

# Roary: rapid large-scale prokaryote pan genome analysis

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Draft Genome Sequence of Triclosan-Resistant Cystic Fibrosis Isolate <i>Achromobacter xylosoxidans</i> CF304. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
3	Microevolution of Monophasic <i>Salmonella</i> Typhimurium during Epidemic, United Kingdom, 2005–2010. <i>Emerging Infectious Diseases</i> , 2016, 22, 617-624.	2.0	158
4	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	1.0	470
5	The diversity of <i>Klebsiella pneumoniae</i> surface polysaccharides. <i>Microbial Genomics</i> , 2016, 2, e000073.	1.0	185
6	Molecular Characterization of <i>Salmonella</i> Serovars Anatum and Ealing Associated with Two Historical Outbreaks, Linked to Contaminated Powdered Infant Formula. <i>Frontiers in Microbiology</i> , 2016, 7, 1664.	1.5	2
7	Diversity of the Germination Apparatus in <i>Clostridium botulinum</i> Groups I, II, III, and IV. <i>Frontiers in Microbiology</i> , 2016, 7, 1702.	1.5	25
8	Glucose Metabolism via the Entner-Doudoroff Pathway in <i>Campylobacter</i> : A Rare Trait that Enhances Survival and Promotes Biofilm Formation in Some Isolates. <i>Frontiers in Microbiology</i> , 2016, 7, 1877.	1.5	30
9	The <i>Campylobacter jejuni</i> Oxidative Stress Regulator RrpB Is Associated with a Genomic Hypervariable Region and Altered Oxidative Stress Resistance. <i>Frontiers in Microbiology</i> , 2016, 07, 2117.	1.5	32
10	Two cases of serotypeable and non-serotypeable variants of <i>Streptococcus pneumoniae</i> detected simultaneously during invasive disease. <i>BMC Microbiology</i> , 2016, 16, 126.	1.3	2
11	Comparative Genomic and Phenotypic Characterization of Pathogenic and Non-Pathogenic Strains of <i>Xanthomonas arboricola</i> Reveals Insights into the Infection Process of Bacterial Spot Disease of Stone Fruits. <i>PLoS ONE</i> , 2016, 11, e0161977.	1.1	31
12	Genomic Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> in a Neonatal Intensive Care Unit. <i>PLoS ONE</i> , 2016, 11, e0164397.	1.1	25
13	Genomic analysis of <i>Salmonella enterica</i> serotype Paratyphi A during an outbreak in Cambodia, 2013–2015. <i>Microbial Genomics</i> , 2016, 2, e000092.	1.0	24
14	Genome analysis of <i>Campylobacter concisus</i> strains from patients with inflammatory bowel disease and gastroenteritis provides new insights into pathogenicity. <i>Scientific Reports</i> , 2016, 6, 38442.	1.6	31
15	A genome-wide association study identifies a horizontally transferred bacterial surface adhesin gene associated with antimicrobial resistant strains. <i>Scientific Reports</i> , 2016, 6, 37811.	1.6	19
16	Draft Genome Sequence of the Bacteriophage vB_Eco_slurp01. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
17	Genomic analysis of nontypeable pneumococci causing invasive pneumococcal disease in South Africa, 2003–2013. <i>BMC Genomics</i> , 2016, 17, 470.	1.2	15
18	Pneumococcal protein antigen serology varies with age and may predict antigenic profile of colonizing isolates. <i>Journal of Infectious Diseases</i> , 2017, 215, jiw628.	1.9	18
19	Rapid scoring of genes in microbial pan-genome-wide association studies with Scoary. <i>Genome Biology</i> , 2016, 17, 238.	3.8	472

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20	Comparison of 432 <i>Pseudomonas</i> strains through integration of genomic, functional, metabolic and expression data. <i>Scientific Reports</i> , 2016, 6, 38699.	1.6	53
21	Comparative genomics reveals <i>Lysinibacillus sphaericus</i> group comprises a novel species. <i>BMC Genomics</i> , 2016, 17, 709.	1.2	18
22	Advances in Understanding Bacterial Pathogenesis Gained from Whole-Genome Sequencing and Phylogenetics. <i>Cell Host and Microbe</i> , 2016, 19, 599-610.	5.1	60
23	CYP101J2, CYP101J3, and CYP101J4, 1,8-Cineole-Hydroxylating Cytochrome P450 Monooxygenases from <i>Sphingobium yanoikuyae</i> Strain B2. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6507-6517.	1.4	12
24	Transmission of <i>Staphylococcus aureus</i> from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5910-5917.	1.4	30
25	Genomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium from Wild Passerines in England and Wales. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6728-6735.	1.4	51
26	Recent independent emergence of multiple multidrug-resistant <i>Serratia marcescens</i> clones within the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1101-1109.	2.4	74
27	Recombination in <i>Streptococcus pneumoniae</i> Lineages Increase with Carriage Duration and Size of the Polysaccharide Capsule. <i>MBio</i> , 2016, 7, .	1.8	50
28	Persistence of a dominant bovine lineage of group <i>Streptococcus</i> reveals genomic signatures of host adaptation. <i>Environmental Microbiology</i> , 2016, 18, 4216-4229.	1.8	38
29	Multiple major disease-associated clones of <i>Legionella pneumophila</i> have emerged recently and independently. <i>Genome Research</i> , 2016, 26, 1555-1564.	2.4	72
30	Evaluation of an Optimal Epidemiological Typing Scheme for <i>Legionella pneumophila</i> with Whole-Genome Sequence Data Using Validation Guidelines. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2135-2148.	1.8	46
31	Distinct <i>Salmonella</i> Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , 2016, 48, 1211-1217.	9.4	191
32	Genomic and phenotypic characterization of the species <i>Acinetobacter venetianus</i> . <i>Scientific Reports</i> , 2016, 6, 21985.	1.6	23
33	Support vector machine applied to predict the zoonotic potential of <i>E. coli</i> O157 cattle isolates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11312-11317.	3.3	55
34	The novel 2016 WHO <i>Neisseria gonorrhoeae</i> reference strains for global quality assurance of laboratory investigations: phenotypic, genetic and reference genome characterization. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3096-3108.	1.3	246
35	The dissemination of multidrug-resistant <i>Enterobacter cloacae</i> throughout the UK and Ireland. <i>Nature Microbiology</i> , 2016, 1, 16173.	5.9	24
36	PGADB-builder: A web service tool for creating pan-genome allele database for molecular fine typing. <i>Scientific Reports</i> , 2016, 6, 36213.	1.6	62
37	BPGA- an ultra-fast pan-genome analysis pipeline. <i>Scientific Reports</i> , 2016, 6, 24373.	1.6	771

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38	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016, 1, 16027.	5.9	65
39	Genome-based characterization of hospital-adapted <i>Enterococcus faecalis</i> lineages. <i>Nature Microbiology</i> , 2016, 1, .	5.9	65
40	A decade of genomic history for healthcare-associated <i>Enterococcus faecium</i> in the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1388-1396.	2.4	96
41	Complete Genome Sequences of Two Marine <i>Vibrio cholerae</i> Strains Isolated from the South Coast of Sweden. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
42	Whole genome sequence analysis indicates recent diversification of mammal-associated <i>Campylobacter fetus</i> and implicates a genetic factor associated with H2S production. <i>BMC Genomics</i> , 2016, 17, 713.	1.2	18
43	Understanding pneumococcal serotype 1 biology through population genomic analysis. <i>BMC Infectious Diseases</i> , 2016, 16, 649.	1.3	22
44	Comparative Genomics of Carriage and Disease Isolates of <i>Streptococcus pneumoniae</i> Serotype 22F Reveals Lineage-Specific Divergence and Niche Adaptation. <i>Genome Biology and Evolution</i> , 2016, 8, 1243-1251.	1.1	8
45	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	9.0	328
46	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124
47	The complete genome sequence of <i>Cronobacter sakazakii</i> ATCC 29544T, a food-borne pathogen, isolated from a child's throat. <i>Cut Pathogens</i> , 2017, 9, 2.	1.6	12
48	Complete genome sequence of the heavy metal resistant bacterium <i>Agromyces aureus</i> AR33T and comparison with related Actinobacteria. <i>Standards in Genomic Sciences</i> , 2017, 12, 2.	1.5	15
49	Fallacy of the Unique Genome: Sequence Diversity within Single <i>Helicobacter pylori</i> Strains. <i>MBio</i> , 2017, 8, .	1.8	64
50	Evolution and Epidemiology of Multidrug-Resistant <i>Klebsiella pneumoniae</i> in the United Kingdom and Ireland. <i>MBio</i> , 2017, 8, .	1.8	97
51	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. <i>Genetics</i> , 2017, 206, 363-376.	1.2	65
52	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	2.4	540
53	Genomic Epidemiology of Penicillin-Nonsusceptible Pneumococci with Nonvaccine Serotypes Causing Invasive Disease in the United States. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1104-1115.	1.8	44
54	Whole genome sequences of three Clade 3 <i>Clostridium difficile</i> strains carrying binary toxin genes in China. <i>Scientific Reports</i> , 2017, 7, 43555.	1.6	21
55	Pneumococcal prophages are diverse, but not without structure or history. <i>Scientific Reports</i> , 2017, 7, 42976.	1.6	62

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56	Genomic landscape of extended-spectrum $\beta$ -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1602-1609.	1.3	46
57	Diversity and Function of Endophytic Microbial Community of Plants with Economical Potential. , 2017, , 209-243.		12
58	Complex Routes of Nosocomial Vancomycin-Resistant <i>Enterococcus faecium</i> Transmission Revealed by Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 64, 886-893.	2.9	93
59	Persistent <i>Listeria monocytogenes</i> strains isolated from mussel production facilities form more biofilm but are not linked to specific genetic markers. <i>International Journal of Food Microbiology</i> , 2017, 256, 45-53.	2.1	50
60	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
61	Diversity and Benefits of Microorganisms from the Tropics. , 2017, , .		14
62	<i>Neisseria</i> genomics: current status and future perspectives. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	23
63	Phenotypic diversity and genotypic flexibility of <i>Burkholderia cenocepacia</i> during long-term chronic infection of cystic fibrosis lungs. <i>Genome Research</i> , 2017, 27, 650-662.	2.4	64
64	Origin and Evolution of the Kiwifruit Canker Pandemic. <i>Genome Biology and Evolution</i> , 2017, 9, 932-944.	1.1	106
65	Genomic characterization of Nontuberculous Mycobacteria. <i>Scientific Reports</i> , 2017, 7, 45258.	1.6	176
66	Comparative genomics analysis of five <i>Psychrobacter</i> strains isolated from world-wide habitats reveal high intra-genus variations. <i>Extremophiles</i> , 2017, 21, 581-589.	0.9	9
67	Use of pan-genome analysis for the identification of lineage-specific genes of <i>Helicobacter pylori</i> . <i>FEMS Microbiology Letters</i> , 2017, 364, fnw296.	0.7	24
68	Benzalkonium tolerance genes and outcome in <i>Listeria monocytogenes</i> meningitis. <i>Clinical Microbiology and Infection</i> , 2017, 23, 265.e1-265.e7.	2.8	87
69	Outbreak of <i>Klebsiella pneumoniae</i> Carbapenemase-Producing <i>Citrobacter freundii</i> at a Tertiary Acute Care Facility in Miami, Florida. <i>Infection Control and Hospital Epidemiology</i> , 2017, 38, 320-326.	1.0	21
70	Protracted Regional Dissemination of GIM-1-Producing <i>Serratia marcescens</i> in Western Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	6
71	Metagenomic assessment of the interplay between the environment and the genetic diversification of <i>Acinetobacter</i> . <i>Environmental Microbiology</i> , 2017, 19, 5010-5024.	1.8	24
72	Geographically widespread honeybee gut symbiont subgroups show locally distinct antibiotic-resistant patterns. <i>Molecular Ecology</i> , 2017, 26, 6590-6607.	2.0	26
73	Conjugation-Mediated Horizontal Gene Transfer of <i>Clostridium perfringens</i> Plasmids in the Chicken Gastrointestinal Tract Results in the Formation of New Virulent Strains. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	28

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74	Complete Genome Sequence of Mycobacterium chimaera Strain CDC2015-22-71. Genome Announcements, 2017, 5, .	0.8	6
75	Large-scale comparative metagenomics of <i>Blastocystis</i> , a common member of the human gut microbiome. ISME Journal, 2017, 11, 2848-2863.	4.4	136
76	Molecular epidemiology of Epizootic haematopoietic necrosis virus (EHNV). Virology, 2017, 511, 320-329.	1.1	2
77	Large-Scale Phylogenomics of the <i>Lactobacillus casei</i> Group Highlights Taxonomic Inconsistencies and Reveals Novel Clade-Associated Features. MSystems, 2017, 2, .	1.7	79
78	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. Clinical Microbiology Reviews, 2017, 30, 1015-1063.	5.7	310
79	Genomic Characterization of Urethritis-Associated <i>Neisseria meningitidis</i> Shows that a Wide Range of <i>N. meningitidis</i> Strains Can Cause Urethritis. Journal of Clinical Microbiology, 2017, 55, 3374-3383.	1.8	24
80	Parallel Evolution of Group B <i>Streptococcus</i> Hypervirulent Clonal Complex 17 Unveils New Pathoadaptive Mutations. MSystems, 2017, 2, .	1.7	31
81	Alterations of <i>GMP</i> turnover proteins modulate semi-constitutive <i>rdar</i> biofilm formation in commensal and uropathogenic <i>Escherichia coli</i> . MicrobiologyOpen, 2017, 6, e00508.	1.2	25
82	Complete Genome Sequence of Mycobacterium chimaera SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. Genome Announcements, 2017, 5, .	0.8	3
83	Community outbreaks of group A <i>Streptococcus</i> revealed by genome sequencing. Scientific Reports, 2017, 7, 8554.	1.6	26
84	Systematic longitudinal survey of invasive <i>Escherichia coli</i> in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. Genome Research, 2017, 27, 1437-1449.	2.4	231
85	Multi-drug resistant <i>Klebsiella pneumoniae</i> strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations. Scientific Reports, 2017, 7, 3534.	1.6	22
86	Plasmids of Distinct IncK Lineages Show Compatible Phenotypes. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	28
87	A review of bioinformatics platforms for comparative genomics. Recent developments of the EDGAR 2.0 platform and its utility for taxonomic and phylogenetic studies. Journal of Biotechnology, 2017, 261, 2-9.	1.9	22
88	Recombination of Virulence Genes in Divergent <i>Acidovorax avenae</i> Strains That Infect a Common Host. Molecular Plant-Microbe Interactions, 2017, 30, 813-828.	1.4	15
89	Genomic epidemiology of global <i>Klebsiella pneumoniae</i> carbapenemase (KPC)-producing <i>Escherichia coli</i> . Scientific Reports, 2017, 7, 5917.	1.6	108
90	<i>Brucella</i> Genetic Variability in Wildlife Marine Mammals Populations Relates to Host Preference and Ocean Distribution. Genome Biology and Evolution, 2017, 9, 1901-1912.	1.1	26
91	Genomic characterization of an extensively-drug resistance <i>Salmonella enterica</i> serotype Indiana strain harboring bla <sub>NDM-1</sub> gene isolated from a chicken carcass in China. Microbiological Research, 2017, 204, 48-54.	2.5	23

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92	A Prospective Cohort Multicenter Study of Molecular Epidemiology and Phylogenomics of <i>Staphylococcus aureus</i> Bacteremia in Nine Latin American Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	95
93	Whole-Genome Sequencing of Human Clinical <i>Klebsiella pneumoniae</i> Isolates Reveals Misidentification and Misunderstandings of <i>Klebsiella pneumoniae</i> , <i>Klebsiella variicola</i> , and <i>Klebsiella quasipneumoniae</i> . <i>MSphere</i> , 2017, 2, .	1.3	139
94	The Divided Bacterial Genome: Structure, Function, and Evolution. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	2.9	190
95	Pathogenicity Locus, Core Genome, and Accessory Gene Contributions to <i>Clostridium difficile</i> Virulence. <i>MBio</i> , 2017, 8, .	1.8	51
96	Comparative genome analysis of the vineyard weed endophyte <i>Pseudomonas viridiflava</i> CDRTc14 showing selective herbicidal activity. <i>Scientific Reports</i> , 2017, 7, 17336.	1.6	24
97	Genomic Variation and Evolution of <i>Vibrio parahaemolyticus</i> ST36 over the Course of a Transcontinental Epidemic Expansion. <i>MBio</i> , 2017, 8, .	1.8	53
98	Constraints on lateral gene transfer in promoting fimbrial usher protein diversity and function. <i>Open Biology</i> , 2017, 7, 170144.	1.5	10
99	Identification of genetic variants of <i>Brucella</i> spp. through genome-wide association studies. <i>Infection, Genetics and Evolution</i> , 2017, 56, 92-98.	1.0	8
100	Whole genome sequencing of ESBL-producing <i>Escherichia coli</i> isolated from patients, farm waste and canals in Thailand. <i>Genome Medicine</i> , 2017, 9, 81.	3.6	73
101	Global phylogenetic analysis of <i>Escherichia coli</i> and plasmids carrying the <i>mcr-1</i> gene indicates bacterial diversity but plasmid restriction. <i>Scientific Reports</i> , 2017, 7, 15364.	1.6	230
102	Distinct <i>Campylobacter fetus</i> lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. <i>Nature Communications</i> , 2017, 8, 1367.	5.8	56
103	Genomic history of the seventh pandemic of cholera in Africa. <i>Science</i> , 2017, 358, 785-789.	6.0	255
104	Integrated view of <i>Vibrio cholerae</i> in the Americas. <i>Science</i> , 2017, 358, 789-793.	6.0	128
105	Evolution and comparative genomics of pAQU-like conjugative plasmids in <i>Vibrio</i> species. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2503-2506.	1.3	11
106	Parallel Evolution of Two Clades of an Atlantic-Endemic Pathogenic Lineage of <i>Vibrio parahaemolyticus</i> by Independent Acquisition of Related Pathogenicity Islands. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	27
107	Genomic Epidemiology of NDM-1-Encoding Plasmids in Latin American Clinical Isolates Reveals Insights into the Evolution of Multidrug Resistance. <i>Genome Biology and Evolution</i> , 2017, 9, 1725-1741.	1.1	48
108	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	3.5	168
109	Evolution of the <i>Staphylococcus argenteus</i> ST2250 Clone in Northeastern Thailand Is Linked with the Acquisition of Livestock-Associated Staphylococcal Genes. <i>MBio</i> , 2017, 8, .	1.8	44

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110	Emergence and spread of a new community-genotype methicillin-resistant <i>Staphylococcus aureus</i> clone in Colombia. <i>BMC Infectious Diseases</i> , 2017, 17, 108.	1.3	6
111	Comparative genomic analysis reveals genetic features related to the virulence of <i>Bacillus cereus</i> FORC_013. <i>Gut Pathogens</i> , 2017, 9, 29.	1.6	7
112	Detection, isolation and characterization of <i>Fusobacterium gastrois</i> sp. nov. colonizing the stomach of pigs. <i>Systematic and Applied Microbiology</i> , 2017, 40, 42-50.	1.2	40
113	Genomic analysis of 495 vancomycin-resistant <i>Enterococcus faecium</i> reveals broad dissemination of a <i>vanA</i> plasmid in more than 19 clones from Copenhagen, Denmark. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 40-47.	1.3	40
114	Population Structure and Local Adaptation of MAC Lung Disease Agent <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 2403-2417.	1.1	75
115	Computational Methods in Microbial Population Genomics. <i>Population Genomics</i> , 2017, , 3-29.	0.2	2
116	Population Structure of Multidrug-Resistant <i>Klebsiella oxytoca</i> within Hospitals across the United Kingdom and Ireland Identifies Sharing of Virulence and Resistance Genes with <i>K. pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 574-584.	1.1	35
117	Genome sequencing of 39 <i>Akkermansia muciniphila</i> isolates reveals its population structure, genomic and functional diversity, and global distribution in mammalian gut microbiotas. <i>BMC Genomics</i> , 2017, 18, 800.	1.2	111
118	Multiple Locus Variable-Number Tandem-Repeat and Single-Nucleotide Polymorphism-Based <i>Brucella</i> Typing Reveals Multiple Lineages in <i>Brucella melitensis</i> Currently Endemic in China. <i>Frontiers in Veterinary Science</i> , 2017, 4, 215.	0.9	14
119	Next-Generation Sequencing, Bioinformatics, and Infectious Diseases. , 2017, , 405-420.		0
120	Pan-genome Analyses of the Species <i>Salmonella enterica</i> , and Identification of Genomic Markers Predictive for Species, Subspecies, and Serovar. <i>Frontiers in Microbiology</i> , 2017, 8, 1345.	1.5	74
121	Determination of <i>Elizabethkingia</i> Diversity by MALDI-TOF Mass Spectrometry and Whole-Genome Sequencing. <i>Emerging Infectious Diseases</i> , 2017, 23, 320-323.	2.0	28
122	Molecular Characterization of <i>Corynebacterium diphtheriae</i> Outbreak Isolates, South Africa, March–June 2015. <i>Emerging Infectious Diseases</i> , 2017, 23, 1308-1315.	2.0	36
123	Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory. <i>Emerging Infectious Diseases</i> , 2017, 23, 1441-1445.	2.0	40
124	How to Name and Classify Your Phage: An Informal Guide. <i>Viruses</i> , 2017, 9, 70.	1.5	323
125	Complete Genome Sequence and Comparative Analysis of <i>Staphylococcus condimentii</i> DSM 11674, a Potential Starter Culture Isolated from Soy Sauce Mash. <i>Frontiers in Bioengineering and Biotechnology</i> , 2017, 5, 56.	2.0	1
126	Genome Dynamics of <i>Escherichia coli</i> during Antibiotic Treatment: Transfer, Loss, and Persistence of Genetic Elements In situ of the Infant Gut. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 126.	1.8	46
127	Genome Analysis of <i>Clostridium difficile</i> PCR Ribotype 014 Lineage in Australian Pigs and Humans Reveals a Diverse Genetic Repertoire and Signatures of Long-Range Interspecies Transmission. <i>Frontiers in Microbiology</i> , 2016, 7, 2138.	1.5	117



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129	The Promise of Whole Genome Pathogen Sequencing for the Molecular Epidemiology of Emerging Aquaculture Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 121.	1.5	80
130	Genetic Characterization of the Exceptionally High Heat Resistance of the Non-toxic Surrogate <i>Clostridium sporogenes</i> PA 3679. <i>Frontiers in Microbiology</i> , 2017, 8, 545.	1.5	17
131	Pan-Genomic Analysis Permits Differentiation of Virulent and Non-virulent Strains of <i>Xanthomonas arboricola</i> That Cohabit <i>Prunus</i> spp. and Elucidate Bacterial Virulence Factors. <i>Frontiers in Microbiology</i> , 2017, 8, 573.	1.5	38
132	Comparative Metagenomics of the Polymicrobial Black Band Disease of Corals. <i>Frontiers in Microbiology</i> , 2017, 8, 618.	1.5	27
133	Evolution of <i>Acinetobacter baumannii</i> In Vivo: International Clone II, More Resistance to Ceftazidime, Mutation in <i>ptk</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1256.	1.5	29
134	In-silico Taxonomic Classification of 373 Genomes Reveals Species Misidentification and New Genospecies within the Genus <i>Pseudomonas</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1296.	1.5	43
135	Whole Genome Sequencing of Danish <i>Staphylococcus argenteus</i> Reveals a Genetically Diverse Collection with Clear Separation from <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1512.	1.5	59
136	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
137	The Bacterial Species <i>Campylobacter jejuni</i> Induce Diverse Innate Immune Responses in Human and Avian Intestinal Epithelial Cells. <i>Frontiers in Microbiology</i> , 2017, 8, 1840.	1.5	17
138	Pathogenicity of Human ST23 <i>Streptococcus agalactiae</i> to Fish and Genomic Comparison of Pathogenic and Non-pathogenic Isolates. <i>Frontiers in Microbiology</i> , 2017, 8, 1933.	1.5	8
139	Comparative Genomics of Facultative Bacterial Symbionts Isolated from European <i>Orius</i> Species Reveals an Ancestral Symbiotic Association. <i>Frontiers in Microbiology</i> , 2017, 8, 1969.	1.5	11
140	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
141	Antibiotic Resistance-Susceptibility Profiles of <i>Streptococcus thermophilus</i> Isolated from Raw Milk and Genome Analysis of the Genetic Basis of Acquired Resistances. <i>Frontiers in Microbiology</i> , 2017, 8, 2608.	1.5	20
142	Bacteriophages are the major drivers of <i>Shigella flexneri</i> serotype 1c genome plasticity: a complete genome analysis. <i>BMC Genomics</i> , 2017, 18, 722.	1.2	10
143	Genomic confirmation of vancomycin-resistant <i>Enterococcus</i> transmission from deceased donor to liver transplant recipient. <i>PLoS ONE</i> , 2017, 12, e0170449.	1.1	16
144	Within-host whole genome analysis of an antibiotic resistant <i>Pseudomonas aeruginosa</i> strain sub-type in cystic fibrosis. <i>PLoS ONE</i> , 2017, 12, e0172179.	1.1	31
145	Genomic analyses of the ancestral Manila family of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2017, 12, e0175330.	1.1	8
146	Development of a real-time PCR for detection of <i>Staphylococcus pseudintermedius</i> using a novel automated comparison of whole-genome sequences. <i>PLoS ONE</i> , 2017, 12, e0183925.	1.1	20

#	ARTICLE	IF	CITATIONS
147	Pf16 and phiPMW: Expanding the realm of <i>Pseudomonas putida</i> bacteriophages. <i>PLoS ONE</i> , 2017, 12, e0184307.	1.1	7
148	Evidence for the evolutionary steps leading to <i>mecA</i> -mediated $\beta$ -lactam resistance in staphylococci. <i>PLoS Genetics</i> , 2017, 13, e1006674.	1.5	63
149	Minimal genetic change in <i>Vibrio cholerae</i> in Mozambique over time: Multilocus variable number tandem repeat analysis and whole genome sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005671.	1.3	31
150	Pan-genome and phylogeny of <i>Bacillus cereus sensu lato</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 176.	3.2	92
151	Within-host evolution of <i>Enterococcus faecium</i> during longitudinal carriage and transition to bloodstream infection in immunocompromised patients. <i>Genome Medicine</i> , 2017, 9, 119.	3.6	26
152	Genome analysis of <i>Clostridium perfringens</i> isolates from healthy and necrotic enteritis infected chickens and turkeys. <i>BMC Research Notes</i> , 2017, 10, 270.	0.6	21
153	<i>Mycoplasma genitalium</i> : whole genome sequence analysis, recombination and population structure. <i>BMC Genomics</i> , 2017, 18, 993.	1.2	35
154	Genomic insights into a sustained national outbreak of <i>Yersinia pseudotuberculosis</i> . <i>Genome Biology and Evolution</i> , 2016, 8, evw285.	1.1	31
155	Draft Genome Sequence of the 1,2-Dichloroethane-Utilizing <i>Micrococcus</i> sp. Strain NDB3Y10, Isolated from an Australian Bore Well Producing Coal Seam Gas. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
156	Phylogenetic Analysis of <i>Klebsiella pneumoniae</i> from Hospitalized Children, Pakistan. <i>Emerging Infectious Diseases</i> , 2017, 23, 1872-1875.	2.0	32
157	Adaptation in a Fibronectin Binding Autolysin of <i>Staphylococcus saprophyticus</i> . <i>MSphere</i> , 2017, 2, .	1.3	9
158	Genomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium DT160 Associated with a 14-Year Outbreak, New Zealand, 1998–2012. <i>Emerging Infectious Diseases</i> , 2017, 23, 906-913.	2.0	31
159	De novo assembly of genomes from long sequence reads reveals uncharted territories of <i>Propionibacterium freudenreichii</i> . <i>BMC Genomics</i> , 2017, 18, 790.	1.2	16
160	Metabolic phenotype of clinical and environmental <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> isolates. <i>PeerJ</i> , 2017, 5, e2833.	0.9	2
161	Evaluating the use of whole-genome sequencing for outbreak investigations in the lack of closely related reference genome. <i>Infection, Genetics and Evolution</i> , 2018, 59, 1-6.	1.0	7
162	Piggy: a rapid, large-scale pan-genome analysis tool for intergenic regions in bacteria. <i>GigaScience</i> , 2018, 7, 1-11.	3.3	59
163	First detection and genomics analysis of KPC-2-producing <i>Citrobacter</i> isolates from river sediments. <i>Environmental Pollution</i> , 2018, 235, 931-937.	3.7	42
164	Microbiological quality and antimicrobial resistance characterization of <i>Salmonella</i> spp. in fresh milk value chains in Ghana. <i>International Journal of Food Microbiology</i> , 2018, 277, 41-49.	2.1	32

#	ARTICLE	IF	CITATIONS
165	Novel sequencing technologies to support industrial biotechnology. FEMS Microbiology Letters, 2018, 365, .	0.7	15
166	High genetic diversity of extended-spectrum $\beta$ -lactamases producing <i>Escherichia coli</i> in feces of horses. Veterinary Microbiology, 2018, 219, 117-122.	0.8	14
167	Genomic analysis of oral <i>Campylobacter concisus</i> strains identified a potential bacterial molecular marker associated with active Crohn's disease. Emerging Microbes and Infections, 2018, 7, 1-14.	3.0	25
168	Horizontal antimicrobial resistance transfer drives epidemics of multiple <i>Shigella</i> species. Nature Communications, 2018, 9, 1462.	5.8	121
169	Homologous Recombination between Genetically Divergent <i>Campylobacter fetus</i> Lineages Supports Host-Associated Speciation. Genome Biology and Evolution, 2018, 10, 716-722.	1.1	16
170	Two Groups of Cocirculating, Epidemic <i>Clostridioides difficile</i> Strains Microdiversify through Different Mechanisms. Genome Biology and Evolution, 2018, 10, 982-998.	1.1	8
171	Origin, evolution, and distribution of the molecular machinery for biosynthesis of sialylated lipooligosaccharide structures in <i>Campylobacter coli</i> . Scientific Reports, 2018, 8, 3028.	1.6	13
172	Genome Sequencing Links Persistent Outbreak of Legionellosis in Sydney (New South Wales, Australia) to an Emerging Clone of <i>Legionella pneumophila</i> Sequence Type 211. Applied and Environmental Microbiology, 2018, 84, .	1.4	10
173	<i>In Situ</i> Analyses Directly in Diarrheal Stool Reveal Large Variations in Bacterial Load and Active Toxin Expression of Enterotoxigenic <i>Escherichia coli</i> and <i>Vibrio cholerae</i> . MSphere, 2018, 3, .	1.3	14
174	Comparative genome analysis reveals a complex population structure of <i>Legionella pneumophila</i> subspecies. Infection, Genetics and Evolution, 2018, 59, 172-185.	1.0	15
175	Pan-Genome Storage and Analysis Techniques. Methods in Molecular Biology, 2018, 1704, 29-53.	0.4	24
176	Comparative Genomics for Prokaryotes. Methods in Molecular Biology, 2018, 1704, 55-78.	0.4	15
177	A primer on microbial bioinformatics for nonbioinformaticians. Clinical Microbiology and Infection, 2018, 24, 342-349.	2.8	52
178	Genome-Based Analysis of <i>Enterococcus faecium</i> Bacteremia Associated with Recurrent and Mixed-Strain Infection. Journal of Clinical Microbiology, 2018, 56, .	1.8	14
179	Zoonotic Transfer of <i>Clostridium difficile</i> Harboring Antimicrobial Resistance between Farm Animals and Humans. Journal of Clinical Microbiology, 2018, 56, .	1.8	102
180	Phandango: an interactive viewer for bacterial population genomics. Bioinformatics, 2018, 34, 292-293.	1.8	468
181	Identification of a novel botulinum neurotoxin gene cluster in <i>Enterococcus</i> . FEBS Letters, 2018, 592, 310-317.	1.3	82
182	Transfer of a bla CTX-M-1-carrying plasmid between different <i>Escherichia coli</i> strains within the human gut explored by whole genome sequencing analyses. Scientific Reports, 2018, 8, 280.	1.6	28

#	ARTICLE	IF	CITATIONS
183	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	1.2	51
184	Comparative Genomics of Bacteriophage of the Genus <i>Seuratvirus</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 72-76.	1.1	41
185	Whole genome sequencing options for bacterial strain typing and epidemiologic analysis based on single nucleotide polymorphism versus gene-by-gene <sup>44</sup> based approaches. <i>Clinical Microbiology and Infection</i> , 2018, 24, 350-354.	2.8	373
186	ClustAGE: a tool for clustering and distribution analysis of bacterial accessory genomic elements. <i>BMC Bioinformatics</i> , 2018, 19, 150.	1.2	40
187	Exploring the arthritogenicity of <i>Streptococcus dysgalactiae</i> subspecies <i>equisimilis</i> . <i>BMC Microbiology</i> , 2018, 18, 17.	1.3	8
188	Invasive Methicillin-Resistant <i>Staphylococcus aureus</i> USA500 Strains from the U.S. Emerging Infections Program Constitute Three Geographically Distinct Lineages. <i>MSphere</i> , 2018, 3, .	1.3	46
189	Leptospiral Genomics and Pathogenesis. <i>Current Topics in Microbiology and Immunology</i> , 2018, 415, 189-214.	0.7	6
190	Single-cell metagenomics: challenges and applications. <i>Protein and Cell</i> , 2018, 9, 501-510.	4.8	70
191	Carbapenem-Resistant Hypervirulent <i>Klebsiella pneumoniae</i> of Sequence Type 36. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	66
192	Whole-Genome Sequencing of <i>Aggregatibacter</i> Species Isolated from Human Clinical Specimens and Description of <i>Aggregatibacter kilianii</i> sp. nov. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	25
193	Low genomic diversity of <i>Legionella pneumophila</i> within clinical specimens. <i>Clinical Microbiology and Infection</i> , 2018, 24, 1020.e1-1020.e4.	2.8	5
194	A Novel <i>Glaesserella</i> sp. Isolated from Pigs with Severe Respiratory Infections Has a Mosaic Genome with Virulence Factors Putatively Acquired by Horizontal Transfer. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
195	Landscape-Scale Factors Affecting the Prevalence of <i>Escherichia coli</i> in Surface Soil Include Land Cover Type, Edge Interactions, and Soil pH. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	25
196	panX: pan-genome analysis and exploration. <i>Nucleic Acids Research</i> , 2018, 46, e5-e5.	6.5	241
197	A fatal outbreak of ST11 carbapenem-resistant hypervirulent <i>Klebsiella pneumoniae</i> in a Chinese hospital: a molecular epidemiological study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 37-46.	4.6	683
198	Revisiting the taxonomy of the genus <i>Elizabethkingia</i> using whole-genome sequencing, optical mapping, and MALDI-TOF, along with proposal of three novel <i>Elizabethkingia</i> species: <i>Elizabethkingia bruuniana</i> sp. nov., <i>Elizabethkingia ursingii</i> sp. nov., and <i>Elizabethkingia occulta</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> . 2018. 111. 55-72.	0.7	91
199	Integration of Comparative Genomics with Genome-Scale Metabolic Modeling to Investigate Strain-Specific Phenotypical Differences. <i>Methods in Molecular Biology</i> , 2018, 1716, 151-175.	0.4	4
201	Invasive Disease Caused Simultaneously by Dual Serotypes of <i>Streptococcus pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	13

#	ARTICLE	IF	CITATIONS
202	INNUENDO: A cross-sectoral platform for the integration of genomics in the surveillance of food-borne pathogens. EFSA Supporting Publications, 2018, 15, 1498E.	0.3	56
203	Genomic epidemiology of methicillin-resistant <i>Staphylococcus aureus</i> ST22 widespread in communities of the Gaza Strip, 2009. <i>Eurosurveillance</i> , 2018, 23, .	3.9	25
204	Genomic Analysis of <i>Rhodococcus</i> sp. Br-6, a Bromate Reducing Bacterium Isolated From Soil in Chiba, Japan. <i>Journal of Genomics</i> , 2018, 6, 122-126.	0.6	0
205	Sputum &Moraxella catarrhalis strains exhibit diversity within and between COPD subjects. <i>International Journal of COPD</i> , 2018, Volume 13, 3663-3667.	0.9	4
206	<i>Bordetella pertussis</i> population dynamics and phylogeny in Japan after adoption of acellular pertussis vaccines. <i>Microbial Genomics</i> , 2018, 4, .	1.0	21
207	Genome Sequencing and Pan-Genome Analysis of 23 <i>Coralococcus</i> spp. Strains Reveal Unexpected Diversity, With Particular Plasticity of Predatory Gene Sets. <i>Frontiers in Microbiology</i> , 2018, 9, 3187.	1.5	68
208	Developing Inclusivity and Exclusivity Panels for Testing Diagnostic and Detection Tools Targeting <i>Burkholderia pseudomallei</i> , the Causative Agent of Melioidosis. <i>Journal of AOAC INTERNATIONAL</i> , 2018, 101, 1920-1926.	0.7	5
209	Patients with Chronic Obstructive Pulmonary Disease harbour a variation of <i>Haemophilus</i> species. <i>Scientific Reports</i> , 2018, 8, 14734.	1.6	14
210	Whole genome sequencing for investigations of meningococcal outbreaks in the United States: a retrospective analysis. <i>Scientific Reports</i> , 2018, 8, 15803.	1.6	20
211	Genetic analysis of invasive <i>Escherichia coli</i> in Scotland reveals determinants of healthcare-associated versus community-acquired infections. <i>Microbial Genomics</i> , 2018, 4, .	1.0	33
212	Genome analysis of clinical multilocus sequence Type 11 <i>Klebsiella pneumoniae</i> from China. <i>Microbial Genomics</i> , 2018, 4, .	1.0	52
213	Genome-wide identification of geographical segregated genetic markers in <i>Salmonella enterica</i> serovar Typhimurium variant 4,[5],12:-. <i>Scientific Reports</i> , 2018, 8, 15251.	1.6	30
214	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	2.1	74
215	Examination of Australian <i>Streptococcus suis</i> isolates from clinically affected pigs in a global context and the genomic characterisation of ST1 as a predictor of virulence. <i>Veterinary Microbiology</i> , 2018, 226, 31-40.	0.8	16
216	The Enterococcus Cassette Chromosome, a Genomic Variation Enabler in Enterococci. <i>MSphere</i> , 2018, 3, .	1.3	7
217	Genome-wide analysis of <i>Streptococcus pneumoniae</i> serogroup 19 in the decade after the introduction of pneumococcal conjugate vaccines in Australia. <i>Scientific Reports</i> , 2018, 8, 16969.	1.6	14
218	A fast and agnostic method for bacterial genome-wide association studies: Bridging the gap between k-mers and genetic events. <i>PLoS Genetics</i> , 2018, 14, e1007758.	1.5	144
219	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of <i>Staphylococcus aureus</i> strains in a paediatric hospital. <i>Genome Medicine</i> , 2018, 10, 82.	3.6	54

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220	Metagenomics-Based, Strain-Level Analysis of <i>Escherichia coli</i> From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018, 9, 2559.	1.5	37
221	Genomes of <i>Escherichia coli</i> bacteraemia isolates originating from urinary tract foci contain more virulence-associated genes than those from non-urinary foci and neutropaenic hosts. <i>Journal of Infection</i> , 2018, 77, 534-543.	1.7	9
222	Genome Sequences and Comparative Analysis of Two Extended-Spectrum Extensively-Drug Resistant <i>Mycobacterium tuberculosis</i> Strains. <i>Frontiers in Pharmacology</i> , 2018, 9, 1492.	1.6	2
223	<i>Enterococcus faecium</i> TIR-Domain Genes Are Part of a Gene Cluster Which Promotes Bacterial Survival in Blood. <i>International Journal of Microbiology</i> , 2018, 2018, 1-17.	0.9	7
224	Species Designations Belie Phenotypic and Genotypic Heterogeneity in Oral Streptococci. <i>MSystems</i> , 2018, 3, .	1.7	45
225	Effect of Vaccination on Pneumococci Isolated from the Nasopharynx of Healthy Children and the Middle Ear of Children with Otitis Media in Iceland. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	26
226	Complement Susceptibility in Relation to Genome Sequence of Recent <i>Klebsiella pneumoniae</i> Isolates from Thai Hospitals. <i>MSphere</i> , 2018, 3, .	1.3	25
227	Prediction of antibiotic resistance in <i>Escherichia coli</i> from large-scale pan-genome data. <i>PLoS Computational Biology</i> , 2018, 14, e1006258.	1.5	127
228	PanDelos: a dictionary-based method for pan-genome content discovery. <i>BMC Bioinformatics</i> , 2018, 19, 437.	1.2	13
229	Genomic traits of <i>Klebsiella oxytoca</i> DSM 29614, an uncommon metal-nanoparticle producer strain isolated from acid mine drainages. <i>BMC Microbiology</i> , 2018, 18, 198.	1.3	5
230	Genome-wide comparison of <i>Corynebacterium diphtheriae</i> isolates from Australia identifies differences in the Pan-genomes between respiratory and cutaneous strains. <i>BMC Genomics</i> , 2018, 19, 869.	1.2	23
231	Co-culture of a Novel Fermentative Bacterium, <i>Lucifera butyrca</i> gen. nov. sp. nov., With the Sulfur Reducer <i>Desulfurella amilii</i> for Enhanced Sulfidogenesis. <i>Frontiers in Microbiology</i> , 2018, 9, 3108.	1.5	22
232	Unveiling the Multilocus Sequence Typing (MLST) Schemes and Core Genome Phylogenies for Genotyping <i>Chlamydia trachomatis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1854.	1.5	23
233	Revisiting the Taxonomy of the Genus <i>Arcobacter</i> : Getting Order From the Chaos. <i>Frontiers in Microbiology</i> , 2018, 9, 2077.	1.5	245
234	Comparative genomics of phenotypic antimicrobial resistances in methicillin-resistant <i>Staphylococcus pseudintermedius</i> of canine origin. <i>Veterinary Microbiology</i> , 2018, 225, 125-131.	0.8	32
235	Five novel carbapenem-hydrolysing OXA-type $\beta$ -lactamase groups are intrinsic in <i>Acinetobacter</i> spp.. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3279-3284.	1.3	6
236	Genome hypermobility by lateral transduction. <i>Science</i> , 2018, 362, 207-212.	6.0	187
237	Genomic heterogeneity differentiates clinical and environmental subgroups of <i>Legionella pneumophila</i> sequence type 1. <i>PLoS ONE</i> , 2018, 13, e0206110.	1.1	9

#	ARTICLE	IF	CITATIONS
238	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
239	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.	0.9	42
240	Genetic Signatures of Dairy <i>Lactobacillus casei</i> Group. <i>Frontiers in Microbiology</i> , 2018, 9, 2611.	1.5	20
241	Conversion of Methionine to Cysteine in <i>Lactobacillus paracasei</i> Depends on the Highly Mobile <i>cysK-ctl-cysE</i> Gene Cluster. <i>Frontiers in Microbiology</i> , 2018, 9, 2415.	1.5	10
242	Capsular Switching and ICE Transformation Occurred in Human <i>Streptococcus agalactiae</i> ST19 With High Pathogenicity to Fish. <i>Frontiers in Veterinary Science</i> , 2018, 5, 281.	0.9	3
243	An investigation into the Omp85 protein BamK in hypervirulent <i>Klebsiella pneumoniae</i> , and its role in outer membrane biogenesis. <i>Molecular Microbiology</i> , 2018, 109, 584-599.	1.2	5
244	<i>Staphylococcus aureus</i> from patients with chronic rhinosinusitis show minimal genetic association between polyp and non-polyp phenotypes. <i>BMC Ear, Nose and Throat Disorders</i> , 2018, 18, 16.	2.6	8
245	Comparative Genomics and in vitro Infection of Field Clonal Isolates of <i>Brucella melitensis</i> Biovar 3 Did Not Identify Signature of Host Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 2505.	1.5	6
246	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
247	High genomic variability in the plant pathogenic bacterium <i>Pectobacterium parmentieri</i> deciphered from de novo assembled complete genomes. <i>BMC Genomics</i> , 2018, 19, 751.	1.2	28
248	First whole genome sequencing of Russian isolate of <i>Capnocytophaga canimorsus</i> , opportunistic pathogen causing lethal sepsis. <i>Microbial Pathogenesis</i> , 2018, 125, 493-496.	1.3	0
249	Antagonistic Pleiotropy in the Bifunctional Surface Protein FadL (OmpP1) during Adaptation of <i>Haemophilus influenzae</i> to Chronic Lung Infection Associated with Chronic Obstructive Pulmonary Disease. <i>MBio</i> , 2018, 9, .	1.8	39
250	Whole genome sequencing reveals the emergence of a <i>Pseudomonas aeruginosa</i> shared strain sub-lineage among patients treated within a single cystic fibrosis centre. <i>BMC Genomics</i> , 2018, 19, 644.	1.2	16
251	Creation and Characterization of a Genomically Hybrid Strain in the Nitrogen-Fixing Symbiotic Bacterium <i>Sinorhizobium meliloti</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 2365-2378.	1.9	24
252	A New Freshwater Cyanosiphovirus Harboring Integrase. <i>Frontiers in Microbiology</i> , 2018, 9, 2204.	1.5	26
253	Conserved collateral antibiotic susceptibility networks in diverse clinical strains of <i>Escherichia coli</i> . <i>Nature Communications</i> , 2018, 9, 3673.	5.8	76
254	Role of plasmid plasticity and mobile genetic elements in the entomopathogen <i>Bacillus thuringiensis</i> serovar israelensis. <i>FEMS Microbiology Reviews</i> , 2018, 42, 829-856.	3.9	33
255	Emergence of soil bacterial ecotypes along a climate gradient. <i>Environmental Microbiology</i> , 2018, 20, 4112-4126.	1.8	32

