <i>Aquaculture Journal</i> , 2022, 2, 269-284.	0.7	2
1709	First report of a multidrug-resistant <i>Salmonella enterica</i> Serovar <i>Infantis</i> carrying pESI megaplasmid isolated from marine shrimp in India. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 31, 248-251.	0.9	1
1710	Whole-genome sequencing for food safety. , 2023, , 854-870.		0
1711	Emergence of sulphonamide resistance in azithromycin-resistant pediatric strains of <i>Salmonella</i> Typhi and Paratyphi A: A genomics insight. <i>Gene</i> , 2023, 851, 146995.	1.0	5
1712	<i>Zobellella iuensis</i> sp. nov., an aerobic denitrifying bacterium isolated from activated sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
1714	The novel oligopeptide utilizing species <i>Anaeropeptidivorans aminofermentans</i> M3/9T, its role in anaerobic digestion and occurrence as deduced from large-scale fragment recruitment analyses. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1715	Pan-genomic analysis of <i>Corynebacterium amycolatum</i> gives insights into molecular mechanisms underpinning the transition to a pathogenic phenotype. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
1716	The mechanism of phosphate solubilizing of <i>Pseudomonas</i> sp. TC952 and its solubilizing process on TC removal. <i>Environmental Science and Pollution Research</i> , 0, , .	2.7	1
1717	Complete Genomes of Three <i>Pseudomonas aeruginosa</i> Bacteriophages, Kara-mokiny 1, Kara-mokiny 2, and Kara-mokiny 3. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1718	Isolation, characterization, and genomic analysis of vB_PaeS_TUMS_P81, a lytic bacteriophage against <i>Pseudomonas aeruginosa</i> . <i>Virus Genes</i> , 2023, 59, 132-141.	0.7	3
1719	Mobile resistome of microbial communities and antimicrobial residues from drinking water supply systems in Rio de Janeiro, Brazil. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
1720	Are Enterobacteriaceae and Enterococcus Isolated from Powdered Infant Formula a Hazard for Infants? A Genomic Analysis. <i>Foods</i> , 2022, 11, 3556.	1.9	2
1721	Metagenomic insights into microorganisms and antibiotic resistance genes of waste antibiotic fermentation residues along production, storage and treatment processes. <i>Journal of Environmental Sciences</i> , 2024, 136, 45-55.	3.2	4
1722	Comparative virulence and antimicrobial resistance distribution of <i>Streptococcus suis</i> isolates obtained from the United States. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
1723	Next-Generation Sequencing Approaches to Predicting Antimicrobial Susceptibility Testing Results. <i>Clinics in Laboratory Medicine</i> , 2022, 42, 557-572.	0.7	5
1724	Dual Network Contrastive Learning for Predicting Microbe-Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 3469-3481.	1.9	0

#	ARTICLE	IF	CITATIONS
1725	Comparative genomic analysis of ovine and other host associated isolates of <i>Staphylococcus aureus</i> exhibit the important role of mobile genetic elements and virulence factors in host adaptation. <i>Gene</i> , 2023, 855, 147131.	1.0	1
1726	Profile and actual transmissibility of Carbapenem resistance genes: Intracellular and extracellular DNA in hospital wastewater. <i>Journal of Environmental Management</i> , 2023, 329, 117085.	3.8	3
1727	BacARscan: an <i>in silico</i> resource to discern diversity in antibiotic resistance genes. <i>Biology Methods and Protocols</i> , 2022, 7, .	1.0	0
1728	Effects of <i>Klebsiella pneumoniae</i> Bacteriophages on IRAK3 Knockdown/Knockout THP-1 Monocyte Cell Lines. <i>Viruses</i> , 2022, 14, 2582.	1.5	2
1729	Broad-Spectrum Salmonella Phages PSE-D1 and PST-H1 Controls Salmonella in Foods. <i>Viruses</i> , 2022, 14, 2647.	1.5	6
1730	Comparative Genomic Analysis of a Multidrug-Resistant <i>Staphylococcus hominis</i> ShoR14 Clinical Isolate from Terengganu, Malaysia, Led to the Discovery of Novel Mobile Genetic Elements. <i>Pathogens</i> , 2022, 11, 1406.	1.2	2
1732	Distribution Patterns of Antibiotic Resistance Genes and Their Bacterial Hosts in a Manure Lagoon of a Large-Scale Swine Finishing Facility. <i>Microorganisms</i> , 2022, 10, 2301.	1.6	5
1733	The pan-genome of the emerging multidrug-resistant pathogen <i>Corynebacterium striatum</i> . <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	4
1734	Integrative metagenomic and metabolomic analyses reveal the role of gut microbiota in antibody-mediated renal allograft rejection. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	5
1735	Whole-genome sequencing (WGS) analysis of <i>Brucella suis</i> biovar 2 isolated from domestic pigs in Egypt for epidemiological and genetic diversity tracing. <i>Veterinary Microbiology</i> , 2023, 277, 109637.	0.8	1
1736	<i>Staphylococcus aureus</i> Breast Implant Infection Isolates Display Recalcitrance To Antibiotic Pocket Irrigants. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
1737	Genomic analysis and biological characterization of a novel Schitoviridae phage infecting <i>Vibrio alginolyticus</i> . <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 749-768.	1.7	4
1738	Metagenomic-based surveillance systems for antibiotic resistance in non-clinical settings. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
1739	Complete Genomic Sequences of Two <i>Aeromonas hydrophila</i> Isolates Derived from Diseased Fish in South Korea. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
1740	Isolation, characterization, and genomic analysis of vB_PaeP_TUMS_P121, a new lytic bacteriophage infecting <i>Pseudomonas aeruginosa</i> . <i>Archives of Virology</i> , 2023, 168, .	0.9	1
1741	<i>Campylobacter majalis</i> sp. nov. and <i>Campylobacter suis</i> sp. nov., novel <i>Campylobacter</i> species isolated from porcine gastrointestinal mucosa. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
1742	MNNMDA: Predicting human microbe-disease association via a method to minimize matrix nuclear norm. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 1414-1423.	1.9	9
1743	Genomic diversity, pathogenicity and antimicrobial resistance of <i>Escherichia coli</i> isolated from poultry in the southern United States. <i>BMC Microbiology</i> , 2023, 23, .	1.3	4

#	ARTICLE	IF	CITATIONS
1744	Deciphering basic and key traits of antibiotic resistome in influent and effluent of hospital wastewater treatment systems. <i>Water Research</i> , 2023, 231, 119614.	5.3	23
1745	Resolving colistin resistance and heteroresistance in <i>Enterobacter</i> species. <i>Nature Communications</i> , 2023, 14, .	5.8	11
1746	Determination of Virulence-Associated Genes and Antimicrobial Resistance Profiles in <i>Brucella</i> Isolates Recovered from Humans and Animals in Iran Using NGS Technology. <i>Pathogens</i> , 2023, 12, 82.	1.2	6
1747	The DNA Phosphorothioation Restriction-Modification System Influences the Antimicrobial Resistance of Pathogenic Bacteria. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
1748	Clinical and genomic analysis of hypermucoviscous <i>Klebsiella pneumoniae</i> isolates: Identification of new hypermucoviscosity associated genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
1749	A symbiotic bacterium of Antarctic fish reveals environmental adaptability mechanisms and biosynthetic potential towards antibacterial and cytotoxic activities. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
1750	Multi-Omics Data Analysis for Inflammation Disease Research: Correlation Analysis, Causal Analysis and Network Analysis. <i>Translational Bioinformatics</i> , 2023, , 101-118.	0.0	0
1751	Whole-Genome and Plasmid Comparative Analysis of <i>Campylobacter jejuni</i> from Human Patients in Toyama, Japan, from 2015 to 2019. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
1752	Genomic characterization and assessment of pathogenic potential of <i>Legionella</i> spp. isolates from environmental monitoring. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