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256	Comparative Secretome Analyses of Human and Zoonotic <i>Staphylococcus aureus</i> Isolates CC8, CC22, and CC398. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2412-2433.	2.5	29
257	PGAweb: A Web Server for Bacterial Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 1910.	1.5	24
258	Genome Sequencing Reveals a Large and Diverse Repertoire of Antimicrobial Peptides. <i>Frontiers in Microbiology</i> , 2018, 9, 2012.	1.5	34
259	Genomic Characterization of Sulphite Reducing Bacteria Isolated From the Dairy Production Chain. <i>Frontiers in Microbiology</i> , 2018, 9, 1507.	1.5	9
260	Characterizing Mobilized Virulence Factors and Multidrug Resistance Genes in Carbapenemase-Producing <i>Klebsiella pneumoniae</i> in a Sri Lankan Hospital. <i>Frontiers in Microbiology</i> , 2018, 9, 2044.	1.5	13
261	High-resolution in situ transcriptomics of <i>Pseudomonas aeruginosa</i> unveils genotype independent patho-phenotypes in cystic fibrosis lungs. <i>Nature Communications</i> , 2018, 9, 3459.	5.8	88
262	Conserved Genome Organization and Core Transcriptome of the <i>Lactobacillus acidophilus</i> Complex. <i>Frontiers in Microbiology</i> , 2018, 9, 1834.	1.5	7
263	Whole-Genome Sequencing and Bioinformatic Analysis of Isolates from Foodborne Illness Outbreaks of <i>Campylobacter jejuni</i> and <i>Salmonella enterica</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	29
264	Genomic analyses reveal two distinct lineages of <i>Corynebacterium ulcerans</i> strains. <i>New Microbes and New Infections</i> , 2018, 25, 7-13.	0.8	17
265	Towards a congruent reclassification and nomenclature of the thermophilic species of the genus <i>Pseudothermotoga</i> within the order Thermotogales. <i>Systematic and Applied Microbiology</i> , 2018, 41, 555-563.	1.2	24
266	Genome Variation and Molecular Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium Pathovariants. <i>Infection and Immunity</i> , 2018, 86, .	1.0	93
267	Complete Closed Genome Sequence of Nontoxigenic Invasive <i>Corynebacterium diphtheriae</i> bv. mitis Strain ISS 3319. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
268	Draft Genome Sequence of a Potentially Novel <i>Streptococcus</i> Species Belonging to the <i>Streptococcus mitis</i> Group. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
269	The impact of serotype-specific vaccination on phylodynamic parameters of <i>Streptococcus pneumoniae</i> and the pneumococcal pan-genome. <i>PLoS Pathogens</i> , 2018, 14, e1006966.	2.1	25
270	Comparative genomics of <i>Campylobacter concisus</i> : Analysis of clinical strains reveals genome diversity and pathogenic potential. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-17.	3.0	25
271	A pan-genome-based machine learning approach for predicting antimicrobial resistance activities of the <i>Escherichia coli</i> strains. <i>Bioinformatics</i> , 2018, 34, i89-i95.	1.8	72
272	Pan4Draft: A Computational Tool to Improve the Accuracy of Pan-Genomic Analysis Using Draft Genomes. <i>Scientific Reports</i> , 2018, 8, 9670.	1.6	14
273	Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2018, 14, e1007333.	1.5	73



#	ARTICLE	IF	CITATIONS
274	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006566.	1.3	50
275	Macroevolution of gastric <i>Helicobacter</i> species unveils interspecies admixture and time of divergence. <i>ISME Journal</i> , 2018, 12, 2518-2531.	4.4	35
276	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. <i>Nature Genetics</i> , 2018, 50, 951-955.	9.4	37
277	Genomic analysis of a <i>Raoultella ornithinolytica</i> strain causing prosthetic joint infection in an immunocompetent patient. <i>Scientific Reports</i> , 2018, 8, 9462.	1.6	10
278	Epidemiology and natural history of <i>Pseudomonas aeruginosa</i> airway infections in non-cystic fibrosis bronchiectasis. <i>ERJ Open Research</i> , 2018, 4, 00162-2017.	1.1	14
279	Investigation of recombination-intense viral groups and their genes in the Earth's virome. <i>Scientific Reports</i> , 2018, 8, 11496.	1.6	14
280	PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. <i>BMC Bioinformatics</i> , 2018, 19, 246.	1.2	9
281	Detection of <i>Legionella anisa</i> in Water from Hospital Dental Chair Units and Molecular Characterization by Whole-Genome Sequencing. <i>Microorganisms</i> , 2018, 6, 71.	1.6	16
282	Whole genome sequencing and phylogenetic analysis of strains of the agent of Lyme disease <i>Borrelia burgdorferi</i> from Canadian emergence zones. <i>Scientific Reports</i> , 2018, 8, 10552.	1.6	34
283	<i>Superficieibacter electus</i> gen. nov., sp. nov., an Extended-Spectrum $\beta$ -Lactamase Possessing Member of the Enterobacteriaceae Family, Isolated From Intensive Care Unit Surfaces. <i>Frontiers in Microbiology</i> , 2018, 9, 1629.	1.5	14
284	Construction and Characterization of Synthetic Bacterial Community for Experimental Ecology and Evolution. <i>Frontiers in Genetics</i> , 2018, 9, 312.	1.1	28
285	Global Scale Dissemination of ST93: A Divergent <i>Staphylococcus aureus</i> Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. <i>Frontiers in Microbiology</i> , 2018, 9, 1453.	1.5	29
286	A GWAS on <i>Helicobacter pylori</i> strains points to genetic variants associated with gastric cancer risk. <i>BMC Biology</i> , 2018, 16, 84.	1.7	55
287	Genetic Separation of <i>Listeria monocytogenes</i> Causing Central Nervous System Infections in Animals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 20.	1.8	22
288	Population Genomics of <i>Francisella tularensis</i> subsp. <i>holarctica</i> and its Implication on the Eco-Epidemiology of Tularemia in Switzerland. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 89.	1.8	34
289	The Novel Phages phiCD5763 and phiCD2955 Represent Two Groups of Big Plasmidial Siphoviridae Phages of <i>Clostridium difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 26.	1.5	18
290	Comparative Genomics of Completely Sequenced <i>Lactobacillus helveticus</i> Genomes Provides Insights into Strain-Specific Genes and Resolves Metagenomics Data Down to the Strain Level. <i>Frontiers in Microbiology</i> , 2018, 9, 63.	1.5	73
291	<i>Pantoea ananatis</i> Genetic Diversity Analysis Reveals Limited Genomic Diversity as Well as Accessory Genes Correlated with Onion Pathogenicity. <i>Frontiers in Microbiology</i> , 2018, 9, 184.	1.5	48

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292	Genome Sequencing of Extended-Spectrum $\hat{I}^2$ -Lactamase (ESBL)-Producing <i>Klebsiella pneumoniae</i> Isolated from Pigs and Abattoir Workers in Cameroon. <i>Frontiers in Microbiology</i> , 2018, 9, 188.	1.5	38
293	Characterization of Asymptomatic Bacteriuria <i>Escherichia coli</i> Isolates in Search of Alternative Strains for Efficient Bacterial Interference against Uropathogens. <i>Frontiers in Microbiology</i> , 2018, 9, 214.	1.5	24
294	A Comparative Genomic Analysis Provides Novel Insights Into the Ecological Success of the Monophasic <i>Salmonella</i> Serovar 4,[5],12:i:-. <i>Frontiers in Microbiology</i> , 2018, 9, 715.	1.5	65
295	Genome-Wide Comparative Functional Analyses Reveal Adaptations of <i>Salmonella</i> sv. Newport to a Plant Colonization Lifestyle. <i>Frontiers in Microbiology</i> , 2018, 9, 877.	1.5	22
296	Comparative Genomics of the Herbivore Gut Symbiont <i>Lactobacillus reuteri</i> Reveals Genetic Diversity and Lifestyle Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 1151.	1.5	49
297	Identification of a New Antimicrobial Resistance Gene Provides Fresh Insights Into Pleuromutilin Resistance in <i>Brachyspira hyodysenteriae</i> , Aetiological Agent of Swine Dysentery. <i>Frontiers in Microbiology</i> , 2018, 9, 1183.	1.5	28
298	Identification of Novel Biomarkers for Priority Serotypes of Shiga Toxin-Producing <i>Escherichia coli</i> and the Development of Multiplex PCR for Their Detection. <i>Frontiers in Microbiology</i> , 2018, 9, 1321.	1.5	7
299	The evolution of ecological facilitation within mixed-species biofilms in the mouse gastrointestinal tract. <i>ISME Journal</i> , 2018, 12, 2770-2784.	4.4	34
300	Evolution of tigecycline- and colistin-resistant CRKP (carbapenem-resistant <i>Klebsiella</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 Td (p 1-11.	3.0	47
301	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , 2018, 9, 2703.	5.8	205
302	Genetic and Phylogenetic Characteristics of <i>Pasteurella multocida</i> Isolates From Different Host Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1408.	1.5	53
303	Whole Genome Sequence and Comparative Genomics Analysis of Multi-drug Resistant Environmental <i>Staphylococcus epidermidis</i> ST59. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2225-2230.	0.8	21
304	Profiling microbial strains in urban environments using metagenomic sequencing data. <i>Biology Direct</i> , 2018, 13, 9.	1.9	29
305	Global Distribution of Invasive Serotype 35D <i>Streptococcus pneumoniae</i> Isolates following Introduction of 13-Valent Pneumococcal Conjugate Vaccine. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	12
306	The orphan germinant receptor protein GerXAO (but not GerX3b) is essential for L-alanine induced germination in <i>Clostridium botulinum</i> Group II. <i>Scientific Reports</i> , 2018, 8, 7060.	1.6	6
307	Genomic survey of <i>Clostridium difficile</i> reservoirs in the East of England implicates environmental contamination of wastewater treatment plants by clinical lineages. <i>Microbial Genomics</i> , 2018, 4, .	1.0	19
308	Microevolution of epidemiological highly relevant non-O157 enterohemorrhagic <i>Escherichia coli</i> of serogroups O26 and O111. <i>International Journal of Medical Microbiology</i> , 2018, 308, 1085-1095.	1.5	7
309	Phylogenomics of colistin-susceptible and resistant XDR <i>Acinetobacter baumannii</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2952-2959.	1.3	41

#	ARTICLE	IF	CITATIONS
310	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
311	Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent <i>Staphylococcus aureus</i> bacteraemia. <i>Genome Medicine</i> , 2018, 10, 65.	3.6	49
312	Genomic characterization of NDM-1 and 5, and OXA-181 carbapenemases in uropathogenic <i>Escherichia coli</i> isolates from Riyadh, Saudi Arabia. <i>PLoS ONE</i> , 2018, 13, e0201613.	1.1	34
313	Evolution of Sequence Type 4821 Clonal Complex Meningococcal Strains in China from Prequinolone to Quinolone Era, 1972–2013. <i>Emerging Infectious Diseases</i> , 2018, 24, 683-690.	2.0	11
314	Whole genome sequencing of the monomorphic pathogen <i>Mycobacterium bovis</i> reveals local differentiation of cattle clinical isolates. <i>BMC Genomics</i> , 2018, 19, 2.	1.2	36
315	SLING: a tool to search for linked genes in bacterial datasets. <i>Nucleic Acids Research</i> , 2018, 46, e128.	6.5	18
316	Real-Time Analysis and Visualization of Pathogen Sequence Data. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	25
317	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium <i>Ensifer</i> sp. M14. <i>Genes</i> , 2018, 9, 379.	1.0	25
319	Microevolution of <i>Streptococcus agalactiae</i> ST-261 from Australia Indicates Dissemination via Imported Tilapia and Ongoing Adaptation to Marine Hosts or Environment. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	33
320	Complete genomic characterization of two <i>Escherichia coli</i> lineages responsible for a cluster of carbapenem-resistant infections in a Chinese hospital. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2340-2346.	1.3	44
321	<i>Ca. Endozoicomonas cretensis</i> : A Novel Fish Pathogen Characterized by Genome Plasticity. <i>Genome Biology and Evolution</i> , 2018, 10, 1363-1374.	1.1	10
322	Applications of genomics to slow the spread of multidrug-resistant <i>Neisseria gonorrhoeae</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 93-109.	1.8	31
323	Evaluation of Rapid Library Preparation Protocols for Whole Genome Sequencing Based Outbreak Investigation. <i>Frontiers in Public Health</i> , 2019, 7, 241.	1.3	32
324	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
325	Integrated genomic epidemiology and phenotypic profiling of <i>Clostridium difficile</i> across intra-hospital and community populations in Colombia. <i>Scientific Reports</i> , 2019, 9, 11293.	1.6	12
326	Rapid phenotypic evolution in multidrug-resistant <i>Klebsiella pneumoniae</i> hospital outbreak strains. <i>Microbial Genomics</i> , 2019, 5, .	1.0	25
327	Comparative genomic and functional analysis of <i>Akkermansia muciniphila</i> and closely related species. <i>Genes and Genomics</i> , 2019, 41, 1253-1264.	0.5	33
328	cano-wgMLST_BacCompare: A Bacterial Genome Analysis Platform for Epidemiological Investigation and Comparative Genomic Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 1687.	1.5	22

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329	Adaptation of host transmission cycle during <i>Clostridium difficile</i> speciation. <i>Nature Genetics</i> , 2019, 51, 1315-1320.	9.4	41
330	Isolates from Colonic Spirochetosis in Humans Show High Genomic Divergence and Potential Pathogenic Features but Are Not Detected Using Standard Primers for the Human Microbiota. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	12
331	Novel Probiotic Mechanisms of the Oral Bacterium <i>Streptococcus</i> sp. A12 as Explored with Functional Genomics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
332	Population Gene Introgression and High Genome Plasticity for the Zoonotic Pathogen <i>Streptococcus agalactiae</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 2572-2590.	3.5	36
333	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
334	The impact of antimicrobials on gonococcal evolution. <i>Nature Microbiology</i> , 2019, 4, 1941-1950.	5.9	91
335	Passive Filtration, Rapid Scanning Electron Microscopy, and Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry for <i>Treponema</i> Culture and Identification from the Oral Cavity. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	14
336	Emerging challenges of whole-genome-sequencing–powered epidemiological surveillance of globally distributed clonal groups of bacterial infections, giving <i>Acinetobacter baumannii</i> ST195 as an example. <i>International Journal of Medical Microbiology</i> , 2019, 309, 151339.	1.5	14
337	The diversity, evolution and ecology of <i>Salmonella</i> in venomous snakes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007169.	1.3	16
338	Genomic analysis unveils important aspects of population structure, virulence, and antimicrobial resistance in <i>Klebsiella aerogenes</i> . <i>FEBS Journal</i> , 2019, 286, 3797-3810.	2.2	27
339	<i>Xanthomonas citri</i> subsp. <i>citri</i> and <i>Xanthomonas arboricola</i> pv. <i>pruni</i> : Comparative analysis of two pathogens producing similar symptoms in different host plants. <i>PLoS ONE</i> , 2019, 14, e0219797.	1.1	7
340	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing <i>Enterobacterales</i> in Victoria, Australia, 2012 to 2016. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	56
341	Genetic diversity, virulence factors and farm-to-table spread pattern of <i>Vibrio parahaemolyticus</i> food-associated isolates. <i>Food Microbiology</i> , 2019, 84, 103270.	2.1	38
342	Pangloss: A Tool for Pan-Genome Analysis of Microbial Eukaryotes. <i>Genes</i> , 2019, 10, 521.	1.0	14
343	Genomic Comparison of <i>Lactobacillus helveticus</i> Strains Highlights Probiotic Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1380.	1.5	50
344	Comparative genomics identifies potential virulence factors in <i>Clostridium tertium</i> and <i>C. paraputrificum</i> . <i>Virulence</i> , 2019, 10, 657-676.	1.8	13
345	Global-level population genomics reveals differential effects of geography and phylogeny on horizontal gene transfer in soil bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15200-15209.	3.3	85
346	Extensively Drug-Resistant <i>Pseudomonas aeruginosa</i> ST309 Harboring Tandem Guiana Extended Spectrum $\beta$ -Lactamase Enzymes: A Newly Emerging Threat in the United States. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz273.	0.4	36

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347	Genomic Features of <i>Vibrio parahaemolyticus</i> from Lebanon and Comparison to Globally Diverse Strains by Whole-Genome Sequencing. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 778-787.	0.8	7
348	Genomic and Seasonal Variations among Aquatic Phages Infecting the Baltic Sea Gammaproteobacterium <i>Rheinheimeria</i> sp. Strain BAL341. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
349	An Outbreak of KPC-Producing <i>Klebsiella pneumoniae</i> Linked with an Index Case of Community-Acquired KPC-Producing Isolate: Epidemiological Investigation and Whole Genome Sequencing Analysis. <i>Microbial Drug Resistance</i> , 2019, 25, 1475-1483.	0.9	7
350	Genotypic and Phenotypic Characterization of Antimicrobial Resistance in <i>Neisseria gonorrhoeae</i> : a Cross-Sectional Study of Isolates Recovered from Routine Urine Cultures in a High-Incidence Setting. <i>MSphere</i> , 2019, 4, .	1.3	8
351	Comparative Genomics of Marine Sponge-Derived <i>Streptomyces</i> spp. Isolates SM17 and SM18 With Their Closest Terrestrial Relatives Provides Novel Insights Into Environmental Niche Adaptations and Secondary Metabolite Biosynthesis Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1713.	1.5	25
352	Identification of a Novel Plasmid Lineage Associated With the Dissemination of Metallo- $\beta$ -Lactamase Genes Among <i>Pseudomonads</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1504.	1.5	10
353	Epidemic of carbapenem-resistant <i>Klebsiella pneumoniae</i> in Europe is driven by nosocomial spread. <i>Nature Microbiology</i> , 2019, 4, 1919-1929.	5.9	476
354	Coherence of <i>Microcystis</i> species revealed through population genomics. <i>ISME Journal</i> , 2019, 13, 2887-2900.	4.4	51
355	Genetically diverse <i>Pseudomonas aeruginosa</i> populations display similar transcriptomic profiles in a cystic fibrosis explanted lung. <i>Nature Communications</i> , 2019, 10, 3397.	5.8	68
356	Genomic Features of High-Priority <i>Salmonella enterica</i> Serovars Circulating in the Food Production Chain, Brazil, 2000–2016. <i>Scientific Reports</i> , 2019, 9, 11058.	1.6	61
357	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	6.5	36
358	Genomewide Assessment of <i>Mycobacterium tuberculosis</i> Conditionally Essential Metabolic Pathways. <i>MSystems</i> , 2019, 4, .	1.7	59
359	Long-Term Intra-host Evolution of Methicillin Resistant <i>Staphylococcus aureus</i> Among Cystic Fibrosis Patients With Respiratory Carriage. <i>Frontiers in Genetics</i> , 2019, 10, 546.	1.1	24
360	In silico Identification of Serovar-Specific Genes for <i>Salmonella</i> Serotyping. <i>Frontiers in Microbiology</i> , 2019, 10, 835.	1.5	18
361	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	5.8	41
362	The biology of IncI2 plasmids shown by whole-plasmid multi-locus sequence typing. <i>Plasmid</i> , 2019, 106, 102444.	0.4	10
363	Segmented Filamentous Bacteria Prevent and Cure Rotavirus Infection. <i>Cell</i> , 2019, 179, 644-658.e13.	13.5	106
364	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

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365	Genomic characterization of <i>Vibrio parahaemolyticus</i> from Pacific white shrimp and rearing water in Malaysia reveals novel sequence types and structural variation in genomic regions containing the <i>Photorhabdus</i> insect-related (Pir) toxin-like genes. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	6
366	Can Insertion Sequences Proliferation Influence Genomic Plasticity? Comparative Analysis of <i>Acinetobacter baumannii</i> Sequence Type 78, a Persistent Clone in Italian Hospitals. <i>Frontiers in Microbiology</i> , 2019, 10, 2080.	1.5	23
367	Spatiotemporal dynamics of multidrug resistant bacteria on intensive care unit surfaces. <i>Nature Communications</i> , 2019, 10, 4569.	5.8	39
368	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	5.1	274
369	Disruption of <i>hmgA</i> by DNA Duplication is Responsible for Hyperpigmentation in a <i>Vibrio anguillarum</i> Strain. <i>Scientific Reports</i> , 2019, 9, 14589.	1.6	2
370	Antimicrobial resistance genotypes and phenotypes of <i>Campylobacter jejuni</i> isolated in Italy from humans, birds from wild and urban habitats, and poultry. <i>PLoS ONE</i> , 2019, 14, e0223804.	1.1	55
371	Novel model-based clustering reveals ecologically differentiated bacterial genomes across a large climate gradient. <i>Ecology Letters</i> , 2019, 22, 2077-2086.	3.0	3
372	PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. <i>GigaScience</i> , 2019, 8, .	3.3	152
373	Genomic comparison of diverse <i>Salmonella</i> serovars isolated from swine. <i>PLoS ONE</i> , 2019, 14, e0224518.	1.1	25
374	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen <i>Klebsiella pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 3240-3251.	1.1	18
375	Red-Brown Pigmentation of <i>Acidipropionibacterium jensenii</i> Is Tied to Haemolytic Activity and <i>cyl</i> -Like Gene Cluster. <i>Microorganisms</i> , 2019, 7, 512.	1.6	10
376	Detection of Genome Sequence Outliers Across Pan-Genomes. , 2019, , .		0
377	Large-scale genome analysis of bovine commensal <i>Escherichia coli</i> reveals that bovine-adapted <i>E. coli</i> lineages are serving as evolutionary sources of the emergence of human intestinal pathogenic strains. <i>Genome Research</i> , 2019, 29, 1495-1505.	2.4	39
378	Genetic and metabolic signatures of <i>Salmonella enterica</i> subsp. <i>enterica</i> associated with animal sources at the pangenomic scale. <i>BMC Genomics</i> , 2019, 20, 814.	1.2	29
379	Description of <i>Klebsiella spallanzanii</i> sp. nov. and of <i>Klebsiella pasteurii</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2019, 10, 2360.	1.5	49
380	A Simple and Robust Statistical Method to Define Genetic Relatedness of Samples Related to Outbreaks at the Genomic Scale – Application to Retrospective <i>Salmonella</i> Foodborne Outbreak Investigations. <i>Frontiers in Microbiology</i> , 2019, 10, 2413.	1.5	17
381	WGS based study of the population structure of <i>Salmonella enterica</i> serovar <i>Infantis</i> . <i>BMC Genomics</i> , 2019, 20, 870.	1.2	63
382	Case report: whole genome sequencing based investigation of maternal-neonatal listeriosis in Sichuan, China. <i>BMC Infectious Diseases</i> , 2019, 19, 893.	1.3	15

#	ARTICLE	IF	CITATIONS
383	Insights into the genome structure of four acetogenic bacteria with specific reference to the Woodâ€™Ljungdahl pathway. <i>MicrobiologyOpen</i> , 2019, 8, e938.	1.2	16
384	Prophages and satellite prophages are widespread in <i>Streptococcus</i> and may play a role in pneumococcal pathogenesis. <i>Nature Communications</i> , 2019, 10, 4852.	5.8	64
385	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
386	The recombination-cold region as an epidemiological marker of recombinogenic opportunistic pathogen <i>Mycobacterium avium</i> . <i>BMC Genomics</i> , 2019, 20, 752.	1.2	7
387	Molecular Evolution of Extensively Drug-Resistant (XDR) <i>Pseudomonas aeruginosa</i> Strains From Patients and Hospital Environment in a Prolonged Outbreak. <i>Frontiers in Microbiology</i> , 2019, 10, 1742.	1.5	10
388	Phylogenetic Analysis of Multi-Drug Resistant <i>Klebsiella pneumoniae</i> Strains From Duodenoscope Biofilm: Microbiological Surveillance and Reprocessing Improvements for Infection Prevention. <i>Frontiers in Public Health</i> , 2019, 7, 219.	1.3	14
389	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019, 7, 119.	4.9	65
390	Machine Learning Approaches for Epidemiological Investigations of Food-Borne Disease Outbreaks. <i>Frontiers in Microbiology</i> , 2019, 10, 1722.	1.5	22
391	Rapid detection of <i>Listeria monocytogenes</i> sequence type 121 strains using a novel multiplex PCR assay. <i>LWT - Food Science and Technology</i> , 2019, 116, 108474.	2.5	11
392	Phylogenomics Reveals Clear Cases of Misclassification and Genus-Wide Phylogenetic Markers for <i>Acinetobacter</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2531-2541.	1.1	60
393	Phenotypic and genotypic characterization of linezolid-resistant <i>Enterococcus faecium</i> from the USA and Pakistan. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3445-3452.	1.3	33
394	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
395	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7Â years in a single center. <i>Genome Biology</i> , 2019, 20, 184.	3.8	22
396	Whole-genome sequencing as an improved means of investigating <i>Neisseria gonorrhoeae</i> treatment failures. <i>Sexual Health</i> , 2019, 16, 500.	0.4	2
397	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. <i>Nature Medicine</i> , 2019, 25, 1442-1452.	15.2	255
398	In Silico Analysis of <i>Gardnerella</i> Genomespecies Detected in the Setting of Bacterial Vaginosis. <i>Clinical Chemistry</i> , 2019, 65, 1375-1387.	1.5	24
399	Emergence and Characterization of a Novel IncP-6 Plasmid Harboring blaKPCâ€™2 and qnrS2 Genes in <i>Aeromonas taiwanensis</i> Isolates. <i>Frontiers in Microbiology</i> , 2019, 10, 2132.	1.5	17
400	Colistin resistance emerges in pandrug-resistant <i>Klebsiella pneumoniae</i> epidemic clones in Rio de Janeiro, Brazil. <i>International Journal of Antimicrobial Agents</i> , 2019, 54, 579-586.	1.1	31

#	ARTICLE	IF	CITATIONS
401	Using the wax moth larva <i>Galleria mellonella</i> infection model to detect emerging bacterial pathogens. PeerJ, 2019, 6, e6150.	0.9	24
402	Persistent metagenomic signatures of early-life hospitalization and antibiotic treatment in the infant gut microbiota and resistome. Nature Microbiology, 2019, 4, 2285-2297.	5.9	191
403	Key evolutionary events in the emergence of a globally disseminated, carbapenem resistant clone in the Escherichia coli ST410 lineage. Communications Biology, 2019, 2, 322.	2.0	36
404	Isolation of five Enterobacteriaceae species harbouring bla <sub>NDM-1</sub> and mcr-1 plasmids from a single paediatric patient. PLoS ONE, 2019, 14, e0221960.	1.1	19
405	Genome Investigation of a Cariogenic Pathogen with Implications in Cardiovascular Diseases. Indian Journal of Microbiology, 2019, 59, 451-459.	1.5	0
406	Whole-Genome Sequencing Redefines Shewanella Taxonomy. Frontiers in Microbiology, 2019, 10, 1861.	1.5	46
407	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. Genome Biology and Evolution, 2019, 11, 2750-2766.	1.1	70
408	Gene Tags Assessment by Comparative Genomics (GTACG): A User-Friendly Framework for Bacterial Comparative Genomics. Frontiers in Genetics, 2019, 10, 725.	1.1	4
409	The Genomics of Streptococcus Pneumoniae Carriage Isolates from UK Children and Their Household Contacts, Pre-PCV7 to Post-PCV13. Genes, 2019, 10, 687.	1.0	16
410	Comparative Genomic Analysis of Staphylococcus haemolyticus Reveals Key to Hospital Adaptation and Pathogenicity. Frontiers in Microbiology, 2019, 10, 2096.	1.5	33
411	A hybrid sub-lineage of Listeria monocytogenes comprising hypervirulent isolates. Nature Communications, 2019, 10, 4283.	5.8	76
412	Genomic epidemiology of Iranian <i>Bordetella pertussis</i> : 50 years after the implementation of whole cell vaccine. Emerging Microbes and Infections, 2019, 8, 1416-1427.	3.0	23
413	ICEKp2: description of an integrative and conjugative element in Klebsiella pneumoniae, co-occurring and interacting with ICEKp1. Scientific Reports, 2019, 9, 13892.	1.6	10
414	Genome Mining Coupled with OSMAC-Based Cultivation Reveal Differential Production of Surugamide A by the Marine Sponge Isolate Streptomyces sp. SM17 When Compared to Its Terrestrial Relative S. albidoflavus J1074. Microorganisms, 2019, 7, 394.	1.6	21
415	Shiga toxin sub-type 2a increases the efficiency of Escherichia coli O157 transmission between animals and restricts epithelial regeneration in bovine enteroids. PLoS Pathogens, 2019, 15, e1008003.	2.1	42
416	simurg: simulate bacterial pangenomes in R. Bioinformatics, 2020, 36, 1273-1274.	1.8	5
417	Geography Shapes the Population Genomics of Salmonella enterica Dublin. Genome Biology and Evolution, 2019, 11, 2220-2231.	1.1	23
418	Inferring bacterial recombination rates from large-scale sequencing datasets. Nature Methods, 2019, 16, 199-204.	9.0	58



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419	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
420	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	2.4	258
421	One Health Genomic Surveillance of <i>Escherichia coli</i> Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. <i>MBio</i> , 2019, 10, .	1.8	130
422	In silico Identification of Novel Toxin Homologs and Associated Mobile Genetic Elements in <i>Clostridium perfringens</i> . <i>Pathogens</i> , 2019, 8, 16.	1.2	15
423	Diversity and Population Overlap between Avian and Human <i>Escherichia coli</i> Belonging to Sequence Type 95. <i>MSphere</i> , 2019, 4, .	1.3	57
424	Phylogenetic relationship of prophages is affected by CRISPR selection in Group A <i>Streptococcus</i> . <i>BMC Microbiology</i> , 2019, 19, 24.	1.3	12
425	Complete genome sequence of <i>Salmonella enterica</i> serovar Sendai shows H antigen convergence with S. Miami and recent divergence from S. Paratyphi A. <i>BMC Genomics</i> , 2019, 20, 398.	1.2	4
426	A core genome approach that enables prospective and dynamic monitoring of infectious outbreaks. <i>Scientific Reports</i> , 2019, 9, 7808.	1.6	8
427	Genome analysis of methicillin-resistant <i>Staphylococcus aureus</i> isolated from pigs: Detection of the clonal lineage ST398 in Cameroon and South Africa. <i>Zoonoses and Public Health</i> , 2019, 66, 512-525.	0.9	13
428	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	9.4	120
429	A century of gray: A genomic locus found in 2 distinct <i>Pseudomonas</i> spp. is associated with historical and contemporary color defects in dairy products worldwide. <i>Journal of Dairy Science</i> , 2019, 102, 5979-6000.	1.4	20
430	'Candidatus <i>Ornithobacterium hominis</i> ': insights gained from draft genomes obtained from nasopharyngeal swabs. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
431	Recent mixing of <i>Vibrio parahaemolyticus</i> populations. <i>ISME Journal</i> , 2019, 13, 2578-2588.	4.4	41
432	Whole-genome comparative analysis of <i>Campylobacter jejuni</i> strains isolated from patients with diarrhea in northeastern Poland. <i>Gut Pathogens</i> , 2019, 11, 32.	1.6	24
433	Long-read based de novo assembly of low-complexity metagenome samples results in finished genomes and reveals insights into strain diversity and an active phage system. <i>BMC Microbiology</i> , 2019, 19, 143.	1.3	104
434	Repeated Isolation of Extended-Spectrum-β-Lactamase-Positive <i>Escherichia coli</i> Sequence Types 648 and 131 from Community Wastewater Indicates that Sewage Systems Are Important Sources of Emerging Clones of Antibiotic-Resistant Bacteria. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	29
435	Variability in Genomic and Virulent Properties of <i>Porphyromonas gingivalis</i> Strains Isolated From Healthy and Severe Chronic Periodontitis Individuals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 246.	1.8	19
436	Extensive genome analysis of <i>Coxiella burnetii</i> reveals limited evolution within genomic groups. <i>BMC Genomics</i> , 2019, 20, 441.	1.2	31

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437	Filling the gap between collection, transport and storage of the human gut microbiota. <i>Scientific Reports</i> , 2019, 9, 8327.	1.6	18
438	Hypervirulent <i>Listeria monocytogenes</i> clones'™ adaption to mammalian gut accounts for their association with dairy products. <i>Nature Communications</i> , 2019, 10, 2488.	5.8	157
439	Type I interferon induced by TLR2-TLR4-MyD88-TRIF-IRF3 controls <i>Mycobacterium abscessus</i> subsp. <i>abscessus</i> persistence in murine macrophages via nitric oxide. <i>International Journal of Medical Microbiology</i> , 2019, 309, 307-318.	1.5	16
440	Complete genome sequence and characterization of virulence genes in Lancefield group C <i>Streptococcus dysgalactiae</i> isolated from farmed amberjack ( <i>Seriola dumerili</i> ). <i>Microbiology and Immunology</i> , 2019, 63, 243-250.	0.7	5
441	Biofilm formation, virulence and antimicrobial resistance of different <i>Campylobacter jejuni</i> isolates from a poultry slaughterhouse. <i>Food Microbiology</i> , 2019, 83, 193-199.	2.1	32
442	Genomic metrics made easy: what to do and where to go in the new era of bacterial taxonomy. <i>Critical Reviews in Microbiology</i> , 2019, 45, 182-200.	2.7	65
443	Not Just a Pathogen? Description of a Plant-Beneficial <i>Pseudomonas syringae</i> Strain. <i>Frontiers in Microbiology</i> , 2019, 10, 1409.	1.5	55
444	Microbiota of human precolostrum and its potential role as a source of bacteria to the infant mouth. <i>Scientific Reports</i> , 2019, 9, 8435.	1.6	51
445	Characterization and rapid identification of phylogroup G in <i>Escherichia coli</i> , a lineage with high virulence and antibiotic resistance potential. <i>Environmental Microbiology</i> , 2019, 21, 3107-3117.	1.8	152
446	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
447	Genomic Epidemiology and Phenotyping Reveal on-Farm Persistence and Cold Adaptation of Raw Milk Outbreak-Associated <i>Yersinia pseudotuberculosis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1049.	1.5	13
448	Molecular epidemiology study of a nosocomial <i>Moraxella catarrhalis</i> outbreak in a neurological rehabilitation unit. <i>Journal of Hospital Infection</i> , 2019, 103, 27-34.	1.4	4
449	Complete Assembly of <i>Escherichia coli</i> Sequence Type 131 Genomes Using Long Reads Demonstrates Antibiotic Resistance Gene Variation within Diverse Plasmid and Chromosomal Contexts. <i>MSphere</i> , 2019, 4, .	1.3	27
450	Phylogenomic Investigation of IncI1- $\beta$ Plasmids Harboring <i>bla</i> <sub>CMY-2</sub> and <i>bla</i> <sub>SHV-12</sub> in <i>Salmonella enterica</i> and <i>Escherichia coli</i> in Multiple Countries. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	14
451	Genomic sequence analysis reveals diversity of Australian <i>Xanthomonas</i> species associated with bacterial leaf spot of tomato, capsicum and chilli. <i>BMC Genomics</i> , 2019, 20, 310.	1.2	17
452	The Cano-eMLST Program: An Approach for the Calculation of Canonical Extended Multi-Locus Sequence Typing, Making Comparison of Genetic Differences Among Bunches of Bacterial Strains. <i>Microorganisms</i> , 2019, 7, 98.	1.6	2
453	Unprecedented Diversity of Lactococcal Group 936 Bacteriophages Revealed by Amplicon Sequencing of the Portal Protein Gene. <i>Viruses</i> , 2019, 11, 443.	1.5	7
454	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 169-182.	3.0	8

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455	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	2.7	168
456	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
457	Diversification of Colonization Factors in a Multidrug-Resistant <i>Escherichia coli</i> Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019, 10, .	1.8	106
458	Nosocomial bloodstream infection and the emerging carbapenem-resistant pathogen <i>Ralstonia insidiosa</i> . <i>BMC Infectious Diseases</i> , 2019, 19, 334.	1.3	33
459	Genomic Analysis of <i>Pseudomonas</i> sp. Strain SCT, an Iodate-Reducing Bacterium Isolated from Marine Sediment, Reveals a Possible Use for Bioremediation. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1321-1329.	0.8	6
460	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
461	Strain- and Species-Level Variation in the Microbiome of Diabetic Wounds Is Associated with Clinical Outcomes and Therapeutic Efficacy. <i>Cell Host and Microbe</i> , 2019, 25, 641-655.e5.	5.1	192
462	Plasmids of <i>Shigella flexneri</i> serotype 1c strain Y394 provide advantages to bacteria in the host. <i>BMC Microbiology</i> , 2019, 19, 86.	1.3	7
463	OrthoVenn2: a web server for whole-genome comparison and annotation of orthologous clusters across multiple species. <i>Nucleic Acids Research</i> , 2019, 47, W52-W58.	6.5	661
464	High-resolution mapping reveals that microniches in the gastric glands control <i>Helicobacter pylori</i> colonization of the stomach. <i>PLoS Biology</i> , 2019, 17, e3000231.	2.6	72
465	Genomic Diversity and Recombination among <i>Xylella fastidiosa</i> Subspecies. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	63
466	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of <i>Klebsiella pneumoniae</i> . <i>PLoS Genetics</i> , 2019, 15, e1008114.	1.5	228
467	Accessory genome of the multi-drug resistant ocular isolate of <i>Pseudomonas aeruginosa</i> PA34. <i>PLoS ONE</i> , 2019, 14, e0215038.	1.1	20
468	Agricultural Origins of a Highly Persistent Lineage of Vancomycin-Resistant <i>Enterococcus faecalis</i> in New Zealand. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
469	Detection of vancomycin-resistant <i>Enterococcus faecium</i> hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment. <i>Genome Research</i> , 2019, 29, 626-634.	2.4	40
470	Riding the wave of genomics to investigate aquatic coliphage diversity and activity. <i>Environmental Microbiology</i> , 2019, 21, 2112-2128.	1.8	33
471	Genomic and Functional Analysis of Emerging Virulent and Multidrug-Resistant <i>Escherichia coli</i> Lineage Sequence Type 648. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	71
472	PanRV: Pangenome-reverse vaccinology approach for identifications of potential vaccine candidates in microbial pangenome. <i>BMC Bioinformatics</i> , 2019, 20, 123.	1.2	80

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473	Inference of Convergent Gene Acquisition Among <i>Pseudomonas syringae</i> Strains Isolated From Watermelon, Cantaloupe, and Squash. <i>Frontiers in Microbiology</i> , 2019, 10, 270.	1.5	17
474	Culture of Clinical Specimens Reveals Extensive Diversity of <i>Legionella pneumophila</i> Strains in Arizona. <i>MSphere</i> , 2019, 4, .	1.3	8
475	Characterization of Clinically Relevant Strains of Extended-Spectrum $\beta$ -Lactamase-Producing <i>Klebsiella pneumoniae</i> Occurring in Environmental Sources in a Rural Area of China by Using Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2019, 10, 211.	1.5	25
476	Genomic Analyses of >3,100 Nasopharyngeal Pneumococci Revealed Significant Differences Between Pneumococci Recovered in Four Different Geographical Regions. <i>Frontiers in Microbiology</i> , 2019, 10, 317.	1.5	9
477	Genome mining identifies cepacin as a plant-protective metabolite of the biopesticidal bacterium <i>Burkholderia ambifaria</i> . <i>Nature Microbiology</i> , 2019, 4, 996-1005.	5.9	106
478	Adaptive Strategies of the Candidate Probiotic <i>E.Âcoli</i> Nissle in the Mammalian Gut. <i>Cell Host and Microbe</i> , 2019, 25, 499-512.e8.	5.1	94
479	In-host evolution of <i>Staphylococcus epidermidis</i> in a pacemaker-associated endocarditis resulting in increased antibiotic tolerance. <i>Nature Communications</i> , 2019, 10, 1149.	5.8	64
480	The complete genome and methylome of <i>Helicobacter pylori</i> hpNEAfrica strain HP14039. <i>Gut Pathogens</i> , 2019, 11, 7.	1.6	5
481	Molecular characterization and evolution of the first outbreak of vancomycin-resistant <i>Enterococcus faecium</i> in Western Australia. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 814-819.	1.1	12
482	Proposal of <i>Lysobacter pythonis</i> sp. nov. isolated from royal pythons ( <i>Python regius</i> ). <i>Systematic and Applied Microbiology</i> , 2019, 42, 326-333.	1.2	10
483	Identifying genes associated with invasive disease in <i>S. pneumoniae</i> by applying a machine learning approach to whole genome sequence typing data. <i>Scientific Reports</i> , 2019, 9, 4049.	1.6	18
484	Weakly haemolytic variants of <i>Brachyspira hyodysenteriae</i> newly emerged in Europe belong to a distinct subclade with unique genetic properties. <i>Veterinary Research</i> , 2019, 50, 21.	1.1	10
485	Survival Mechanisms of <i>Campylobacter hepaticus</i> Identified by Genomic Analysis and Comparative Transcriptomic Analysis of in vivo and in vitro Derived Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 107.	1.5	21
486	Livestock-Associated MRSA CC1 in Norway; Introduction to Pig Farms, Zoonotic Transmission, and Eradication. <i>Frontiers in Microbiology</i> , 2019, 10, 139.	1.5	30
487	Comparative genomic analysis of 127 <i>Escherichia coli</i> strains isolated from domestic animals with diarrhea in China. <i>BMC Genomics</i> , 2019, 20, 212.	1.2	10
488	Host adaptation and convergent evolution increases antibiotic resistance without loss of virulence in a major human pathogen. <i>PLoS Pathogens</i> , 2019, 15, e1007218.	2.1	56
489	TORMES: an automated pipeline for whole bacterial genome analysis. <i>Bioinformatics</i> , 2019, 35, 4207-4212.	1.8	82
490	The history, genome and biology of NCTC 30: a non-pandemic <i>Vibrio cholerae</i> isolate from World War One. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182025.	1.2	18

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491	Multiple Recombination Events Drive the Current Genetic Structure of <i>Xanthomonas perforans</i> in Florida. <i>Frontiers in Microbiology</i> , 2019, 10, 448.	1.5	42
492	High quality reference genomes for toxigenic and non-toxigenic <i>Vibrio cholerae</i> serogroup O139. <i>Scientific Reports</i> , 2019, 9, 5865.	1.6	13
493	Satellite tracking of gulls and genomic characterization of faecal bacteria reveals environmentally mediated acquisition and dispersal of antimicrobial-resistant <i>Escherichia coli</i> on the Kenai Peninsula, Alaska. <i>Molecular Ecology</i> , 2019, 28, 2531-2545.	2.0	29
494	WGS of 1058 <i>Enterococcus faecium</i> from Copenhagen, Denmark, reveals rapid clonal expansion of vancomycin-resistant clone ST80 combined with widespread dissemination of a <i>vanA</i> -containing plasmid and acquisition of a heterogeneous accessory genome. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1776-1785.	1.3	43
495	Within-farm prevalence and environmental distribution of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in farmed mink ( <i>Neovison vison</i> ). <i>Veterinary Microbiology</i> , 2019, 231, 80-86.	0.8	10
496	Within-Species Genomic Variation and Variable Patterns of Recombination in the Tetracycline Producer <i>Streptomyces rimosus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 552.	1.5	25
497	Comparative Genomic Analysis Reveals the Potential Risk of <i>Vibrio parahaemolyticus</i> Isolated From Ready-To-Eat Foods in China. <i>Frontiers in Microbiology</i> , 2019, 10, 186.	1.5	25
498	Genome plasticity favours double chromosomal Tn4401b- <i>bla</i> KPC-2 transposon insertion in the <i>Pseudomonas aeruginosa</i> ST235 clone. <i>BMC Microbiology</i> , 2019, 19, 45.	1.3	24
499	Description of <i>Klebsiella africanensis</i> sp. nov., <i>Klebsiella variicola</i> subsp. <i>atropicalensis</i> subsp. nov. and <i>Klebsiella variicola</i> subsp. <i>variicola</i> subsp. nov.. <i>Research in Microbiology</i> , 2019, 170, 165-170.	1.0	92
500	Genome Analysis of <i>Shigella flexneri</i> Serotype 3b Strain SFL1520 Reveals Significant Horizontal Gene Acquisitions Including a Multidrug Resistance Cassette. <i>Genome Biology and Evolution</i> , 2019, 11, 776-785.	1.1	9
501	Longitudinal Study of Shiga Toxin-Producing <i>Escherichia coli</i> and <i>Campylobacter jejuni</i> on Finnish Dairy Farms and in Raw Milk. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	17
502	Circulation of Plasmids Harboring Resistance Genes to Quinolones and/or Extended-Spectrum Cephalosporins in Multiple <i>Salmonella enterica</i> Serotypes from Swine in the United States. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	16
503	Remodeling of pSK1 Family Plasmids and Enhanced Chlorhexidine Tolerance in a Dominant Hospital Lineage of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	18
504	Draft Genome Sequence of <i>Chromatium okenii</i> Isolated from the Stratified Alpine Lake Cadagno. <i>Scientific Reports</i> , 2019, 9, 1936.	1.6	16
505	Genomic analysis of <i>Klebsiella pneumoniae</i> isolates from Malawi reveals acquisition of multiple ESBL determinants across diverse lineages. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1223-1232.	1.3	36
506	Evolutionary Model of Cluster Divergence of the Emergent Marine Pathogen <i>Vibrio vulnificus</i> : From Genotype to Ecotype. <i>MBio</i> , 2019, 10, .	1.8	41
507	Genome Mining and Comparative Analysis of <i>Streptococcus intermedius</i> Causing Brain Abscess in a Child. <i>Pathogens</i> , 2019, 8, 22.	1.2	13
508	Resistance mechanisms and population structure of highly drug resistant <i>Klebsiella</i> in Pakistan during the introduction of the carbapenemase NDM-1. <i>Scientific Reports</i> , 2019, 9, 2392.	1.6	45

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509	Draft Whole-Genome Sequences of <i>Xylella fastidiosa</i> subsp. <i>fastidiosa</i> Strains TPD3 and TPD4, Isolated from Grapevines in Hou-li, Taiwan. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
510	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019, 10, .	1.8	19
511	Genomic analysis on broiler-associated <i>Clostridium perfringens</i> strains and exploratory caecal microbiome investigation reveals key factors linked to poultry necrotic enteritis. <i>Animal Microbiome</i> , 2019, 1, 12.	1.5	29
512	Molecular Signatures Related to the Virulence of <i>Bacillus cereus</i> Sensu Lato, a Leading Cause of Devastating Endophthalmitis. <i>MSystems</i> , 2019, 4, .	1.7	4
513	Study protocol: characterising the clinical, epidemiological and aetiological aspects of leptospirosis in Sri Lanka: a hospital based clinico-epidemiological study. <i>BMJ Open</i> , 2019, 9, e027850.	0.8	14
514	Whole-Genome Sequencing of <i>Mycobacterium tilburgii</i> Strain MEPHI. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
515	Reanalysis of <i>Lactobacillus paracasei</i> Lbs2 Strain and Large-Scale Comparative Genomics Places Many Strains into Their Correct Taxonomic Position. <i>Microorganisms</i> , 2019, 7, 487.	1.6	14
516	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
517	Development of a multi-locus typing scheme for an Enterobacteriaceae linear plasmid that mediates inter-species transfer of flagella. <i>PLoS ONE</i> , 2019, 14, e0218638.	1.1	15
518	Multi-strain Tn-Seq reveals common daptomycin resistance determinants in <i>Staphylococcus aureus</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007862.	2.1	68
519	Pan-genome diversification and recombination in <i>Cronobacter sakazakii</i> , an opportunistic pathogen in neonates, and insights to its xerotolerant lifestyle. <i>BMC Microbiology</i> , 2019, 19, 306.	1.3	12
520	Whole Genome Sequencing of <i>Aggregatibacter actinomycetemcomitans</i> Cultured from Blood Stream Infections Reveals Three Major Phylogenetic Groups Including a Novel Lineage Expressing Serotype a Membrane O Polysaccharide. <i>Pathogens</i> , 2019, 8, 256.	1.2	13
521	An <i>Escherichia coli</i> ST131 pangenome atlas reveals population structure and evolution across 4,071 isolates. <i>Scientific Reports</i> , 2019, 9, 17394.	1.6	71
522	A Complete Genome Screening Program of Clinical Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates Identifies the Origin and Progression of a Neonatal Intensive Care Unit Outbreak. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	16
523	Comparative genomics of eight <i>Lactobacillus buchneri</i> strains isolated from food spoilage. <i>BMC Genomics</i> , 2019, 20, 902.	1.2	12
524	Distinct Phenotypic and Genomic Signatures Underlie Contrasting Pathogenic Potential of <i>Staphylococcus epidermidis</i> Clonal Lineages. <i>Frontiers in Microbiology</i> , 2019, 10, 1971.	1.5	32
525	VCGIDB: A Database and Web Resource for the Genomic Islands from <i>Vibrio cholerae</i> . <i>Pathogens</i> , 2019, 8, 261.	1.2	5
526	deltaRpkM: an R package for a rapid detection of differential gene presence between related bacterial genomes. <i>BMC Bioinformatics</i> , 2019, 20, 621.	1.2	3

#	ARTICLE	IF	CITATIONS
527	Genomic analyses of <i>Burkholderia cenocepacia</i> reveal multiple species with differential host-adaptation to plants and humans. <i>BMC Genomics</i> , 2019, 20, 803.	1.2	47
528	Modification of the genome topology network and its application to the comparison of group B <i>Streptococcus</i> genomes. <i>BMC Genomics</i> , 2019, 20, 886.	1.2	0
529	Isolation and comparative genomics of <i>Mycobacterium tuberculosis</i> isolates from cattle and their attendants in South India. <i>Scientific Reports</i> , 2019, 9, 17892.	1.6	14
530	Genetic variation associated with infection and the environment in the accidental pathogen <i>Burkholderia pseudomallei</i> . <i>Communications Biology</i> , 2019, 2, 428.	2.0	19
531	Genome-Wide Identification of Myxobacterial Predation Genes and Demonstration of Formaldehyde Secretion as a Potentially Predation-Resistant Trait of <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2650.	1.5	32
532	Residual Variation Intolerance Score Detects Loci Under Selection in Neuroinvasive <i>Listeria monocytogenes</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2702.	1.5	1
533	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
534	Genetic determinants of genus-level glycan diversity in a bacterial protein glycosylation system. <i>PLoS Genetics</i> , 2019, 15, e1008532.	1.5	16
535	Genomic insights into <i>Vibrio cholerae</i> O1 responsible for cholera epidemics in Tanzania between 1993 and 2017. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007934.	1.3	21
536	SureSelect targeted enrichment, a new cost effective method for the whole genome sequencing of <i>Candidatus Liberibacter asiaticus</i> . <i>Scientific Reports</i> , 2019, 9, 18962.	1.6	10
537	Search for Ancestral Features in Genomes of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> Strains Isolated from the Relict Legume <i>Vavilovia formosa</i> . <i>Genes</i> , 2019, 10, 990.	1.0	8
538	Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. <i>Nature</i> , 2019, 574, 117-121.	13.7	617
539	High-resolution genome-wide analysis is essential for the identification of ambiguous <i>Aeromonas</i> strains. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	4
540	Prevalence of <i>Shigella boydii</i> in Bangladesh: Isolation and Characterization of a Rare Phage MK-13 That Can Robustly Identify Shigellosis Caused by <i>Shigella boydii</i> Type 1. <i>Frontiers in Microbiology</i> , 2019, 10, 2461.	1.5	9
541	Genome investigations show host adaptation and transmission of LA-MRSA CC398 from pigs into Danish healthcare institutions. <i>Scientific Reports</i> , 2019, 9, 18655.	1.6	51
542	Emergence of NDM-1- and CTX-M-3-Producing <i>Raoultella ornithinolytica</i> in Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2019, 10, 2678.	1.5	11
543	Biofilm Formation of <i>Listeria monocytogenes</i> Strains Under Food Processing Environments and Pan-Genome-Wide Association Study. <i>Frontiers in Microbiology</i> , 2019, 10, 2698.	1.5	83
544	Clonal expansion of a virulent <i>Streptococcus suis</i> serotype 9 lineage distinguishable from carriage subpopulations. <i>Scientific Reports</i> , 2019, 9, 15429.	1.6	11

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545	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019, 10, .	1.8	50
546	Enrichment of <i>Marinobacter</i> sp. and Halophilic Homoacetogens at the Biocathode of Microbial Electrosynthesis System Inoculated With Red Sea Brine Pool. <i>Frontiers in Microbiology</i> , 2019, 10, 2563.	1.5	24
547	Some strains that have converged to infect <i>Prunus</i> spp. trees are members of distinct <i>Pseudomonas syringae</i> genomospecies and ecotypes as revealed by in silico genomic comparison. <i>Archives of Microbiology</i> , 2019, 201, 67-80.	1.0	6
548	Multidisciplinary approaches for studying rhizobium-“legume symbioses. <i>Canadian Journal of Microbiology</i> , 2019, 65, 1-33.	0.8	77
549	Population Genetics and Characterization of <i>Campylobacter jejuni</i> Isolates from Western Jackdaws and Game Birds in Finland. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
550	Insights from genome-wide approaches to identify variants associated to phenotypes at pan-genome scale: Application to <i>L. monocytogenes</i> ' ability to grow in cold conditions. <i>International Journal of Food Microbiology</i> , 2019, 291, 181-188.	2.1	38
551	Insights into the population structure and pan-genome of <i>Haemophilus influenzae</i> . <i>Infection, Genetics and Evolution</i> , 2019, 67, 126-135.	1.0	38
552	Diversity and distribution of <i>Klebsiella</i> capsules in <i>Escherichia coli</i> . <i>Environmental Microbiology Reports</i> , 2019, 11, 107-117.	1.0	15
553	Genome-resolved metagenomic analysis reveals roles of microbial community members in full-scale seawater reverse osmosis plant. <i>Water Research</i> , 2019, 149, 263-271.	5.3	31
554	Pan-genomic analysis provides novel insights into the association of <i>E.coli</i> with human host and its minimal genome. <i>Bioinformatics</i> , 2019, 35, 1987-1991.	1.8	22
555	Pangenomic Approach To Understanding Microbial Adaptations within a Model Built Environment, the International Space Station, Relative to Human Hosts and Soil. <i>MSystems</i> , 2019, 4, .	1.7	34
556	Metagenomic profiling of ticks: Identification of novel rickettsial genomes and detection of tick-borne canine parvovirus. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0006805.	1.3	27
557	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , 2019, 176, 649-662.e20.	13.5	1,087
558	Cystic Fibrosis-Associated <i>Stenotrophomonas maltophilia</i> Strain-Specific Adaptations and Responses to pH. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	11
559	Chromids Aid Genome Expansion and Functional Diversification in the Family <i>Burkholderiaceae</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 562-574.	3.5	34
560	Limited contribution of non-intensive chicken farming to ESBL-producing <i>Escherichia coli</i> colonization in humans in Vietnam: an epidemiological and genomic analysis. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 561-570.	1.3	35
561	Persistence and Microevolution of <i>Pseudomonas aeruginosa</i> in the Cystic Fibrosis Lung: A Single-Patient Longitudinal Genomic Study. <i>Frontiers in Microbiology</i> , 2018, 9, 3242.	1.5	27
562	Phylogenomic Analysis of Extraintestinal Pathogenic <i>Escherichia coli</i> Sequence Type 1193, an Emerging Multidrug-Resistant Clonal Group. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	64



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563	Whole genome sequencing of toxigenic <i>Clostridium difficile</i> in asymptomatic carriers: insights into possible role in transmission. <i>Journal of Hospital Infection</i> , 2019, 102, 125-134.	1.4	15
564	Reinfection with <i>Streptococcus suis</i> analysed by whole genome sequencing. <i>Zoonoses and Public Health</i> , 2019, 66, 179-183.	0.9	4
565	Import of community-associated, methicillin-resistant <i>Staphylococcus aureus</i> to Europe through skin and soft-tissue infection in intercontinental travellers, 2011–2016. <i>Clinical Microbiology and Infection</i> , 2019, 25, 739-746.	2.8	35
566	Draft genome Sequence of Phosphate-Accumulating Bacterium <i>Acinetobacter tandoii</i> SC36 from a Mangrove Wetland Ecosystem Provides Insights into Elements of Phosphorus Removal. <i>Current Microbiology</i> , 2019, 76, 207-212.	1.0	7
567	A full-ocean-depth rated modular lander and pressure-retaining sampler capable of collecting hadal-endemic microbes under in situ conditions. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 143, 50-57.	0.6	52
568	From proteins to polysaccharides: lifestyle and genetic evolution of <i>Coprothermobacter proteolyticus</i> . <i>ISME Journal</i> , 2019, 13, 603-617.	4.4	30
569	Investigation of an outbreak caused by antibiotic-sensitive <i>Klebsiella oxytoca</i> in a neonatal intensive care unit in Norway. <i>Acta Paediatrica, International Journal of Paediatrics</i> , 2019, 108, 76-82.	0.7	15
570	Metagenomic analysis of intestinal mucosa revealed a specific eukaryotic gut virome signature in early-diagnosed inflammatory bowel disease. <i>Gut Microbes</i> , 2019, 10, 149-158.	4.3	70
571	Systematic analysis of supervised machine learning as an effective approach to predicate $\beta$ -lactam resistance phenotype in <i>Streptococcus pneumoniae</i> . <i>Briefings in Bioinformatics</i> , 2020, 21, 1347-1355.	3.2	8
572	Cross-transmission Is Not the Source of New <i>Mycobacterium abscessus</i> Infections in a Multicenter Cohort of Cystic Fibrosis Patients. <i>Clinical Infectious Diseases</i> , 2020, 70, 1855-1864.	2.9	48
573	Horizontal Gene Transfer. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	8
574	Early Signals of Vaccine-driven Perturbation Seen in Pneumococcal Carriage Population Genomic Data. <i>Clinical Infectious Diseases</i> , 2020, 70, 1294-1303.	2.9	9
575	PADS Arsenal: a database of prokaryotic defense systems related genes. <i>Nucleic Acids Research</i> , 2020, 48, D590-D598.	6.5	25
576	Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 417-428.	3.5	27
577	Genomic and metabolic features of <i>Lactobacillus sakei</i> as revealed by its pan-genome and the metatranscriptome of kimchi fermentation. <i>Food Microbiology</i> , 2020, 86, 103341.	2.1	39
578	In vitro and in vivo characterisation of <i>Listeria monocytogenes</i> outbreak isolates. <i>Food Control</i> , 2020, 107, 106784.	2.8	19
579	Genomic Analysis of Multidrug-Resistant <i>Escherichia coli</i> from Surface Water in Northeast Georgia, United States: Presence of an ST131 Epidemic Strain Containing <i>bla</i> <sub>CTX-M-15</sub> on a Phage-Like Plasmid. <i>Microbial Drug Resistance</i> , 2020, 26, 447-455.	0.9	4
580	Comparative genomics of a subset of Adherent/Invasive <i>Escherichia coli</i> strains isolated from individuals without inflammatory bowel disease. <i>Genomics</i> , 2020, 112, 1813-1820.	1.3	16

#	ARTICLE	IF	CITATIONS
581	The Green Revolution shaped the population structure of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . ISME Journal, 2020, 14, 492-505.	4.4	29
582	Engineering bacteriocin-mediated resistance against the plant pathogen <i>Pseudomonas syringae</i> . Plant Biotechnology Journal, 2020, 18, 1296-1306.	4.1	32
583	Comparative genomic analysis reveals a high prevalence of inter-species in vivo transfer of carbapenem-resistance plasmids in patients with haematological malignancies. Clinical Microbiology and Infection, 2020, 26, 780.e1-780.e8.	2.8	21
584	Alteration of antibiotic regimen as an additional control measure in suspected multi-drug-resistant <i>Enterobacter cloacae</i> outbreak in a neonatal intensive care unit. Journal of Hospital Infection, 2020, 104, 144-149.	1.4	13
585	Pan-genome analysis of <i>Riemerella anatipestifer</i> reveals its genomic diversity and acquired antibiotic resistance associated with genomic islands. Functional and Integrative Genomics, 2020, 20, 307-320.	1.4	8
586	Computational Framework for High-Quality Production and Large-Scale Evolutionary Analysis of Metagenome Assembled Genomes. Molecular Biology and Evolution, 2020, 37, 593-598.	3.5	11
587	Evolutionary relationships among bifidobacteria and their hosts and environments. BMC Genomics, 2020, 21, 26.	1.2	26
588	Genome Sequence and Characterization of Coliphage vB_Eco_SLUR29. Phage, 2020, 1, 38-44.	0.8	3
589	Whole genome sequencing of <i>Borrelia miyamotoi</i> isolate Izh-4: reference for a complex bacterial genome. BMC Genomics, 2020, 21, 16.	1.2	26
590	The transferability and evolution of NDM-1 and KPC-2 co-producing <i>Klebsiella pneumoniae</i> from clinical settings. EBioMedicine, 2020, 51, 102599.	2.7	87
591	Current status of pan-genome analysis for pathogenic bacteria. Current Opinion in Biotechnology, 2020, 63, 54-62.	3.3	54
592	Estimating Pangenomes with Roary. Molecular Biology and Evolution, 2020, 37, 933-939.	3.5	39
593	Genome-Wide Profiling of Enterotoxigenic <i>Staphylococcus aureus</i> Strains Used for the Production of Naturally Contaminated Cheeses. Genes, 2020, 11, 33.	1.0	9
594	Cultivated <i>Escherichia coli</i> diversity in intestinal microbiota of Crohn's disease patients and healthy individuals: Whole genome data. Data in Brief, 2020, 28, 104948.	0.5	9
595	Breast milk-derived human milk oligosaccharides promote <i>Bifidobacterium</i> interactions within a single ecosystem. ISME Journal, 2020, 14, 635-648.	4.4	220
596	Emergence of a Plant Pathogen in Europe Associated with Multiple Intercontinental Introductions. Applied and Environmental Microbiology, 2020, 86, .	1.4	57
597	Genotypic study of <i>Citrobacter koseri</i> , an emergent platelet contaminant since 2012 in France. Transfusion, 2020, 60, 245-249.	0.8	3
598	Comparative Genomics Screen Identifies Microbe-Associated Molecular Patterns from <i>Candidatus Liberibacter</i> spp. That Elicit Immune Responses in Plants. Molecular Plant-Microbe Interactions, 2020, 33, 539-552.	1.4	11

#	ARTICLE	IF	CITATIONS
599	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
601	Clonal expansion of colistin-resistant <i>Acinetobacter baumannii</i> isolates in Cape Town, South Africa. <i>International Journal of Infectious Diseases</i> , 2020, 91, 94-100.	1.5	24
602	Comparative Pangenomics of the Mammalian Gut Commensal <i>Bifidobacterium longum</i> . <i>Microorganisms</i> , 2020, 8, 7.	1.6	23
603	Screening of <i>Lactobacillus salivarius</i> strains from the feces of Chinese populations and the evaluation of their effects against intestinal inflammation in mice. <i>Food and Function</i> , 2020, 11, 221-235.	2.1	38
604	First Steps in the Analysis of Prokaryotic Pan-Genomes. <i>Bioinformatics and Biology Insights</i> , 2020, 14, 117793222093806.	1.0	48
605	Molecular Characteristics and Zoonotic Potential of <i>Salmonella Weltevreden</i> From Cultured Shrimp and Tilapia in Vietnam and China. <i>Frontiers in Microbiology</i> , 2020, 11, 1985.	1.5	15
606	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
607	Genomics of the Argentinian cholera epidemic elucidate the contrasting dynamics of epidemic and endemic <i>Vibrio cholerae</i> . <i>Nature Communications</i> , 2020, 11, 4918.	5.8	12
608	<i>Haloferax profundus</i> sp. nov. and <i>Haloferax marisrubri</i> sp. nov., Isolated from the Discovery Deep Brine-Seawater Interface in the Red Sea. <i>Microorganisms</i> , 2020, 8, 1475.	1.6	1
609	Phenotypic and Genotypic Characterization of <i>Streptococcus mutans</i> Strains Isolated from Endodontic Infections. <i>Journal of Endodontics</i> , 2020, 46, 1876-1883.	1.4	8
610	Genomic Characteristics of Invasive <i>Streptococcus pneumoniae</i> Serotype 1 in New Caledonia Prior to the Introduction of PCV13. <i>Bioinformatics and Biology Insights</i> , 2020, 14, 117793222096210.	1.0	2
611	Newly Explored <i>Faecalibacterium</i> Diversity Is Connected to Age, Lifestyle, Geography, and Disease. <i>Current Biology</i> , 2020, 30, 4932-4943.e4.	1.8	72
612	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
613	A database for risk assessment and comparative genomic analysis of foodborne <i>Vibrio parahaemolyticus</i> in China. <i>Scientific Data</i> , 2020, 7, 321.	2.4	8
614	Large scale genome reconstructions illuminate <i>Wolbachia</i> evolution. <i>Nature Communications</i> , 2020, 11, 5235.	5.8	71
615	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. <i>PLoS ONE</i> , 2020, 15, e0239677.	1.1	13
616	The New <i>Klebsiella pneumoniae</i> ST152 Variants with Hypermucoviscous Phenotype Isolated from Renal Transplant Recipients with Asymptomatic Bacteriuria: Genetic Characteristics by WGS. <i>Genes</i> , 2020, 11, 1189.	1.0	10
617	Integrated Phenotypic-Genotypic Analysis of Candidate Probiotic <i>Weissella cibaria</i> Strains Isolated from Dairy Cows in Kuwait. <i>Probiotics and Antimicrobial Proteins</i> , 2021, 13, 809-823.	1.9	8

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618	Comparative genomics of ocular <i>Pseudomonas aeruginosa</i> strains from keratitis patients with different clinical outcomes. <i>Genomics</i> , 2020, 112, 4769-4776.	1.3	12
619	Investigation of Outbreaks of Extended-Spectrum Beta-Lactamase-Producing <i>Klebsiella Pneumoniae</i> in Three Neonatal Intensive Care Units Using Whole Genome Sequencing. <i>Antibiotics</i> , 2020, 9, 705.	1.5	13
620	Molecular and epidemiological surveillance of polymyxin-resistant <i>Klebsiella pneumoniae</i> strains isolated from Brazil with multiple <i>mgrB</i> gene mutations. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151448.	1.5	17
621	Distinctive gene and protein characteristics of extremely piezophilic <i>Colwellia</i> . <i>BMC Genomics</i> , 2020, 21, 692.	1.2	27
622	Lipopolysaccharide O structure of adherent and invasive <i>Escherichia coli</i> regulates intestinal inflammation via complement C3. <i>PLoS Pathogens</i> , 2020, 16, e1008928.	2.1	12
623	<i>Escherichia coli</i> Sequence Type 457 Is an Emerging Extended-Spectrum-β-Lactam-Resistant Lineage with Reservoirs in Wildlife and Food-Producing Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	30
624	Newly Emerged Serotype 1c of <i>Shigella flexneri</i> : Multiple Origins and Changing Drug Resistance Landscape. <i>Genes</i> , 2020, 11, 1042.	1.0	1
625	Development of a High-Resolution Single-Nucleotide Polymorphism Strain-Typing Assay Using Whole Genome-Based Analyses for the <i>Lactobacillus acidophilus</i> Probiotic Strain. <i>Microorganisms</i> , 2020, 8, 1445.	1.6	4
626	Comparative Genomics and Pan-Genomics of the Myxococcaceae, including a Description of Five Novel Species: <i>Myxococcus eversor</i> sp. nov., <i>Myxococcus llanfairpwllgwyngyllgogerychwyrndrobwlllantysiliogogochensis</i> sp. nov., <i>Myxococcus vastator</i> sp. nov., <i>Pyxidicoccus caerfyrddinensis</i> sp. nov., and <i>Pyxidicoccus trucidator</i> sp. nov.. <i>Genome Biology and Evolution</i> , 2020, 12, 2289-2302.	1.1	48
627	Microbiota Supplementation with <i>Bifidobacterium</i> and <i>Lactobacillus</i> Modifies the Preterm Infant Gut Microbiota and Metabolome: An Observational Study. <i>Cell Reports Medicine</i> , 2020, 1, 100077.	3.3	119
628	Myanmar <i>Burkholderia pseudomallei</i> strains are genetically diverse and originate from Asia with phylogenetic evidence of reintroductions from neighbouring countries. <i>Scientific Reports</i> , 2020, 10, 16260.	1.6	11
629	GenAPI: a tool for gene absence-presence identification in fragmented bacterial genome sequences. <i>BMC Bioinformatics</i> , 2020, 21, 320.	1.2	19
630	<i>Escherichia coli</i> ST8196 is a novel, locally evolved, and extensively drug resistant pathogenic lineage within the ST131 clonal complex. <i>Emerging Microbes and Infections</i> , 2020, 9, 1780-1792.	3.0	3
631	First description of antimicrobial resistance in carbapenem-susceptible <i>Klebsiella pneumoniae</i> after imipenem treatment, driven by outer membrane remodeling. <i>BMC Microbiology</i> , 2020, 20, 218.	1.3	14
632	Completed Genomic Sequence of <i>Bacillus thuringiensis</i> HER1410 Reveals a Cry-Containing Chromosome, Two Megaplasms, and an Integrative Plasmidial Prophage. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2927-2939.	0.8	20
633	Antimicrobial Resistance in Wildlife in Guadeloupe (French West Indies): Distribution of a Single blaCTX-1/Inc11/ST3 Plasmid Among Humans and Wild Animals. <i>Frontiers in Microbiology</i> , 2020, 11, 1524.	1.5	25
634	Genomic and Phenotypic Analysis of an ESBL-Producing <i>E. coli</i> ST1159 Clonal Lineage From Wild Birds in Mongolia. <i>Frontiers in Microbiology</i> , 2020, 11, 1699.	1.5	7
635	Application of Whole Genome Sequencing and Pan-Family Multi-Locus Sequence Analysis to Characterize Relationships Within the Family <i>Brucellaceae</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1329.	1.5	17

#	ARTICLE	IF	CITATIONS
636	Molecular characterization of <i>Neisseria meningitidis</i> isolates recovered from patients with invasive meningococcal disease in Colombia from 2013 to 2016. <i>PLoS ONE</i> , 2020, 15, e0234475.	1.1	8
637	<i>Methanobrevibacter smithii</i> Archaemia in Febrile Patients With Bacteremia, Including Those With Endocarditis. <i>Clinical Infectious Diseases</i> , 2021, 73, e2571-e2579.	2.9	19
638	Multidrug-Resistant <i>Proteus mirabilis</i> Strain with Cointegrate Plasmid. <i>Microorganisms</i> , 2020, 8, 1775.	1.6	13
639	Multidrug-Resistant Hypervirulent <i>Klebsiella pneumoniae</i> Found Persisting Silently in Infant Gut Microbiota. <i>International Journal of Microbiology</i> , 2020, 2020, 1-6.	0.9	3
640	Genetic Variation in <i>Neisseria meningitidis</i> Does Not Influence Disease Severity in Meningococcal Meningitis. <i>Frontiers in Medicine</i> , 2020, 7, 594769.	1.2	8
641	Disease Diagnostics and Potential Coinfections by <i>Vibrio coralliilyticus</i> During an Ongoing Coral Disease Outbreak in Florida. <i>Frontiers in Microbiology</i> , 2020, 11, 569354.	1.5	55
642	Contribution of biofilm formation genetic locus, <i>pgaABCD</i> , to antibiotic resistance development in gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1842992.	4.3	9
643	Two New Cases of Pulmonary Infection by <i>Mycobacterium shigaense</i> , Japan. <i>Emerging Infectious Diseases</i> , 2020, 26, 2728-2732.	2.0	1
644	Quantitative Microbial Risk Assessment Based on Whole Genome Sequencing Data: Case of <i>Listeria monocytogenes</i> . <i>Microorganisms</i> , 2020, 8, 1772.	1.6	13
645	<i>Bartonella gabonensis</i> sp. nov., a new bartonella species from savannah rodent <i>Lophuromys</i> sp. in Franceville, Gabon. <i>New Microbes and New Infections</i> , 2020, 38, 100796.	0.8	5
646	Gene duplication drives genome expansion in a major lineage of Thaumarchaeota. <i>Nature Communications</i> , 2020, 11, 5494.	5.8	55
647	CAPRIB: a user-friendly tool to study amino acid changes and selection for the exploration of intra-genus evolution. <i>BMC Genomics</i> , 2020, 21, 832.	1.2	2
648	The Epidome - a species-specific approach to assess the population structure and heterogeneity of <i>Staphylococcus epidermidis</i> colonization and infection. <i>BMC Microbiology</i> , 2020, 20, 362.	1.3	8
649	Population genomics and antimicrobial resistance in <i>Corynebacterium diphtheriae</i> . <i>Genome Medicine</i> , 2020, 12, 107.	3.6	47
650	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
651	Genomic patterns and characterizations of chromosomally-encoded <i>mcr-1</i> in <i>Escherichia coli</i> populations. <i>Gut Pathogens</i> , 2020, 12, 55.	1.6	10
652	Emergence of a Clinical <i>Escherichia coli</i> Sequence Type 131 Strain Carrying a Chromosomal <i>blaKPC</i> <sup>2</sup> Gene. <i>Frontiers in Microbiology</i> , 2020, 11, 586764.	1.5	4
653	Genomic Characterization of <i>Salmonella</i> Minnesota Clonal Lineages Associated with Poultry Production in Brazil. <i>Animals</i> , 2020, 10, 2043.	1.0	10

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654	Limited Genetic Diversity of bla <sub>CMY-2</sub> -Containing Inc11-pST12 Plasmids from Enterobacteriaceae of Human and Broiler Chicken Origin in The Netherlands. <i>Microorganisms</i> , 2020, 8, 1755.	1.6	1
655	The assessment of leading traits in the taxonomy of the <i>Bacillus cereus</i> group. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 2223-2242.	0.7	9
656	Metagenomic Association Analysis of Gut Symbiont <i>Limosilactobacillus reuteri</i> Without Host-Specific Genome Isolation. <i>Frontiers in Microbiology</i> , 2020, 11, 585622.	1.5	4
657	Genome-based characterization of two Colombian clinical <i>Providencia rettgeri</i> isolates co-harboring NDM-1, VIM-2, and other $\beta$ -lactamases. <i>BMC Microbiology</i> , 2020, 20, 345.	1.3	12
658	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
659	Preliminary view of the global distribution and spread of the tet(X) family of tetracycline resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2797-2803.	1.3	22
660	Comparative Genomic Analysis of Rapidly Evolving SARS-CoV-2 Reveals Mosaic Pattern of Phylogeographical Distribution. <i>MSystems</i> , 2020, 5, .	1.7	60
661	Genetic Diversity Among <i>Mycobacterium avium</i> Subspecies Revealed by Analysis of Complete Genome Sequences. <i>Frontiers in Microbiology</i> , 2020, 11, 1701.	1.5	21
662	ICEs Are the Main Reservoirs of the Ciprofloxacin-Modifying <i>crpP</i> Gene in <i>Pseudomonas aeruginosa</i> . <i>Genes</i> , 2020, 11, 889.	1.0	13
663	Comparative genomics of canine <i>Lactobacillus reuteri</i> reveals adaptation to a shared environment with humans. <i>Genes and Genomics</i> , 2020, 42, 1107-1116.	0.5	5
664	Culturable diversity of bacterial endophytes associated with medicinal plants of the Western Ghats, India. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	18
665	Genetic and Phenotypic Factors Associated with Persistent Shedding of Shiga Toxin-Producing <i>Escherichia coli</i> by Beef Cattle. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	7
666	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	1.7	82
667	Description of <i>Komagataeibacter melaceti</i> sp. nov. and <i>Komagataeibacter melomenus</i> sp. nov. Isolated from Apple Cider Vinegar. <i>Microorganisms</i> , 2020, 8, 1178.	1.6	34
668	Comparative Genomics of <i>Microbacterium</i> Species to Reveal Diversity, Potential for Secondary Metabolites and Heavy Metal Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 1869.	1.5	29
669	<i>Georgenia faecalis</i> sp. nov. isolated from the faeces of Tibetan antelope. <i>Journal of Microbiology</i> , 2020, 58, 734-740.	1.3	1
670	Host Range Determinants of <i>Pseudomonas savastanoi</i> Pathovars of Woody Hosts Revealed by Comparative Genomics and Cross-Pathogenicity Tests. <i>Frontiers in Plant Science</i> , 2020, 11, 973.	1.7	24
671	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	3.8	419

#	ARTICLE	IF	CITATIONS
672	Type I-F CRISPR-Cas Distribution and Array Dynamics in <i>Legionella pneumophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1039-1050.	0.8	12
673	Complete Genomic Analysis of <i>Enterococcus faecium</i> Heat-Resistant Strain Developed by Two-Step Adaptation Laboratory Evolution Method. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 828.	2.0	8
674	Phylogenomic Classification and Biosynthetic Potential of the Fossil Fuel-Biodesulfurizing <i>Rhodococcus</i> Strain IGTS8. <i>Frontiers in Microbiology</i> , 2020, 11, 1417.	1.5	24
675	NAuRA: Genomic Tool to Identify Staphylococcal Enterotoxins in <i>Staphylococcus aureus</i> Strains Responsible for FoodBorne Outbreaks. <i>Frontiers in Microbiology</i> , 2020, 11, 1483.	1.5	22
676	Concurrent Infection of Skunk Adenovirus-1, <i>Listeria monocytogenes</i> , and a Regionally Specific Clade of Canine Distemper Virus in One Gray Fox ( <i>Urocyon cinereoargenteus</i> ) and Concurrent Listeriosis and Canine Distemper in a Second Gray Fox. <i>Pathogens</i> , 2020, 9, 591.	1.2	11
677	High diversity and variability of pipolins among a wide range of pathogenic <i>Escherichia coli</i> strains. <i>Scientific Reports</i> , 2020, 10, 12452.	1.6	7
678	A Diverse Panel of Clinical <i>Acinetobacter baumannii</i> for Research and Development. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	39
679	Succession of <i>Bifidobacterium longum</i> Strains in Response to a Changing Early Life Nutritional Environment Reveals Dietary Substrate Adaptations. <i>IScience</i> , 2020, 23, 101368.	1.9	26
680	Acquisition and Adaptation of Ultra-small Parasitic Reduced Genome Bacteria to Mammalian Hosts. <i>Cell Reports</i> , 2020, 32, 107939.	2.9	152
681	Completion of draft bacterial genomes by long-read sequencing of synthetic genomic pools. <i>BMC Genomics</i> , 2020, 21, 519.	1.2	11
682	Relationships among streptococci from the mitis group, misidentified as <i>Streptococcus pneumoniae</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2020, 39, 1865-1878.	1.3	7
683	<i>Enterococci</i> 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
684	Core and Accessory Genome Comparison of Australian and International Strains of O157 Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 566415.	1.5	3
685	Identification of a Novel Plasmid-Borne Gentamicin Resistance Gene in Nontyphoidal <i>Salmonella</i> Isolated from Retail Turkey. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	6
686	MDACP: A Pathogen Genome and Metagenome Analysis Cloud Platform. <i>Frontiers in Genetics</i> , 2020, 11, 1007.	1.1	1
687	A novel <i>Thermotoga</i> strain TFO isolated from a Californian petroleum reservoir phylogenetically related to <i>Thermotoga petrophila</i> and <i>T. naphthophila</i> , two thermophilic anaerobic isolates from a Japanese reservoir: Taxonomic and genomic considerations. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126132.	1.2	6
688	<i>AmpR</i> Increases the Virulence of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> by Regulating the Initial Step of Capsule Synthesis. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 3431-3441.	1.1	6
689	<i>Streptococcus pneumoniae</i> Serotype 12F-CC4846 and Invasive Pneumococcal Disease after Introduction of 13-Valent Pneumococcal Conjugate Vaccine, Japan, 2015–2017. <i>Emerging Infectious Diseases</i> , 2020, 26, 2660-2668.	2.0	5

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690	Differences in Blood-Derived <i>Francisella tularensis</i> Type B Strains from Clinical Cases of Tularemia. <i>Microorganisms</i> , 2020, 8, 1515.	1.6	3
691	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. <i>Communications Biology</i> , 2020, 3, 559.	2.0	11
692	Accurate reconstruction of bacterial pan- and core genomes with PEPPAN. <i>Genome Research</i> , 2020, 30, 1667-1679.	2.4	56
693	Phylogenetic and Evolutionary Analysis Reveals the Recent Dominance of Ciprofloxacin-Resistant <i>Shigella sonnei</i> and Local Persistence of <i>S. flexneri</i> Clones in India. <i>MSphere</i> , 2020, 5, .	1.3	5
694	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 5374.	5.8	40
695	Multidrug-Resistant CTX-M and CMY-2 Producing <i>Escherichia coli</i> Isolated from Healthy Household Dogs from the Great Metropolitan Area, Costa Rica. <i>Microbial Drug Resistance</i> , 2020, 26, 1421-1428.	0.9	7
696	Population Analysis of <i>Staphylococcus aureus</i> Reveals a Cryptic, Highly Prevalent Superantigen SEIW That Contributes to the Pathogenesis of Bacteremia. <i>MBio</i> , 2020, 11, .	1.8	14
697	The level of antimicrobial resistance of sewage isolates is higher than that of river isolates in different <i>Escherichia coli</i> lineages. <i>Scientific Reports</i> , 2020, 10, 17880.	1.6	12
698	High prevalence of <i>mcr-1</i> -encoded colistin resistance in commensal <i>Escherichia coli</i> from broiler chicken in Bangladesh. <i>Scientific Reports</i> , 2020, 10, 18637.	1.6	28
699	Pathogenic <i>Escherichia coli</i> Possess Elevated Growth Rates under Exposure to Sub-Inhibitory Concentrations of Azithromycin. <i>Antibiotics</i> , 2020, 9, 735.	1.5	5
700	Comparative Genome Analysis of <i>Bifidobacterium longum</i> subsp. <i>infantis</i> Strains Reveals Variation in Human Milk Oligosaccharide Utilization Genes among Commercial Probiotics. <i>Nutrients</i> , 2020, 12, 3247.	1.7	46
701	Strong oral plaque microbiome signatures for dental implant diseases identified by strain-resolution metagenomics. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 47.	2.9	54
702	Molecular characteristics of <i>Staphylococcus aureus</i> associated prosthetic joint infections after hip fractures treated with hemiarthroplasty: a retrospective genome-wide association study. <i>Scientific Reports</i> , 2020, 10, 16553.	1.6	4
703	Genomic analysis of European bovine <i>Staphylococcus aureus</i> from clinical versus subclinical mastitis. <i>Scientific Reports</i> , 2020, 10, 18172.	1.6	45
704	Reclassification of the Taxonomic Framework of Orders <i>Cellvibrionales</i> , <i>Oceanospirillales</i> , <i>Pseudomonadales</i> , and <i>Alteromonadales</i> in Class <i>Gammaproteobacteria</i> through Phylogenomic Tree Analysis. <i>MSystems</i> , 2020, 5, .	1.7	50
705	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
706	Characterization of integrated prophages within diverse species of clinical nontuberculous mycobacteria. <i>Virology Journal</i> , 2020, 17, 124.	1.4	22
707	Whole Genome Sequencing Reveals Virulence Potentials of <i>Helicobacter pylori</i> Strain KE21 Isolated from a Kenyan Patient with Gastric Signet Ring Cell Carcinoma. <i>Toxins</i> , 2020, 12, 556.	1.5	10



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708	High precision <i>Neisseria gonorrhoeae</i> variant and antimicrobial resistance calling from metagenomic Nanopore sequencing. <i>Genome Research</i> , 2020, 30, 1354-1363.	2.4	27
709	Investigation of a <i>Staphylococcus argenteus</i> Strain Involved in a Chronic Prosthetic-Joint Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6245.	1.8	7
710	Multi-omic Analysis of the Interaction between <i>Clostridioides difficile</i> Infection and Pediatric Inflammatory Bowel Disease. <i>Cell Host and Microbe</i> , 2020, 28, 422-433.e7.	5.1	45
711	Integrated chromosomal and plasmid sequence analyses reveal diverse modes of carbapenemase gene spread among <i>Klebsiella pneumoniae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25043-25054.	3.3	97
712	Diversity of the Genomes and Neurotoxins of Strains of <i>Clostridium botulinum</i> Group I and <i>Clostridium sporogenes</i> Associated with Foodborne, Infant and Wound Botulism. <i>Toxins</i> , 2020, 12, 586.	1.5	32
713	Genotype-phenotype correlation of $\beta$ -lactamase-producing uropathogenic <i>Escherichia coli</i> (UPEC) strains from Bangladesh. <i>Scientific Reports</i> , 2020, 10, 14549.	1.6	11
714	Twentieth-century emergence of antimicrobial resistant human- and bovine-associated <i>Salmonella enterica</i> serotype Typhimurium lineages in New York State. <i>Scientific Reports</i> , 2020, 10, 14428.	1.6	10
715	Complete Genome Sequence of Strain BB001, a Novel Epibiont Bacterium from the Candidate Phylum Saccharibacteria (TM7). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
716	Gut microorganisms act together to exacerbate inflammation in spinal cords. <i>Nature</i> , 2020, 585, 102-106.	13.7	153
717	Genomic Surveillance of Ceftriaxone-Resistant <i>Escherichia coli</i> in Western New York Suggests the Extended-Spectrum $\beta$ -Lactamase blaCTX-M-27 Is Emerging on Distinct Plasmids in ST38. <i>Frontiers in Microbiology</i> , 2020, 11, 1747.	1.5	16
718	Antibiotic Resistance Characteristics of <i>Pseudomonas aeruginosa</i> Isolated from Keratitis in Australia and India. <i>Antibiotics</i> , 2020, 9, 600.	1.5	26
719	Benchmarking hybrid assembly approaches for genomic analyses of bacterial pathogens using Illumina and Oxford Nanopore sequencing. <i>BMC Genomics</i> , 2020, 21, 631.	1.2	40
720	New insights into the biodiversity of coliphages in the intestine of poultry. <i>Scientific Reports</i> , 2020, 10, 15220.	1.6	13
721	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
722	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
723	Prevalence and Distribution Characteristics of bla <sub>KPC-2</sub> and bla <sub>NDM-1</sub> Genes in <i>Klebsiella pneumoniae</i> . <i>Infection and Drug Resistance</i> . 2020. Volume 13. 2901-2910.	1.1	22
724	The binding mechanism of the virulence factor <i>Streptococcus suis</i> adhesin P subtype to globotetraosylceramide is associated with systemic disease. <i>Journal of Biological Chemistry</i> , 2020, 295, 14305-14324.	1.6	10
725	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 4126.	5.8	51