1753	Metagenomic sequencing combined with flow cytometry facilitated a novel microbial risk assessment framework for bacterial pathogens in municipal wastewater without cultivation. , 2023, 2, .		5
1754	Molecular surveillance of multidrug-resistant Gram-negative bacteria in Ukrainian patients, Germany, March to June 2022. <i>Eurosurveillance</i> , 2023, 28, .	3.9	11
1755	Whole Genome-Based Characterization of Multidrug Resistant <i>Enterobacter</i> and <i>Klebsiella aerogenes</i> Isolates from Lebanon. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	11
1756	Î²-LacFamPred: An online tool for prediction and classification of Î²-lactamase class, subclass, and family. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
1757	A Genome of Temperate <i>Enterococcus</i> Bacteriophage Placed in a Space of Pooled Viral Dark Matter Sequences. <i>Viruses</i> , 2023, 15, 216.	1.5	0
1758	<i>Terrisporobacter hibernicus</i> sp. nov., isolated from bovine faeces in Northern Ireland. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
1759	Environmental contamination with highly resistant microorganisms after relocating to a new hospital building with 100% single-occupancy rooms: A prospective observational before-and-after study with a three-year follow-up. <i>International Journal of Hygiene and Environmental Health</i> , 2023, 248, 114106.	2.1	4
1760	Antibiotic Susceptibility, Resistance Gene Determinants and Corresponding Genomic Regions in <i>Lactobacillus amylovorus</i> Isolates Derived from Wild Boars and Domestic Pigs. <i>Microorganisms</i> , 2023, 11, 103.	1.6	3
1761	Genomic diversification of the specialized parasite of the fungus-growing ant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4

#	ARTICLE	IF	CITATIONS
1762	Hybrid Genomic Analysis of Salmonella enterica Serovar Enteritidis SE3 Isolated from Polluted Soil in Brazil. Microorganisms, 2023, 11, 111.	1.6	2
1763	ARGs-OAP v3.0: Antibiotic-Resistance Gene Database Curation and Analysis Pipeline Optimization. Engineering, 2022, , .	3.2	12
1764	Genome Sequence Resource of <i>Fusarium proliferatum</i> f. sp. <i>malus domestica</i> MR5, the Causative Agent of Apple Replant Disease. Plant Disease, 0, , .	0.7	0
1765	Analysis of Whole-Genome Sequences of Pathogenic Gram-Positive and Gram-Negative Isolates from the Same Hospital Environment to Investigate Common Evolutionary Trends Associated with Horizontal Gene Exchange, Mutations and DNA Methylation Patterning. Microorganisms, 2023, 11, 323.	1.6	3
1766	Nanopore-based enrichment of antimicrobial resistance genes – a case-based study. GigaByte, 0, 2023, 1-15.	0.0	3
1767	Phenotypic and Genomic Characterization of Nine String-Positive Carbapenem-Resistant Acinetobacter baumannii Isolates from Israel. Microbiology Spectrum, 2023, 11, .	1.2	1
1768	Enrichment of drug resistance genes in human pathogenic bacteria showing antimicrobial resistance. , 2023, , 41-60.		0
1769	Rumen and Fecal Microbiota Characteristics of Qinchuan Cattle with Divergent Residual Feed Intake. Microorganisms, 2023, 11, 358.	1.6	1
1770	Identification of genes influencing the evolution of Escherichia coli ST372 in dogs and humans. Microbial Genomics, 2023, 9, .	1.0	1
1772	Phylogeography of Francisella tularensis subspecies holarctica and epidemiology of tularemia in Switzerland. Frontiers in Microbiology, 0, 14, .	1.5	2
1773	Extended chloramination significantly enriched intracellular antibiotic resistance genes in drinking water treatment plants. Water Research, 2023, 232, 119689.	5.3	7
1774	Genomic Characterization of Carbapenem-Resistant Acinetobacter baumannii (CRAB) in Mechanically Ventilated COVID-19 Patients and Impact of Infection Control Measures on Reducing CRAB Circulation during the Second Wave of the SARS-CoV-2 Pandemic in Milan, Italy. Microbiology Spectrum, 2023, 11, .	1.2	4
1775	Microplastics exhibit accumulation and horizontal transfer of antibiotic resistance genes. Journal of Environmental Management, 2023, 336, 117632.	3.8	10