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726	Fine capsule variation affects bacteriophage susceptibility in <i>Klebsiella pneumoniae</i> ST258. <i>FASEB Journal</i> , 2020, 34, 10801-10817.	0.2	17
727	Trophic cooperation promotes bacterial survival of <i>Staphylococcus aureus</i> and <i>Pseudomonas aeruginosa</i> . <i>ISME Journal</i> , 2020, 14, 3093-3105.	4.4	39
728	A Biological Inventory of Prophages in <i>A. baumannii</i> Genomes Reveal Distinct Distributions in Classes, Length, and Genomic Positions. <i>Frontiers in Microbiology</i> , 2020, 11, 579802.	1.5	38
729	Horizontally acquired papGII-containing pathogenicity islands underlie the emergence of invasive uropathogenic <i>Escherichia coli</i> lineages. <i>Nature Communications</i> , 2020, 11, 5968.	5.8	42
730	Pandemic <i>Vibrio cholerae</i> shuts down site-specific recombination to retain an interbacterial defence mechanism. <i>Nature Communications</i> , 2020, 11, 6246.	5.8	17
731	Comparative genomics of <i>Klebsiella michiganensis</i> BD177 and related members of <i>Klebsiella</i> sp. reveal the symbiotic relationship with <i>Bactrocera dorsalis</i> . <i>BMC Genetics</i> , 2020, 21, 138.	2.7	5
732	The Influence of Biofilms on Carbapenem Susceptibility and Patient Outcome in Device Associated <i>K. pneumoniae</i> Infections: Insights Into Phenotype vs Genome-Wide Analysis and Correlation. <i>Frontiers in Microbiology</i> , 2020, 11, 591679.	1.5	28
733	Survey and Sequence Characterization of Bovine Mastitis-Associated <i>Escherichia coli</i> in Dairy Herds. <i>Frontiers in Veterinary Science</i> , 2020, 7, 582297.	0.9	7
734	Functional and Genomic Characterization of <i>Ligilactobacillus salivarius</i> TUCO-L2 Isolated From Lama glama Milk: A Promising Immunobiotic Strain to Combat Infections. <i>Frontiers in Microbiology</i> , 2020, 11, 608752.	1.5	12
735	Antimicrobial Resistance and in silico Virulence Profiling of <i>Aliarcobacter butzleri</i> Strains From German Water Poultry. <i>Frontiers in Microbiology</i> , 2020, 11, 617685.	1.5	6
736	Carriage and Gene Content Variability of the pESI-Like Plasmid Associated with <i>Salmonella Infantis</i> Recently Established in United States Poultry Production. <i>Genes</i> , 2020, 11, 1516.	1.0	25
737	Identification of Nitrogen Fixation Genes in <i>Lactococcus</i> Isolated from Maize Using Population Genomics and Machine Learning. <i>Microorganisms</i> , 2020, 8, 2043.	1.6	15
738	Detection and elimination of a novel non-toxigenic <i>Clostridioides difficile</i> strain from the microbiota of a mouse colony. <i>Gut Microbes</i> , 2020, 12, 1851999.	4.3	4
739	Identification of New <i>Helicobacter pylori</i> Subpopulations in Native Americans and Mestizos From Peru. <i>Frontiers in Microbiology</i> , 2020, 11, 601839.	1.5	7
740	Comprehensive Genomic Investigation of Adaptive Mutations Driving the Low-Level Oxacillin Resistance Phenotype in <i>Staphylococcus aureus</i> . <i>MBio</i> , 2020, 11, .	1.8	27
741	A <i>Klebsiella pneumoniae</i> ST307 outbreak clone from Germany demonstrates features of extensive drug resistance, hypermucoviscosity, and enhanced iron acquisition. <i>Genome Medicine</i> , 2020, 12, 113.	3.6	82
742	Comparative genomics of <i>Helicobacter pullorum</i> from different countries. <i>Gut Pathogens</i> , 2020, 12, 56.	1.6	7
743	Antimicrobial Resistance and Genomic Characterization of OXA-48- and CTX-M-15-Co-Producing Hypervirulent <i>Klebsiella pneumoniae</i> ST23 Recovered from Nosocomial Outbreak. <i>Antibiotics</i> , 2020, 9, 862.	1.5	27

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744	Benchmarking Long-Read Assemblers for Genomic Analyses of Bacterial Pathogens Using Oxford Nanopore Sequencing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9161.	1.8	26
745	Comparative Genomics of <i>Xanthomonas citri</i> pv. <i>citri</i> A* Pathotype Reveals Three Distinct Clades with Varying Plasmid Distribution. <i>Microorganisms</i> , 2020, 8, 1947.	1.6	4
746	An integrated model system to gain mechanistic insights into biofilm-associated antimicrobial resistance in <i>Pseudomonas aeruginosa</i> MPAO1. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 46.	2.9	31
747	An Earliest Endosymbiont, <i>Wolbachia massiliensis</i> sp. nov., Strain PL13 from the Bed Bug ( <i>Cimex</i> ) Tj ETQq1 1 0.784314 rgBT /Overlooked 8064.	1.8	23
748	Cooperative Interaction of <i>Janthinobacterium</i> sp. SLB01 and <i>Flavobacterium</i> sp. SLB02 in the Diseased Sponge <i>Lubomirskia baicalensis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 8128.	1.8	7
749	Selection of Immunobiotic <i>Ligilactobacillus salivarius</i> Strains from the Intestinal Tract of Wakame-Fed Pigs: Functional and Genomic Studies. <i>Microorganisms</i> , 2020, 8, 1659.	1.6	21
750	<i>Mycoplasma bovis</i> in Nordic European Countries: Emergence and Dominance of a New Clone. <i>Pathogens</i> , 2020, 9, 875.	1.2	14
751	Comparative Genome Analysis of 33 <i>Chlamydia</i> Strains Reveals Characteristic Features of <i>Chlamydia Psittaci</i> and Closely Related Species. <i>Pathogens</i> , 2020, 9, 899.	1.2	24
752	Carbapenemase-Producing Gram-Negative Bacteria from American Crows in the United States. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	7
753	Population Genomic Analysis of <i>Mycoplasma bovis</i> Elucidates Geographical Variations and Genes associated with Host-Types. <i>Microorganisms</i> , 2020, 8, 1561.	1.6	13
754	Epidemiology of <i>Salmonella enterica</i> Serovar Dublin in Cattle and Humans in Denmark, 1996 to 2016: a Retrospective Whole-Genome-Based Study. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	20
755	Plasmids Shaped the Recent Emergence of the Major Nosocomial Pathogen <i>Enterococcus faecium</i> . <i>MBio</i> , 2020, 11, .	1.8	91
756	Phylogenomic Insights into Diversity and Evolution of Nonpathogenic <i>Xanthomonas</i> Strains Associated with Citrus. <i>MSphere</i> , 2020, 5, .	1.3	18
757	Deciphering the Structural Diversity and Classification of the Mobile Tigecycline Resistance Gene <i>tet(X)</i> -Bearing Plasmidome among Bacteria. <i>MSystems</i> , 2020, 5, .	1.7	85
758	A Genomic Toolkit for the Mechanistic Dissection of Intractable Human Gut Bacteria. <i>Cell Host and Microbe</i> , 2020, 27, 1001-1013.e9.	5.1	39
759	Comparative genomics in infectious disease. <i>Current Opinion in Microbiology</i> , 2020, 53, 61-70.	2.3	11
760	Dissemination of Quinolone-Resistant <i>Escherichia coli</i> in the Norwegian Broiler and Pig Production Chains and Possible Persistence in the Broiler Production Environment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
761	Deciphering the Cold Adaptive Mechanisms in <i>Pseudomonas psychrophila</i> MTCC12324 Isolated from the Arctic at 79° N. <i>Current Microbiology</i> , 2020, 77, 2345-2355.	1.0	14

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762	Prevalence and genomic characterization of <i>Salmonella</i> Weltevreden in commercial pig feed. <i>Veterinary Microbiology</i> , 2020, 246, 108725.	0.8	18
763	Revisiting the Metabolic Capabilities of <i>Bifidobacterium longum</i> subsp. <i>longum</i> and <i>Bifidobacterium longum</i> subsp. <i>infantis</i> from a Glycoside Hydrolase Perspective. <i>Microorganisms</i> , 2020, 8, 723.	1.6	11
764	Large-scale network analysis captures biological features of bacterial plasmids. <i>Nature Communications</i> , 2020, 11, 2452.	5.8	78
765	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
766	Genome Comparison Identifies Different <i>Bacillus</i> Species in a Bast Fibre-Retting Bacterial Consortium and Provides Insights into Pectin Degrading Genes. <i>Scientific Reports</i> , 2020, 10, 8169.	1.6	22
767	Linking Comparative Genomics of Nine Potato-Associated <i>Pseudomonas</i> Isolates With Their Differing Biocontrol Potential Against Late Blight. <i>Frontiers in Microbiology</i> , 2020, 11, 857.	1.5	32
768	Genomic profiling of antimicrobial resistance genes in clinical isolates of <i>Salmonella</i> Typhi from patients infected with Typhoid fever in India. <i>Scientific Reports</i> , 2020, 10, 8299.	1.6	41
769	Molecular Typing, Characterization of Antimicrobial Resistance, Virulence Profiling and Analysis of Whole-Genome Sequence of Clinical <i>Klebsiella pneumoniae</i> Isolates. <i>Antibiotics</i> , 2020, 9, 261.	1.5	29
770	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
771	Genomic variation among closely related <i>Vibrio alginolyticus</i> strains is located on mobile genetic elements. <i>BMC Genomics</i> , 2020, 21, 354.	1.2	19
772	Evolution of vancomycin-resistant <i>Enterococcus faecium</i> during colonization and infection in immunocompromised pediatric patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11703-11714.	3.3	36
773	Rhesus macaques are most likely the ancestral source of <i>Helicobacter suis</i> infection in pigs and not cynomolgus macaques. <i>Helicobacter</i> , 2020, 25, e12689.	1.6	1
774	Genotypic and Phenotypic Characterization of Fecal <i>Staphylococcus epidermidis</i> Isolates Suggests Plasticity to Adapt to Different Human Body Sites. <i>Frontiers in Microbiology</i> , 2020, 11, 688.	1.5	19
775	Pan-Genomic Analysis of <i>Clostridium botulinum</i> Group II (Non-Proteolytic <i>C. botulinum</i> ) Associated with Foodborne Botulism and Isolated from the Environment. <i>Toxins</i> , 2020, 12, 306.	1.5	20
776	Dynamics of mcr-1 prevalence and mcr-1-positive <i>Escherichia coli</i> after the cessation of colistin use as a feed additive for animals in China: a prospective cross-sectional and whole genome sequencing-based molecular epidemiological study. <i>Lancet Microbe</i> , The, 2020, 1, e34-e43.	3.4	85
777	Genome sequence analysis of multidrug-resistant <i>Mycobacterium tuberculosis</i> from Malaysia. <i>Scientific Data</i> , 2020, 7, 135.	2.4	4
778	Within-species variation in OMV cargo proteins: the <i>Myxococcus xanthus</i> OMV pan-proteome. <i>Molecular Omics</i> , 2020, 16, 387-397.	1.4	28
779	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

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780	Prophage-Mediated Disruption of Genetic Competence in <i>Staphylococcus pseudintermedius</i> . <i>MSystems</i> , 2020, 5, .	1.7	24
781	Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. <i>Nature Communications</i> , 2020, 11, 2610.	5.8	190
782	Pangenome Graphs. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 139-162.	2.5	148
783	Antimicrobial Resistance in <i>Salmonella enterica</i> Serovar Paratyphi B Variant Java in Poultry from Europe and Latin America. <i>Emerging Infectious Diseases</i> , 2020, 26, 1164-1173.	2.0	11
784	Comparison of Antimicrobial Resistance and Pan-Genome of Clinical and Non-Clinical <i>Enterococcus cecorum</i> from Poultry Using Whole-Genome Sequencing. <i>Foods</i> , 2020, 9, 686.	1.9	13
785	Determining the Genetic Characteristics of Resistance and Virulence of the <i>Staphylococcus epidermidis</i> Cluster Group Through Pan-Genome Analysis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 274.	1.8	16
786	Pan-GWAS of <i>Streptococcus agalactiae</i> Highlights Lineage-Specific Genes Associated with Virulence and Niche Adaptation. <i>MBio</i> , 2020, 11, .	1.8	47
787	Lateral Gene Transfer Shapes Diversity of <i>Gardnerella</i> spp.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 293.	1.8	18
788	A Novel Inducible Prophage from <i>Burkholderia vietnamiensis</i> G4 Is Widely Distributed across the Species and Has Lytic Activity against Pathogenic <i>Burkholderia</i> . <i>Viruses</i> , 2020, 12, 601.	1.5	8
789	Simultaneous Nasal Carriage by Methicillin-Resistant and Methicillin Susceptible <i>Staphylococcus aureus</i> of Lineage ST398 in a Live Pig Transporter. <i>Pathogens</i> , 2020, 9, 401.	1.2	4
790	Population genomics of <i>Staphylococcus pseudintermedius</i> in companion animals in the United States. <i>Communications Biology</i> , 2020, 3, 282.	2.0	29
791	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
792	Genetic Diversity of <i>Xylella fastidiosa</i> Plasmids Assessed by Comparative Genomics. <i>Tropical Plant Pathology</i> , 2020, 45, 342-360.	0.8	8
793	Interest of bacterial pangenome analyses in clinical microbiology. <i>Microbial Pathogenesis</i> , 2020, 149, 104275.	1.3	12
794	Structure and Evolution of <i>Acinetobacter baumannii</i> Plasmids. <i>Frontiers in Microbiology</i> , 2020, 11, 1283.	1.5	59
795	Detection of heterogeneous vancomycin intermediate resistance in MRSA isolates from Latin America. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2424-2431.	1.3	8
796	Overall changes in the transcriptome of <i>Escherichia coli</i> O26:H11 induced by a subinhibitory concentration of ciprofloxacin. <i>Journal of Applied Microbiology</i> , 2020, 129, 1577-1588.	1.4	12
797	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48

#	ARTICLE	IF	CITATIONS
798	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	3.8	72
799	Comparative Genome Analyses of Wild Type- and Quinolone Resistant <i>Escherichia coli</i> Indicate Dissemination of QREC in the Norwegian Broiler Breeding Pyramid. <i>Frontiers in Microbiology</i> , 2020, 11, 938.	1.5	5
800	A Modular Metagenomics Pipeline Allowing for the Inclusion of Prior Knowledge Using the Example of Anaerobic Digestion. <i>Microorganisms</i> , 2020, 8, 669.	1.6	1
801	A sister lineage of the <i>Mycobacterium tuberculosis</i> complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020, 11, 2917.	5.8	136
802	Genetic and Functional Analyses of Virulence Potential of an <i>Escherichia coli</i> O157:H7 Strain Isolated From Super-Shedder Cattle. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 271.	1.8	14
803	Complete Genome Sequences of <i>Micrococcus luteus</i> Strains NCCP 15687 and NCCP 16831, Isolated in South Korea. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
804	Novel <i>Erwinia persicina</i> Infecting Phage Midgardsormr38 Within the Context of Temperate <i>Erwinia</i> Phages. <i>Frontiers in Microbiology</i> , 2020, 11, 1245.	1.5	6
805	Lethal Outcome of Leptospirosis in Southern Russia: Characterization of <i>Leptospira interrogans</i> Isolated from a Deceased Teenager. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 4238.	1.2	3
806	Whole-Genome Analysis of Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 398 Strains Isolated From Patients With Bacteremia in China. <i>Journal of Infectious Diseases</i> , 2020, 221, S220-S228.	1.9	13
807	Molecular Characteristics of <i>Klebsiella pneumoniae</i> Isolates From Outpatients in Sentinel Hospitals, Beijing, China, 2010–2019. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 85.	1.8	12
808	<i>Neisseria gonorrhoeae</i> Population Genomics: Use of the Gonococcal Core Genome to Improve Surveillance of Antimicrobial Resistance. <i>Journal of Infectious Diseases</i> , 2020, 222, 1816-1825.	1.9	36
809	A highly conserved complete accessory <i>Escherichia coli</i> type III secretion system 2 is widespread in bloodstream isolates of the ST69 lineage. <i>Scientific Reports</i> , 2020, 10, 4135.	1.6	12
810	Novel Insights into the Classification of Staphylococcal $\beta$ -Lactamases in Relation to the Cefazolin Inoculum Effect. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	13
811	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
812	Four European <i>Salmonella</i> Typhimurium datasets collected to develop WGS-based source attribution methods. <i>Scientific Data</i> , 2020, 7, 75.	2.4	16
813	WhatsGNU: a tool for identifying proteomic novelty. <i>Genome Biology</i> , 2020, 21, 58.	3.8	15
814	The CRISPR-Cas systems were selectively inactivated during evolution of <i>Bacillus cereus</i> group for adaptation to diverse environments. <i>ISME Journal</i> , 2020, 14, 1479-1493.	4.4	32
815	PPanGGOLiN: Depicting microbial diversity via a partitioned pangenome graph. <i>PLoS Computational Biology</i> , 2020, 16, e1007732.	1.5	102

#	ARTICLE	IF	CITATIONS
816	Pan-transcriptomics and its applications. , 2020, , 343-356.		2
817	Phylogenetic relationship between Australian <i>Fusarium oxysporum</i> isolates and resolving the species complex using the multispecies coalescent model. <i>BMC Genomics</i> , 2020, 21, 248.	1.2	25
818	Host and body site-specific adaptation of <i>Lactobacillus crispatus</i> genomes. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa001.	1.5	21
819	Genome-resolved metagenomics to study co-occurrence patterns and intraspecific heterogeneity among plant pathogen metapopulations. <i>Environmental Microbiology</i> , 2020, 22, 2693-2708.	1.8	19
820	An Integrated Multi-Disciplinary Perspective for Addressing Challenges of the Human Gut Microbiome. <i>Metabolites</i> , 2020, 10, 94.	1.3	13
821	Genomic Stability of Composite SCCmec ACME and COMER-Like Genetic Elements in <i>Staphylococcus epidermidis</i> Correlates With Rate of Excision. <i>Frontiers in Microbiology</i> , 2020, 11, 166.	1.5	12
822	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
823	Population structure and adaptation of a bacterial pathogen in California grapevines. <i>Environmental Microbiology</i> , 2020, 22, 2625-2638.	1.8	26
824	Comparative genomic analysis reveals high intra-serovar plasticity within <i>Salmonella</i> Napoli isolated in 2005–2017. <i>BMC Genomics</i> , 2020, 21, 202.	1.2	12
825	Host-glycan metabolism is regulated by a species-conserved two-component system in <i>Streptococcus pneumoniae</i> . <i>PLoS Pathogens</i> , 2020, 16, e1008332.	2.1	10
826	Clinical and Genomic Epidemiology of Carbapenem-Nonsusceptible <i>Citrobacter</i> spp. at a Tertiary Health Care Center over 2 Decades. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	21
827	Municipal Wastewater Surveillance Revealed a High Community Disease Burden of a Rarely Reported and Possibly Subclinical <i>Salmonella enterica</i> Serovar Derby Strain. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	19
828	Genomic Characterization of mcr-1-carrying <i>Salmonella enterica</i> Serovar 4,[5],12:i:- ST 34 Clone Isolated From Pigs in China. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 663.	2.0	42
829	Genomic Surveillance Enables Suitability Assessment of <i>Salmonella</i> Gene Targets Used for Culture-Independent Diagnostic Testing. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	5
830	A novel <i>Borrelia</i> species, intermediate between Lyme disease and relapsing fever groups, in neotropical passerine-associated ticks. <i>Scientific Reports</i> , 2020, 10, 10596.	1.6	32
831	Phylogenomic characterisation of a novel corynebacterial species pathogenic to animals. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1225-1239.	0.7	13
832	<i>Staphylococcus</i> Agr virulence is critical for epidermal colonization and associates with atopic dermatitis development. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	62
833	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

#	ARTICLE	IF	CITATIONS
834	Comparative Genome-Centric Analysis of Freshwater and Marine ANAMMOX Cultures Suggests Functional Redundancy in Nitrogen Removal Processes. <i>Frontiers in Microbiology</i> , 2020, 11, 1637.	1.5	37
835	Stool Samples of Acute Diarrhea Inpatients as a Reservoir of ST11 Hypervirulent KPC-2-Producing <i>Klebsiella pneumoniae</i> . <i>MSystems</i> , 2020, 5, .	1.7	42
836	<p><em>Characterization of a Novel <em>mcr-8.2</em>-Bearing Plasmid in ST395 <em>Klebsiella pneumoniae</em> of Chicken Origin</p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1781-1784.	1.1	5
837	Genotypic and Phenotypic Diversity of <i>Staphylococcus aureus</i> Isolates from Cystic Fibrosis Patient Lung Infections and Their Interactions with <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2020, 11, .	1.8	45
838	Increasing incidence of group B streptococcus neonatal infections in the Netherlands is associated with clonal expansion of CC17 and CC23. <i>Scientific Reports</i> , 2020, 10, 9539.	1.6	25
839	Genomic epidemiology and carbon metabolism of <i>Escherichia coli</i> serogroup O145 reflect contrasting phylogenies. <i>PLoS ONE</i> , 2020, 15, e0235066.	1.1	3
840	Genomic analysis of <i>Escherichia coli</i> strains isolated from diseased chicken in the Czech Republic. <i>BMC Veterinary Research</i> , 2020, 16, 189.	0.7	30
841	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
842	A bioinformatic approach to identify core genome difference between <i>Salmonella Pullorum</i> and <i>Salmonella Enteritidis</i> . <i>Infection, Genetics and Evolution</i> , 2020, 85, 104446.	1.0	3
843	Phylogeographical Analyses and Antibiotic Resistance Genes of <i>Acinetobacter johnsonii</i> Highlight Its Clinical Relevance. <i>MSphere</i> , 2020, 5, .	1.3	13
844	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
845	Genomic analyses of multidrug-resistant <i>Salmonella</i> Indiana, Typhimurium, and Enteritidis isolates using MinION and MiSeq sequencing technologies. <i>PLoS ONE</i> , 2020, 15, e0235641.	1.1	16
846	Dynamics of mobile genetic elements of <i>Listeria monocytogenes</i> persisting in ready-to-eat seafood processing plants in France. <i>BMC Genomics</i> , 2020, 21, 130.	1.2	59
847	Comparative genomics of multidrug-resistant <i>Enterococcus</i> spp. isolated from wastewater treatment plants. <i>BMC Microbiology</i> , 2020, 20, 20.	1.3	31
848	Taxonomic Organization of the Family Brucellaceae Based on a Phylogenomic Approach. <i>Frontiers in Microbiology</i> , 2019, 10, 3083.	1.5	33
849	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
850	Whole-Genome Sequencing of <i>Corynebacterium diphtheriae</i> Isolates Recovered from an Inner-City Population Demonstrates the Predominance of a Single Molecular Strain. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	13
851	Using comparative genomics to understand molecular features of carbapenem-resistant <i>Acinetobacter baumannii</i> from South Korea causing invasive infections and their clinical implications. <i>PLoS ONE</i> , 2020, 15, e0229416.	1.1	13



#	ARTICLE	IF	CITATIONS
852	First Indian report on genome-wide comparison of multidrug-resistant <i>Escherichia coli</i> from blood stream infections. <i>PLoS ONE</i> , 2020, 15, e0220428.	1.1	33
853	<i>Escherichia coli</i> O8:H8 Carrying a Novel Variant of the Heat-Labile Enterotoxin LT2 Gene Caused Outbreaks of Diarrhea. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa021.	0.4	5
854	Whole genome sequencing reveals extended natural transformation in <i>Campylobacter</i> impacting diagnostics and the pathogens adaptive potential. <i>Scientific Reports</i> , 2020, 10, 3686.	1.6	24
855	First evidence of production of the lantibiotic nisin P. <i>Scientific Reports</i> , 2020, 10, 3738.	1.6	35
856	A three-year whole genome sequencing perspective of <i>Enterococcus faecium</i> sepsis in Australia. <i>PLoS ONE</i> , 2020, 15, e0228781.	1.1	14
857	<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
858	Fecal IgA Levels Are Determined by Strain-Level Differences in <i>Bacteroides ovatus</i> and Are Modifiable by Gut Microbiota Manipulation. <i>Cell Host and Microbe</i> , 2020, 27, 467-475.e6.	5.1	124
859	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
860	Comparative genomics: Dominant coral-bacterium <i>Endozoicomonas acroporae</i> metabolizes dimethylsulfoniopropionate (DMSP). <i>ISME Journal</i> , 2020, 14, 1290-1303.	4.4	96
861	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism calling pipelines. <i>GigaScience</i> , 2020, 9, .	3.3	92
862	A Proteogenomic Resource Enabling Integrated Analysis of <i>Listeria</i> Genotype-Phenotype Relationships. <i>Journal of Proteome Research</i> , 2020, 19, 1647-1662.	1.8	10
863	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	4.4	74
864	Extensive Genomic Rearrangements along with Distinct Mobilome and TALome are Associated with Extreme Pathotypes of a Rice Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 3951-3956.	1.1	2
865	Comparative Analysis of <i>Lactobacillus gasseri</i> and <i>Lactobacillus crispatus</i> Isolated From Human Urogenital and Gastrointestinal Tracts. <i>Frontiers in Microbiology</i> , 2019, 10, 3146.	1.5	41
866	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
867	<i>Lactobacillus rhamnosus</i> GG Genomic and Phenotypic Stability in an Industrial Production Process. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	13
868	A competence-regulated toxin-antitoxin system in <i>Haemophilus influenzae</i> . <i>PLoS ONE</i> , 2020, 15, e0217255.	1.1	5
869	A Real-Time PCR Screening Assay for Rapid Detection of <i>Listeria Monocytogenes</i> Outbreak Strains. <i>Foods</i> , 2020, 9, 67.	1.9	10

#	ARTICLE	IF	CITATIONS
870	Genetic Determinants of Trehalose Utilization Are Not Associated With Severe Clostridium difficile Infection Outcome. Open Forum Infectious Diseases, 2020, 7, ofz548.	0.4	19
871	A snapshot of diversity: Intraclonal variation of Escherichia coli clones as commensals and pathogens. International Journal of Medical Microbiology, 2020, 310, 151401.	1.5	7
872	Comparative genomic analysis reveals an "open" pan-genome of African swine fever virus. Transboundary and Emerging Diseases, 2020, 67, 1553-1562.	1.3	22
873	Distinct but Intertwined Evolutionary Histories of Multiple Salmonella enterica Subspecies. MSystems, 2020, 5, .	1.7	24
874	Bacillus subtilis strain GOT9 confers enhanced tolerance to drought and salt stresses in Arabidopsis thaliana and Brassica campestris. Plant Physiology and Biochemistry, 2020, 148, 359-367.	2.8	58
875	Mechanisms of $\beta$ -lactam resistance of Streptococcus uberis isolated from bovine mastitis cases. Veterinary Microbiology, 2020, 242, 108592.	0.8	18
876	Focal duodenal necrosis in chickens: attempts to reproduce the disease experimentally and diagnostic considerations. Journal of Veterinary Diagnostic Investigation, 2020, 32, 268-276.	0.5	2
877	Host-Specific Evolutionary and Transmission Dynamics Shape the Functional Diversification of Staphylococcus epidermidis in Human Skin. Cell, 2020, 180, 454-470.e18.	13.5	102
878	High quality 3C de novo assembly and annotation of a multidrug resistant ST-111 Pseudomonas aeruginosa genome: Benchmark of hybrid and non-hybrid assemblers. Scientific Reports, 2020, 10, 1392.	1.6	32
879	Genomic Characterization of Antibiotic Resistant Escherichia coli Isolated From Domestic Chickens in Pakistan. Frontiers in Microbiology, 2019, 10, 3052.	1.5	23
880	Stepwise evolution and convergent recombination underlie the global dissemination of carbapenemase-producing Escherichia coli. Genome Medicine, 2020, 12, 10.	3.6	40
881	The Wild Mouse (Micromys minutus): Reservoir of a Novel Campylobacter jejuni Strain. Frontiers in Microbiology, 2019, 10, 3066.	1.5	6
882	A novel tigeicycline resistance gene, tet(X6), on an SXT/R391 integrative and conjugative element in a Proteus genomospecies 6 isolate of retail meat origin. Journal of Antimicrobial Chemotherapy, 2020, 75, 1159-1164.	1.3	70
883	Diversity and Host Interactions among Virulent and Temperate Baltic Sea Flavobacterium Phages. Viruses, 2020, 12, 158.	1.5	11
884	Hybrid Genome Assembly and Annotation of a Pandrug-Resistant Klebsiella pneumoniae Strain Using Nanopore and Illumina Sequencing. Infection and Drug Resistance, 2020, Volume 13, 199-206.	1.1	26
885	Xanthomonas diversity, virulence and plant-pathogen interactions. Nature Reviews Microbiology, 2020, 18, 415-427.	13.6	182
886	The Pangenome. , 2020, , .		32
887	Abundance of Colistin-Resistant, OXA-23- and ArmA-Producing Acinetobacter baumannii Belonging to International Clone 2 in Greece. Frontiers in Microbiology, 2020, 11, 668.	1.5	29

#	ARTICLE	IF	CITATIONS
888	Atypical <i>Salmonella enterica</i> Serovars in Murine and Human Macrophage Infection Models. <i>Infection and Immunity</i> , 2020, 88, .	1.0	6
889	Description of Three Novel Members in the Family Geobacteraceae, <i>Oryzomonas japonicum</i> gen. nov., sp. nov., <i>Oryzomonas sagensis</i> sp. nov., and <i>Oryzomonas ruber</i> sp. nov.. <i>Microorganisms</i> , 2020, 8, 634.	1.6	29
890	Bioinformatics approaches applied in pan-genomics and their challenges. , 2020, , 43-64.		1
891	Pan-omics focused to Crick's central dogma. , 2020, , 1-41.		3
892	Genomic characteristics of clinically important ST11 <i>Klebsiella pneumoniae</i> strains worldwide. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 519-526.	0.9	36
893	Genomic Epidemiology of Vancomycin-Resistant <i>Enterococcus faecium</i> (VREfm) in Latin America: Revisiting The Global VRE Population Structure. <i>Scientific Reports</i> , 2020, 10, 5636.	1.6	39
894	Type II and type IV toxin-antitoxin systems show different evolutionary patterns in the global <i>Klebsiella pneumoniae</i> population. <i>Nucleic Acids Research</i> , 2020, 48, 4357-4370.	6.5	14
895	Genomic Landscape of <i>Ornithobacterium rhinotracheale</i> in Commercial Turkey Production in the United States. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	4
896	Genomic Epidemiology and Evolution of Diverse Lineages of Clinical <i>Campylobacter jejuni</i> Cocirculating in New Hampshire, USA, 2017. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	5
897	<i>Paenibacillus odorifer</i> , the Predominant <i>Paenibacillus</i> Species Isolated from Milk in the United States, Demonstrates Genetic and Phenotypic Conservation of Psychrotolerance but Clade-Associated Differences in Nitrogen Metabolic Pathways. <i>MSphere</i> , 2020, 5, .	1.3	9
898	Genomics of <i>Serratia marcescens</i> Isolates Causing Outbreaks in the Same Pediatric Unit 47 Years Apart: Position in an Updated Phylogeny of the Species. <i>Frontiers in Microbiology</i> , 2020, 11, 451.	1.5	18
899	Integrated Comparative Genomic Analysis and Phenotypic Profiling of <i>Pseudomonas aeruginosa</i> Isolates From Crude Oil. <i>Frontiers in Microbiology</i> , 2020, 11, 519.	1.5	9
900	Comparative Genome Analysis of Hungarian and Global Strains of <i>Salmonella infantis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 539.	1.5	19
901	Genomic and Phenotypic Analyses of <i>Acinetobacter baumannii</i> Isolates From Three Tertiary Care Hospitals in Thailand. <i>Frontiers in Microbiology</i> , 2020, 11, 548.	1.5	26
902	Biological Machine Learning Combined with <i>Campylobacter</i> Population Genomics Reveals Virulence Gene Allelic Variants Cause Disease. <i>Microorganisms</i> , 2020, 8, 549.	1.6	12
903	Metagenomic growth rate inferences of strains in situ. <i>Science Advances</i> , 2020, 6, eaaz2299.	4.7	19
904	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
905	Draft Genome Sequences of <i>Bifidobacterium animalis</i> Consecutively Isolated from Healthy Japanese Individuals. <i>Journal of Genomics</i> , 2020, 8, 37-42.	0.6	0

#	ARTICLE	IF	CITATIONS
906	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. <i>ISME Journal</i> , 2020, 14, 1834-1846.	4.4	43
907	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist <i>Stenotrophomonas maltophilia</i> . <i>Nature Communications</i> , 2020, 11, 2044.	5.8	76
908	Persistent contamination of raw milk by <i>Campylobacter jejuni</i> ST-883. <i>PLoS ONE</i> , 2020, 15, e0231810.	1.1	25
909	Complete genome sequence and comparative genomic analysis of hyper-aerotolerant <i>Campylobacter lari</i> strain SCHS02 isolated from duck for its potential pathogenicity. <i>Microbial Pathogenesis</i> , 2020, 142, 104110.	1.3	6
910	Reverse vaccinology and drug target identification through pan-genomics. , 2020, , 317-333.		5
911	Fecal Carriage of Extended-Spectrum-β <sup>2</sup> -Lactamase/AmpC-Producing <i>Escherichia coli</i> in Horses. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
912	Emergence of a Novel <i>Salmonella enterica</i> Serotype Reading Clonal Group Is Linked to Its Expansion in Commercial Turkey Production, Resulting in Unanticipated Human Illness in North America. <i>MSphere</i> , 2020, 5, .	1.3	22
913	Prevalence and Characteristics of Extended-Spectrum-β <sup>2</sup> -Lactamase-Producing and Carbapenemase-Producing <i>Enterobacteriaceae</i> from Freshwater Fish and Pork in Wet Markets of Hong Kong. <i>MSphere</i> , 2020, 5, .	1.3	18
914	Caries-Associated Biosynthetic Gene Clusters in <i>Streptococcus mutans</i> . <i>Journal of Dental Research</i> , 2020, 99, 969-976.	2.5	13
915	The Genomic Context for the Evolution and Transmission of Community-Associated <i>Staphylococcus aureus</i> ST59 Through the Food Chain. <i>Frontiers in Microbiology</i> , 2020, 11, 422.	1.5	21
916	Whole Genome Sequencing Differentiates Presumptive Extended Spectrum Beta-Lactamase Producing <i>Escherichia coli</i> along Segments of the One Health Continuum. <i>Microorganisms</i> , 2020, 8, 448.	1.6	25
917	Whole-Genome Sequencing-Based Characteristics in Extended-Spectrum Beta-Lactamase-Producing <i>Escherichia coli</i> Isolated from Retail Meats in Korea. <i>Microorganisms</i> , 2020, 8, 508.	1.6	6
918	Genomic Characterization of the Novel <i>Bartonella refiksaydamii</i> sp. Isolated from the Blood of a <i>Crocidura suaveolens</i> (Pallas, 1811). <i>Vector-Borne and Zoonotic Diseases</i> , 2021, 21, 432-440.	0.6	11
919	Applying Genomics to Track Antimicrobial Resistance in the Food Chain. , 2021, , 188-211.		3
920	Toward a high-quality pan-genome landscape of <i>Bacillus subtilis</i> by removal of confounding strains. <i>Briefings in Bioinformatics</i> , 2021, 22, 1951-1971.	3.2	46
921	Identification of Natural Mutations Responsible for Altered Infection Phenotypes of <i>Salmonella enterica</i> Clinical Isolates by Using Cell Line Infection Screens. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	4
922	IS <sub>26</sub> -mediated amplification of <i>bla</i> <sub>OXA-1</sub> and <i>bla</i> <sub>CTX-M-15</sub> 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
923	Characterization of <i>Bacillus cereus</i> sensu lato isolates from milk for consumption; phylogenetic identity, potential for spoilage and disease. <i>Food Microbiology</i> , 2021, 93, 103604.	2.1	14

#	ARTICLE	IF	CITATIONS
924	Characterization of <i>isa</i> (D), a Novel Gene Responsible for Resistance to Lincosamides, Streptogramins A, and Pleuromutilins in Fish Pathogenic <i>Lactococcus garvieae</i> Serotype II. Microbial Drug Resistance, 2021, 27, 301-310.	0.9	8
925	Mass drug administration with azithromycin for trachoma elimination and the population structure of <i>Streptococcus pneumoniae</i> in the nasopharynx. Clinical Microbiology and Infection, 2021, 27, 864-870.	2.8	3
926	A unified catalog of 204,938 reference genomes from the human gut microbiome. Nature Biotechnology, 2021, 39, 105-114.	9.4	628
927	Genomic and phenotypic analysis of siderophore-producing <i>Rhodococcus qingshengii</i> strain S10 isolated from an arid weathered serpentine rock environment. Archives of Microbiology, 2021, 203, 855-860.	1.0	6
928	Population Genomics of Bacterial Plant Pathogens. Phytopathology, 2021, 111, 23-31.	1.1	10
929	Genomic Characterization of Emerging Bacterial Uropathogen <i>Neisseria meningitidis</i> , Which Was Misidentified as <i>Neisseria gonorrhoeae</i> by Nucleic Acid Amplification Testing. Journal of Clinical Microbiology, 2021, 59, .	1.8	13
930	Isolation of Harveyi clade <i>Vibrio</i> spp. collected in aquaculture farms: How can the identification issue be addressed?. Journal of Microbiological Methods, 2021, 180, 106106.	0.7	11
931	Whole-genome sequencing of clinical <i>Clostridioides difficile</i> isolates reveals molecular epidemiology and discrepancies with conventional laboratory diagnostic testing. Journal of Hospital Infection, 2021, 108, 64-71.	1.4	5
932	The novel outer membrane protein from OprD/Occ family is associated with hypervirulence of carbapenem resistant <i>Acinetobacter baumannii</i> ST2/KL22. Virulence, 2021, 12, 1-11.	1.8	9
933	PCR identification of <i>Salmonella</i> serovars for the E serogroup based on novel specific targets obtained by pan-genome analysis. LWT - Food Science and Technology, 2021, 145, 110535.	2.5	7
934	GenSeizer: a Multiplex PCR-Based Targeted Gene Sequencing Platform for Rapid and Accurate Identification of Major <i>Mycobacterium</i> Species. Journal of Clinical Microbiology, 2021, 59, .	1.8	9
935	Phylogenetic and Biogeographic Patterns of <i>Vibrio parahaemolyticus</i> Strains from North America Inferred from Whole-Genome Sequence Data. Applied and Environmental Microbiology, 2021, 87, .	1.4	6
936	Isolation and genomic characterization of the ibuprofen-degrading bacterium <i>Sphingomonas</i> strain <i>MPO218</i> . Environmental Microbiology, 2021, 23, 267-280.	1.8	20
937	The changing epidemiology of carbapenemase-producing <i>Klebsiella pneumoniae</i> in Italy: toward polyclonal evolution with emergence of high-risk lineages. Journal of Antimicrobial Chemotherapy, 2021, 76, 355-361.	1.3	43
938	SNP-based genotyping and whole-genome sequencing reveal previously unknown genetic diversity in <i>Xanthomonas vasicola</i> pv. <i>musacearum</i> , causal agent of banana xanthomonas wilt, in its presumed Ethiopian origin. Plant Pathology, 2021, 70, 534-543.	1.2	3
939	Comparative genome analysis of global and Russian strains of community-acquired methicillin-resistant <i>Staphylococcus aureus</i> ST22, a Gaza clone™. International Journal of Antimicrobial Agents, 2021, 57, 106264.	1.1	9
940	Time-calibrated genomic evolution of a monomorphic bacterium during its establishment as an endemic crop pathogen. Molecular Ecology, 2021, 30, 1823-1835.	2.0	9
941	The <i>Roseobacter</i> -Group Bacterium <i>Phaeobacter</i> as a Safe Probiotic Solution for Aquaculture. Applied and Environmental Microbiology, 2021, 87, e0258120.	1.4	22

#	ARTICLE	IF	CITATIONS
942	Genome Reduction Is Associated with Bacterial Pathogenicity across Different Scales of Temporal and Ecological Divergence. <i>Molecular Biology and Evolution</i> , 2021, 38, 1570-1579.	3.5	50
943	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
944	Real-time PCR identification of <i>Listeria monocytogenes</i> serotype 4c using primers for novel target genes obtained by comparative genomic analysis. <i>LWT - Food Science and Technology</i> , 2021, 138, 110774.	2.5	10
945	Community-led, integrated, reproducible multi-omics with <i>anvi</i> ™. <i>Nature Microbiology</i> , 2021, 6, 3-6.	5.9	370
946	Stepwise evolution of <i>Salmonella</i> Typhimurium ST313 causing bloodstream infection in Africa. <i>Nature Microbiology</i> , 2021, 6, 327-338.	5.9	68
947	Polyclonality, Shared Strains, and Convergent Evolution in Chronic Cystic Fibrosis <i>&lt;i&gt;Staphylococcus aureus&lt;/i&gt;</i> Airway Infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021, 203, 1127-1137.	2.5	33
948	Bacteriophages that infect Gram-negative bacteria as source of signal-arrest-release motif lysins. <i>Research in Microbiology</i> , 2021, 172, 103794.	1.0	11
949	Diverse lineages of multidrug resistant clinical <i>Salmonella enterica</i> and a cryptic outbreak in New Hampshire, USA revealed from a year-long genomic surveillance. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104645.	1.0	6
950	Mining of novel target genes through pan-genome analysis for multiplex PCR differentiation of the major <i>Listeria monocytogenes</i> serotypes. <i>International Journal of Food Microbiology</i> , 2021, 339, 109026.	2.1	8
951	The population genetics of pathogenic <i>Escherichia coli</i> . <i>Nature Reviews Microbiology</i> , 2021, 19, 37-54.	13.6	268
952	Comparative genome analysis of 12 <i>Shigella sonnei</i> strains: virulence, resistance, and their interactions. <i>International Microbiology</i> , 2021, 24, 83-91.	1.1	1
953	<i>&lt;i&gt;CoreCruncher&lt;/i&gt;</i> : Fast and Robust Construction of Core Genomes in Large Prokaryotic Data Sets. <i>Molecular Biology and Evolution</i> , 2021, 38, 727-734.	3.5	17
954	Challenges in gene-oriented approaches for pangenome content discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
955	Whole genome analysis unveils genetic diversity and potential virulence determinants in <i>&lt;i&gt;Vibrio parahaemolyticus&lt;/i&gt;</i> associated with disease outbreak among cultured <i>&lt;i&gt;Litopenaeus vannamei&lt;/i&gt;</i> (Pacific white shrimp) in India. <i>Virulence</i> , 2021, 12, 1936-1949.	1.8	15
958	The utility of <i>Escherichia coli</i> as a contamination indicator for rural drinking water: Evidence from whole genome sequencing. <i>PLoS ONE</i> , 2021, 16, e0245910.	1.1	28
959	Genetic Diversity of Clinical <i>Bordetella Pertussis</i> ST2 Strains in comparison with Vaccine Reference Strains of India. <i>Journal of Genomics</i> , 2021, 9, 38-42.	0.6	1
960	Emergence of MDR invasive <i>&lt;i&gt;Neisseria meningitidis&lt;/i&gt;</i> in El Salvador, 2017â€“19. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1155-1159.	1.3	9
961	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

#	ARTICLE	IF	CITATIONS
962	Higher genome variability within metabolism genes associates with recurrent <i>Clostridium difficile</i> infection. <i>BMC Microbiology</i> , 2021, 21, 36.	1.3	7
964	Comparative Genomics of <i>Leuconostoc carnosum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 605127.	1.5	11
966	Analyses of publicly available <i>Hungatella hathewayi</i> genomes revealed genetic distances indicating they belong to more than one species. <i>Virulence</i> , 2021, 12, 1950-1964.	1.8	6
967	Multidrug Resistant <i>Klebsiella pneumoniae</i> ST101 Clone Survival Chain From Inpatients to Hospital Effluent After Chlorine Treatment. <i>Frontiers in Microbiology</i> , 2020, 11, 610296.	1.5	28
968	AMR-Diag: Neural network based genotype-to-phenotype prediction of resistance towards $\beta$ -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
969	metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. <i>Nucleic Acids Research</i> , 2021, 49, e126-e126.	6.5	50
971	Recent technological advancements in studying biodegradation of polycyclic aromatic hydrocarbons through theoretical approaches. , 2021, , 435-453.		0
972	Cryptic prophages within a <i>Streptococcus pyogenes</i> genotype emm4 lineage. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
974	Microbiota control of maternal behavior regulates early postnatal growth of offspring. <i>Science Advances</i> , 2021, 7, .	4.7	13
975	Rapid Genomic Characterization and Global Surveillance of <i>Klebsiella</i> Using Pathogenwatch. <i>Clinical Infectious Diseases</i> , 2021, 73, S325-S335.	2.9	47
976	Fungicidal Activity of Volatile Organic Compounds Emitted by <i>Burkholderia gladioli</i> Strain BBB-01. <i>Molecules</i> , 2021, 26, 745.	1.7	16
977	Predicting Host Association for Shiga Toxin-Producing <i>E. coli</i> Serogroups by Machine Learning. <i>Methods in Molecular Biology</i> , 2021, 2291, 99-117.	0.4	1
978	A Compendium of Bioinformatic Tools for Bacterial Pangenomics to Be Used by Wet-Lab Scientists. <i>Methods in Molecular Biology</i> , 2021, 2242, 233-243.	0.4	3
979	Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. <i>Methods in Molecular Biology</i> , 2021, 2242, 91-112.	0.4	0
980	Whole Genome Analysis of Environmental <i>Pseudomonas mendocina</i> Strains: Virulence Mechanisms and Phylogeny. <i>Genes</i> , 2021, 12, 115.	1.0	3
981	Taxonomic Evaluation of the <i>Heyndrickxia</i> (Basonym <i>Bacillus</i> ) <i>sporothermodurans</i> Group (H.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 246.	1.6	2
982	Emergence and Transmission of Daptomycin and Vancomycin-Resistant Enterococci Between Patients and Hospital Rooms. <i>Clinical Infectious Diseases</i> , 2021, 73, 2306-2313.	2.9	12
983	Antibiotic Resistance and Phylogeny of <i>Pseudomonas</i> spp. Isolated over Three Decades from Chicken Meat in the Norwegian Food Chain. <i>Microorganisms</i> , 2021, 9, 207.	1.6	24

#	ARTICLE	IF	CITATIONS
984	Gene Presence/Absence Variation analysis of coronavirus family displays its pan-genomic diversity. International Journal of Biological Sciences, 2021, 17, 3717-3727.	2.6	5
985	Kill and cure: genomic phylogeny and bioactivity of Burkholderia gladioli bacteria capable of pathogenic and beneficial lifestyles. Microbial Genomics, 2021, 7, .	1.0	24
986	Long-read metagenomics using PromethION uncovers oral bacteriophages and their interaction with host bacteria. Nature Communications, 2021, 12, 27.	5.8	45
987	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. Methods in Molecular Biology, 2021, 2242, 205-220.	0.4	5
988	Identification of the key characteristics of <i>Bifidobacterium longum</i> strains for the alleviation of ulcerative colitis. Food and Function, 2021, 12, 3476-3492.	2.1	23
989	Comparative analysis of genomic characteristics, fitness and virulence of MRSA ST398 and ST9 isolated from China and Germany. Emerging Microbes and Infections, 2021, 10, 1481-1494.	3.0	11
990	Comprehensive genomic analysis reveals virulence factors and antibiotic resistance genes in Pantoea agglomerans KM1, a potential opportunistic pathogen. PLoS ONE, 2021, 16, e0239792.	1.1	21
991	Whole genomic comparative analysis of Streptococcus pneumoniae serotype 1 isolates causing invasive and non-invasive infections among children under 5 years in Casablanca, Morocco. BMC Genomics, 2021, 22, 39.	1.2	2
992	Measurable Genomic Changes in Mycobacterium avium subsp. hominissuis after Long-Term Adaptation in Acanthamoeba lenticulata and Reduced Persistence in Macrophages. Journal of Bacteriology, 2021, 203, .	1.0	5
993	Distinct clonal lineages and within-host diversification shape invasive Staphylococcus epidermidis populations. PLoS Pathogens, 2021, 17, e1009304.	2.1	41
994	Proposed virulence-associated genes of Streptococcus suis isolates from the United States serve as predictors of pathogenicity. Porcine Health Management, 2021, 7, 22.	0.9	13
996	Complete Genome Sequence of a Clinical Campylobacter Isolate Identical to a Novel Campylobacter Species. Microbiology Resource Announcements, 2021, 10, .	0.3	2
997	Environmental Spread of Extended Spectrum Beta-Lactamase (ESBL) Producing <i>Escherichia coli</i> and ESBL Genes among Children and Domestic Animals in Ecuador. Environmental Health Perspectives, 2021, 129, 27007.	2.8	43
998	Essential Amino Acid Enrichment and Positive Selection Highlight Endosymbiont's Role in a Global Virus-Vectoring Pest. MSystems, 2021, 6, .	1.7	3
999	Genes Influencing Phage Host Range in Staphylococcus aureus on a Species-Wide Scale. MSphere, 2021, 6, .	1.3	19
1000	Comparative Genomics Analysis Demonstrated a Link Between Staphylococci Isolated From Different Sources: A Possible Public Health Risk. Frontiers in Microbiology, 2021, 12, 576696.	1.5	4
1001	Complete Genome Sequencing of Acinetobacter baumannii AC1633 and Acinetobacter nosocomialis AC1530 Unveils a Large Multidrug-Resistant Plasmid Encoding the NDM-1 and OXA-58 Carbapenemases. MSphere, 2021, 6, .	1.3	14
1002	Genomic and Chemical Diversity of Bacillus subtilis Secondary Metabolites against Plant Pathogenic Fungi. MSystems, 2021, 6, .	1.7	55



#	ARTICLE	IF	CITATIONS
1003	Comprehensive genomics depict accessory genes encoding pathogenicity and biofilm determinants in <i>Enterococcus faecalis</i> . <i>Future Microbiology</i> , 2021, 16, 143-157.	1.0	2
1004	Isolation and Characterization of <i>Kingella bonacorsii</i> sp. nov., A Novel <i>Kingella</i> Species Detected in a Stable Periodontitis Subject. <i>Pathogens</i> , 2021, 10, 240.	1.2	3
1006	Comparative genomics of <i>Staphylococcus epidermidis</i> from prosthetic-joint infections and nares highlights genetic traits associated with antimicrobial resistance, not virulence. <i>Microbial Genomics</i> , 2021, 7, .	1.0	19
1008	Comparative Genomics of <i>Mycobacterium avium</i> Subspecies Paratuberculosis Sheep Strains. <i>Frontiers in Veterinary Science</i> , 2021, 8, 637637.	0.9	7
1009	<i>Escherichia ruysiae</i> sp. nov., a novel Gram-stain-negative bacterium, isolated from a faecal sample of an international traveller. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	24
1010	Genomic Investigation of Virulence Potential in Shiga Toxin <i>Escherichia coli</i> (STEC) Strains From a Semi-Hard Raw Milk Cheese. <i>Frontiers in Microbiology</i> , 2020, 11, 629189.	1.5	5
1012	Nonadditive Transcriptomic Signatures of Genotype-by-Genotype Interactions during the Initiation of Plant-Rhizobium Symbiosis. <i>MSystems</i> , 2021, 6, .	1.7	26
1014	The Distribution of Several Genomic Virulence Determinants Does Not Corroborate the Established Serotyping Classification of <i>Bacillus thuringiensis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2244.	1.8	6
1015	Approaches for characterizing and tracking hospital-associated multidrug-resistant bacteria. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 2585-2606.	2.4	21
1016	Information Detection and Data Denoising Method Using Nano Electrode Array Sensor. <i>Journal of Nanoelectronics and Optoelectronics</i> , 2021, 16, 303-311.	0.1	0
1017	Comparative phenotypic, genotypic and genomic analyses of <i>Bacillus thuringiensis</i> associated with foodborne outbreaks in France. <i>PLoS ONE</i> , 2021, 16, e0246885.	1.1	29
1018	First Report of an Extensively Drug-Resistant ST23 <i>Klebsiella pneumoniae</i> of Capsular Serotype K1 Co-Producing CTX-M-15, OXA-48 and ArmA in Spain. <i>Antibiotics</i> , 2021, 10, 157.	1.5	17
1019	Plant NLR diversity: the known unknowns of pan-NLRomes. <i>Plant Cell</i> , 2021, 33, 814-831.	3.1	99
1020	cognac: rapid generation of concatenated gene alignments for phylogenetic inference from large, bacterial whole genome sequencing datasets. <i>BMC Bioinformatics</i> , 2021, 22, 70.	1.2	10
1021	A comprehensive and high-quality collection of <i>Escherichia coli</i> genomes and their genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	38
1022	Continental-Scale Gene Flow Prevents Allopatric Divergence of Pelagic Freshwater Bacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	50
1023	PlasmidHawk improves lab of origin prediction of engineered plasmids using sequence alignment. <i>Nature Communications</i> , 2021, 12, 1167.	5.8	11
1024	A novel vieuvirus from multidrug-resistant <i>Acinetobacter baumannii</i> . <i>Archives of Virology</i> , 2021, 166, 1401-1408.	0.9	6

#	ARTICLE	IF	CITATIONS
1025	Clonal spread of multi-resistant <i>Gallibacterium anatis</i> isolates among Iranian broilers and layers. <i>Veterinary Research</i> , 2021, 52, 27.	1.1	14
1026	Phylogeny of <i>Salmonella enterica</i> subspecies <i>arizonae</i> by whole-genome sequencing reveals high incidence of polyphyly and low phase I H antigen variability. <i>Microbial Genomics</i> , 2021, 7, .	1.0	3
1028	Epidemiological analysis of pneumococcal strains isolated at Yangon Children's Hospital in Myanmar via whole-genome sequencing-based methods. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
1029	Detection of Key Proteins in Obstetric Preeclampsia by Nanocomposites Using Gold Nanoparticles/ DNA/Methylene Blue. <i>Science of Advanced Materials</i> , 2021, 13, 321-330.	0.1	3
1030	Microbiota restoration reduces antibiotic-resistant bacteria gut colonization in patients with recurrent <i>Clostridioides difficile</i> infection from the open-label PUNCH CD study. <i>Genome Medicine</i> , 2021, 13, 28.	3.6	51
1031	<i>Salmonella</i> Genomics and Population Analyses Reveal High Inter- and Intraserovar Diversity in Freshwater. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	18
1032	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
1033	Sequence characterisation and novel insights into bovine mastitis-associated <i>Streptococcus uberis</i> in dairy herds. <i>Scientific Reports</i> , 2021, 11, 3046.	1.6	16
1034	Staphylococcal Enterotoxin Gene Cluster: Prediction of Enterotoxin (SEG and SEI) Production and of the Source of Food Poisoning on the Basis of <i>Sal</i> <sup>2</sup> Typing. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0266220.	1.4	14
1036	Molecular Epidemiology and Clone Transmission of Carbapenem-Resistant <i>Acinetobacter baumannii</i> in ICU Rooms. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 633817.	1.8	20
1037	Binnacle: Using Scaffolds to Improve the Contiguity and Quality of Metagenomic Bins. <i>Frontiers in Microbiology</i> , 2021, 12, 638561.	1.5	2
1039	Genomic Epidemiology and Evolution of <i>Escherichia coli</i> in Wild Animals in Mexico. <i>MSphere</i> , 2021, 6, .	1.3	19
1040	Colonization with <i>Staphylococcus aureus</i> and <i>Klebsiella pneumoniae</i> causes infections in a Vietnamese intensive care unit. <i>Microbial Genomics</i> , 2021, 7, .	1.0	10
1041	Comparative Genomic Analysis of <i>Mycobacteriaceae</i> Reveals Horizontal Gene Transfer-Mediated Evolution of the CRISPR-Cas System in the <i>Mycobacterium tuberculosis</i> Complex. <i>MSystems</i> , 2021, 6, .	1.7	11
1042	A novel DNA chromatography method to discriminate <i>Mycobacterium abscessus</i> subspecies and macrolide susceptibility. <i>EBioMedicine</i> , 2021, 64, 103187.	2.7	16
1043	Population Genomic Analysis of <i>Listeria monocytogenes</i> From Food Reveals Substrate-Specific Genome Variation. <i>Frontiers in Microbiology</i> , 2021, 12, 620033.	1.5	6
1046	Overview of bioinformatic methods for analysis of antibiotic resistome from genome and metagenome data. <i>Journal of Microbiology</i> , 2021, 59, 270-280.	1.3	16
1047	Evolutionary Dynamics Based on Comparative Genomics of Pathogenic <i>Escherichia coli</i> Lineages Harboring Polyketide Synthase ( <i>pks</i> ) Island. <i>MBio</i> , 2021, 12, .	1.8	10

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1048	Limosilactobacillus balticus sp. nov., Limosilactobacillus agrestis sp. nov., Limosilactobacillus albertensis sp. nov., Limosilactobacillus rudii sp. nov. and Limosilactobacillus fastidiosus sp. nov., five novel Limosilactobacillus species isolated from the vertebrate gastrointestinal tract, and proposal of six subspecies of Limosilactobacillus reuteri adapted to the gastrointestinal tract of specific vertebrate hosts. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	60
1049	Molecular investigation of an outbreak associated with total parenteral nutrition contaminated with NDM-producing <i>Leclercia adecarboxylata</i> . BMC Infectious Diseases, 2021, 21, 235.	1.3	10
1053	Evolutionary Genomic and Bacterial Genome-Wide Association Study of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> and Dairy Cattle Johne's Disease Phenotypes. Applied and Environmental Microbiology, 2021, 87, .	1.4	4
1054	Characterization of multidrug-resistant <i>Acinetobacter baumannii</i> strain ATCC BAA1605 using whole-genome sequencing. BMC Research Notes, 2021, 14, 83.	0.6	8
1055	Whole-Genome Sequencing and Comparative Genomics of Three <i>Helicobacter pylori</i> Strains Isolated from the Stomach of a Patient with Adenocarcinoma. Pathogens, 2021, 10, 331.	1.2	5
1058	A Test for the Rapid Detection of the Cefazolin Inoculum Effect in Methicillin-Susceptible <i>Staphylococcus aureus</i> . Journal of Clinical Microbiology, 2021, 59, .	1.8	6
1059	Market Chickens as a Source of Antibiotic-Resistant <i>Escherichia coli</i> in a Peri-Urban Community in Lima, Peru. Frontiers in Microbiology, 2021, 12, 635871.	1.5	27
1060	Genetic characterisation of a subset of <i>Campylobacter jejuni</i> isolates from clinical and poultry sources in Ireland. PLoS ONE, 2021, 16, e0246843.	1.1	8
1061	Characterization of antimicrobial-resistant Gram-negative bacteria that cause neonatal sepsis in seven low- and middle-income countries. Nature Microbiology, 2021, 6, 512-523.	5.9	146
1062	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
1063	Protein-Coding Genes of <i>Helicobacter pylori</i> Predominantly Present Purifying Selection though Many Membrane Proteins Suffer from Selection Pressure: A Proposal to Analyze Bacterial Pangenomes. Genes, 2021, 12, 377.	1.0	3
1064	Genome Sequencing of five <i>Lactocaseibacillus</i> Strains and Analysis of Type I and II Toxin-Antitoxin System Distribution. Microorganisms, 2021, 9, 648.	1.6	7
1066	Gill microbiome structure and function in the chemosymbiotic coastal lucinid <i>Stewartia floridana</i> . FEMS Microbiology Ecology, 2021, 97, .	1.3	2
1067	Evolutionary histories and antimicrobial resistance in <i>Shigella flexneri</i> and <i>Shigella sonnei</i> in Southeast Asia. Communications Biology, 2021, 4, 353.	2.0	17
1068	Isolation and Description of <i>Catonella massiliensis</i> sp. nov., a Novel <i>Catonella</i> Species, Isolated from a Stable Periodontitis Subject. Pathogens, 2021, 10, 367.	1.2	5
1071	GABA-Producing <i>Lactococcus lactis</i> Strains Isolated from Camel's Milk as Starters for the Production of GABA-Enriched Cheese. Foods, 2021, 10, 633.	1.9	17
1072	Identification of Novel Sensitive and Reliable Serovar-Specific Targets for PCR Detection of <i>Salmonella</i> Serovars Hadar and Albany by Pan-Genome Analysis. Frontiers in Microbiology, 2021, 12, 605984.	1.5	8
1073	A Roadmap for Genome-Based Phage Taxonomy. Viruses, 2021, 13, 506.	1.5	268

#	ARTICLE	IF	CITATIONS
1074	Comparative in silico genome analysis of <i>Clostridium perfringens</i> unravels stable phylogroups with different genome characteristics and pathogenic potential. <i>Scientific Reports</i> , 2021, 11, 6756.	1.6	16
1075	Isolation and Characterisation of Bacteriophages with Activity against Invasive Non-Typhoidal Salmonella Causing Bloodstream Infection in Malawi. <i>Viruses</i> , 2021, 13, 478.	1.5	8
1076	Genomic Analysis of <i>Staphylococcus aureus</i> of the Lineage CC130, Including mecC-Carrying MRSA and MSSA Isolates Recovered of Animal, Human, and Environmental Origins. <i>Frontiers in Microbiology</i> , 2021, 12, 655994.	1.5	12
1077	Genomic Characterization of <i>Campylobacter jejuni</i> Adapted to the Guinea Pig ( <i>Cavia porcellus</i> ) Host. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 607747.	1.8	5
1078	Taxonomic Identification of Different Species of the Genus <i>Aeromonas</i> by Whole-Genome Sequencing and Use of Their Species-Specific $\beta$ -Lactamases as Phylogenetic Markers. <i>Antibiotics</i> , 2021, 10, 354.	1.5	6
1081	Transmission, adaptation and geographical spread of the <i>Pseudomonas aeruginosa</i> Liverpool epidemic strain. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12
1082	Tetracycline Resistance Mediated by <i>tetM</i> (M) Has Variable Integrative Conjugative Element Composition in <i>Mycoplasma hominis</i> Strains Isolated in the United Kingdom from 2005 to 2015. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	13
1083	Machine learning predicts and provides insights into milk acidification rates of <i>Lactococcus lactis</i> . <i>PLoS ONE</i> , 2021, 16, e0246287.	1.1	7
1084	<i>Pseudomonas aeruginosa</i> PA80 is a cystic fibrosis isolate deficient in RhlRI quorum sensing. <i>Scientific Reports</i> , 2021, 11, 5729.	1.6	10
1085	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
1087	ESBL and AmpC $\beta$ -Lactamase Encoding Genes in <i>E. coli</i> From Pig and Pig Farm Workers in Vietnam and Their Association With Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2021, 12, 629139.	1.5	16
1090	Evidence of gene nucleotide composition favoring replication and growth in a fastidious plant pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
1093	Survival of <i>Salmonella</i> Under Heat Stress is Associated with the Presence/Absence of CRISPR Cas Genes and Iron Levels. <i>Current Microbiology</i> , 2021, 78, 1741-1751.	1.0	5
1094	Spatiotemporal persistence of multiple, diverse clades and toxins of <i>Corynebacterium diphtheriae</i> . <i>Nature Communications</i> , 2021, 12, 1500.	5.8	22
1095	Allopatric Plant Pathogen Population Divergence following Disease Emergence. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
1096	The global dissemination of hospital clones of <i>Enterococcus faecium</i> . <i>Genome Medicine</i> , 2021, 13, 52.	3.6	33
1097	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
1098	Genomics of an endemic cystic fibrosis <i>Burkholderia multivorans</i> strain reveals low within-patient evolution but high between-patient diversity. <i>PLoS Pathogens</i> , 2021, 17, e1009418.	2.1	11

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1099	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
1100	WGS Analysis of Clonal and Plasmidic Epidemiology of Colistin-Resistance Mediated by <i>mcr</i> Genes in the Poultry Sector in Lebanon. <i>Frontiers in Microbiology</i> , 2021, 12, 624194.	1.5	24
1101	The genetic variation landscape of African swine fever virus reveals frequent positive selection and adaptive flexibility. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 2703-2721.	1.3	10
1102	Activity of imipenem/relebactam against a Spanish nationwide collection of carbapenemase-producing Enterobacterales. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1498-1510.	1.3	27
1103	Unexpected genomic, biosynthetic and species diversity of <i>Streptomyces</i> bacteria from bats in Arizona and New Mexico, USA. <i>BMC Genomics</i> , 2021, 22, 247.	1.2	2
1104	Genomic and phenotypic diversity of <i>Enterococcus faecalis</i> isolated from endophthalmitis. <i>PLoS ONE</i> , 2021, 16, e0250084.	1.1	8
1106	New Genotype of <i>Yersinia pestis</i> Found in Live Rodents in Yunnan Province, China. <i>Frontiers in Microbiology</i> , 2021, 12, 628335.	1.5	5
1107	Unravelling the Molecular Mechanisms Underlying the Protective Effect of Lactate on the High-Pressure Resistance of <i>Listeria monocytogenes</i> . <i>Biomolecules</i> , 2021, 11, 677.	1.8	6
1108	Exploring the industrial potential of <i>Lactobacillus delbrueckii</i> ssp. <i>bulgaricus</i> by population genomics and genome-wide association study analysis. <i>Journal of Dairy Science</i> , 2021, 104, 4044-4055.	1.4	10
1109	Presence of Broad-Spectrum Beta-Lactamase-Producing Enterobacteriaceae in Zoo Mammals. <i>Microorganisms</i> , 2021, 9, 834.	1.6	9
1110	Genomic investigation of antimicrobial resistance determinants and virulence factors in <i>Salmonella enterica</i> serovars isolated from contaminated food and human stool samples in Brazil. <i>International Journal of Food Microbiology</i> , 2021, 343, 109091.	2.1	15
1111	Non-oral <i>Prevotella</i> stepping into the spotlight. <i>Anaerobe</i> , 2021, 68, 102321.	1.0	14
1112	Draft Genome Assemblies of Two <i>Campylobacter novaezeelandiae</i> and Four Unclassified Thermophilic <i>Campylobacter</i> Isolates from Canadian Agricultural Surface Water. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1113	Evolution and genomic insight into methicillin-resistant <i>Staphylococcus aureus</i> ST9 in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1703-1711.	1.3	11
1114	Accessory Genome Dynamics and Structural Variation of <i>Shigella</i> from Persistent Infections. <i>MBio</i> , 2021, 12, .	1.8	7
1115	Genomic diversity and molecular epidemiology of <i>Pasteurella multocida</i> . <i>PLoS ONE</i> , 2021, 16, e0249138.	1.1	36
1116	Genome and Pangenome Analysis of <i>Lactobacillus hilgardii</i> FLUBâ€”A New Strain Isolated from Mead. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3780.	1.8	2
1117	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

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1118	The complete genome sequence of <i>Listeria monocytogenes</i> strain S2542 and expression of selected genes under high-pressure processing. <i>BMC Research Notes</i> , 2021, 14, 137.	0.6	1
1119	Whole genome-based characterisation of antimicrobial resistance and genetic diversity in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> from ruminants. <i>Scientific Reports</i> , 2021, 11, 8998.	1.6	25
1120	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021, 184, 2053-2067.e18.	13.5	167
1121	Evolutionary stasis of a deep subsurface microbial lineage. <i>ISME Journal</i> , 2021, 15, 2830-2842.	4.4	23
1122	Vegetable-Derived Carbapenemase-Producing High-Risk <i>Klebsiella pneumoniae</i> ST15 and <i>Acinetobacter baumannii</i> ST2 Clones in Japan: Coexistence of <i>bla</i> <sub>NDM-1</sub> , <i>bla</i> <sub>OXA-66</sub> , <i>bla</i> <sub>OXA-72</sub> , and an <i>AbaR4</i> -Like Resistance Island in the Same Sample. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
1123	Genomic insights into persistence of <i>Listeria</i> species in the food processing environment. <i>Journal of Applied Microbiology</i> , 2021, 131, 2082-2094.	1.4	35
1124	Local Adaptation of <i>Legionella pneumophila</i> within a Hospital Hot Water System Increases Tolerance to Copper. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
1125	A Mycobacterial Systems Resource for the Research Community. <i>MBio</i> , 2021, 12, .	1.8	20
1127	Genomic Characterization of <i>Salmonella typhimurium</i> DT104 Strains Associated with Cattle and Beef Products. <i>Pathogens</i> , 2021, 10, 529.	1.2	7
1128	Patient and Microbial Genomic Factors Associated with Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Extraintestinal Colonization and Infection. <i>MSystems</i> , 2021, 6, .	1.7	16
1129	Multiple concurrent and convergent stages of genome reduction in bacterial symbionts across a stink bug family. <i>Scientific Reports</i> , 2021, 11, 7731.	1.6	7
1130	Population genomics and antimicrobial resistance dynamics of <i>Escherichia coli</i> in wastewater and river environments. <i>Communications Biology</i> , 2021, 4, 457.	2.0	20
1131	Insights on the Evolutionary Genomics of the <i>Blautia</i> Genus: Potential New Species and Genetic Content Among Lineages. <i>Frontiers in Microbiology</i> , 2021, 12, 660920.	1.5	33
1133	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021, 13, 61.	3.6	63
1134	Comparative genomics and physiological investigation supported safety, cold adaptation, efficient hydrolytic and plant growth-promoting potential of psychrotrophic <i>Glutamicibacter arilaitensis</i> LJH19, isolated from night-soil compost. <i>BMC Genomics</i> , 2021, 22, 307.	1.2	17
1135	Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic <i>Escherichia coli</i> (ETEC) circulating in modern time. <i>Scientific Reports</i> , 2021, 11, 9256.	1.6	12
1136	Genetic features of the <i>poxA</i> linezolid resistance gene in human enterococci from France. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1978-1985.	1.3	14
1137	Prophages integrating into prophages: A mechanism to accumulate type III secretion effector genes and duplicate Shiga toxin-encoding prophages in <i>Escherichia coli</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009073.	2.1	14

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1138	Re-Emergence of Salmonellosis in Hog Farms: Outbreak and Bacteriological Characterization. <i>Microorganisms</i> , 2021, 9, 947.	1.6	10
1139	Multi-Drug Resistant Plasmids with ESBL/AmpC and mcr-5.1 in Paraguayan Poultry Farms: The Linkage of Antibiotic Resistance and Hatcheries. <i>Microorganisms</i> , 2021, 9, 866.	1.6	6
1140	Genomic Characterization of <i>Salmonella enterica</i> Isolates From Retail Meat in Beijing, China. <i>Frontiers in Microbiology</i> , 2021, 12, 636332.	1.5	23
1141	Two <i>Acinetobacter baumannii</i> Isolates Obtained From a Fatal Necrotizing Fasciitis Infection Display Distinct Genomic and Phenotypic Characteristics in Comparison to Type Strains. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 635673.	1.8	7
1143	Cocultivation of an ultrasmall environmental parasitic bacterium with lytic ability against bacteria associated with wastewater foams. <i>Nature Microbiology</i> , 2021, 6, 703-711.	5.9	43
1144	In-Host Emergence of Linezolid Resistance in a Complex Pattern of Toxic Shock Syndrome Toxin-1-Positive Methicillin-Resistant <i>Staphylococcus aureus</i> Colonization in Siblings with Cystic Fibrosis. <i>Toxins</i> , 2021, 13, 317.	1.5	6
1145	New Sequence Type ST3449 in Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Isolates from a Cystic Fibrosis Patient. <i>Antibiotics</i> , 2021, 10, 491.	1.5	5
1146	Evidence for continental-scale dispersal of antimicrobial resistant bacteria by landfill-foraging gulls. <i>Science of the Total Environment</i> , 2021, 764, 144551.	3.9	30
1147	Horsing Around: <i>Escherichia coli</i> ST1250 of Equine Origin Harboring Epidemic IncHI1/ST9 Plasmid with <i>bla</i> <sub>CTX-M-1</sub> and an Operon for Short-Chain Fructooligosaccharide Metabolism. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	5
1148	Exploring the Antibiotic Resistance Burden in Livestock, Livestock Handlers and Their Non-Livestock Handling Contacts: A One Health Perspective. <i>Frontiers in Microbiology</i> , 2021, 12, 651461.	1.5	17
1149	Microbiota-associated risk factors for asymptomatic gut colonisation with multi-drug-resistant organisms in a Dutch nursing home. <i>Genome Medicine</i> , 2021, 13, 54.	3.6	19
1150	Genomics reveals the novel species placement of industrial contaminant isolates incorrectly identified as <i>Burkholderia lata</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
1151	Frequency, Local Dynamics, and Genomic Characteristics of ESBL-Producing <i>Escherichia coli</i> Isolated From Specimens of Hospitalized Horses. <i>Frontiers in Microbiology</i> , 2021, 12, 671676.	1.5	10
1152	Genomic context of the two integrons of ST-111 <i>Pseudomonas aeruginosa</i> AG1: A VIM-2-carrying old-acquaintance and a novel IMP-18-carrying integron. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104740.	1.0	7
1153	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
1154	A pan-genome method to determine core regions of the <i>Bacillus subtilis</i> and <i>Escherichia coli</i> genomes. <i>F1000Research</i> , 2021, 10, 286.	0.8	5
1155	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	4.7	47
1157	Horizontal transfer and evolution of wall teichoic acid gene cassettes in <i>Bacillus subtilis</i> . <i>F1000Research</i> , 2021, 10, 354.	0.8	4

#	ARTICLE	IF	CITATIONS
1158	EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure. <i>Nucleic Acids Research</i> , 2021, 49, W185-W192.	6.5	65
1159	The auxin-producing <i>Bacillus thuringiensis</i> RZ2MS9 promotes the growth and modifies the root architecture of tomato ( <i>Solanum lycopersicum</i> cv. Micro-Tom). <i>Archives of Microbiology</i> , 2021, 203, 3869-3882.	1.0	49
1160	Phylogenomic analysis and characterization of carbon monoxide utilization genes in the family Phyllobacteriaceae with reclassification of <i>Aminobacter carboxidus</i> (Meyer et al. 1993, HÄrrdt et al.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 TF 5 Microbiology</i> , 2021, 44, 126199.	1.2	8
1161	Combining comparative genomic analysis with machine learning reveals some promising diagnostic markers to identify five common pathogenic non-tuberculous mycobacteria. <i>Microbial Biotechnology</i> , 2021, 14, 1539-1549.	2.0	8
1162	<i>Chryseobacterium schmidteae</i> sp. nov. a novel bacterial species isolated from planarian <i>Schmidtea mediterranea</i> . <i>Scientific Reports</i> , 2021, 11, 11002.	1.6	10
1163	Prevalence, genomic characteristics, and transmission dynamics of mcr-1-positive <i>Salmonella enterica</i> Typhimurium from patients with infectious diarrhea. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151501.	1.5	8
1164	Isolation and Characterization of <i>Streptococcus</i> Mutans Phage as a Possible Treatment Agent for Caries. <i>Viruses</i> , 2021, 13, 825.	1.5	19
1165	Whole-Genome sequencing and comparative genomics of <i>Mycobacterium</i> spp. from farmed Atlantic and coho salmon in Chile. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1323-1336.	0.7	1
1166	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen <i>Mycobacterium kansasii</i> . <i>Nature Communications</i> , 2021, 12, 2491.	5.8	20
1167	Quantitative Detection of <i>Bifidobacterium longum</i> Strains in Feces Using Strain-Specific Primers. <i>Microorganisms</i> , 2021, 9, 1159.	1.6	9
1168	Emergence and Expansion of a Carbapenem-Resistant <i>Pseudomonas aeruginosa</i> Clone Are Associated with Plasmid-Borne <i>bla</i> KPC-2 and Virulence-Related Genes. <i>MSystems</i> , 2021, 6, .	1.7	33
1169	Isolation and Characterization of <i>Capnocytophaga bilenii</i> sp. nov., a Novel <i>Capnocytophaga</i> Species Detected in a Gingivitis Subject. <i>Pathogens</i> , 2021, 10, 547.	1.2	2
1170	Pan-Genome Analysis Reveals Host-Specific Functional Divergences in <i>Burkholderia gladioli</i> . <i>Microorganisms</i> , 2021, 9, 1123.	1.6	13
1171	Risk factors for acquisition of colistin-resistant <i>Klebsiella pneumoniae</i> and expansion of a colistin-resistant ST307 epidemic clone in hospitals in Marseille, France, 2014 to 2017. <i>Eurosurveillance</i> , 2021, 26, .	3.9	5
1172	Transmission Dynamics of Shiga Toxin-Producing <i>Escherichia coli</i> in New Zealand Cattle from Farm to Slaughter. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	3
1173	Distinguishing <i>bla</i> KPC Gene-Containing IncF Plasmids from Epidemiologically Related and Unrelated <i>Enterobacteriaceae</i> Based on Short- and Long-Read Sequence Data. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	4
1174	ProkEvo: an automated, reproducible, and scalable framework for high-throughput bacterial population genomics analyses. <i>PeerJ</i> , 2021, 9, e11376.	0.9	4
1176	Extensive Comparative Genomic Analysis of <i>Enterococcus faecalis</i> and <i>Enterococcus faecium</i> Reveals a Direct Association between the Absence of CRISPR-Cas Systems, the Presence of Anti-Endonuclease ( <i>ardA</i> ) and the Acquisition of Vancomycin Resistance in <i>E. faecium</i> . <i>Microorganisms</i> , 2021, 9, 1118.	1.6	6





#	ARTICLE	IF	CITATIONS
1197	Loop-mediated isothermal amplification (LAMP) for rapid detection of Salmonella in foods based on new molecular targets. <i>LWT - Food Science and Technology</i> , 2021, 142, 110999.	2.5	23
1198	Comparative Genomic Analysis of the Foodborne Pathogen <i>Burkholderia gladioli</i> pv. <i>cocovenenans</i> Harboring a Bongkrekic Acid Biosynthesis Gene Cluster. <i>Frontiers in Microbiology</i> , 2021, 12, 628538.	1.5	10
1199	Case Report: A New <i>Mycobacterium ulcerans</i> Genotype Causing Buruli Ulcer in CÔte d'Ivoire. <i>American Journal of Tropical Medicine and Hygiene</i> , 2021, 104, 1782-1783.	0.6	0
1200	Development of a One-Step Multiplex PCR Assay for Differential Detection of Four species ( <i>Enterobacter cloacae</i> , <i>Enterobacter hormaechei</i> , <i>Enterobacter roggkampii</i> , and <i>Enterobacter kobei</i> ) Belonging to <i>Enterobacter cloacae</i> Complex With Clinical Significance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 677089.	1.8	18
1201	PAN2HGENE tool for comparative analysis and identifying new gene products. <i>PLoS ONE</i> , 2021, 16, e0252414.	1.1	6
1203	Comparative genomics reveals an SNP potentially leading to phenotypic diversity of <i>Salmonella enterica</i> serovar <i>Enteritidis</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	3
1204	Evidence for Selection in the Abundant Accessory Gene Content of a Prokaryote Pangenome. <i>Molecular Biology and Evolution</i> , 2021, 38, 3697-3708.	3.5	21
1205	Genome-wide insights into population structure and host specificity of <i>Campylobacter jejuni</i> . <i>Scientific Reports</i> , 2021, 11, 10358.	1.6	18
1206	Specific metagenomic asset drives the spontaneous fermentation of Italian sausages. <i>Food Research International</i> , 2021, 144, 110379.	2.9	13
1208	Phylogenomic Characterization of a Novel <i>Corynebacterium</i> Species Associated with Fatal Diphtheritic Stomatitis in Endangered Yellow-Eyed Penguins. <i>MSystems</i> , 2021, 6, e0032021.	1.7	10
1209	Genomic and Transcriptomic Analysis of Colistin-Susceptible and Colistin-Resistant Isolates Identify Two-Component System EvgS/EvgA Associated with Colistin Resistance in <i>Escherichia coli</i> . <i>Infection and Drug Resistance</i> , 2021, Volume 14, 2437-2447.	1.1	2
1210	Genomic signatures of adaptation to natural settings in non-typhoidal <i>Salmonella enterica</i> Serovars Saintpaul, Thompson and Weltevreden. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104771.	1.0	5
1211	<i>gfpA</i> and <i>chiA</i> genes are not uniformly distributed amongst diverse <i>Vibrio cholerae</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
1212	Higher Prevalence of <i>Bacteroides fragilis</i> in Crohn's Disease Exacerbations and Strain-Dependent Increase of Epithelial Resistance. <i>Frontiers in Microbiology</i> , 2021, 12, 598232.	1.5	18
1214	Genomic analysis of <i>Neisseria elongata</i> isolate from a patient with infective endocarditis. <i>FEBS Open Bio</i> , 2021, 11, 1987-1996.	1.0	1
1215	Major genetic discontinuity and novel toxigenic species in <i>Clostridioides difficile</i> taxonomy. <i>ELife</i> , 2021, 10, .	2.8	50
1216	Comparative genomic analysis of <i>Mycoplasma anatis</i> strains. <i>Genes and Genomics</i> , 2021, 43, 1327-1337.	0.5	2
1217	The global emergence of a novel <i>Streptococcus suis</i> clade associated with human infections. <i>EMBO Molecular Medicine</i> , 2021, 13, e13810.	3.3	33

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1218	Precision Methylome and In Vivo Methylation Kinetics Characterization of <i>Klebsiella pneumoniae</i> . Genomics, Proteomics and Bioinformatics, 2022, 20, 418-434.	3.0	13
1219	Next-Generation Sequencing for Whole-Genome Characterization of <i>Weissella cibaria</i> UTNGt210 Strain Originated From Wild <i>Solanum quitoense</i> Lam. Fruits: An Atlas of Metabolites With Biotechnological Significance. Frontiers in Microbiology, 2021, 12, 675002.	1.5	11
1220	Evolutionary, genomic, and biogeographic characterization of two novel xenobiotics-degrading strains affiliated with <i>Dechloromonas</i> . Heliyon, 2021, 7, e07181.	1.4	12
1221	Characterisation of Bacteriophage-Encoded Depolymerases Selective for Key <i>Klebsiella pneumoniae</i> Capsular Exopolysaccharides. Frontiers in Cellular and Infection Microbiology, 2021, 11, 686090.	1.8	14
1222	Influence of Taxonomic and Functional Content of Microbial Communities on the Quality of Fermented Cocoa Pulp-Bean Mass. Applied and Environmental Microbiology, 2021, 87, e0042521.	1.4	9
1224	The Rhizobacterium <i>Pseudomonas alcaligenes</i> AVO110 Induces the Expression of Biofilm-Related Genes in Response to <i>Rosellinia necatrix</i> Exudates. Microorganisms, 2021, 9, 1388.	1.6	4
1225	Variability of the response of human vaginal <i>Lactobacillus crispatus</i> to 17 $\beta$ -estradiol. Scientific Reports, 2021, 11, 11533.	1.6	5
1226	Evolutionary responses to codon usage of horizontally transferred genes in <i>Pseudomonas aeruginosa</i> : gene retention, amelioration and compensatory evolution. Microbial Genomics, 2021, 7, .	1.0	9
1228	Genome-Inferred Correspondence between Phylogeny and Metabolic Traits in the Wild <i>Drosophila</i> Gut Microbiome. Genome Biology and Evolution, 2021, 13, .	1.1	5
1229	Multi-Omics Approach Reveals the Potential Core Vaccine Targets for the Emerging Foodborne Pathogen <i>Campylobacter jejuni</i> . Frontiers in Microbiology, 2021, 12, 665858.	1.5	7
1231	rMAP: the Rapid Microbial Analysis Pipeline for ESKAPE bacterial group whole-genome sequence data. Microbial Genomics, 2021, 7, .	1.0	6
1232	Bioinformatics tools used for whole-genome sequencing analysis of <i>Neisseria gonorrhoeae</i> : a literature review. Briefings in Functional Genomics, 2022, 21, 78-89.	1.3	3
1234	Unraveling the world of halophilic and halotolerant bacteria in cheese by combining cultural, genomic and metagenomic approaches. International Journal of Food Microbiology, 2021, 358, 109312.	2.1	16
1236	Protective effects of different <i>Bacteroides vulgatus</i> strains against lipopolysaccharide-induced acute intestinal injury, and their underlying functional genes. Journal of Advanced Research, 2022, 36, 27-37.	4.4	53
1237	Zetaproteobacteria Pan-Genome Reveals Candidate Gene Cluster for Twisted Stalk Biosynthesis and Export. Frontiers in Microbiology, 2021, 12, 679409.	1.5	9
1238	<i>Escherichia coli</i> Causing Recurrent Urinary Tract Infections: Comparison to Non-Recurrent Isolates and Genomic Adaptation in Recurrent Infections. Microorganisms, 2021, 9, 1416.	1.6	14
1239	<i>Staphylococcus saprophyticus</i> From Clinical and Environmental Origins Have Distinct Biofilm Composition. Frontiers in Microbiology, 2021, 12, 663768.	1.5	12
1240	Subtypes, resistance and virulence platforms in extended-drug resistant <i>Acinetobacter baumannii</i> Romanian isolates. Scientific Reports, 2021, 11, 13288.	1.6	16

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1241	Whole-Genome Sequencing and Machine Learning Analysis of <i>Staphylococcus aureus</i> from Multiple Heterogeneous Sources in China Reveals Common Genetic Traits of Antimicrobial Resistance. <i>MSystems</i> , 2021, 6, e0118520.	1.7	17
1242	Identification of new serovar-specific detection targets against salmonella B serogroup using large-scale comparative genomics. <i>Food Control</i> , 2021, 124, 107862.	2.8	5
1243	Genome-wide association studies reveal candidate genes associated to bacteraemia caused by ST93-IV CA-MRSA. <i>BMC Genomics</i> , 2021, 22, 418.	1.2	0
1245	Genomic epidemiology of methicillin-resistant and -susceptible <i>Staphylococcus aureus</i> from bloodstream infections. <i>BMC Infectious Diseases</i> , 2021, 21, 589.	1.3	13
1246	<i>Staphylococcus saprophyticus</i> Causing Infections in Humans Is Associated with High Resistance to Heavy Metals. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0268520.	1.4	9
1247	Genomic Information on Linezolid-Resistant Sequence-Type 398 Livestock-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Isolated from a Pig. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 378-387.	0.8	4
1248	Comparative metagenomic analysis of the vaginal microbiome in healthy women. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 77-84.	1.8	11
1250	Phylogenetically closely related pseudomonads isolated from arthropods exhibit differential insect-killing abilities and genetic variations in insecticidal factors. <i>Environmental Microbiology</i> , 2021, 23, 5378-5394.	1.8	13
1252	Mining genome traits that determine the different gut colonization potential of <i>Lactobacillus</i> and <i>Bifidobacterium</i> species. <i>Microbial Genomics</i> , 2021, 7, .	1.0	14
1254	Transcriptomics differentiate two novel bioactive strains of <i>Paenibacillus</i> sp. isolated from the perennial ryegrass seed microbiome. <i>Scientific Reports</i> , 2021, 11, 15545.	1.6	6
1255	Phenotypic and Genotypic Characterization of Novel Polyvalent Bacteriophages With Potent In Vitro Activity Against an International Collection of Genetically Diverse <i>Staphylococcus aureus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 698909.	1.8	8
1257	Genomic insights into methicillin-resistant <i>Staphylococcus pseudintermedius</i> isolates from dogs and humans of the same sequence types reveals diversity in prophages and pathogenicity islands. <i>PLoS ONE</i> , 2021, 16, e0254382.	1.1	8
1259	Comparative genomic analysis of <i>Escherichia coli</i> isolates from cases of bovine clinical mastitis identifies nine specific pathotype marker genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
1260	Phylogeography and resistome of pneumococcal meningitis in West Africa before and after vaccine introduction. <i>Microbial Genomics</i> , 2021, 7, .	1.0	0
1261	Pangenome analyses of LuxS-coding genes and enzymatic repertoires in cocoa-related lactic acid bacteria. <i>Genomics</i> , 2021, 113, 1659-1670.	1.3	7
1262	Pangenome analysis and virulence profiling of <i>Streptococcus intermedius</i> . <i>BMC Genomics</i> , 2021, 22, 522.	1.2	7
1264	Discerning the role of a functional arsenic-resistance cassette in the evolution and adaptation of a rice pathogen. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
1266	Pangenomic Analysis of <i>Dickeya dianthicola</i> Strains Related to the Outbreak of Blackleg and Soft Rot of Potato in USA. <i>Plant Disease</i> , 2021, , PDIS03210587RE.	0.7	5