1776	Coal-source acid mine drainage reduced the soil multidrug-dominated antibiotic resistome but increased the heavy metal(loid) resistome and energy production-related metabolism. Science of the Total Environment, 2023, 873, 162330.	3.9	1
1777	First reported detection of the mobile colistin resistance genes, mcr-8 and mcr-9, in the Irish environment. Science of the Total Environment, 2023, 876, 162649.	3.9	2
1778	Application of nematicide avermectin enriched antibiotic-resistant bacteria and antibiotic resistance genes in farmland soil. Environmental Research, 2023, 227, 115802.	3.7	5
1779	Lebanese fermented goat milk products: From tradition to meta-omics. Food Research International, 2023, 168, 112762.	2.9	4
1780	Genomic characterization of endemic diarrheagenic Escherichia coli and Escherichia albertii from infants with diarrhea in Vietnam. PLoS Neglected Tropical Diseases, 2023, 17, e0011259.	1.3	1

#	ARTICLE	IF	CITATIONS
1781	Metagenomic analysis characterizes resistomes of an acidic, multimetal(loid)-enriched coal source mine drainage treatment system. <i>Journal of Hazardous Materials</i> , 2023, 448, 130898.	6.5	2
1782	Airborne antibiotic resistome and human health risk in railway stations during COVID-19 pandemic. <i>Environment International</i> , 2023, 172, 107784.	4.8	3
1783	Bioinformatics toolbox for exploring target mutation-induced drug resistance. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	4
1785	Metagenomic Insights for Antimicrobial Resistance Surveillance in Soils with Different Land Uses in Brazil. <i>Antibiotics</i> , 2023, 12, 334.	1.5	0
1786	Effects of levodopa on gut bacterial antibiotic resistance in Parkinsonâ€™s disease rat. <i>Frontiers in Aging Neuroscience</i> , 0, 15, .	1.7	1
1788	Complete genome sequence data of two <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Gallinarum: A 9R vaccine strain and a virulent Brazilian field strain. <i>Data in Brief</i> , 2023, 47, 108959.	0.5	1
1789	HyperVR: a hybrid deep ensemble learning approach for simultaneously predicting virulence factors and antibiotic resistance genes. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	4
1790	A Highly Effective Bacteriophage-1252 to Control Multiple Serovars of <i>Salmonella enterica</i> . <i>Foods</i> , 2023, 12, 797.	1.9	0
1791	Genomic insights into antibiotic resistance and mobilome of lactic acid bacteria and bifidobacteria. <i>Life Science Alliance</i> , 2023, 6, e202201637.	1.3	2
1792	Comparative Genomics Identifies Novel Genetic Changes Associated with Oxacillin, Vancomycin and Daptomycin Susceptibility in ST100 Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Antibiotics</i> , 2023, 12, 372.	1.5	2
1793	Diverse Populations of <i>Staphylococcus pseudintermedius</i> Colonize the Skin of Healthy Dogs. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
1794	Comparison of the gut microbiome and resistome in captive African and Asian elephants on the same diet. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	1
1795	Genomic insights into <i>Cronobacter</i> spp. recovered from food and human clinical cases in Zhejiang province, China (2008â€“2021). <i>Journal of Applied Microbiology</i> , 2023, 134, .	1.4	1
1796	Genomic Islands Identified in Highly Resistant <i>Serratia</i> sp. HRI: A Pathway to Discover New Disinfectant Resistance Elements. <i>Microorganisms</i> , 2023, 11, 515.	1.6	1
1798	Whole-genome-based characterization of <i>Campylobacter jejuni</i> from human patients with gastroenteritis collected over an 18 year period reveals increasing prevalence of antimicrobial resistance. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
1799	Genetic-Phenotype Analysis of <i>Bifidobacterium bifidum</i> and Its Glycoside Hydrolase Gene Distribution at Different Age Groups. <i>Foods</i> , 2023, 12, 922.	1.9	2
1800	Pilot Study on the Action of <i>Thymus vulgaris</i> Essential Oil in Treating the Most Common Bacterial Contaminants and <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Derby in Poultry Litter. <i>Antibiotics</i> , 2023, 12, 436.	1.5	2
1801	Comparative Genomics of <i>Halobacterium salinarum</i> Strains Isolated from Salted Foods Reveals Protechnological Genes for Food Applications. <i>Microorganisms</i> , 2023, 11, 587.	1.6	1

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1802	In Vitro Activity of Ceftolozane-Tazobactam against <i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> and <i>Pseudomonas aeruginosa</i> Obtained from Blood Cultures from Sentinel Public Hospitals in South Africa. <i>Antibiotics</i> , 2023, 12, 453.	1.5	1
1803	Clonal Expansion of Multidrug-Resistant <i>Streptococcus dysgalactiae</i> Subspecies <i>equisimilis</i> Causing Bacteremia, Japan, 2005–2021. <i>Emerging Infectious Diseases</i> , 2023, 29, 528-539.	2.0	6
1804	Molecular characteristics and antibiotic resistance mechanisms of clindamycin-resistant <i>Streptococcus agalactiae</i> isolates in China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
1805	Recommendations for the use of metagenomics for routine monitoring of antibiotic resistance in wastewater and impacted aquatic environments. <i>Critical Reviews in Environmental Science and Technology</i> , 2023, 53, 1731-1756.	6.6	4
1806	Population-level impacts of antibiotic usage on the human gut microbiome. <i>Nature Communications</i> , 2023, 14, .	5.8	15
1807	Whole-Genome Sequencing-Based Resistome Analysis of Nosocomial Multidrug-Resistant Non-Fermenting Gram-Negative Pathogens from the Balkans. <i>Microorganisms</i> , 2023, 11, 651.	1.6	4
1808	Trophic level and proteobacteria abundance drive antibiotic resistance levels in fish from coastal New England. <i>Animal Microbiome</i> , 2023, 5, .	1.5	3
1809	Genetic Characterization of <i>Listeria</i> from Food of Non-Animal Origin Products and from Producing and Processing Companies in Bavaria, Germany. <i>Foods</i> , 2023, 12, 1120.	1.9	3
1810	Genome Analysis of <i>Pseudomonas aeruginosa</i> Strains from Chronically Infected Patients with High Levels of Persister Formation. <i>Pathogens</i> , 2023, 12, 426.	1.2	3
1811	Comparative genomic analysis of <i>Stenotrophomonas maltophilia</i> unravels their genetic variations and versatility trait. <i>Journal of Applied Genetics</i> , 2023, 64, 351-360.	1.0	1
1812	Genetic comparison of <i>Brucella</i> spp. and <i>Ochrobactrum</i> spp. erroneously included into the genus <i>Brucella</i> confirms separate genera. <i>German Journal of Veterinary Research</i> , 2023, 3, 31-37.	0.4	4
1813	Whole-genome Study of Carbapenem-resistant <i>Acinetobacter baumannii</i> Virulence and Resistance. <i>Iranian Journal of Medical Microbiology</i> , 2023, 17, 90-102.	0.1	0
1815	Genomic Characterization of <i>Staphylococcus aureus</i> in Wildlife. <i>Animals</i> , 2023, 13, 1064.	1.0	6
1816	Dissemination of carbapenemase-producing Enterobacterales in Ireland from 2012 to 2017: a retrospective genomic surveillance study. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
1817	Microbial diversity and antimicrobial resistance in faecal samples from acute medical patients assessed through metagenomic sequencing. <i>PLoS ONE</i> , 2023, 18, e0282584.	1.1	1
1818	Elucidating the genomic history of commercially used <i>Bacillus thuringiensis</i> subsp. <i>tenebrionis</i> strain NB176. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
1820	Complete Genome Sequence and Analysis of a ST573 Multidrug-Resistant Methicillin-Resistant <i>Staphylococcus aureus</i> SauR3 Clinical Isolate from Terengganu, Malaysia. <i>Pathogens</i> , 2023, 12, 502.	1.2	2
1821	Identification and Characterization of OXA-232-Producing Sequence Type 231 Multidrug Resistant <i>Klebsiella pneumoniae</i> Strains Causing Bloodstream Infections in China. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1

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1822	Classification for β -lactamases: historical perspectives. <i>Expert Review of Anti-Infective Therapy</i> , 2023, 21, 513-522.	2.0	4
1823	First report of coexistence of blaKPC-2-, blaNDM-1- and mcr-9-carrying plasmids in a clinical carbapenem-resistant <i>Enterobacter hormaechei</i> isolate. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