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1267	Chloroplast Genome Sequencing, Comparative Analysis, and Discovery of Unique Cytoplasmic Variants in Pomegranate ( <i>Punica granatum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 704075.	1.1	10
1268	Phenotypic and Genetic Comparison of a Plant-Internalized and an Animal-Isolated <i>Salmonella</i> Choleraesuis Strain. <i>Microorganisms</i> , 2021, 9, 1554.	1.6	1
1270	Comparative genomics of <i>Edwardsiella ictaluri</i> revealed four distinct host-specific genotypes and thirteen potential vaccine candidates. <i>Genomics</i> , 2021, 113, 1976-1987.	1.3	10
1271	Evidence for the existence of a new genus <i>Chlamydiifrater</i> gen. nov. inside the family Chlamydiaceae with two new species isolated from flamingo ( <i>Phoenicopterus roseus</i> ): <i>Chlamydiifrater phoenicopteri</i> sp. nov. and <i>Chlamydiifrater volucris</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126200.	1.2	24
1272	A Molecular-Beacon-Based Multiplex Real-Time PCR Assay To Distinguish <i>Mycobacterium abscessus</i> Subspecies and Determine Macrolide Susceptibility. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0045521.	1.8	11
1273	Functional pangenome analysis reveals high virulence plasticity of <i>Aliarcobacter butzleri</i> and affinity to human mucus. <i>Genomics</i> , 2021, 113, 2065-2076.	1.3	11
1274	Whole-Genome Comparative Analysis Reveals Association Between <i>Salmonella</i> Genomic Variation and Egg Production Systems. <i>Frontiers in Veterinary Science</i> , 2021, 8, 666767.	0.9	2
1276	Identification of a Novel Plasmid-Mediated Carbapenemase-Encoding Gene, <i>bla</i> <sub>VMB-2</sub> , in <i>Vibrio diabolicus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0020621.	1.4	7
1277	Biofilm associated genotypes of multiple antibiotic resistant <i>Pseudomonas aeruginosa</i> . <i>BMC Genomics</i> , 2021, 22, 572.	1.2	11
1278	Investigation of the Genomic and Pathogenic Features of the Potentially Zoonotic <i>Streptococcus parasuis</i> . <i>Pathogens</i> , 2021, 10, 834.	1.2	8
1279	Interstrain Variability of Human Vaginal <i>Lactobacillus crispatus</i> for Metabolism of Biogenic Amines and Antimicrobial Activity against Urogenital Pathogens. <i>Molecules</i> , 2021, 26, 4538.	1.7	8
1280	MRSA strains with distinct accessory genes predominate at different ages in cystic fibrosis. <i>Pediatric Pulmonology</i> , 2021, 56, 2868-2878.	1.0	6
1281	PCR and multiplex PCR assays for the detection of <i>Cronobacter</i> species using specific targets obtained by a bioinformatics approach. <i>Food Control</i> , 2021, 125, 107896.	2.8	11
1282	Genomic Analysis of <i>Staphylococcus aureus</i> Isolates Associated With Peracute Non-gangrenous or Gangrenous Mastitis and Comparison With Other Mastitis-Associated <i>Staphylococcus aureus</i> Isolates. <i>Frontiers in Microbiology</i> , 2021, 12, 688819.	1.5	8
1283	Characterization, Pathogenicity, Phylogeny, and Comparative Genomic Analysis of <i>Pseudomonas tolaasii</i> Strains Isolated from Various Mushrooms in China. <i>Phytopathology</i> , 2022, 112, 521-534.	1.1	2
1284	Comprehensive pan-genome analysis of <i>Lactiplantibacillus plantarum</i> complete genomes. <i>Journal of Applied Microbiology</i> , 2022, 132, 592-604.	1.4	26
1286	Absence of Host-Specific Genes in Canine and Human <i>Staphylococcus pseudintermedius</i> as Inferred from Comparative Genomics. <i>Antibiotics</i> , 2021, 10, 854.	1.5	8
1287	The Tetracycline Resistance Gene, <i>tet</i> (W) in <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Follows Phylogeny and Differs From <i>tet</i> (W) in Other Species. <i>Frontiers in Microbiology</i> , 2021, 12, 658943.	1.5	11

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1288	Dynamics of Baltic Sea phages driven by environmental changes. <i>Environmental Microbiology</i> , 2021, 23, 4576-4594.	1.8	5
1289	Temperature and Nutrient Limitations Decrease Transfer of Conjugative IncP-1 Plasmid pJKK5 to Wild <i>Escherichia coli</i> Strains. <i>Frontiers in Microbiology</i> , 2021, 12, 656250.	1.5	20
1290	Whole-genome sequencing of <i>Pseudomonas</i> sp. TAE6080, a strain capable of inhibiting <i>Staphylococcus epidermidis</i> biofilm. <i>Marine Genomics</i> , 2021, 60, 100887.	0.4	3
1291	Genomic Landscape and Phenotypic Assessment of <i>Cronobacter sakazakii</i> Isolated From Raw Material, Environment, and Production Facilities in Powdered Infant Formula Factories in China. <i>Frontiers in Microbiology</i> , 2021, 12, 686189.	1.5	13
1292	Generation of Infectious Mimivirus Virions Through Inoculation of Viral DNA Within <i>Acanthamoeba castellanii</i> Shows Involvement of Five Proteins, Essentially Uncharacterized. <i>Frontiers in Microbiology</i> , 2021, 12, 677847.	1.5	0
1293	Targeted capture and sequencing of <i>Orientia tsutsugamushi</i> genomes from chiggers and humans. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104818.	1.0	6
1294	Genomic analysis of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 from cattle and pork-production related environments. <i>Npj Science of Food</i> , 2021, 5, 15.	2.5	6
1295	In vivo evolution of an emerging zoonotic bacterial pathogen in an immunocompromised human host. <i>Nature Communications</i> , 2021, 12, 4495.	5.8	6
1297	Genomic characterization of sporadic isolates of the dominant clone of <i>Mycobacterium abscessus</i> subspecies <i>massiliense</i> . <i>Scientific Reports</i> , 2021, 11, 15336.	1.6	11
1298	Ranking 67 Florida Reefs for Survival of <i>Acropora cervicornis</i> Outplants. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
1299	Comparative genome analysis of <i>Alkalihalobacillus okhensis</i> Kh10-101ÂT reveals insights into adaptive mechanisms for halo-alkali tolerance. <i>3 Biotech</i> , 2021, 11, 392.	1.1	4
1300	The <i>mutL</i> Gene as a Genome-Wide Taxonomic Marker for High Resolution Discrimination of <i>Lactiplantibacillus plantarum</i> and Its Closely Related Taxa. <i>Microorganisms</i> , 2021, 9, 1570.	1.6	2
1301	The dissemination of antimicrobial resistance determinants in surface water sources in Lebanon. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	5
1302	Polar bearâ€adapted <i>Ursidibacter maritimus</i> are remarkably conserved after generations in captivity. <i>Molecular Ecology</i> , 2021, 30, 4497-4504.	2.0	0
1303	<i>Pseudomonas lactucae</i> sp. nov., a pathogen causing bacterial rot of lettuce in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
1304	Delivery of Metabolically Neuroactive Probiotics to the Human Gut. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9122.	1.8	3
1305	Using genomics to examine the persistence of <i>Streptococcus pneumoniae</i> serotype 19A in Ireland and the emergence of a sub-clade associated with vaccine failures. <i>Vaccine</i> , 2021, 39, 5064-5073.	1.7	9
1306	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

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1307	Mobile Elements Harboring Heavy Metal and Bacitracin Resistance Genes Are Common among <i>Listeria monocytogenes</i> Strains Persisting on Dairy Farms. <i>MSphere</i> , 2021, 6, e0038321.	1.3	17
1308	Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clones from Wild Chimpanzees and Termites in Senegal. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0255720.	1.4	13
1310	Recent Evolution and Genomic Profile of <i>Salmonella enterica</i> Serovar Heidelberg Isolates from Poultry Flocks in Brazil. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0103621.	1.4	16
1311	Characterization of <i>Campylobacter</i> spp. Strains Isolated From Wild Birds in Turkey. <i>Frontiers in Microbiology</i> , 2021, 12, 712106.	1.5	8
1312	Evolutionary and Functional Analysis of Coagulase Positivity among the Staphylococci. <i>MSphere</i> , 2021, 6, e0038121.	1.3	9
1313	<i>Nitrogeniibacter mangrovi</i> gen. nov., sp. nov., a novel anaerobic and aerobic denitrifying betaproteobacterium and reclassification of <i>Azoarcus pumilus</i> as <i>Aromatoleum pumilum</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	13
1314	Machine Learning Prediction of Resistance to Subinhibitory Antimicrobial Concentrations from <i>Escherichia coli</i> Genomes. <i>MSystems</i> , 2021, 6, e0034621.	1.7	6
1315	The Resistome and Mobilome of Multidrug-Resistant <i>Staphylococcus sciuri</i> C2865 Unveil a Transferable Trimethoprim Resistance Gene, Designated <i>dfrE</i> , Spread Unnoticed. <i>MSystems</i> , 2021, 6, e0051121.	1.7	7
1316	Population Genomics of <i>emm4</i> Group A <i>Streptococcus</i> Reveals Progressive Replacement with a Hypervirulent Clone in North America. <i>MSystems</i> , 2021, 6, e0049521.	1.7	5
1319	<i>Prevotella copri</i> increases fat accumulation in pigs fed with formula diets. <i>Microbiome</i> , 2021, 9, 175.	4.9	100
1322	Rephine.r: a pipeline for correcting gene calls and clusters to improve phage pangenomes and phylogenies. <i>PeerJ</i> , 2021, 9, e11950.	0.9	2
1323	The genomic epidemiology of multi-drug resistant invasive non-typhoidal <i>Salmonella</i> in selected sub-Saharan African countries. <i>BMJ Global Health</i> , 2021, 6, e005659.	2.0	16
1324	Captive Common Marmosets ( <i>Callithrix jacchus</i> ) Are Colonized throughout Their Lives by a Community of <i>Bifidobacterium</i> Species with Species-Specific Genomic Content That Can Support Adaptation to Distinct Metabolic Niches. <i>MBio</i> , 2021, 12, e0115321.	1.8	8
1326	<i>Akkermansia muciniphila</i> Exerts Strain-Specific Effects on DSS-Induced Ulcerative Colitis in Mice. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 698914.	1.8	27
1327	Characterization of FRI carbapenemase-producing <i>Enterobacter</i> spp. isolated from a hospital and the environment in Osaka, Japan. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 3061-3062.	1.3	8
1328	Genome-based studies indicate that the <i>Enterococcus faecium</i> Clade B strains belong to <i>Enterococcus lactis</i> species and lack of the hospital infection associated markers. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	35
1329	Occurrence of major and minor pathogens in calves diagnosed with bovine respiratory disease. <i>Veterinary Microbiology</i> , 2021, 259, 109135.	0.8	18
1330	Genome-wide association study identifies the virulence-associated marker in <i>Streptococcus suis</i> serotype 2. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104894.	1.0	6

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1331	Genetic Background and Antibiotic Resistance Profiles of <i>K. pneumoniae</i> NDM-1 Strains Isolated from UTI, ABU, and the GI Tract, from One Hospital in Poland, in Relation to Strains Nationally and Worldwide. <i>Genes</i> , 2021, 12, 1285.	1.0	4
1334	Accessory Genomic Epidemiology of Cocirculating <i>Acinetobacter baumannii</i> Clones. <i>MSystems</i> , 2021, 6, e0062621.	1.7	15
1335	Complete Genome Sequencing and Comparative Analysis of <i>Citrobacter koseri</i> CKNJ, a Strain Isolated from a Patient with Endogenous Endophthalmitis. <i>Japanese Journal of Infectious Diseases</i> , 2022, 75, 148-155.	0.5	0
1337	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
1338	Whole Genome Sequencing of Pediatric <i>Klebsiella pneumoniae</i> Strains Reveals Important Insights Into Their Virulence-Associated Traits. <i>Frontiers in Microbiology</i> , 2021, 12, 711577.	1.5	11
1339	Draft Genome Sequence of <i>Bacillus velezensis</i> Strain Marseille-Q1230, Isolated from a Stool Sample from a Severely Malnourished Child. <i>Microbiology Resource Announcements</i> , 2021, 10, e0051421.	0.3	3
1340	Genomic insights into the diversity, virulence and resistance of <i>Klebsiella pneumoniae</i> extensively drug resistant clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
1342	Characterization of Emerging Pathogens Carrying blaKPC-2 Gene in IncP-6 Plasmids Isolated From Urban Sewage in Argentina. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 722536.	1.8	10
1343	A Combination of Metagenomic and Cultivation Approaches Reveals Hypermutator Phenotypes within <i>Vibrio cholerae</i> -Infected Patients. <i>MSystems</i> , 2021, 6, e0088921.	1.7	8
1344	Comparative genomics of <i>Salmonella enterica</i> subsp. <i>diarizonae</i> serovar 61:k:1,5,(7) reveals lineage-specific host adaptation of ST432. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
1346	Evolution of <i>Acinetobacter baumannii</i> in Clinical Bacteremia Patients. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 3553-3562.	1.1	3
1347	Genomic attributes differ between <i>Vibrio parahaemolyticus</i> environmental and clinical isolates including pathotypes. <i>Environmental Microbiology Reports</i> , 2022, 14, 365-375.	1.0	2
1348	Multilevel Genome Typing Describes Short- and Long-Term <i>Vibrio cholerae</i> Molecular Epidemiology. <i>MSystems</i> , 2021, 6, e0013421.	1.7	6
1349	The worm affair: fidelity and environmental adaptation in symbiont species that co-occur in vestimentiferan tubeworms. <i>Environmental Microbiology Reports</i> , 2021, 13, 744-752.	1.0	3
1350	Discovery of the <i>Pseudomonas</i> Polyene Protegencin by a Phylogeny-Guided Study of Polyene Biosynthetic Gene Cluster Diversity. <i>MBio</i> , 2021, 12, e0071521.	1.8	16
1351	Comparative Transcriptomic Analysis of <i>Staphylococcus aureus</i> Associated with Periprosthetic Joint Infection under in Vivo and in Vitro Conditions. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 986-999.	1.2	4
1353	Whole genome sequencing reveals the genomic diversity, taxonomic classification, and evolutionary relationships of the genus <i>Nocardia</i> . <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009665.	1.3	12
1354	Genome-Scale Metabolic Models and Machine Learning Reveal Genetic Determinants of Antibiotic Resistance in <i>Escherichia coli</i> and Unravel the Underlying Metabolic Adaptation Mechanisms. <i>MSystems</i> , 2021, 6, e0091320.	1.7	26



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1355	Development, Phenotypic Characterization and Genomic Analysis of a <i>Francisella tularensis</i> Panel for Tularemia Vaccine Testing. <i>Frontiers in Microbiology</i> , 2021, 12, 725776.	1.5	3
1356	Genomic Epidemiology and Global Population Structure of Exfoliative Toxin A-Producing <i>Staphylococcus aureus</i> Strains Associated With Staphylococcal Scalded Skin Syndrome. <i>Frontiers in Microbiology</i> , 2021, 12, 663831.	1.5	8
1357	Environmental stress leads to genome streamlining in a widely distributed species of soil bacteria. <i>ISME Journal</i> , 2022, 16, 423-434.	4.4	36
1359	Spontaneous Mutants of <i>Streptococcus sanguinis</i> with Defects in the Glucose-Phosphotransferase System Show Enhanced Post-Exponential-Phase Fitness. <i>Journal of Bacteriology</i> , 2021, 203, e0037521.	1.0	6
1360	<i>Corynebacterium hindlerae</i> sp. nov., derived from a human granuloma, which forms black colonies and black halos on modified Tinsdale medium but is not closely related to <i>Corynebacterium diphtheriae</i> and related taxa. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
1361	Genome-driven elucidation of phage-host interplay and impact of phage resistance evolution on bacterial fitness. <i>ISME Journal</i> , 2022, 16, 533-542.	4.4	32
1363	Comparative genomics reveals environmental adaptation differences between <i>Cronobacter</i> species. <i>Food Research International</i> , 2021, 147, 110541.	2.9	3
1364	<i>Xanthomonas sontii</i> sp. nov., a non-pathogenic bacterium isolated from healthy basmati rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo 0.7 22	0.7	22
1366	Molecular Characterisation of Vancomycin-Resistant <i>Enterococcus faecium</i> Isolates Belonging to the Lineage ST117/CT24 Causing Hospital Outbreaks. <i>Frontiers in Microbiology</i> , 2021, 12, 728356.	1.5	7
1367	Re-Emergence and Spread of Haemorrhagic Septicaemia in Germany: The Wolf as a Vector?. <i>Microorganisms</i> , 2021, 9, 1999.	1.6	1
1368	Metagenomic analysis of ancient dental calculus reveals unexplored diversity of oral archaeal <i>Methanobrevibacter</i> . <i>Microbiome</i> , 2021, 9, 197.	4.9	18
1369	Towards a better understanding of the bacterial pan-genome. <i>Acta Universitatis Lodzianis Folia Biologica Et Oecologica</i> , 0, 17, 84-96.	1.0	1
1370	Widespread prevalence and molecular epidemiology of tet(X4) and mcr-1 harboring <i>Escherichia coli</i> isolated from chickens in Pakistan. <i>Science of the Total Environment</i> , 2022, 806, 150689.	3.9	17
1371	Pan-Genome Portrait of <i>Bacillus mycoides</i> Provides Insights into the Species Ecology and Evolution. <i>Microbiology Spectrum</i> , 2021, 9, e0031121.	1.2	4
1372	Comparative Genomic Analysis of Novel <i>Bifidobacterium longum</i> subsp. <i>longum</i> Strains Reveals Functional Divergence in the Human Gut Microbiota. <i>Microorganisms</i> , 2021, 9, 1906.	1.6	11
1373	A role for arthropods as vectors of multidrug-resistant Enterobacterales in surgical site infections from South Asia. <i>Nature Microbiology</i> , 2021, 6, 1259-1270.	5.9	16
1374	Genetic Determinants of Stress Resistance in Desiccated <i>Salmonella enterica</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0168321.	1.4	8
1375	Comparative Genomic Features of &lt;i>Streptococcus canis</i> Based on Pan-Genome Orthologous Group Analysis According to Sequence Type. <i>Japanese Journal of Infectious Diseases</i> , 2022, 75, 269-276.	0.5	2

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1376	Whole genome sequencing reveals great diversity of <i>Vibrio</i> spp in prawns at retail. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
1377	The E phylogroup of <i>Escherichia coli</i> is highly diverse and mimics the whole <i>E. coli</i> species population structure. <i>Environmental Microbiology</i> , 2021, 23, 7139-7151.	1.8	16
1378	Homologous <i>Escherichia coli</i> Identified in Cerebrospinal Fluid and Bloodstream. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 674235.	1.8	2
1380	Analysis of Draft Genome Resources of Thirty-Three Canadian Strains of <i>Pseudomonas syringae</i> pv. <i>tomato</i> Isolated Between 1992 and 2008 Reveals Achromobactin Virulence Cluster that Is Absent in the Reference Strain DC3000. <i>Phytopathology</i> , 2022, 112, 968-972.	1.1	1
1381	Genomic stability among O3:K6V. <i>parahaemolyticus</i> pandemic strains isolated between 1996 to 2012 in American countries. <i>BMC Genomic Data</i> , 2021, 22, 38.	0.7	3
1382	The Hidden Genomic Diversity, Specialized Metabolite Capacity, and Revised Taxonomy of <i>Burkholderia Sensu Lato</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 726847.	1.5	16
1383	Clinical and Bacterial Characteristics of <i>Klebsiella pneumoniae</i> Affecting 30-Day Mortality in Patients With Bloodstream Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 688989.	1.8	11
1384	<i>Bacillus velezensis</i> stimulates resident rhizosphere <i>Pseudomonas stutzeri</i> for plant health through metabolic interactions. <i>ISME Journal</i> , 2022, 16, 774-787.	4.4	125
1385	Longitudinal Genomic Characterization of Carbapenemase-producing Enterobacteriaceae (CPE) Reveals Changing Pattern of CPE Isolated in Hong Kong Hospitals. <i>International Journal of Antimicrobial Agents</i> , 2021, 58, 106430.	1.1	5
1386	Colonized Niche, Evolution and Function Signatures of <i>Bifidobacterium pseudolongum</i> within <i>Bifidobacterium</i> Genus. <i>Foods</i> , 2021, 10, 2284.	1.9	6
1387	Clinical Molecular and Genomic Epidemiology of <i>Morganella morganii</i> in China. <i>Frontiers in Microbiology</i> , 2021, 12, 744291.	1.5	9
1388	Pandora: nucleotide-resolution bacterial pan-genomics with reference graphs. <i>Genome Biology</i> , 2021, 22, 267.	3.8	26
1389	A pan-genome method to determine core regions of the <i>Bacillus subtilis</i> and <i>Escherichia coli</i> genomes. <i>F1000Research</i> , 2021, 10, 286.	0.8	3
1390	Comparative Genome Analysis and Spore Heat Resistance Assay Reveal a New Component to Population Structure and Genome Epidemiology Within <i>Clostridium perfringens</i> Enterotoxin-Carrying Isolates. <i>Frontiers in Microbiology</i> , 2021, 12, 717176.	1.5	5
1391	Comparative genomics of in vitro and in vivo evolution of probiotics reveals energy restriction not the main evolution driving force in short term. <i>Genomics</i> , 2021, 113, 3373-3380.	1.3	4
1392	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
1393	Genome Analysis of Nicotinamide Adenine Dinucleotide-Independent <i>Mycoplasma synoviae</i> Isolates From Korea. <i>Pathogens</i> , 2021, 10, 1231.	1.2	0
1394	GALAXY Workflow for Bacterial Next-Generation Sequencing De Novo Assembly and Annotation. <i>Current Protocols</i> , 2021, 1, e242.	1.3	6

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1395	Spread of ESC-, carbapenem- and colistin-resistant <i>Escherichia coli</i> clones and plasmids within and between food workers in Lebanon. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 3135-3143.	1.3	18
1397	Identification of <i>Faecalibacterium prausnitzii</i> strains for gut microbiome-based intervention in Alzheimer's-type dementia. <i>Cell Reports Medicine</i> , 2021, 2, 100398.	3.3	42
1398	Molecular analysis of an increase in trimethoprim/sulfamethoxazole-resistant MRSA reveals multiple introductions into a tertiary care hospital, Germany 2012–19. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 77, 38-48.	1.3	7
1399	Surveillance for Colonization, Transmission, and Infection With Methicillin-Susceptible <i>Staphylococcus aureus</i> in a Neonatal Intensive Care Unit. <i>JAMA Network Open</i> , 2021, 4, e2124938.	2.8	22
1400	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
1401	Exploring the Genomic Diversity and Antimicrobial Susceptibility of <i>Bifidobacterium pseudocatenulatum</i> in a Vietnamese Population. <i>Microbiology Spectrum</i> , 2021, 9, e0052621.	1.2	6
1402	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
1404	Evolutionary Trajectories toward Ceftazidime-Avibactam Resistance in <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0057421.	1.4	41
1405	Whole-genome sequence-informed MALDI-TOF MS diagnostics reveal importance of <i>Klebsiella oxytoca</i> group in invasive infections: a retrospective clinical study. <i>Genome Medicine</i> , 2021, 13, 150.	3.6	19
1406	Global Expansion of Linezolid-Resistant Coagulase-Negative Staphylococci. <i>Frontiers in Microbiology</i> , 2021, 12, 661798.	1.5	14
1407	Gene-gene relationships in an <i>Escherichia coli</i> accessory genome are linked to function and mobility. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
1408	Single-colony sequencing reveals microbe-by-microbiome phyllosymbiosis between the cyanobacterium <i>Microcystis</i> and its associated bacteria. <i>Microbiome</i> , 2021, 9, 194.	4.9	27
1409	An object-oriented framework for evolutionary pangenome analysis. <i>Cell Reports Methods</i> , 2021, 1, 100085.	1.4	11
1410	The fall and rise of group B <i>Streptococcus</i> in dairy cattle: reintroduction due to human-to-cattle host jumps?. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12
1411	Genomic insights on DNase production in <i>Streptococcus agalactiae</i> ST17 and ST19 strains. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104969.	1.0	2
1412	Defining nosocomial transmission of <i>Escherichia coli</i> and antimicrobial resistance genes: a genomic surveillance study. <i>Lancet Microbe</i> , The, 2021, 2, e472-e480.	3.4	39
1413	Whole-genome analysis uncovers loss of bla <sub>Z</sub> 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
1414	Genome of <i>Bifidobacterium longum</i> NCIM 5672 provides insights into its acid-tolerance mechanism and probiotic properties. <i>Archives of Microbiology</i> , 2021, 203, 6109-6118.	1.0	9

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1415	Streptococcus pneumoniae serotypes that frequently colonise the human nasopharynx are common recipients of penicillin-binding protein gene fragments from Streptococcus mitis. Microbial Genomics, 2021, 7, .	1.0	5
1416	Genome-wide analysis provides a deeper understanding of the population structure of the Salmonella enterica serotype Paratyphi B complex in Bangladesh. Microbial Genomics, 2021, 7, .	1.0	2
1418	Human gut-derived B. longum subsp. longum strains protect against aging in a d-galactose-induced aging mouse model. Microbiome, 2021, 9, 180.	4.9	22
1419	Pan-Genome of the Genus Streptomyces and Prioritization of Biosynthetic Gene Clusters With Potential to Produce Antibiotic Compounds. Frontiers in Microbiology, 2021, 12, 677558.	1.5	21
1420	Eikenella glucosivorans sp. nov., isolated from a human throat swab, and emendation of the genus Eikenella to include saccharolytic species. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
1422	Genomic and biochemical characterization of antifungal compounds produced by Bacillus subtilis PMB102 against Alternaria brassicicola. Microbiological Research, 2021, 251, 126815.	2.5	18
1423	Heuristic and Hierarchical-Based Population Mining of Salmonella enterica Lineage I Pan-Genomes as a Platform to Enhance Food Safety. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	3
1424	In silico comparative genomics analysis of Lactiplantibacillus plantarum DW12, a potential gamma-aminobutyric acid (GABA)-producing strain. Microbiological Research, 2021, 251, 126833.	2.5	11
1425	Whole-Genome Assessment of Clinical Acinetobacter baumannii Isolates Uncovers Potentially Novel Factors Influencing Carbapenem Resistance. Frontiers in Microbiology, 2021, 12, 714284.	1.5	3
1426	First finding of Streptococcus phocae infections in mink (Neovison vison). Research in Veterinary Science, 2021, 139, 145-151.	0.9	3
1427	Genomic and phenotypic comparison of two Salmonella Typhimurium strains responsible for consecutive salmonellosis outbreaks in New Zealand. International Journal of Medical Microbiology, 2021, 311, 151534.	1.5	2
1428	Characterization of a blaNDM-1-Bearing IncHI5-Like Plasmid From Klebsiella pneumoniae of Infant Origin. Frontiers in Cellular and Infection Microbiology, 2021, 11, 738053.	1.8	9
1429	Characterization of antibiotic resistance and virulence genes of ocular methicillin-resistant Staphylococcus aureus strains through complete genome analysis. Experimental Eye Research, 2021, 212, 108764.	1.2	4
1430	Phylogenetic analysis and population structure of Pseudomonas alloputida. Genomics, 2021, 113, 3762-3773.	1.3	12
1431	Pre-existing T cell-mediated cross-reactivity to SARS-CoV-2 cannot solely be explained by prior exposure to endemic human coronaviruses. Infection, Genetics and Evolution, 2021, 95, 105075.	1.0	37
1432	Protocol for post-processing of bacterial pangenome data using Pagoo pipeline. STAR Protocols, 2021, 2, 100802.	0.5	5
1433	Whole-genome sequencing and antimicrobial resistance analysis of multidrug-resistant Aeromonas veronii strain JC529 from a common carp. Journal of Global Antimicrobial Resistance, 2021, 27, 118-122.	0.9	12
1434	Genomics landscape of 185 Streptococcus thermophilus and identification of fermentation biomarkers. Food Research International, 2021, 150, 110711.	2.9	8

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1435	Host-Dependent Clustering of <i>Campylobacter</i> Strains From Small Mammals in Finland. <i>Frontiers in Microbiology</i> , 2020, 11, 621490.	1.5	5
1436	<i>Bifidobacterium bifidum</i> strains synergize with immune checkpoint inhibitors to reduce tumour burden in mice. <i>Nature Microbiology</i> , 2021, 6, 277-288.	5.9	130
1437	Molecular characterization of carbapenem-resistant and virulent plasmids in <i>Klebsiella pneumoniae</i> from patients with bloodstream infections in China. <i>Emerging Microbes and Infections</i> , 2021, 10, 700-709.	3.0	31
1439	Multiplex PCR for the Identification of Pathogenic <i>Listeria</i> in <i>Flammulina velutipes</i> Plant Based on Novel Specific Targets Revealed by Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , 2020, 11, 634255.	1.5	9
1440	Diagnostic Sequences That Distinguish <i>M. avium</i> Subspecies Strains. <i>Frontiers in Veterinary Science</i> , 2020, 7, 620094.	0.9	2
1441	Intraspecies plasmid and genomic variation of <i>Mycobacterium kansasii</i> revealed by the complete genome sequences of two clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
1442	Integrating pan-genome with metagenome for microbial community profiling. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1458-1466.	1.9	16
1443	Genomic epidemiology of <i>Escherichia coli</i> isolates from a tertiary referral center in Lilongwe, Malawi. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12
1444	Identifying Conjugative Plasmids and Integrative Conjugative Elements with CONJscan. <i>Methods in Molecular Biology</i> , 2020, 2075, 265-283.	0.4	51
1445	A Review of Pangenome Tools and Recent Studies. , 2020, , 89-112.		21
1446	First Report of Isolation and Genome Sequence of <i>L. petauri</i> Strain from a Rainbow Trout Lactococcosis Outbreak. <i>Current Microbiology</i> , 2020, 77, 1089-1096.	1.0	21
1447	Genome recovery and metatranscriptomic confirmation of functional acetate-oxidizing bacteria from enriched anaerobic biogas digesters. <i>Environmental Pollution</i> , 2020, 265, 114843.	3.7	42
1448	Exploring tet(X)-bearing tigecycline-resistant bacteria of swine farming environments. <i>Science of the Total Environment</i> , 2020, 733, 139306.	3.9	47
1449	<i>Aliarcobacter vitoriensis</i> sp. nov., isolated from carrot and urban wastewater. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126091.	1.2	17
1450	Characterization of <i>Acinetobacter chengduensis</i> sp. nov., isolated from hospital sewage and capable of acquisition of carbapenem resistance genes. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126092.	1.2	14
1451	Pan-transcriptomic analysis identified common differentially expressed genes of <i>Acinetobacter baumannii</i> in response to polymyxin treatments. <i>Molecular Omics</i> , 2020, 16, 327-338.	1.4	7
1452	Signatures of cytoplasmic proteins in the exoproteome distinguish community- and hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> USA300 lineages. <i>Virulence</i> , 2017, 8, 891-907.	1.8	19
1453	Antimicrobial resistance and gene regulation in Enteroaggregative <i>Escherichia coli</i> from Egyptian children with diarrhoea: Similarities and differences. <i>Virulence</i> , 2021, 12, 57-74.	1.8	13

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1454	panRGP: a pangenome-based method to predict genomic islands and explore their diversity. <i>Bioinformatics</i> , 2020, 36, i651-i658.	1.8	26
1455	Symbiotic and Nonsymbiotic Members of the Genus <i>Ensifer</i> (syn. <i>Sinorhizobium</i> ) Are Separated into Two Clades Based on Comparative Genomics and High-Throughput Phenotyping. <i>Genome Biology and Evolution</i> , 2020, 12, 2521-2534.	1.1	30
1456	PanACoTA: a modular tool for massive microbial comparative genomics. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa106.	1.5	26
1457	<i>Streptococcus bovimastitidis</i> sp. nov., isolated from a dairy cow with mastitis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 21-27.	0.8	12
1458	<i>Listeria costaricensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 844-850.	0.8	39
1459	<i>Anaerobacillus isosaccharinicus</i> sp. nov., an alkaliphilic bacterium which degrades isosaccharinic acid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3666-3671.	0.8	17
1460	<i>Campylobacter blaseri</i> sp. nov., isolated from common seals ( <i>Phoca vitulina</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1787-1794.	0.8	22
1461	Whole-genome-based revisit of <i>Phototribus</i> phylogeny: proposal for the elevation of most <i>Phototribus</i> subspecies to the species level and description of one novel species <i>Phototribus bodei</i> sp. nov., and one novel subspecies <i>Phototribus laumondii</i> subsp. <i>clarkei</i> subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2664-2681.	0.8	132
1462	<i>Listeria goaensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3285-3291.	0.8	38
1463	<i>Staphylococcus cornubiensis</i> sp. nov., a member of the <i>Staphylococcus intermedius</i> Group (SIG). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3404-3408.	0.8	31
1464	<i>Listeria thailandensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 74-81.	0.8	55
1465	<i>Anaerobacillus alkaliphilus</i> sp. nov., a novel alkaliphilic and moderately halophilic bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 631-637.	0.8	19
1466	<i>Microbulbifer flavimaris</i> sp. nov., a halophilic Gammaproteobacteria isolated from marine sediment of the Yellow Sea, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1135-1141.	0.8	8
1467	<i>Vagococcus bubulae</i> sp. nov., isolated from ground beef, and <i>Vagococcus vulneris</i> sp. nov., isolated from a human foot wound. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2268-2276.	0.8	26
1468	<i>Leptospira yasudae</i> sp. nov. and <i>Leptospira stimsonii</i> sp. nov., two new species of the pathogenic group isolated from environmental sources. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1450-1456.	0.8	43
1469	Genome-based analyses indicate that <i>Serratia marcescens</i> subsp. <i>marcescens</i> and <i>Serratia marcescens</i> subsp. <i>sakuensis</i> do not merit separation to subspecies status. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3924-3926.	0.8	6
1470	<i>Campylobacter armoricus</i> sp. nov., a novel member of the <i>Campylobacter lari</i> group isolated from surface water and stools from humans with enteric infection. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3969-3979.	0.8	17
1471	Genome-based reclassification of <i>Lactobacillus casei</i> : emended classification and description of the species <i>Lactobacillus zeae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3755-3762.	0.8	36

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1472	<i>Streptococcus downii</i> sp. nov., isolated from the oral cavity of a teenager with Down syndrome. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4098-4104.	0.8	13
1473	<i>Dickeya oryzae</i> sp. nov., isolated from the roots of rice. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4171-4178.	0.8	51
1474	<i>Acinetobacter portensis</i> sp. nov. and <i>Acinetobacter guerrae</i> sp. nov., isolated from raw meat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4544-4554.	0.8	16
1475	Six novel species of the obligate marine actinobacterium <i>Salinispora</i> , <i>Salinispora cortesiana</i> sp. nov., <i>Salinispora fenicalii</i> sp. nov., <i>Salinispora goodfellowii</i> sp. nov., <i>Salinispora mooreana</i> sp. nov., <i>Salinispora oceanensis</i> sp. nov. and <i>Salinispora vitiensis</i> sp. nov., and emended description of the genus <i>Salinispora</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4668-4682.	0.8	40
1476	<i>Listeria valentina</i> sp. nov., isolated from a water trough and the faeces of healthy sheep. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5868-5879.	0.8	47
1477	<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
1478	Closed genome sequences of <i>Staphylococcus lloydii</i> sp. nov. and <i>Staphylococcus durrellii</i> sp. nov. isolated from captive fruit bats ( <i>Pteropus livingstonii</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	18
1479	Enhanced infectivity of strains of <i>Helicobacter pylori</i> isolated from children compared with parental strains. <i>Journal of Medical Microbiology</i> , 2019, 68, 633-641.	0.7	3
1480	Directional gene flow and ecological separation in <i>Yersinia enterocolitica</i> . <i>Microbial Genomics</i> , 2015, 1, e000030.	1.0	16
1481	Robust high-throughput prokaryote de novo assembly and improvement pipeline for Illumina data. <i>Microbial Genomics</i> , 2016, 2, e000083.	1.0	208
1482	Short-term evolution of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 between two food-borne outbreaks. <i>Microbial Genomics</i> , 2016, 2, e000084.	1.0	45
1483	Putatively novel serotypes and the potential for reduced vaccine effectiveness: capsular locus diversity revealed among 5405 pneumococcal genomes. <i>Microbial Genomics</i> , 2016, 2, 000090.	1.0	41
1484	Whole genome analysis of <i>Yersinia ruckeri</i> isolated over 27 years in Australia and New Zealand reveals geographical endemism over multiple lineages and recent evolution under host selection. <i>Microbial Genomics</i> , 2016, 2, e000095.	1.0	21
1485	Patchy promiscuity: machine learning applied to predict the host specificity of <i>Salmonella enterica</i> and <i>Escherichia coli</i> . <i>Microbial Genomics</i> , 2017, 3, e000135.	1.0	46
1486	Whole-genome sequencing of bloodstream <i>Staphylococcus aureus</i> isolates does not distinguish bacteraemia from endocarditis. <i>Microbial Genomics</i> , 2017, 3, .	1.0	21
1487	The lytic Myoviridae of Enterobacteriaceae form tight recombining assemblages separated by discontinuities in genome average nucleotide identity and lateral gene flow. <i>Microbial Genomics</i> , 2018, 4, .	1.0	3
1488	PANINI: Pangenome Neighbour Identification for Bacterial Populations. <i>Microbial Genomics</i> , 2019, 5, .	1.0	27
1489	Spatial structuring of a <i>Legionella pneumophila</i> population within the water system of a large occupational building. <i>Microbial Genomics</i> , 2018, 4, .	1.0	6

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1490	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	1.0	18
1491	Pan-genome analyses of model fungal species. <i>Microbial Genomics</i> , 2019, 5, .	1.0	59
1492	Genomic correlates of extraintestinal infection are linked with changes in cell morphology in <i>Campylobacter jejuni</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	6
1493	Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. <i>Microbial Genomics</i> , 2019, 5, .	1.0	12
1494	Caribbean multi-centre study of <i>Klebsiella pneumoniae</i> : whole-genome sequencing, antimicrobial resistance and virulence factors. <i>Microbial Genomics</i> , 2019, 5, .	1.0	19
1495	Global phylogenomics of multidrug-resistant <i>Salmonella enterica</i> serotype Kentucky ST198. <i>Microbial Genomics</i> , 2019, 5, .	1.0	69
1496	Not all <i>Pseudomonas aeruginosa</i> are equal: strains from industrial sources possess uniquely large multireplicon genomes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	26
1497	Analysis of genetic recombination and the pan-genome of a highly recombinogenic bacteriophage species. <i>Microbial Genomics</i> , 2019, 5, .	1.0	12
1498	The speciation and hybridization history of the genus <i>Salmonella</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	13
1499	Large-scale and significant expression from pseudogenes in <i>Sodalis glossinidius</i> – a facultative bacterial endosymbiont. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
1500	A cluster of melioidosis infections in hatchling saltwater crocodiles ( <i>Crocodylus porosus</i> ) resolved using genome-wide comparison of a common north Australian strain of <i>Burkholderia pseudomallei</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	7
1501	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	171
1502	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
1503	Comparative genomic analysis identifies X-factor (haemin)-independent <i>Haemophilus haemolyticus</i> : a formal re-classification of ' <i>Haemophilus intermedius</i> '. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
1504	Pangenome of <i>Acinetobacter baumannii</i> uncovers two groups of genomes, one of them with genes involved in CRISPR/Cas defence systems associated with the absence of plasmids and exclusive genes for biofilm formation. <i>Microbial Genomics</i> , 2019, 5, .	1.0	42
1505	O-antigen biosynthesis gene clusters of <i>Escherichia albertii</i> : their diversity and similarity to <i>Escherichia coli</i> gene clusters and the development of an O-genotyping method. <i>Microbial Genomics</i> , 2019, 5, .	1.0	27
1506	A guide to machine learning for bacterial host attribution using genome sequence data. <i>Microbial Genomics</i> , 2019, 5, .	1.0	26
1507	Differential dynamics and impacts of prophages and plasmids on the pangenome and virulence factor repertoires of Shiga toxin-producing <i>Escherichia coli</i> O145:H28. <i>Microbial Genomics</i> , 2020, 6, .	1.0	28



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1508	Coinfinder: detecting significant associations and dissociations in pangenomes. <i>Microbial Genomics</i> , 2020, 6, .	1.0	40
1509	Origin, maintenance and spread of antibiotic resistance genes within plasmids and chromosomes of bloodstream isolates of <i>Escherichia coli</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	20
1510	Visualizing variation within Global Pneumococcal Sequence Clusters (GPSCs) and country population snapshots to contextualize pneumococcal isolates. <i>Microbial Genomics</i> , 2020, 6, .	1.0	25
1511	Bayesian reconstruction of <i>Mycobacterium tuberculosis</i> transmission networks in a high incidence area over two decades in Malawi reveals associated risk factors and genomic variants. <i>Microbial Genomics</i> , 2020, 6, .	1.0	18
1512	AB_SA: Accessory genes-Based Source Attribution “ tracing the source of <i>Salmonella enterica</i> Typhimurium environmental strains. <i>Microbial Genomics</i> , 2020, 6, .	1.0	7
1513	Assessing the genomic relatedness and evolutionary rates of persistent verotoxigenic <i>Escherichia coli</i> serotypes within a closed beef herd in Canada. <i>Microbial Genomics</i> , 2020, 6, .	1.0	4
1514	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
1515	Microevolution in the major outer membrane protein OmpA of <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	19
1516	Genomic analyses of <i>Staphylococcus aureus</i> clonal complex 45 isolates does not distinguish nasal carriage from bacteraemia. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
1517	Whole-genome analyses reveal gene content differences between nontypeable <i>Haemophilus influenzae</i> isolates from chronic obstructive pulmonary disease compared to other clinical phenotypes. <i>Microbial Genomics</i> , 2020, 6, .	1.0	10
1518	Comparative genome analysis of <i>Erysipelothrix rhusiopathiae</i> isolated from domestic pigs and wild boars suggests host adaptation and selective pressure from the use of antibiotics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	4
1519	Diversification in immunogenicity genes caused by selective pressures in invasive meningococci. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
1520	Comparing serotyping with whole-genome sequencing for subtyping of non-typhoidal <i>Salmonella enterica</i> : a large-scale analysis of 37 serotypes with a public health impact in the USA. <i>Microbial Genomics</i> , 2020, 6, .	1.0	11
1521	Forensic genomics of a novel <i>Klebsiella quasipneumoniae</i> type from a neonatal intensive care unit in China reveals patterns of colonization, evolution and epidemiology. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
1522	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
1523	Analysis of complete <i>Campylobacter concisus</i> genomes identifies genomospecies features, secretion systems and novel plasmids and their association with severe ulcerative colitis. <i>Microbial Genomics</i> , 2020, 6, .	1.0	13
1524	Genomic analysis of trimethoprim-resistant extraintestinal pathogenic <i>Escherichia coli</i> and recurrent urinary tract infections. <i>Microbial Genomics</i> , 2020, 6, .	1.0	17
1525	Comprehensive genome analyses of <i>Sellimonas intestinalis</i> , a potential biomarker of homeostasis gut recovery. <i>Microbial Genomics</i> , 2020, 6, .	1.0	28

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1526	Reclassification of the biocontrol agents <i>Bacillus subtilis</i> BY-2 and Tu-100 as <i>Bacillus velezensis</i> and insights into the genomic and specialized metabolite diversity of the species. <i>Microbiology (United Kingdom)</i> , 2020, 152, 1-10.	1.7	10
1636	Transient Silencing of Antibiotic Resistance by Mutation Represents a Significant Potential Source of Unanticipated Therapeutic Failure. <i>MBio</i> , 2019, 10, .	1.8	39
1637	Horizontal Gene Transfer to a Defensive Symbiont with a Reduced Genome in a Multipartite Beetle Microbiome. <i>MBio</i> , 2020, 11, .	1.8	52
1638	Staphylococcal Protein A ( <i>spa</i> ) Locus Is a Hot Spot for Recombination and Horizontal Gene Transfer in <i>Staphylococcus pseudintermedius</i> . <i>MSphere</i> , 2020, 5, .	1.3	16
1639	Impacts of local population history and ecology on the evolution of a globally dispersed pathogen. <i>BMC Genomics</i> , 2020, 21, 369.	1.2	19
1640	Genome-wide association studies of <i>Shigella</i> spp. and Enteroinvasive <i>Escherichia coli</i> isolates demonstrate an absence of genetic markers for prediction of disease severity. <i>BMC Genomics</i> , 2020, 21, 138.	1.2	11
1641	Whole genome sequence comparison of avian pathogenic <i>Escherichia coli</i> from acute and chronic salpingitis of egg laying hens. <i>BMC Veterinary Research</i> , 2020, 16, 148.	0.7	13
1642	Pangenome guided pharmacophore modelling of enterohemorrhagic <i>Escherichia coli</i> <i>stx2A</i> . <i>F1000Research</i> , 2019, 8, 33.	0.8	5
1643	On the transformation of MinHash-based uncorrected distances into proper evolutionary distances for phylogenetic inference. <i>F1000Research</i> , 2020, 9, 1309.	0.8	20
1644	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 0, 3, 33.	0.9	18
1645	Daptomycin treatment impacts resistance in off-target populations of vancomycin-resistant <i>Enterococcus faecium</i> . <i>PLoS Biology</i> , 2020, 18, e3000987.	2.6	13
1646	Speciation trajectories in recombining bacterial species. <i>PLoS Computational Biology</i> , 2017, 13, e1005640.	1.5	24
1647	Diversity and distribution of nuclease bacteriocins in bacterial genomes revealed using Hidden Markov Models. <i>PLoS Computational Biology</i> , 2017, 13, e1005652.	1.5	52
1648	Major role of iron uptake systems in the intrinsic extra-intestinal virulence of the genus <i>Escherichia</i> revealed by a genome-wide association study. <i>PLoS Genetics</i> , 2020, 16, e1009065.	1.5	56
1649	A Phylogenetic and Phenotypic Analysis of <i>Salmonella enterica</i> Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004446.	1.3	59
1650	<i>Salmonella</i> identified in pigs in Kenya and Malawi reveals the potential for zoonotic transmission in emerging pork markets. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008796.	1.3	17
1651	Phylogenetic analyses and antimicrobial resistance profiles of <i>Campylobacter</i> spp. from diarrhoeal patients and chickens in Botswana. <i>PLoS ONE</i> , 2018, 13, e0194481.	1.1	37
1652	Shotgun metagenome sequencing identification of a set of genes encoded by <i>Actinomyces</i> associated with medication-related osteonecrosis of the jaw. <i>PLoS ONE</i> , 2020, 15, e0241676.	1.1	4