1824	The COVID-19 Pandemic Sparked Off a Large-Scale Outbreak of Carbapenem-Resistant <i>Acinetobacter baumannii</i> from the Endemic Strains at an Italian Hospital. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3
1825	Metabiotics Signature through Genome Sequencing and In Vitro Inhibitory Assessment of a Novel <i>Lactococcus lactis</i> Strain UTNCys6-1 Isolated from Amazonian Camu-Camu Fruits. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6127.	1.8	2
1826	Worldwide Dissemination of blaKPC Gene by Novel Mobilization Platforms in <i>Pseudomonas aeruginosa</i> : A Systematic Review. <i>Antibiotics</i> , 2023, 12, 658.	1.5	9
1827	Gram-negative bacteria and lipopolysaccharides as risk factors for the occurrence of diabetic foot. <i>Journal of Clinical Endocrinology and Metabolism</i> , 0, , .	1.8	0
1828	Genomic Characterization and Genetic Profiles of <i>Salmonella Gallinarum</i> Strains Isolated from Layers with Fowl Typhoid in Colombia. <i>Genes</i> , 2023, 14, 823.	1.0	1
1829	<i>Streptococcus canis</i> genomic epidemiology reveals the potential for zoonotic transfer. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
1830	Aerosol partitioning potential of bacteria presenting antimicrobial resistance from different stages of a small decentralized septic treatment system. <i>Aerosol Science and Technology</i> , 2023, 57, 517-531.	1.5	3
1832	First insights into antimicrobial resistance, toxigenic profiles, and genetic diversity in <i>Bacillus cereus</i> isolated from Chinese sausages. <i>LWT - Food Science and Technology</i> , 2023, 181, 114717.	2.5	2
1833	Molecular characterization and comparative genomic analysis of <i>Acinetobacter baumannii</i> isolated from the community and the hospital: an epidemiological study in Segamat, Malaysia. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
1834	Whole genome sequencing to study antimicrobial resistance and RTX virulence genes in equine <i>Actinobacillus</i> isolates. <i>Veterinary Research</i> , 2023, 54, .	1.1	2
1835	A methodology for the selection and characterization of riboflavin-overproducing <i>Weissella cibaria</i> strains after treatment with roseoflavin. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
1836	A survey on antimicrobial resistance genes of frequently used probiotic bacteria, 1901 to 2022. <i>Eurosurveillance</i> , 2023, 28, .	3.9	5
1837	<i>Brevundimonas brasiliensis</i> sp. nov.: a New Multidrug-Resistant Species Isolated from a Patient in Brazil. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
1838	Outbreak report of polymyxin-carbapenem-resistant <i>Klebsiella pneumoniae</i> causing untreatable infections evidenced by synergy tests and bacterial genomes. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
1839	Elucidating the role of two types of essential oils in regulating antibiotic resistance in soil. <i>Journal of Hazardous Materials</i> , 2023, 454, 131443.	6.5	1
1840	CARD*Shark: automated prioritization of literature curation for the Comprehensive Antibiotic Resistance Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2023, 2023, .	1.4	1

#	ARTICLE	IF	CITATIONS
1860	MAIRA: Protein-based Analysis of MinION Reads on a Laptop. <i>Methods in Molecular Biology</i> , 2023, , 223-234.	0.4	0
1924	Artificial intelligence for natural product drug discovery. <i>Nature Reviews Drug Discovery</i> , 2023, 22, 895-916.	21.5	16
1945	Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Livestock Diseases and Management</i> , 2023, , 215-230.	0.5	0
2001	Recent advances in combatting bacterial infections <i>via</i> well-designed metallacycles/metallacages. <i>Dalton Transactions</i> , 2024, 53, 3434-3444.	1.6	0
2009	BE-AI: A Beaconized Platform with Machine Learning Capabilities. <i>IFMBE Proceedings</i> , 2024, , 105-114.	0.2	0
2015	TGC-ARG: Predicting Antibiotic Resistance through Transformer-based Modeling and Contrastive Learning. , 2023, , .		0