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1653	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
1654	Genomic investigation of a suspected outbreak of <i>Legionella pneumophila</i> ST82 reveals undetected heterogeneity by the present gold-standard methods, Denmark, July to November 2014. <i>Eurosurveillance</i> , 2017, 22, .	3.9	13
1655	Air-conditioner cooling towers as complex reservoirs and continuous source of <i>Legionella pneumophila</i> infection evidenced by a genomic analysis study in 2017, Switzerland. <i>Eurosurveillance</i> , 2019, 24, .	3.9	28
1656	Two multi-fragment recombination events resulted in the $\beta$ -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
1657	Multilevel genome typing: genomics-guided scalable resolution typing of microbial pathogens. <i>Eurosurveillance</i> , 2020, 25, .	3.9	12
1658	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
1659	Genetic Diversity of norA, Coding for a Main Efflux Pump of <i>Staphylococcus aureus</i> . <i>Frontiers in Genetics</i> , 2018, 9, 710.	1.1	58
1660	Whole-Genome Sequences of Five <i>Acinetobacter baumannii</i> Strains From a Child With Leukemia M2. <i>Frontiers in Microbiology</i> , 2019, 10, 132.	1.5	24
1661	Genomic Insight into <i>Pediococcus acidilactici</i> HN9, a Potential Probiotic Strain Isolated from the Traditional Thai-Style Fermented Beef Nhang. <i>Microorganisms</i> , 2021, 9, 50.	1.6	18
1662	<i>Helicobacter pylori</i> in ancient human remains. <i>World Journal of Gastroenterology</i> , 2019, 25, 6289-6298.	1.4	13
1663	Comparative genome analysis of 15 clinical <i>Shigella flexneri</i> strains regarding virulence and antibiotic resistance. <i>AIMS Microbiology</i> , 2019, 5, 205-222.	1.0	9
1664	Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of <i>Rickettsia typhi</i> in a Resource-Limited Setting. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 102, 408-414.	0.6	22
1665	Phenotype inference in an <i>Escherichia coli</i> strain panel. <i>ELife</i> , 2017, 6, .	2.8	38
1666	The landscape of coadaptation in <i>Vibrio parahaemolyticus</i> . <i>ELife</i> , 2020, 9, .	2.8	14
1667	Analysis of 44 <i>Vibrio anguillarum</i> genomes reveals high genetic diversity. <i>PeerJ</i> , 2020, 8, e10451.	0.9	8
1668	Genome sequencing and analysis of the first complete genome of <i>Lactobacillus kunkeei</i> strain MP2, an <i>Apis mellifera</i> gut isolate. <i>PeerJ</i> , 2016, 4, e1950.	0.9	20
1669	Genomic analysis of ST88 community-acquired methicillin resistant <i>Staphylococcus aureus</i> in Ghana. <i>PeerJ</i> , 2017, 5, e3047.	0.9	20
1670	Translating genomics into practice for real-time surveillance and response to carbapenemase-producing <i>Enterobacteriaceae</i> : evidence from a complex multi-institutional KPC outbreak. <i>PeerJ</i> , 2018, 6, e4210.	0.9	66

#	ARTICLE	IF	CITATIONS
1671	<i>Staphylococcus aureus</i> viewed from the perspective of 40,000+ genomes. PeerJ, 2018, 6, e5261.	0.9	66
1672	Improved genome of <i>Agrobacterium radiobacter</i> type strain provides new taxonomic insight into <i>Agrobacterium</i> genomospecies 4. PeerJ, 2019, 7, e6366.	0.9	3
1673	SpeciesPrimer: a bioinformatics pipeline dedicated to the design of qPCR primers for the quantification of bacterial species. PeerJ, 2020, 8, e8544.	0.9	23
1674	Genomic analysis of variability in Delta-toxin levels between <i>Staphylococcus aureus</i> strains. PeerJ, 2020, 8, e8717.	0.9	12
1675	Phenotypic and genomic analysis reveals <i>Riemerella anatipestifer</i> as the potential reservoir of <i>tet(X)</i> variants. Journal of Antimicrobial Chemotherapy, 2022, 77, 374-380.	1.3	17
1677	Pangenomic and functional investigations for dormancy and biodegradation features of an organic pollutant-degrading bacterium <i>Rhodococcus biphenylivorans</i> TG9. Science of the Total Environment, 2022, 809, 151141.	3.9	10
1678	Genomic signatures of host adaptation in group B <i>Salmonella enterica</i> ST416/ST417 from harbour porpoises. Veterinary Research, 2021, 52, 134.	1.1	2
1679	Emergence of 16S rRNA methyltransferases among carbapenemase-producing Enterobacterales in Spain studied by whole-genome sequencing. International Journal of Antimicrobial Agents, 2022, 59, 106456.	1.1	11
1680	Identification of <i>Streptococcus suis</i> putative zoonotic virulence factors: A systematic review and genomic meta-analysis. Virulence, 2021, 12, 2787-2797.	1.8	14
1681	Rapid methicillin resistance diversification in <i>Staphylococcus epidermidis</i> colonizing human neonates. Nature Communications, 2021, 12, 6062.	5.8	6
1683	Distribution of Genes Related to Probiotic Effects Across <i>Lactobacillus rhamnosus</i> Revealed by Population Structure. Probiotics and Antimicrobial Proteins, 2021, , 1.	1.9	0
1684	Transition of Serotype 35B Pneumococci From Commensal to Prevalent Virulent Strain in Children. Frontiers in Cellular and Infection Microbiology, 2021, 11, 744742.	1.8	3
1685	Whole-Genome Sequencing, Phylogenetic and Genomic Analysis of <i>Lactiplantibacillus pentosus</i> L33, a Potential Probiotic Strain Isolated From Fermented Sausages. Frontiers in Microbiology, 2021, 12, 746659.	1.5	24
1687	Extended-Spectrum Beta-Lactamase Producing- <i>Escherichia coli</i> Isolated From Irrigation Waters and Produce in Ecuador. Frontiers in Microbiology, 2021, 12, 709418.	1.5	16
1688	Comparative analysis of integrative and conjugative mobile genetic elements in the genus <i>Mesorhizobium</i> . Microbial Genomics, 2021, 7, .	1.0	13
1689	A genomic epidemiological study shows that prevalence of antimicrobial resistance in Enterobacterales is associated with the livestock host, as well as antimicrobial usage. Microbial Genomics, 2021, 7, .	1.0	20
1690	Clinical Characteristics of Patients and Whole Genome Sequencing-Based Surveillance of <i>Escherichia coli</i> Community-Onset Bloodstream Infections at a Non-tertiary Hospital in CHINA. Frontiers in Microbiology, 2021, 12, 748471.	1.5	3
1691	Ice nucleation in a Gram-positive bacterium isolated from precipitation depends on a polyketide synthase and non-ribosomal peptide synthetase. ISME Journal, 2022, 16, 890-897.	4.4	4

#	ARTICLE	IF	CITATIONS
1692	Genomic Characterisation of <i>Campylobacter jejuni</i> Isolates Recovered During Commercial Broiler Production. <i>Frontiers in Microbiology</i> , 2021, 12, 716182.	1.5	4
1693	RNA Sequencing Elucidates Drug-Specific Mechanisms of Antibiotic Tolerance and Resistance in <i>Mycobacterium abscessus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0150921.	1.4	10
1694	Characterization of Basal Transcriptomes Identifies Potential Metabolic and Virulence-Associated Adaptations Among Diverse Nontyphoidal <i>Salmonella enterica</i> Serovars. <i>Frontiers in Microbiology</i> , 2021, 12, 730411.	1.5	4
1695	Adaptation and genomic erosion in fragmented <i>Pseudomonas aeruginosa</i> populations in the sinuses of people with cystic fibrosis. <i>Cell Reports</i> , 2021, 37, 109829.	2.9	19
1696	<i>Microcoleus</i> (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. <i>Molecular Ecology</i> , 2022, 31, 86-103.	2.0	14
1698	Population genomics reveals distinct temporal association with the emergence of ST1 serotype V Group B <i>Streptococcus</i> and macrolide resistance in North America. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, , AAC0071421.	1.4	3
1699	Adaptation to Endophytic Lifestyle Through Genome Reduction by <i>Kitasatospora</i> sp. SUK42. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 740722.	2.0	4
1701	Applications and challenges of high performance computing in genomics. <i>CCF Transactions on High Performance Computing</i> , 2021, 3, 344-352.	1.1	6
1702	Comparative Genomics of <i>Mycobacterium avium</i> Complex Reveals Signatures of Environment-Specific Adaptation and Community Acquisition. <i>MSystems</i> , 2021, 6, e0119421.	1.7	7
1703	Molecular Mechanisms of Colistin Resistance in <i>Klebsiella pneumoniae</i> in a Tertiary Care Teaching Hospital. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 673503.	1.8	15
1704	PATO: Pangenome Analysis Toolkit. <i>Bioinformatics</i> , 2021, 37, 4564-4566.	1.8	9
1705	In vitro and in vivo activity of new strains of <i>Bacillus subtilis</i> against ESBL-producing <i>Escherichia coli</i> : an experimental study. <i>Journal of Applied Microbiology</i> , 2022, 132, 2270-2279.	1.4	4
1706	Genetic diversity of <i>Salmonella</i> Paratyphi A isolated from enteric fever patients in Bangladesh from 2008 to 2018. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009748.	1.3	10
1708	Plasmids Shape the Current Prevalence of <i>tmxCD1-toprJ1</i> among <i>Klebsiella pneumoniae</i> in Food Production Chains. <i>MSystems</i> , 2021, 6, e0070221.	1.7	26
1710	Myxobacterial Genomics and Post-Genomics: A Review of Genome Biology, Genome Sequences and Related Omics Studies. <i>Microorganisms</i> , 2021, 9, 2143.	1.6	13
1711	A tale of two STs: molecular and clinical epidemiology of MRSA t304 in Norway 2008–2016. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 209-218.	1.3	5
1712	Isolation and description of <i>Selenomonas timonae</i> sp. nov., a novel <i>Selenomonas</i> species detected in a gingivitis patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
1713	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

#	ARTICLE	IF	CITATIONS
1715	Whole-genome sequencing reveals high genetic diversity of <i>Streptococcus uberis</i> isolated from cows with mastitis. <i>BMC Veterinary Research</i> , 2021, 17, 321.	0.7	8
1716	Genomic sequence data of bacterial isolates from pistachio trees and other woody plants in California are inconsistent with a role of <i>Rhodococcus</i> as the causative agent of Pistachio Bushy Top Syndrome. <i>PhytoFrontiers</i> , 0, , .	0.8	0
1717	Pneumococcal pneumonia among shipyard workers: Inside the features of disease onset. <i>Travel Medicine and Infectious Disease</i> , 2021, 44, 102183.	1.5	1
1718	Deep phylo-taxono genomics reveals <i>Xylella</i> as a variant lineage of plant associated <i>Xanthomonas</i> and supports their taxonomic reunification along with <i>Stenotrophomonas</i> and <i>Pseudoxanthomonas</i> . <i>Genomics</i> , 2021, 113, 3989-4003.	1.3	17
1724	Bioinformatics Aspects of Foodborne Pathogen Research. , 2017, , 51-64.		0
1759	Bacterial Pan-Genomics. , 2019, , 21-38.		6
1777	<i>Limosilactobacillus urinaemulieris</i> sp. nov. and <i>Limosilactobacillus portuensis</i> sp. nov. isolated from urine of healthy women. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	10
1793	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
1796	Draft Genome Sequences of <i>Enterococcus faecalis</i> Strains Isolated from Healthy Japanese Individuals. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1797	Genomic differences among carriage and invasive nontypeable pneumococci circulating in South Africa. <i>Microbial Genomics</i> , 2019, 5, .	1.0	0
1808	Two cases of type-a <i>Haemophilus influenzae</i> meningitis within the same week in the same hospital are phylogenetically unrelated but recently exchanged capsule genes. <i>Microbial Genomics</i> , 2020, 6, .	1.0	3
1811	Whole genome sequence and comparative genome analyses of multi-resistant <i>Staphylococcus warneri</i> GD01 isolated from a diseased pig in China. <i>PLoS ONE</i> , 2020, 15, e0233363.	1.1	4
1821	<i>Campylobacter novaezeelandiae</i> sp. nov., isolated from birds and water in New Zealand. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3775-3784.	0.8	14
1825	<i>Prevotella vespertina</i> sp. nov., isolated from an abscess of a hospital patient. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4576-4582.	0.8	9
1831	Xylan utilisation promotes adaptation of <i>Bifidobacterium pseudocatenulatum</i> to the human gastrointestinal tract. <i>ISME Communications</i> , 2021, 1, .	1.7	13
1832	Multidrug Resistance Dynamics in <i>Salmonella</i> in Food Animals in the United States: An Analysis of Genomes from Public Databases. <i>Microbiology Spectrum</i> , 2021, 9, e0049521.	1.2	11
1833	Establishment of a Publicly Available Core Genome Multilocus Sequence Typing Scheme for <i>Clostridium perfringens</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0053321.	1.2	5
1835	Genomic Analysis of a Hospital-Associated Outbreak of <i>Mycobacterium abscessus</i> : Implications on Transmission. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0154721.	1.8	10

#	ARTICLE	IF	CITATIONS
1837	Genomic analysis of group A Streptococcus isolated during a correctional facility outbreak of MRSA in 2004. <i>Jammi, O, .</i>	0.3	0
1838	Genomic convergence between <i>Akkermansia muciniphila</i> in different mammalian hosts. <i>BMC Microbiology, 2021, 21, 298.</i>	1.3	10
1839	Genomic analysis of shiga toxin-containing <i>Escherichia coli</i> O157:H7 isolated from Argentinean cattle. <i>PLoS ONE, 2021, 16, e0258753.</i>	1.1	4
1840	An Effective Preprocessing Method for High-Quality Pan-Genome Analysis of <i>Bacillus subtilis</i> and <i>Escherichia coli</i> . <i>Methods in Molecular Biology, 2022, 2377, 371-390.</i>	0.4	1
1842	Emergence of Tigecycline Nonsusceptible and IMP-4 Carbapenemase-Producing K2-ST65 Hypervirulent <i>Klebsiella pneumoniae</i> in China. <i>Microbiology Spectrum, 2021, 9, e0130521.</i>	1.2	17
1843	The open pan-genome architecture and virulence landscape of <i>Mycobacterium bovis</i> . <i>Microbial Genomics, 2021, 7, .</i>	1.0	9
1844	Genomic Analysis of Prophages from <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Microorganisms, 2021, 9, 2252.</i>	1.6	14
1845	Serotypes, Virulence-Associated Factors, and Antimicrobial Resistance of <i>Streptococcus suis</i> Isolates Recovered From Sick and Healthy Pigs Determined by Whole-Genome Sequencing. <i>Frontiers in Veterinary Science, 2021, 8, 742345.</i>	0.9	10
1846	Molecular Characterization Based on Whole-Genome Sequencing of <i>Streptococcus pneumoniae</i> in Children Living in Southwest China During 2017-2019. <i>Frontiers in Cellular and Infection Microbiology, 2021, 11, 726740.</i>	1.8	12
1847	Genome information of the cellulolytic soil actinobacterium <i>Isophtericola dokdonensis</i> DS-3 and comparative genomic analysis of the genus <i>Isophtericola</i> . <i>Journal of Microbiology, 2021, 59, 1010-1018.</i>	1.3	1
1849	<i>Pseudomonas xionganensis</i> sp. nov., isolated from Baiyangdian Lake in Xiong'an New Area. <i>International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6052-6059.</i>	0.8	5
1853	Co-existence of multiple distinct lineages in <i>Vibrio parahaemolyticus</i> serotype O4:K12. <i>Microbial Genomics, 2020, 6, .</i>	1.0	1
1855	Molecular insights into meningococcal carriage isolates from Burkina Faso 7 years after introduction of a serogroup A meningococcal conjugate vaccine. <i>Microbial Genomics, 2020, 6, .</i>	1.0	0
1856	Evidence of homologous recombination as a driver of diversity in <i>Brachyspira pilosicoli</i> . <i>Microbial Genomics, 2020, 6, .</i>	1.0	2
1858	<i>Pseudoxanthomonas winnipegensis</i> sp. nov., derived from human clinical materials and recovered from cystic fibrosis and other patient types in Canada, and emendation of <i>Pseudoxanthomonas spadix</i> Young et al. 2007. <i>International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6313-6322.</i>	0.8	21
1859	Comparative Genomics and In Vitro Plant Growth Promotion and Biocontrol Traits of Lactic Acid Bacteria from the Wheat Rhizosphere. <i>Microorganisms, 2021, 9, 78.</i>	1.6	24
1863	Evaluating Selective Pressures Driving Clades Differentiation of the <i>Faecalibacterium prausnitzii</i> Complex. <i>SSRN Electronic Journal, 0, .</i>	0.4	0
1864	Characterization of cellular, biochemical and genomic features of the diazotrophic plant growth-promoting bacterium <i>Azospirillum</i> sp. UENF-412522, a novel member of the <i>Azospirillum</i> genus. <i>Microbiological Research, 2022, 254, 126896.</i>	2.5	5

#	ARTICLE	IF	CITATIONS
1866	Bacterial Microevolution and the Pangenome. , 2020, , 129-149.		1
1868	A Comprehensive Analysis of the Global Human Gut Archaeome from a Thousand Genome Catalogue. SSRN Electronic Journal, 0, , .	0.4	0
1869	Complete genome sequence of a methicillin-resistant <i>Staphylococcus schleiferi</i> strain from canine otitis externa in Korea. <i>Journal of Veterinary Science</i> , 2020, 21, e11.	0.5	3
1873	Comparative Genome Analysis of <i>Psychrobacillus</i> Strain PB01, Isolated from an Iceberg. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 237-243.	0.9	6
1879	Metagenomic sequencing of clinical samples reveals a single widespread clone of <i>Lawsonia intracellularis</i> responsible for porcine proliferative enteropathy. <i>Microbial Genomics</i> , 2020, 6, .	1.0	2
1880	Genome Sequence of the Fish Brain Bacterium <i>Clostridium tarantellae</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
1886	Type VI secretion system mutations reduced competitive fitness of classical <i>Vibrio cholerae</i> biotype. <i>Nature Communications</i> , 2021, 12, 6457.	5.8	15
1887	<i>Pseudoalteromonas ostreae</i> sp. nov., a new bacterial species harboured by the flat oyster <i>Ostrea edulis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
1888	Genomic Epidemiology and Characterization of Methicillin-Resistant <i>Staphylococcus aureus</i> from Bloodstream Infections in China. <i>MSystems</i> , 2021, 6, e0083721.	1.7	27
1889	In vivo and in silico Virulence Analysis of <i>Leptospira</i> Species Isolated From Environments and Rodents in Leptospirosis Outbreak Areas in Malaysia. <i>Frontiers in Microbiology</i> , 2021, 12, 753328.	1.5	4
1890	Genome-informed loop-mediated isothermal amplification assay for specific detection of <i>Pectobacterium parmentieri</i> in infected potato tissues and soil. <i>Scientific Reports</i> , 2021, 11, 21948.	1.6	13
1891	Biomolecule sulphation and novel methylations related to Guillain-Barré syndrome-associated <i>Campylobacter jejuni</i> serotype HS:19. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
1892	Genomic analysis of a rare recurrent <i>Listeria monocytogenes</i> prosthetic joint infection indicates a protected niche within biofilm on prosthetic materials. <i>Scientific Reports</i> , 2021, 11, 21864.	1.6	7
1893	Properties of <i>Modestobacter deserti</i> sp. nov., a Kind of Novel Phosphate-Solubilizing Actinobacteria Inhabited in the Desert Biological Soil Crusts. <i>Frontiers in Microbiology</i> , 2021, 12, 742798.	1.5	9
1894	Comparative Genomic Analyses and CRISPR-Cas Characterization of <i>Cutibacterium acnes</i> Provide Insights Into Genetic Diversity and Typing Applications. <i>Frontiers in Microbiology</i> , 2021, 12, 758749.	1.5	8
1900	Genomic epidemiology of methicillin-resistant <i>Staphylococcus aureus</i> ST22 widespread in communities of the Gaza Strip, 2009. <i>Eurosurveillance</i> , 2018, 23, .	3.9	0
1901	Comparative genomic insights into <i>Yersinia hibernica</i> – a commonly misidentified <i>Yersinia enterocolitica</i> -like organism. <i>Microbial Genomics</i> , 2020, 6, .	1.0	1
1909	Population structure of <i>Salmonella enterica</i> serotype Mbandaka reveals similar virulence potential irrespective of source and phylogenomic stratification. <i>F1000Research</i> , 2020, 9, 1142.	0.8	3



#	ARTICLE	IF	CITATIONS
1914	Symbiosis islands of Loteae-nodulating Mesorhizobium comprise three radiating lineages with concordant nod gene complements and nodulation host-range groupings. <i>Microbial Genomics</i> , 2020, 6, .	1.0	7
1915	Pan-genomics of <i>Ochrobactrum</i> species from clinical and environmental origins reveals distinct populations and possible links. <i>Genomics</i> , 2020, 112, 3003-3012.	1.3	8
1923	Investigating hospital <i>Mycobacterium chelonae</i> infection using whole genome sequencing and hybrid assembly. <i>PLoS ONE</i> , 2020, 15, e0236533.	1.1	5
1924	Prediction of <i>Burkholderia pseudomallei</i> DsbA substrates identifies potential virulence factors and vaccine targets. <i>PLoS ONE</i> , 2020, 15, e0241306.	1.1	5
1925	Complete genome sequence and analysis of <i>Alcaligenes faecalis</i> strain Mc250, a new potential plant bioinoculant. <i>PLoS ONE</i> , 2020, 15, e0241546.	1.1	9
1926	Genomic characterization and phylogenetic analysis of <i>Salmonella enterica</i> serovar Javiana. <i>PeerJ</i> , 2020, 8, e10256.	0.9	4
1927	Multi-locus phylogenetic analyses uncover species boundaries and reveal the occurrence of two new entomopathogenic nematode species, <i>Heterorhabditis ruandica</i> n. sp. and <i>Heterorhabditis zacatecana</i> n. sp.. <i>Journal of Nematology</i> , 2021, 53, 1-42.	0.4	14
1928	Genomic insights of <i>Acinetobacter baumannii</i> ST374 reveal wide and increasing resistome and virulome. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105148.	1.0	6
1929	Global Genome Diversity and Recombination in <i>Mycoplasma pneumoniae</i> . <i>Emerging Infectious Diseases</i> , 2022, 28, 111-117.	2.0	4
1930	Genome sequencing of the vermicompost strain <i>Stenotrophomonas maltophilia</i> UENF-4GII and population structure analysis of the <i>S. maltophilia</i> Sm3 genogroup. <i>Microbiological Research</i> , 2022, 255, 126923.	2.5	4
1931	Isolation and characterization of <i>Campylobacter massiliensis</i> sp. nov., a novel <i>Campylobacter</i> species detected in a gingivitis subject. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
1932	Molecular Surveillance of Carbapenem-Resistant Gram-Negative Bacteria in Liver Transplant Candidates. <i>Frontiers in Microbiology</i> , 2021, 12, 791574.	1.5	4
1935	Anatomy of an extensively drug-resistant <i>Klebsiella pneumoniae</i> outbreak in Tuscany, Italy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
1936	A comparative study of pan-genome methods for microbial organisms: <i>Acinetobacter baumannii</i> pan-genome reveals structural variation in antimicrobial resistance-carrying plasmids. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
1937	Complete genome sequencing and comparative genomic analysis of <i>Lactobacillus acidophilus</i> C5 as a potential canine probiotics. <i>Journal of Animal Science and Technology</i> , 2021, 63, 1411-1422.	0.8	4
1938	Identification of CTX-M Type ESBL <i>E. coli</i> from Sheep and Their Abattoir Environment Using Whole-Genome Sequencing. <i>Pathogens</i> , 2021, 10, 1480.	1.2	5
1939	Evolutionary Divergence of the Novel Staphylococcal Species <i>Staphylococcus argenteus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 769642.	1.5	4
1940	<i>Staphylococcus aureus</i> injection drug use-associated bloodstream infections are propagated by community outbreaks of diverse lineages. <i>Communications Medicine</i> , 2021, 1, .	1.9	9

#	ARTICLE	IF	CITATIONS
1942	Genome structural variation in <i>Escherichia coli</i> O157:H7. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
1943	Genomic Characterization of Group A Streptococci Causing Pharyngitis and Invasive Disease in Colorado, USA, June 2016–April 2017. <i>Journal of Infectious Diseases</i> , 2022, 225, 1841-1851.	1.9	8
1944	<i>Microbacterium paulum</i> sp. nov., isolated from microfiltered milk. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
1945	The Genetic Relatedness and Antimicrobial Resistance Patterns of Mastitis-Causing <i>Staphylococcus aureus</i> Strains Isolated from New Zealand Dairy Cattle. <i>Veterinary Sciences</i> , 2021, 8, 287.	0.6	5
1946	Combining pangenome analysis to identify potential cross-protective antigens against avian pathogenic <i>Escherichia coli</i> . <i>Avian Pathology</i> , 2022, 51, 66-75.	0.8	2
1947	Phylo-Taxonogenomics Supports Revision of Taxonomic Status of <i>Xanthomonas</i> Pathovars to <i>Xanthomonas citri</i> . <i>Phytopathology</i> , 2022, 112, 1201-1207.	1.1	9
1949	<i>Enterococcus faecium</i> Regulates Honey Bee Developmental Genes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12105.	1.8	12
1951	Complete Genome Sequence of <i>Salmonella enterica</i> Bacteriophage PRF-SP1. <i>Microbiology Resource Announcements</i> , 2021, 10, e0096521.	0.3	2
1952	Invasive atypical non-typhoidal <i>Salmonella</i> serovars in The Gambia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
1953	The Persistence of <i>Staphylococcus aureus</i> in Pressure Ulcers: A Colonising Role. <i>Genes</i> , 2021, 12, 1883.	1.0	4
1954	Whole-genome epidemiology and characterisation of <i>mcr-1</i> -encoding <i>Escherichia coli</i> in aquatic bird farms from the Pearl River Delta, China, 2019–2020. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106478.	1.1	3
1955	Pangenome inventory of <i>Burkholderia sensu lato</i> , <i>Burkholderia sensu stricto</i> , and the <i>Burkholderia cepacia</i> complex reveals the uniqueness of <i>Burkholderia catarinensis</i> . <i>Genomics</i> , 2022, 114, 398-408.	1.3	13
1956	Systematic Evaluation of Whole-Genome Sequencing Based Prediction of Antimicrobial Resistance in <i>Campylobacter jejuni</i> and <i>C. coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 776967.	1.5	14
1957	Genetic and Phenotypic Diversity of <i>Morganella morganii</i> Isolated From Cheese. <i>Frontiers in Microbiology</i> , 2021, 12, 738492.	1.5	8
1958	Genomic analysis of <i>Elizabethkingia</i> species from aquatic environments: evidence for potential clinical transmission. <i>Current Research in Microbial Sciences</i> , 2021, 3, 100083.	1.4	2
1960	Genomic Investigation and Successful Containment of an Intermittent Common Source Outbreak of OXA-48-Producing <i>Enterobacter cloacae</i> Related to Hospital Shower Drains. <i>Microbiology Spectrum</i> , 2021, 9, e0138021.	1.2	8
1961	High prevalence of multiple antibiotic resistance in clinical <i>E. coli</i> isolates from Bangladesh and prediction of molecular resistance determinants using WGS of an XDR isolate. <i>Scientific Reports</i> , 2021, 11, 22859.	1.6	19
1962	Genomic investigation of a suspected <i>Klebsiella pneumoniae</i> outbreak in a neonatal care unit in sub-Saharan Africa. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8

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1963	Antimicrobial Resistance and Genomic Characterization of Six New Sequence Types in Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Clinical Isolates from Pakistan. <i>Antibiotics</i> , 2021, 10, 1386.	1.5	5
1964	Deciphering the Epidemiological Characteristics and Molecular Features of blaKPCâ€“2- or blaNDMâ€“1-Positive <i>Klebsiella pneumoniae</i> Isolates in a Newly Established Hospital. <i>Frontiers in Microbiology</i> , 2021, 12, 741093.	1.5	11
1965	Antimicrobial Resistance in <i>Enterococcus</i> Spp. Isolated from a Beef Processing Plant and Retail Ground Beef. <i>Microbiology Spectrum</i> , 2021, 9, e0198021.	1.2	10
1966	Vertical Inheritance Facilitates Interspecies Diversification in Biosynthetic Gene Clusters and Specialized Metabolites. <i>MBio</i> , 2021, 12, e0270021.	1.8	23
1967	Emergence and global spread of <i>Listeria monocytogenes</i> main clinical clonal complex. <i>Science Advances</i> , 2021, 7, eabj9805.	4.7	23
1968	Survival Comes at a Cost: A Coevolution of Phage and Its Host Leads to Phage Resistance and Antibiotic Sensitivity of <i>Pseudomonas aeruginosa</i> Multidrug Resistant Strains. <i>Frontiers in Microbiology</i> , 2021, 12, 783722.	1.5	12
1969	Genomic Analysis of Global <i>Staphylococcus argenteus</i> Strains Reveals Distinct Lineages With Differing Virulence and Antibiotic Resistance Gene Content. <i>Frontiers in Microbiology</i> , 2021, 12, 795173.	1.5	10
1970	Development of a high resolution melting method based on a novel molecular target for discrimination between <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> . <i>Food Research International</i> , 2022, 151, 110845.	2.9	10
1971	<i>Mycobacterium fortuitum</i> genomic epidemiology, resistome and virulome. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2022, 116, e210247.	0.8	8
1972	A quantitative framework reveals traditional laboratory growth is a highly accurate model of human oral infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
1973	<i>Staphylococcus ratti</i> sp. nov. Isolated from a Lab Rat. <i>Pathogens</i> , 2022, 11, 51.	1.2	7
1974	The changing molecular epidemiology of <i>Enterococcus faecium</i> harbouring the van operon at a teaching hospital in Western Australia: A fifteen-year retrospective study. <i>International Journal of Medical Microbiology</i> , 2022, 312, 151546.	1.5	0
1975	APTC-EC-2A: A Lytic Phage Targeting Multidrug Resistant <i>E. coli</i> Planktonic Cells and Biofilms. <i>Microorganisms</i> , 2022, 10, 102.	1.6	6
1976	Protective effects of <i>Bacteroides fragilis</i> against lipopolysaccharide-induced systemic inflammation and their potential functional genes. <i>Food and Function</i> , 2022, 13, 1015-1025.	2.1	16
1977	Genomic epidemiology and characterisation of penicillin-sensitive <i>Staphylococcus aureus</i> isolates from invasive bloodstream infections in China: an increasing prevalence and higher diversity in genetic typing be revealed. <i>Emerging Microbes and Infections</i> , 2022, 11, 326-336.	3.0	8
1978	Whole-genome analysis of carbapenem-resistant <i>Acinetobacter baumannii</i> from clinical isolates in Southern Thailand. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 545-558.	1.9	12
1979	Genome analysis of a new biosurfactants source: The Antarctic bacterium <i>Psychrobacter</i> sp. TAE2020. <i>Marine Genomics</i> , 2022, 61, 100922.	0.4	6
1980	In vitro and in vivo evaluation of probiotic properties of <i>Corynebacterium accolens</i> isolated from the human nasal cavity. <i>Microbiological Research</i> , 2022, 255, 126927.	2.5	5

#	ARTICLE	IF	CITATIONS
1981	Parvimonas parva sp. nov., derived from a human genito-urinary lesion. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	5
1983	Genomic Characterization of Carbapenem-Non-susceptible Pseudomonas aeruginosa Clinical Isolates From Saudi Arabia Revealed a Global Dissemination of GES-5-Producing ST235 and VIM-2-Producing ST233 Sub-Lineages. Frontiers in Microbiology, 2021, 12, 765113.	1.5	13
1984	Genomic and Phenotypic Evolution of Tigecycline-Resistant Acinetobacter baumannii in Critically Ill Patients. Microbiology Spectrum, 2022, 10, e0159321.	1.2	7
1987	Frequencies and characteristics of genome-wide recombination in Streptococcus agalactiae, Streptococcus pyogenes, and Streptococcus suis. Scientific Reports, 2022, 12, 1515.	1.6	5
1988	Close genetic linkage between human and companion animal extraintestinal pathogenic Escherichia coli ST127. Current Research in Microbial Sciences, 2022, 3, 100106.	1.4	9
1990	Pathogenomic analyses of Shigella isolates inform factors limiting shigellosis prevention and control across LMICs. Nature Microbiology, 2022, 7, 251-261.	5.9	23
1991	Improved Genomic Identification, Clustering, and Serotyping of Shiga Toxin-Producing Escherichia coli Using Cluster/Serotype-Specific Gene Markers. Frontiers in Cellular and Infection Microbiology, 2021, 11, 772574.	1.8	9
1992	Whole-Genome Sequencing Reveals the High Nosocomial Transmission and Antimicrobial Resistance of Clostridioides difficile in a Single Center in China, a Four-Year Retrospective Study. Microbiology Spectrum, 2022, 10, e0132221.	1.2	8
1993	Genomic evolution of the globally disseminated multidrug-resistant Klebsiella pneumoniae clonal group 147. Microbial Genomics, 2022, 8, .	1.0	22
1995	High-resolution genomic surveillance elucidates a multilayered hierarchical transfer of resistance between WWTP- and human/animal-associated bacteria. Microbiome, 2022, 10, 16.	4.9	18
1996	Comparative genomics of the black rot pathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> and non-pathogenic co-inhabitant <i>Xanthomonas melonis</i> from Trinidad reveal unique pathogenicity determinants and secretion system profiles. PeerJ, 2022, 9, e12632.	0.9	6
1997	Roseobacter group probiotics exhibit differential killing of fish pathogenic Tenacibaculum species. Applied and Environmental Microbiology, 2022, , aem0241821.	1.4	11
1998	Large-scale WGS of carbapenem-resistant <i>Acinetobacter baumannii</i> isolates reveals patterns of dissemination of ST clades associated with antibiotic resistance. Journal of Antimicrobial Chemotherapy, 2022, 77, 934-943.	1.3	5
2000	DNA Methylation in <i>Ensifer</i> Species during Free-Living Growth and during Nitrogen-Fixing Symbiosis with <i>Medicago</i> spp.. MSystems, 2022, 7, e0109221.	1.7	7
2001	Phylogeny and potential virulence of cryptic clade Escherichia coli species complex isolates derived from an arable field trial. Current Research in Microbial Sciences, 2022, 3, 100093.	1.4	0
2002	Interplay between Klebsiella pneumoniae producing KPC-31 and KPC-3 under treatment with high dosage meropenem: a case report. European Journal of Clinical Microbiology and Infectious Diseases, 2022, 41, 495-500.	1.3	10
2003	Description and comparative genomic analysis of a mcr-1-carrying Escherichia coli ST683/CC155 recovered from touristic coastal water in Northeastern Brazil. Infection, Genetics and Evolution, 2022, 97, 105196.	1.0	5
2004	Hyper-aerotolerant Campylobacter coli, an emerging foodborne pathogen, shows differential expressions of oxidative stress-related genes. Veterinary Microbiology, 2022, 264, 109308.	0.8	1

#	ARTICLE	IF	CITATIONS
2006	A novel multiplex PCR method for simultaneous identification of hypervirulent <i>Listeria monocytogenes</i> clonal complex 87 and CC88 strains in China. <i>International Journal of Food Microbiology</i> , 2022, 366, 109558.	2.1	6
2009	<i>Buttiauxella massiliensis</i> sp. nov., Isolated from a Human Bone Infection. <i>Current Microbiology</i> , 2022, 79, 41.	1.0	5
2010	Comparative Genomics of <i>Bacteroides fragilis</i> Group Isolates Reveals Species-Dependent Resistance Mechanisms and Validates Clinical Tools for Resistance Prediction. <i>MBio</i> , 2022, 13, e0360321.	1.8	17
2011	Characterization of phage resistance and phages capable of intestinal decolonization of carbapenem-resistant <i>Klebsiella pneumoniae</i> in mice. <i>Communications Biology</i> , 2022, 5, 48.	2.0	32
2012	Genomic Investigation of Two <i>Acinetobacter baumannii</i> Outbreaks in a Veterinary Intensive Care Unit in The Netherlands. <i>Pathogens</i> , 2022, 11, 123.	1.2	7
2013	Revisiting the intragenomic structure of the genus <i>Pseudomonas</i> with complete whole genome sequence information: Insights into diversity and pathogen-related genetic determinants. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105183.	1.0	6
2015	Genomic Changes within a Subset of IncI2 Plasmids Associated with Dissemination of <i>mcr-1</i> Genes and Other Important Antimicrobial Resistance Determinants. <i>Antibiotics</i> , 2022, 11, 181.	1.5	3
2016	<i>Brenneria goodwinii</i> growth in vitro is improved by competitive interactions with other bacterial species associated with Acute Oak Decline. <i>Current Research in Microbial Sciences</i> , 2022, 3, 100102.	1.4	4
2017	Selective Isolation of <i>Eggerthella lenta</i> from Human Faeces and Characterisation of the Species Prophage Diversity. <i>Microorganisms</i> , 2022, 10, 195.	1.6	9
2018	First report of foodborne botulism due to <i>Clostridium botulinum</i> type A(B) from vegetarian home-canned pate in Hanoi, Vietnam. <i>Anaerobe</i> , 2022, 77, 102514.	1.0	3
2019	Comparative Genomics of Borderline Oxacillin-Resistant <i>Staphylococcus aureus</i> Detected during a Pseudo-outbreak of Methicillin-Resistant <i>S. aureus</i> in a Neonatal Intensive Care Unit. <i>MBio</i> , 2022, 13, e0319621.	1.8	7
2020	Comparative Genome Analysis Reveals Accumulation of Single-Nucleotide Repeats in Pathogenic <i>Escherichia</i> Lineages. <i>Current Issues in Molecular Biology</i> , 2022, 44, 498-504.	1.0	0
2021	The potential of bacteriophages to control <i>Xanthomonas campestris</i> pv. <i>campestris</i> at different stages of disease development. <i>Microbial Biotechnology</i> , 2022, 15, 1762-1782.	2.0	16
2022	F Plasmid Lineages in <i>Escherichia coli</i> ST95: Implications for Host Range, Antibiotic Resistance, and Zoonoses. <i>MSystems</i> , 2022, 7, e0121221.	1.7	20
2023	Investigating Nontuberculous Mycobacteria Transmission at the Colorado Adult Cystic Fibrosis Program. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 205, 1064-1074.	2.5	18
2024	The Resistance Mechanism Governs Physiological Adaptation of <i>Escherichia coli</i> to Growth With Sublethal Concentrations of Carbapenem. <i>Frontiers in Microbiology</i> , 2021, 12, 812544.	1.5	0
2025	Comparative Genome Analysis of Three <i>Komagataeibacter</i> Strains Used for Practical Production of Nata-de-Coco. <i>Frontiers in Microbiology</i> , 2021, 12, 798010.	1.5	1
2026	The interplay between community and hospital <i>Enterococcus faecium</i> clones within health-care settings: a genomic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e133-e141.	3.4	17

#	ARTICLE	IF	CITATIONS
2027	Assessment of selection pressure exerted on genes from complete pangenomes helps to improve the accuracy in the prediction of new genes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
2028	Molecular epidemiology and antimicrobial resistance profiles of <i>Salmonella</i> isolates from dairy heifer calves and adult lactating cows in a Mediterranean pasture-based system of Australia. <i>Journal of Dairy Science</i> , 2022, 105, 1493-1503.	1.4	7
2029	Diversity of carbapenem-resistant <i>Acinetobacter baumannii</i> and bacteriophage-mediated spread of the Oxa23 carbapenemase. <i>Microbial Genomics</i> , 2022, 8, .	1.0	12
2030	Dissemination Routes of Carbapenem and Pan-Aminoglycoside Resistance Mechanisms in Hospital and Urban Wastewater Canalizations of Ghana. <i>MSystems</i> , 2022, 7, e0101921.	1.7	7
2032	Widespread sharing of pneumococcal strains in a rural African setting: proximate villages are more likely to share similar strains that are carried at multiple timepoints. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
2033	Tracing the source and route of uterine colonization by exploring the genetic relationship of <i>Escherichia coli</i> isolated from the reproductive and gastrointestinal tract of dairy cows. <i>Veterinary Microbiology</i> , 2022, 266, 109355.	0.8	4
2034	O145 may be emerging as a predominant serogroup of Avian pathogenic <i>Escherichia coli</i> (APEC) in China. <i>Veterinary Microbiology</i> , 2022, 266, 109358.	0.8	6
2035	Comparative genomic analysis of the first <i>Ehrlichia canis</i> detections in Australia. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 101909.	1.1	12
2036	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
2037	KaruBioNet: a network and discussion group for a better collaboration and structuring of bioinformatics in Guadeloupe (French West Indies). <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	7
2038	Whole genome sequencing-based classification of human-related <i>Haemophilus</i> species and detection of antimicrobial resistance genes. <i>Genome Medicine</i> , 2022, 14, 13.	3.6	6
2039	Genomic analysis reveals high intra-species diversity of <i>Shewanella</i> algae. <i>Microbial Genomics</i> , 2022, 8, .	1.0	6
2040	Development of Loop-Mediated Isothermal Amplification Rapid Diagnostic Assays for the Detection of <i>Klebsiella pneumoniae</i> and Carbapenemase Genes in Clinical Samples. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 794961.	1.6	7
2041	Serial passage in an insect host indicates genetic stability of the human probiotic <i>Escherichia coli</i> Nissle 1917. <i>Evolution, Medicine and Public Health</i> , 2022, 10, 71-86.	1.1	4
2042	<i>Bartonella machadoae</i> sp. nov. isolated from wild rodents in the Pantanal wetland. <i>Acta Tropica</i> , 2022, 229, 106368.	0.9	12
2043	Insights and genetic features of extended-spectrum beta-lactamase producing <i>Escherichia coli</i> isolates from two hospitals in Ghana. <i>Scientific Reports</i> , 2022, 12, 1843.	1.6	14
2044	A role for ColV plasmids in the evolution of pathogenic <i>Escherichia coli</i> ST58. <i>Nature Communications</i> , 2022, 13, 683.	5.8	40
2045	Characterization of Genetic Elements Carrying <i>mcr-1</i> Gene in <i>Escherichia coli</i> from the Community and Hospital Settings in Vietnam. <i>Microbiology Spectrum</i> , 2022, 10, e0135621.	1.2	6

#	ARTICLE	IF	CITATIONS
2046	The evolutionary history of <i>Shigella flexneri</i> serotype 6 in Asia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	3
2047	Cluster-specific gene markers enhance <i>Shigella</i> and enteroinvasive <i>Escherichia coli</i> in silico serotyping. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
2048	Prophages encoding human immune evasion cluster genes are enriched in <i>Staphylococcus aureus</i> isolated from chronic rhinosinusitis patients with nasal polyps. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
2049	Introduction and adaptation of an emerging pathogen to olive trees in Italy. <i>Microbial Genomics</i> , 2021, 7, .	1.0	14
2050	New Delhi Metallo-Beta-Lactamase Facilitates the Emergence of Cefiderocol Resistance in <i>Enterobacter cloacae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0201121.	1.4	42
2051	Comparative Genomes Analysis of Aflatoxin B <sub>1</sub> -Degrading <i>Pseudomonas</i> Strains with Different Degradation Abilities. <i>Science of Advanced Materials</i> , 2022, 14, 111-121.	0.1	1
2052	Comparative genome analysis of the first &i>Listeria monocytogenes</i> core genome multi-locus sequence types CT2050 AND CT2051 strains with their close relatives. <i>AIMS Microbiology</i> , 2022, 8, 61-72.	1.0	1
2053	Comparative genomic analysis of <i>Staphylococcus aureus</i> isolates associated with either bovine intramammary infections or human infections demonstrates the importance of restriction-modification systems in host adaptation. <i>Microbial Genomics</i> , 2022, 8, .	1.0	6
2054	Comparative phylogenomics of ESBL-, AmpC- and carbapenemase-producing <i>Klebsiella pneumoniae</i> originating from companion animals and humans. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 1263-1271.	1.3	18
2055	Comparative Genomic Reveals Clonal Heterogeneity in Persistent <i>Staphylococcus aureus</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 817841.	1.8	1
2056	Molecular Epidemiology of <i>Klebsiella pneumoniae</i> from Clinical Bovine Mastitis in Northern Area of China, 2018–2019. <i>Engineering</i> , 2022, 10, 146-154.	3.2	2
2057	Comparative pangenome analysis of capsulated <i>Haemophilus influenzae</i> serotype f highlights their high genomic stability. <i>Scientific Reports</i> , 2022, 12, 3189.	1.6	0
2059	Biotyping reveals loss of motility in two distinct <i>Yersinia ruckeri</i> lineages exclusive to Norwegian aquaculture. <i>Journal of Fish Diseases</i> , 2022, 45, 641-653.	0.9	5
2060	High Prevalence of <i>Klebsiella pneumoniae</i> in European Food Products: a Multicentric Study Comparing Culture and Molecular Detection Methods. <i>Microbiology Spectrum</i> , 2022, 10, e0237621.	1.2	23
2062	Characterization and genomic analysis of a Demerecviridae phage SP76 with lytic multiple-serotypes of <i>Salmonella</i> . <i>Archives of Microbiology</i> , 2022, 204, 175.	1.0	1
2064	Analysis of global <i>Aeromonas veronii</i> genomes provides novel information on source of infection and virulence in human gastrointestinal diseases. <i>BMC Genomics</i> , 2022, 23, 166.	1.2	15
2065	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
2066	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

#	ARTICLE	IF	CITATIONS
2067	Genomic Epidemiology Insights on NDM-Producing Pathogens Revealed the Pivotal Role of Plasmids on <i>bla</i> <sub>NDM</sub> Transmission. <i>Microbiology Spectrum</i> , 2022, 10, e0215621.	1.2	21
2068	Decoding the Gene Variants of Two Native Probiotic <i>Lactiplantibacillus plantarum</i> Strains through Whole-Genome Resequencing: Insights into Bacterial Adaptability to Stressors and Antimicrobial Strength. <i>Genes</i> , 2022, 13, 443.	1.0	6
2069	Population genomics of the food-borne pathogen <i>Vibrio fluvialis</i> reveals lineage associated pathogenicity-related genetic elements. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
2070	Taxonomic Refinement of <i>Xanthomonas arboricola</i> . <i>Phytopathology</i> , 2022, 112, 1630-1639.	1.1	8
2072	Comparative genomics of 26 complete circular genomes of 18 different serotypes of <i>Actinobacillus pleuropneumoniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
2073	Comparative Whole-Genome Analysis of <i>Neisseria gonorrhoeae</i> Isolates Revealed Changes in the Gonococcal Genetic Island and Specific Genes as a Link to Antimicrobial Resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 831336.	1.8	7
2074	Phenotypic and Genotypic Characterization of a Hypervirulent Carbapenem-Resistant <i>Klebsiella pneumoniae</i> ST17-KL38 Clinical Isolate Harboring the Carbapenemase IMP-4. <i>Microbiology Spectrum</i> , 2022, 10, e0213421.	1.2	15
2075	Pan-genome and resistome analysis of extended-spectrum $\beta$ -lactamase-producing <i>Escherichia coli</i> : A multi-setting epidemiological surveillance study from Malaysia. <i>PLoS ONE</i> , 2022, 17, e0265142.	1.1	7
2076	Genetic Diversity and Pathogenic Features in <i>Klebsiella pneumoniae</i> Isolates from Patients with Pyogenic Liver Abscess and Pneumonia. <i>Microbiology Spectrum</i> , 2022, 10, e0264621.	1.2	7
2077	Pan-Genome Analysis of <i>Laribacter hongkongensis</i> : Virulence Gene Profiles, Carbohydrate-Active Enzyme Prediction, and Antimicrobial Resistance Characterization. <i>Frontiers in Microbiology</i> , 2022, 13, 862776.	1.5	2
2078	Genomic and Phenotypic Insights for Toxigenic Clinical <i>Vibrio cholerae</i> O141. <i>Emerging Infectious Diseases</i> , 2022, 28, 617-624.	2.0	3
2079	Cysteine dependence of <i>Lactobacillus iners</i> is a potential therapeutic target for vaginal microbiota modulation. <i>Nature Microbiology</i> , 2022, 7, 434-450.	5.9	32
2080	Genomic and antigenic diversity of colonizing <i>Klebsiella pneumoniae</i> isolates mirrors that of invasive isolates in Blantyre, Malawi. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
2081	Unraveling the Genotypic and Phenotypic Diversity of the Psychrophilic <i>Clostridium estertheticum</i> Complex, a Meat Spoilage Agent. <i>Frontiers in Microbiology</i> , 2022, 13, 856810.	1.5	4
2082	Healthcare-associated infections caused by chlorhexidine-tolerant <i>Serratia marcescens</i> carrying a promiscuous IncHI2 multi-drug resistance plasmid in a veterinary hospital. <i>PLoS ONE</i> , 2022, 17, e0264848.	1.1	6
2083	The Use of Comparative Genomic Analysis for the Development of Subspecies-Specific PCR Assays for <i>Mycobacterium abscessus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 816615.	1.8	3
2084	Comparative Genomics of Cyclic di-GMP Metabolism and Chemosensory Pathways in <i>Shewanella</i> algae Strains: Novel Bacterial Sensory Domains and Functional Insights into Lifestyle Regulation. <i>MSystems</i> , 2022, 7, e0151821.	1.7	11
2085	Complete Genome Assemblies of All <i>Xanthomonas translucens</i> Pathotype Strains Reveal Three Genetically Distinct Clades. <i>Frontiers in Microbiology</i> , 2021, 12, 817815.	1.5	19



#	ARTICLE	IF	CITATIONS
2086	Benchmarking the topological accuracy of bacterial phylogenomic workflows using in silico evolution. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
2087	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
2090	Recombination resolves the cost of horizontal gene transfer in experimental populations of <i>Helicobacter pylori</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2119010119.	3.3	12
2091	Genome wide association study of <i>Escherichia coli</i> bloodstream infection isolates identifies genetic determinants for the portal of entry but not fatal outcome. <i>PLoS Genetics</i> , 2022, 18, e1010112.	1.5	22
2092	Convergent Evolution of Antibiotic Tolerance in Patients with Persistent Methicillin-Resistant <i>Staphylococcus aureus</i> Bacteremia. <i>Infection and Immunity</i> , 2022, 90, e0000122.	1.0	8
2093	WHO Critical Priority <i>Escherichia coli</i> as One Health Challenge for a Post-Pandemic Scenario: Genomic Surveillance and Analysis of Current Trends in Brazil. <i>Microbiology Spectrum</i> , 2022, 10, e0125621.	1.2	31
2095	Rapid expansion and extinction of antibiotic resistance mutations during treatment of acute bacterial respiratory infections. <i>Nature Communications</i> , 2022, 13, 1231.	5.8	22
2097	Comparative Genomic Analysis Reveals Intestinal Habitat Adaptation of <i>Ligilactobacillus</i> Rich in Prophage and Degrading Cellulase. <i>Molecules</i> , 2022, 27, 1867.	1.7	1
2099	A Polymorphic Gene within the <i>Mycobacterium smegmatis</i> <i>esx1</i> Locus Determines Mycobacterial Self-Identity and Conjugal Compatibility. <i>MBio</i> , 2022, 13, e0021322.	1.8	5
2100	The Role of Plasmid and Resistance Gene Acquisition in the Emergence of ST23 Multi-Drug Resistant, Hypervirulent <i>Klebsiella pneumoniae</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0192921.	1.2	10
2101	Insights From the <i>Lactobacillus johnsonii</i> Genome Suggest the Production of Metabolites With Antibiofilm Activity Against the Pathobiont <i>Candida albicans</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 853762.	1.5	23
2102	Global population structure of the <i>Serratia marcescens</i> complex and identification of hospital-adapted lineages in the complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	8
2103	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
2104	Diversity of blaCTX-M-1-carrying plasmids recovered from <i>Escherichia coli</i> isolated from Canadian domestic animals. <i>PLoS ONE</i> , 2022, 17, e0264439.	1.1	4
2105	A Plasmid With Conserved Phage Genes Helps <i>Klebsiella pneumoniae</i> Defend Against the Invasion of Transferable DNA Elements at the Cost of Reduced Virulence. <i>Frontiers in Microbiology</i> , 2022, 13, 827545.	1.5	2
2106	Deciphering the Potential Coding of Human Cytomegalovirus: New Predicted Transmembrane Proteome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2768.	1.8	5
2107	Persistence and multi-ward dissemination of vancomycin-resistant <i>Enterococcus faecium</i> ST17 clone in hospital settings in Slovakia 2017–2020. <i>International Journal of Antimicrobial Agents</i> , 2022, 59, 106561.	1.1	1
2108	Phylogenetics of Historical Host Switches in a Bacterial Plant Pathogen. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0235621.	1.4	6

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2110	Whole genome sequencing and molecular epidemiology of paediatric <i>Staphylococcus aureus</i> bacteraemia. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 29, 197-206.	0.9	6
2111	Characterization of Silver Resistance and Coexistence of sil Operon with Antibiotic Resistance Genes Among Gram-Negative Pathogens Isolated from Wound Samples by Using Whole-Genome Sequencing. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1425-1437.	1.1	7
2112	A high-quality reference genome for the fish pathogen <i>Streptococcus iniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	0
2113	Comparative Analysis of <i>Bacillus cereus</i> Group Isolates' Resistance Using Disk Diffusion and Broth Microdilution and the Correlation between Antimicrobial Resistance Phenotypes and Genotypes. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0230221.	1.4	8
2114	Genomic characterization of multidrug-resistant <i>Salmonella</i> serovar Kentucky ST198 isolated in poultry flocks in Spain (2011â€“2017). <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
2115	Environmental surveillance of ESBL and carbapenemase-producing gram-negative bacteria in a Ghanaian Tertiary Hospital. <i>Antimicrobial Resistance and Infection Control</i> , 2022, 11, 49.	1.5	10
2116	<i>Salmonella</i> <i>Salamae</i> and <i>S. Waycross</i> isolated from Nile perch in Lake Victoria show limited human pathogenic potential. <i>Scientific Reports</i> , 2022, 12, 4229.	1.6	7
2118	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
2119	Deciphering Genomes: Genetic Signatures of Plant-Associated Micromonospora. <i>Frontiers in Plant Science</i> , 2022, 13, 872356.	1.7	3
2120	Lytic Phages against ST11 K47 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> and the Corresponding Phage Resistance Mechanisms. <i>MSphere</i> , 2022, 7, e0008022.	1.3	7
2121	Genetic Diversity, Distribution, and Genomic Characterization of Antibiotic Resistance and Virulence of Clinical <i>Pseudomonas aeruginosa</i> Strains in Kenya. <i>Frontiers in Microbiology</i> , 2022, 13, 835403.	1.5	12
2122	Comparative analysis of <i>Streptococcus suis</i> genomes identifies novel candidate virulence-associated genes in North American isolates. <i>Veterinary Research</i> , 2022, 53, 23.	1.1	11
2123	Molecular Genetic Characteristics of Plasmid-Borne mcr-9 in <i>Salmonella enterica</i> Serotype Typhimurium and Thompson in Zhejiang, China. <i>Frontiers in Microbiology</i> , 2022, 13, 852434.	1.5	5
2124	Genomic Surveillance of Vancomycin-Resistant <i>Enterococcus faecium</i> Reveals Spread of a Linear Plasmid Conferring a Nutrient Utilization Advantage. <i>MBio</i> , 2022, 13, e0377121.	1.8	11
2125	Genome analysis of <i>Legionella pneumophila</i> ST23 from various countries reveals highly similar strains. <i>Life Science Alliance</i> , 2022, 5, e202101117.	1.3	6
2126	Semi-Quantitative Assay to Measure Urease Activity by Urinary Catheter-Associated Uropathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 859093.	1.8	4
2127	Genomic diversity and antimicrobial resistance among non-typhoidal <i>Salmonella</i> associated with human disease in The Gambia. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
2128	Whole-genome sequencing and gene sharing network analysis powered by machine learning identifies antibiotic resistance sharing between animals, humans and environment in livestock farming. <i>PLoS Computational Biology</i> , 2022, 18, e1010018.	1.5	19

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2129	Comparative Respiratory Tract Microbiome Between Carbapenem-Resistant <i>Acinetobacter baumannii</i> Colonization and Ventilator Associated Pneumonia. <i>Frontiers in Microbiology</i> , 2022, 13, 782210.	1.5	5
2130	Distinct increase in antimicrobial resistance genes among <i>Escherichia coli</i> during 50 years of antimicrobial use in livestock production in China. <i>Nature Food</i> , 2022, 3, 197-205.	6.2	34
2131	Isolation and Characterization of Lytic Bacteriophages Targeting Diverse <i>Enterobacter</i> spp. Clinical Isolates. <i>Phage</i> , 2022, 3, 50-58.	0.8	1
2132	Evidence of Genomic Diversification in a Natural Symbiotic Population Within Its Host. <i>Frontiers in Microbiology</i> , 2022, 13, 854355.	1.5	3
2134	Genomic Characteristics of Recently Recognized <i>Vibrio cholerae</i> El Tor Lineages Associated with Cholera in Bangladesh, 1991 to 2017. <i>Microbiology Spectrum</i> , 2022, 10, e0039122.	1.2	3
2135	Genome-Wide Association Study Reveals Host Factors Affecting Conjugation in <i>Escherichia coli</i> . <i>Microorganisms</i> , 2022, 10, 608.	1.6	3
2136	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
2137	Ficolin-2 Lectin Complement Pathway Mediates Capsule-Specific Innate Immunity Against Invasive Pneumococcal Disease. <i>Frontiers in Immunology</i> , 2022, 13, 841062.	2.2	2
2138	Characterisation of Bacteriophage vB_SmaM_Ps15 Infective to <i>Stenotrophomonas maltophilia</i> Clinical Ocular Isolates. <i>Viruses</i> , 2022, 14, 709.	1.5	0
2139	Role of mobile genetic elements in the global dissemination of the carbapenem resistance gene blaNDM. <i>Nature Communications</i> , 2022, 13, 1131.	5.8	72
2140	Coexistence of <i>tet</i> (X4), <i>mcr-1</i> , and <i>bla</i> <sub>NDM-5</sub> in ST6775 <i>Escherichia coli</i> Isolates of Animal Origin in China. <i>Microbiology Spectrum</i> , 2022, 10, e0019622.	1.2	18
2141	Intracellular <i>Salmonella Paratyphi A</i> is motile and differs in the expression of flagella-chemotaxis, SPI-1 and carbon utilization pathways in comparison to intracellular <i>S. Typhimurium</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010425.	2.1	4
2142	Relationship and distribution of <i>Salmonella enterica</i> serovar I 4,[5],12:i:- strain sequences in the NCBI Pathogen Detection database. <i>BMC Genomics</i> , 2022, 23, 268.	1.2	3
2145	Antimicrobial resistance and genomic relationships of <i>Salmonella enterica</i> from Australian cattle. <i>International Journal of Food Microbiology</i> , 2022, 371, 109672.	2.1	6
2147	Rates of evolutionary change of resident <i>Escherichia coli</i> O157:H7 differ within the same ecological niche. <i>BMC Genomics</i> , 2022, 23, 275.	1.2	3
2148	Comparative Genomic Analysis of a Pantone™ Valentine Leukocidin-Positive ST22 Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> from Pakistan. <i>Antibiotics</i> , 2022, 11, 496.	1.5	6
2150	<i>Escherichia marmotae</i> a Human Pathogen Easily Misidentified as <i>Escherichia coli</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0203521.	1.2	7
2151	Wild Boars as an Indicator of Environmental Spread of ES <sup>2</sup> L-Producing <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 838383.	1.5	6

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2152	Extensive epigenetic modification with large-scale chromosomal and plasmid recombination characterise the <i>Legionella longbeachae</i> serogroup 1 genome. <i>Scientific Reports</i> , 2022, 12, 5810.	1.6	0
2153	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
2154	K-mer based prediction of <i>Clostridioides difficile</i> relatedness and ribotypes. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0
2156	<i>IncP-2</i> -Encoding IncP-6 Plasmids in <i>Citrobacter freundii</i> and <i>Klebsiella variicola</i> Strains from Hospital Sewage in Japan. <i>Applied and Environmental Microbiology</i> , 2022, , e0001922.	1.4	2
2157	Correlation of organic acid tolerance and genotypic characteristics of <i>Listeria monocytogenes</i> food and clinical isolates. <i>Food Microbiology</i> , 2022, 104, 104004.	2.1	10
2158	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
2159	Isolation, characterization, and genome analysis of bacteriophage P929 that could specifically lyase the KL19 capsular type of <i>Klebsiella pneumoniae</i> . <i>Virus Research</i> , 2022, 314, 198750.	1.1	9
2160	Performance of halotolerant bacteria associated with Sahara-inhabiting halophytes <i>Atriplex halimus</i> L. and <i>Lygeum spartum</i> L. ameliorate tomato plant growth and tolerance to saline stress: from selective isolation to genomic analysis of potential determinants. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 16.	1.7	3
2161	Genomic comparisons of <i>Escherichia coli</i> ST131 from Australia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	22
2163	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
2164	Comprehensive Genomic Investigation of Tigecycline Resistance Gene <i>tet(X4)</i> -Bearing Strains Expanding among Different Settings. <i>Microbiology Spectrum</i> , 2021, 9, e0163321.	1.2	27
2165	Evolutionary Processes Driving the Rise and Fall of <i>Staphylococcus aureus</i> ST239, a Dominant Hybrid Pathogen. <i>MBio</i> , 2021, 12, e0216821.	1.8	9
2166	The Darkest Place Is under the Candlestick-Healthy Urogenital Tract as a Source of Worldwide Disseminated Extraintestinal Pathogenic <i>Escherichia coli</i> Lineages. <i>Microorganisms</i> , 2022, 10, 27.	1.6	0
2167	Genome analysis provides insight into hyper-virulence of <i>Streptococcus suis</i> LSM178, a human strain with a novel sequence type 1005. <i>Scientific Reports</i> , 2021, 11, 23919.	1.6	2
2168	Prevalence, Risk Factors, and Genetic Characterization of Extended-Spectrum Beta-Lactamase <i>Escherichia coli</i> Isolated From Healthy Pregnant Women in Madagascar. <i>Frontiers in Microbiology</i> , 2021, 12, 786146.	1.5	9
2169	<i>Enterococcus innesii</i> sp. nov., isolated from the wax moth <i>Galleria mellonella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	9
2170	LASSO-based feature selection for improved microbial and microbiome classification. , 2021, , .		5
2171	Genomic adaptations of <i>Campylobacter jejuni</i> to long-term human colonization. <i>Gut Pathogens</i> , 2021, 13, 72.	1.6	5

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2172	Genomic Characterization of <i>Streptococcus suis</i> Serotype 24 Clonal Complex 221/234 From Human Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 812436.	1.5	7
2173	Identification of multiple transfer units and novel subtypes of <i>tmexCD-toprJ</i> gene clusters in clinical carbapenem-resistant <i>Enterobacter cloacae</i> and <i>Klebsiella oxytoca</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 625-632.	1.3	8
2174	Genome placement of alpha-haemolysin cluster is associated with alpha-haemolysin sequence variation, adhesin and iron acquisition factor profile of <i>Escherichia coli</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
2175	Occurrence and Molecular Characterization of Abundant tet(X) Variants Among Diverse Bacterial Species of Chicken Origin in Jiangsu, China. <i>Frontiers in Microbiology</i> , 2021, 12, 751006.	1.5	5
2176	Not All That Glitters Is Gold: The Paradox of CO-dependent Hydrogenogenesis in <i>Parageobacillus thermoglucosidasius</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 784652.	1.5	5
2177	Genetic differentiation of <i>Xylella fastidiosa</i> following the introduction into Taiwan. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
2178	VasH Contributes to Virulence of <i>Aeromonas hydrophila</i> and Is Necessary to the T6SS-mediated Bactericidal Effect. <i>Frontiers in Veterinary Science</i> , 2021, 8, 793458.	0.9	6
2179	A high-throughput multiplexing and selection strategy to complete bacterial genomes. <i>GigaScience</i> , 2021, 10, .	3.3	13
2180	Pan-Resistome Characterization of Uropathogenic <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Strains Circulating in Uganda and Kenya, Isolated from 2017-2018. <i>Antibiotics</i> , 2021, 10, 1547.	1.5	11
2181	Phage Genome Annotation: Where to Begin and End. <i>Phage</i> , 2021, 2, 183-193.	0.8	17
2184	Comparative genomics of Chinese and international isolates of <i>Escherichia albertii</i> : population structure and evolution of virulence and antimicrobial resistance. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
2185	Deletion of glyceraldehyde-3-phosphate dehydrogenase ( <i>gapN</i> ) in <i>Clostridium saccharoperbutylacetonicum</i> N1-4(HMT) using CLEAVE <sub>2</sub> increases the ATP pool and accelerates solvent production. <i>Microbial Biotechnology</i> , 2021, , .	2.0	1
2186	<i>Neglectibacter timonensis</i> gen. nov., sp. nov. and <i>Scatolibacter rhodanostii</i> gen. nov., sp. nov., two anaerobic bacteria isolated from human stool samples. <i>Archives of Microbiology</i> , 2022, 204, 45.	1.0	6
2187	Genomic Features and Construction of Streamlined Genome Chassis of Nisin Z Producer <i>Lactococcus lactis</i> N8. <i>Microorganisms</i> , 2022, 10, 47.	1.6	10
2188	Phylogenomic Reappraisal of Fatty Acid Biosynthesis, Mycolic Acid Biosynthesis and Clinical Relevance Among Members of the Genus <i>Corynebacterium</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 802532.	1.5	12
2189	Population analysis of <i>Legionella pneumophila</i> reveals a basis for resistance to complement-mediated killing. <i>Nature Communications</i> , 2021, 12, 7165.	5.8	11
2190	Transcriptomic analysis of <i>Streptococcus agalactiae</i> periprosthetic joint infection. <i>MicrobiologyOpen</i> , 2021, 10, e1256.	1.2	3
2191	Possible Dissemination of <i>Escherichia coli</i> Sequence Type 410 Closely Related to B4/H24RxC in Ghana. <i>Frontiers in Microbiology</i> , 2021, 12, 770130.	1.5	7

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2193	Genome reorganization during emergence of host-associated <i>Mycobacterium abscessus</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
2194	Spontaneous Phage Resistance in Avian Pathogenic <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 782757.	1.5	3
2195	“Pseudo-pseudogenes” in bacterial genomes: Proteogenomics reveals a wide but low protein expression of pseudogenes in <i>Salmonella enterica</i> . <i>Nucleic Acids Research</i> , 2022, 50, 5158-5170.	6.5	9
2196	<i>Gordonia</i> species as a rare pathogen isolated from milk of dairy cows with mastitis. <i>Scientific Reports</i> , 2022, 12, 6028.	1.6	2
2197	Isolation and molecular characterization of <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> toxic to lepidopteran pests <i>Spodoptera</i> spp. and <i>Plutella xylostella</i> . <i>Pest Management Science</i> , 2022, 78, 2976-2984.	1.7	3
2198	Amplicon Sequencing of Single-Copy Protein-Coding Genes Reveals Accurate Diversity for Sequence-Discrete Microbiome Populations. <i>Microbiology Spectrum</i> , 2022, 10, e0210521.	1.2	0
2199	Genomic characterisation of an entomopathogenic strain of <i>Serratia ureilytica</i> in the critically endangered phasmid <i>Dryococelus australis</i> . <i>PLoS ONE</i> , 2022, 17, e0265967.	1.1	0
2200	In vitro Synergistic Activities of Fosfomycin in Combination with Other Antimicrobial Agents Against Carbapenem-Resistant <i>Escherichia coli</i> Harboring bla <sub>NDM-1</sub> on the IncN2 Plasmid and a Study of the Genomic Characteristics of These Pathogens. <i>Infection and Drug Resistance</i> , 2022, Volume 15, 1777-1791.	1.1	1
2201	Comparative Genomic Analysis Reveals Potential Pathogenicity and Slow-Growth Characteristics of Genus <i>Brevundimonas</i> and Description of <i>Brevundimonas pishanensis</i> sp. nov.. <i>Microbiology Spectrum</i> , 2022, 10, e0246821.	1.2	5
2202	<i>Bifidobacterium infantis</i> treatment promotes weight gain in Bangladeshi infants with severe acute malnutrition. <i>Science Translational Medicine</i> , 2022, 14, eabk1107.	5.8	61
2203	Comparative genomics analysis of genus <i>Leuconostoc</i> resolves its taxonomy and elucidates its biotechnological importance. <i>Food Microbiology</i> , 2022, 106, 104039.	2.1	11
2204	In-depth genome analysis of <i>Bacillus</i> sp. BH32, a salt stress-tolerant endophyte obtained from a halophyte in a semiarid region. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 3113-3137.	1.7	11
2205	Litter Commensal Bacteria Can Limit the Horizontal Gene Transfer of Antimicrobial Resistance to <i>Salmonella</i> in Chickens. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0251721.	1.4	13
2206	Development of a novel machine learning-based weighted modeling approach to incorporate <i>Salmonella enterica</i> heterogeneity on a genetic scale in a dose-response modeling framework. <i>Risk Analysis</i> , 2022, , .	1.5	1
2209	Phylogenetic Distribution and Evolution of Type VI Secretion System in the Genus <i>Xanthomonas</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 840308.	1.5	5
2210	Comparative genome analysis of <i>Escherichia coli</i> bacteriophages isolated from sewage and chicken meat. <i>Virus Research</i> , 2022, , 198784.	1.1	1
2212	The Minimal Translation Machinery: What We Can Learn From Naturally and Experimentally Reduced Genomes. <i>Frontiers in Microbiology</i> , 2022, 13, 858983.	1.5	2
2214	Piperacillin/tazobactam-resistant, cephalosporin-susceptible <i>Escherichia coli</i> bloodstream infections are driven by multiple acquisition of resistance across diverse sequence types. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3

#	ARTICLE	IF	CITATIONS
2742	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
2743	Occurrence of genes encoding spore germination in <i>Clostridium</i> species that cause meat spoilage. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
2744	Carbapenemase-Producing Extraintestinal Pathogenic <i>Escherichia coli</i> From Argentina: Clonal Diversity and Predominance of Hyperepidemic Clones CC10 and CC131. <i>Frontiers in Microbiology</i> , 2022, 13, 830209.	1.5	6
2745	Optimizing the Parametrization of Homologue Classification in the Pan-Genome Computation for a Bacterial Species: Case Study <i>Streptococcus pyogenes</i> . <i>Methods in Molecular Biology</i> , 2022, 2449, 299-324.	0.4	1
2747	Comparative Genomics Applied to Systematically Assess Pathogenicity Potential in Shiga Toxin-Producing <i>Escherichia coli</i> O145:H28. <i>Microorganisms</i> , 2022, 10, 866.	1.6	7
2748	Isolation and Characterization of Two Lytic Phages Efficient Against Phytopathogenic Bacteria From <i>Pseudomonas</i> and <i>Xanthomonas</i> Genera. <i>Frontiers in Microbiology</i> , 2022, 13, 853593.	1.5	7
2749	Phylogenetic and Phenotypic Analyses of a Collection of Food and Clinical <i>Listeria monocytogenes</i> Isolates Reveal Loss of Function of Sigma B from Several Clonal Complexes. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0005122.	1.4	9
2751	Occurrence of High Levels of Cefiderocol Resistance in Carbapenem-Resistant <i>Escherichia coli</i> before Its Approval in China: a Report from China CRE-Network. <i>Microbiology Spectrum</i> , 2022, 10, e0267021.	1.2	30
2752	Differentiation of <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> Using Genome-Guided MALDI-TOF MS Based on Variations in Ribosomal Proteins. <i>Microorganisms</i> , 2022, 10, 918.	1.6	4
2753	Exploration of the Molecular Mechanisms Underlying the Anti-Photoaging Effect of <i>Limosilactobacillus fermentum</i> XJC60. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 838060.	1.8	9
2754	A deep siamese neural network improves metagenome-assembled genomes in microbiome datasets across different environments. <i>Nature Communications</i> , 2022, 13, 2326.	5.8	47
2755	Comparative genomic analysis of <i>Thermus</i> provides insights into the evolutionary history of an incomplete denitrification pathway. , 0, , .		3
2756	Systems-Based Approach for Optimization of Assembly-Free Bacterial MLST Mapping. <i>Life</i> , 2022, 12, 670.	1.1	0
2757	Discovery of Early-Branching <i>Wolbachia</i> Reveals Functional Enrichment on Horizontally Transferred Genes. <i>Frontiers in Microbiology</i> , 2022, 13, 867392.	1.5	6
2759	Strain Variation in <i>Clostridioides difficile</i> Cytotoxicity Associated with Genomic Variation at Both Pathogenic and Nonpathogenic Loci. <i>MSphere</i> , 2022, 7, .	1.3	3
2760	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
2761	<i>Escherichia coli</i> Strains from Patients with Inflammatory Bowel Diseases have Disease-specific Genomic Adaptations. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 1584-1597.	0.6	5
2762	Comprehensive Analysis Reveals the Genetic and Pathogenic Diversity of <i>Ralstonia solanacearum</i> Species Complex and Benefits Its Taxonomic Classification. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3

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2763	<i>Pseudomonas aeruginosa</i> Detection Using Conventional PCR and Quantitative Real-Time PCR Based on Species-Specific Novel Gene Targets Identified by Pangenome Analysis. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	7
2764	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 900-910.	1.8	9
2765	Cold-adaptive traits identified by comparative genomic analysis of a lipase-producing <i>Pseudomonas</i> sp. HS6 isolated from snow-covered soil of Sikkim Himalaya and molecular simulation of lipase for wide substrate specificity. <i>Current Genetics</i> , 2022, , .	0.8	2
2766	<i>Lentilactobacillus rapi</i> subsp. <i>dabitei</i> subsp. nov., a lactic acid bacterium isolated from naturally fermented dairy product. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	9
2767	Mobility of antimicrobial resistance across serovars and disease presentations in non-typhoidal <i>Salmonella</i> from animals and humans in Vietnam. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
2768	Dressing like a pathogen: Comparative analysis of different <i>Pseudomonas</i> genomospecies wearing different features to infect <i>Corylus avellana</i> . <i>Journal of Phytopathology</i> , 2022, 170, 504-516.	0.5	4
2769	Effect of childhood vaccination and antibiotic use on pneumococcal populations and genome-wide associations with disease among children in Nepal: an observational study. <i>Lancet Microbe</i> , The, 2022, 3, e503-e511.	3.4	2
2770	<i>Helicobacter cinaedi</i> is a human-adapted lineage in the <i>Helicobacter cinaedi/canicola/â€™magdeburgensis</i> â€™™ complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
2771	Genomic characterization of lytic bacteriophages targeting genetically diverse <i>Pseudomonas aeruginosa</i> clinical isolates. <i>IScience</i> , 2022, 25, 104372.	1.9	16
2772	Comparative Genomics Revealed Wide Intra-Species Genetic Heterogeneity and Lineage-Specific Genes of <i>Arkkermansia muciniphila</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0243921.	1.2	3
2773	Psychrotrophic plant beneficial bacteria from the glacial ecosystem of Sikkim Himalaya: Genomic evidence for the cold adaptation and plant growth promotion. <i>Microbiological Research</i> , 2022, 260, 127049.	2.5	11
2774	Characterization of blaNDM-positive Enterobacteriaceae reveals the clonal dissemination of <i>Enterobacter hormaechei</i> coharboring blaNDM and tet(X4) along the pork production chain. <i>International Journal of Food Microbiology</i> , 2022, 372, 109692.	2.1	6
2775	Carriage prevalence and genomic epidemiology of <i>Staphylococcus aureus</i> among Native American children and adults in the Southwestern USA. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
2776	Co-Occurrence of Multidrug Resistant <i>Klebsiella pneumoniae</i> Pathogenic Clones of Human Relevance in an Equine Pneumonia Case. <i>Microbiology Spectrum</i> , 2022, , e0215821.	1.2	3
2777	Sequence-based pangenomic core detection. <i>IScience</i> , 2022, 25, 104413.	1.9	5
2778	High Prevalence of blaCTXMâ€™1/IncI1-Î³3/ST3 Plasmids in Extended-Spectrum Î²-Lactamase-Producing <i>Escherichia coli</i> Isolates Collected From Domestic Animals in Guadeloupe (French West Indies). <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
2779	Genetic and Phenotypic Study of the <i>Pectobacterium versatile</i> Beta-Lactamase, the Enzyme Most Similar to the Plasmid-Encoded TEM-1. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0022022.	1.4	2
2780	Genomic and metabolomic profiling of endolithic <i>Rhodococcus fascians</i> strain S11 isolated from an arid serpentine environment. <i>Archives of Microbiology</i> , 2022, 204, 336.	1.0	1



#	ARTICLE	IF	CITATIONS
2781	Investigating plant disease outbreaks with long-read metagenomics: sensitive detection and highly resolved phylogenetic reconstruction applied to <i>Xylella fastidiosa</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	5
2782	Dissecting <i>Listeria monocytogenes</i> Persistent Contamination in a Retail Market Using Whole-Genome Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, e0018522.	1.2	4
2783	The Emergence of a Multidrug-Resistant and Pathogenic ST42 Lineage of <i>Staphylococcus haemolyticus</i> from a Hospital in China. <i>Microbiology Spectrum</i> , 2022, 10, e0234221.	1.2	6
2784	Using unique ORFan genes as strain-specific identifiers for <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2022, 22, 135.	1.3	2
2785	Genomic analysis of <i>qnr</i> -harbouring <i>IncX</i> plasmids and their transferability within different hosts under induced stress. <i>BMC Microbiology</i> , 2022, 22, 136.	1.3	5
2792	The <i>Neisseria gonorrhoeae</i> Accessory Genome and Its Association with the Core Genome and Antimicrobial Resistance. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	9
2793	Bacterial Adaptation to Venom in Snakes and Arachnida. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	13
2794	Genetic Resistance Determinants in Clinical <i>Acinetobacter pittii</i> Genomes. <i>Antibiotics</i> , 2022, 11, 676.	1.5	2
2796	<i>Furfurilactobacillus mii</i> sp. nov., isolated from fermented cereal foods. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	12
2798	Comparative Whole Genome Analysis of an <i>Anaplasma phagocytophilum</i> Strain Isolated from Norwegian Sheep. <i>Pathogens</i> , 2022, 11, 601.	1.2	4
2799	Multiplex PCR identification of the major <i>Pseudomonas aeruginosa</i> serogroups using specific novel target genes. <i>LWT - Food Science and Technology</i> , 2022, 163, 113567.	2.5	3
2800	Comparative genomic analysis of <i>Leptospira</i> spp. isolated from <i>Rattus norvegicus</i> in Indonesia. <i>Infection, Genetics and Evolution</i> , 2022, 102, 105306.	1.0	1
2801	Phenotypic and Genomic Comparison of <i>Staphylococcus Aureus</i> ; Highlights Virulence and Host Adaptation Favoring the Success of Epidemic Clones. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2802	An Epistatic Network Describes <i>oppA</i> and <i>glgB</i> as Relevant Genes for <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
2803	Comparative genomics of the Western Hemisphere soft tick-borne relapsing fever borreliae highlights extensive plasmid diversity. <i>BMC Genomics</i> , 2022, 23, .	1.2	13
2804	APTC-C-SA01: A Novel Bacteriophage Cocktail Targeting <i>Staphylococcus aureus</i> and MRSA Biofilms. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6116.	1.8	9
2806	Emergence of a High-Risk <i>Klebsiella michiganensis</i> Clone Disseminating Carbapenemase Genes. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
2807	Complete Genome Sequence of <i>Weissella cibaria</i> NH9449 and Comprehensive Comparative-Genomic Analysis: Genomic Diversity and Versatility Trait Revealed. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4

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2809	Pangenome analyses of <i>Bacillus pumilus</i> , <i>Bacillus safensis</i> , and <i>Priestia megaterium</i> exploring the plant-associated features of bacilli strains isolated from canola. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1063-1079.	1.0	19
2810	Emergence of multi-drug-resistant <i>Mycobacterium tuberculosis</i> in Niger: A snapshot based on whole-genome sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010443.	1.3	3
2811	Genomic Characterization of Two <i>Escherichia fergusonii</i> Isolates Harboring <i>mcr-1</i> Gene From Farm Environment. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5
2812	Complete Genome Sequences of Nine <i>Streptococcus pneumoniae</i> Serotype 3 Clonal Complex 180 Strains. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	1
2813	Functional Characterization and Whole-Genome Analysis of an Aflatoxin-Degrading <i>Rhodococcus pyridinivorans</i> Strain. <i>Biology</i> , 2022, 11, 774.	1.3	3
2816	Origin, Phylogeny, and Transmission of the Epidemic Clone ST208 of Carbapenem-Resistant <i>Acinetobacter baumannii</i> on a Global Scale. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
2817	Molecular and metabolic characteristics of wastewater associated <i>Escherichia coli</i> strains. <i>Environmental Microbiology Reports</i> , 2022, 14, 646-654.	1.0	5
2818	Genomic Surveillance of Clinical <i>Pseudomonas aeruginosa</i> Isolates Reveals an Additive Effect of Carbapenemase Production on Carbapenem Resistance. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
2819	<i>Helicobacter pylori</i> genomes reveal Paleolithic human migration to the east end of Asia. <i>IScience</i> , 2022, 25, 104477.	1.9	3
2820	Antibiotic-resistant organisms establish reservoirs in new hospital built environments and are related to patient blood infection isolates. <i>Communications Medicine</i> , 2022, 2, .	1.9	21
2821	Comparative Genomics Provides Insights Into Genetic Diversity of <i>Clostridium tyrobutyricum</i> and Potential Implications for Late Blowing Defects in Cheese. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
2823	Comparative genomic analysis of hypervirulent <i>Aeromonas hydrophila</i> strains from striped catfish ( <i>Pangasianodon hypophthalmus</i> ) in Vietnam. <i>Aquaculture</i> , 2022, 558, 738364.	1.7	4
2824	Virulence and DNA sequence analysis of <i>Cronobacter</i> spp. isolated from infant cereals. <i>International Journal of Food Microbiology</i> , 2022, 376, 109745.	2.1	4
2829	Genomic Diversity of Hospital-Acquired Infections Revealed through Prospective Whole-Genome Sequencing-Based Surveillance. <i>MSystems</i> , 2022, 7, .	1.7	10
2830	Genomic characterization of denitrifying methylotrophic <i>Pseudomonas aeruginosa</i> strain AAK/M5 isolated from municipal solid waste landfill soil. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, .	1.7	3
2831	Endosymbiont population genomics sheds light on transmission mode, partner specificity, and stability of the scaly-foot snail holobiont. <i>ISME Journal</i> , 2022, 16, 2132-2143.	4.4	6
2832	Molecular Evolution and Genomic Insights into Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> Sequence Type 88. <i>Microbiology Spectrum</i> , 0, , .	1.2	2
2834	<i>Xanthomonas bonasiae</i> sp. nov. and <i>Xanthomonas youngii</i> sp. nov., isolated from crown gall tissues. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	16

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2835	Comparative Genomics of Shiga Toxin-Producing <i>Escherichia coli</i> Strains Isolated from Pediatric Patients with and without Hemolytic Uremic Syndrome from 2000 to 2016 in Finland. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	8
2836	Strain Specific Variations in <i>Acinetobacter baumannii</i> Complement Sensitivity. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
2837	Genomic Insights of <i>Enterococcus faecium</i> UC7251, a Multi-Drug Resistant Strain From Ready-to-Eat Food, Highlight the Risk of Antimicrobial Resistance in the Food Chain. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	14
2838	Detection of <i>Pseudomonas aeruginosa</i> Serogroup G Using Real-Time PCR for Novel Target Genes Identified Through Comparative Genomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
2839	Genomic characterization of <i>Streptococcus parasuis</i> , a close relative of <i>Streptococcus suis</i> and also a potential opportunistic zoonotic pathogen. <i>BMC Genomics</i> , 2022, 23, .	1.2	6
2840	<i>Pseudomonas petroselini</i> sp. nov., a pathogen causing bacterial rot of parsley in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
2841	Identification of novel molecular targets for <i>Weissella</i> species-specific real-time PCR based on pangenome analysis. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 4157-4168.	1.7	4
2842	Genomic Insight Into <i>Lactocaseibacillus paracasei</i> SP5, Reveals Genes and Gene Clusters of Probiotic Interest and Biotechnological Potential. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	14
2843	Genomic and Evolutionary Analysis of <i>Salmonella enterica</i> Serovar Kentucky Sequence Type 198 Isolated From Livestock In East Africa. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5
2844	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
2845	Genomic Analysis of Carbapenem-Resistant <i>Comamonas</i> in Water Matrices: Implications for Public Health and Wastewater Treatments. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	10
2846	Comparative genomic analysis revealed genetic divergence between <i>Bifidobacterium catenulatum</i> subspecies present in infant versus adult guts. <i>BMC Microbiology</i> , 2022, 22, .	1.3	6
2847	Genomic and Temporal Trends in Canine ExPEC Reflect Those of Human ExPEC. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11
2848	Differentiated Evolutionary Strategies of Genetic Diversification in Atlantic and Pacific Thaumarchaeal Populations. <i>MSystems</i> , 2022, 7, .	1.7	3
2849	Clustered Regularly Interspaced Short Palindromic Repeats Genotyping of Multidrug-Resistant <i>Salmonella</i> Heidelberg Strains Isolated From the Poultry Production Chain Across Brazil. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
2850	An Outbreak of Human Systemic Anthrax, including One Case of Anthrax Meningitis, Occurred in Calabria Region (Italy): A Description of a Successful One Health Approach. <i>Life</i> , 2022, 12, 909.	1.1	2
2851	Duck sewage source coliphage P762 can lyse STEC and APEC. <i>Virus Genes</i> , 2022, 58, 436-447.	0.7	6
2852	A 16th century <i>Escherichia coli</i> draft genome associated with an opportunistic bile infection. <i>Communications Biology</i> , 2022, 5, .	2.0	2

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2853	<i>Listeria ilorinensis</i> sp. nov., isolated from cow milk cheese in Nigeria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	15
2854	Common and distinctive genomic features of <i>Klebsiella pneumoniae</i> thriving in the natural environment or in clinical settings. <i>Scientific Reports</i> , 2022, 12, .	1.6	18
2855	Contaminated Incubators: Source of a Multispecies <i>Enterobacter</i> Outbreak of Neonatal Sepsis. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
2857	Phylogenetic Characterization and Genome Sequence Analysis of <i>Burkholderia glumae</i> Strains Isolated in Thailand as the Causal Agent of Rice Bacterial Panicle Blight. <i>Pathogens</i> , 2022, 11, 676.	1.2	3
2858	Biofilm formation and genomic features of <i>Listeria monocytogenes</i> strains isolated from meat and dairy industries located in Piedmont (Italy). <i>International Journal of Food Microbiology</i> , 2022, 378, 109784.	2.1	10
2859	Comparative Genomics Reveals the Acquisition of a Novel Transposon Tn.ArsmerS12 by the Plant Growth-Promoting <i>Pantoea eucrina</i> OB49 in Polluted Environments. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2860	Virulence plasmid pINV as a genetic signature for <i>Shigella flexneri</i> phylogeny. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
2861	Evaluation of Fourier Transform Infrared Spectroscopy as a First-Line Typing Tool for the Identification of Extended-Spectrum $\beta$ -Lactamase-Producing <i>Klebsiella pneumoniae</i> Outbreaks in the Hospital Setting. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	11
2862	Whole-Genome Sequence of Multidrug-Resistant Methicillin-Resistant <i>Staphylococcus epidermidis</i> Carrying Biofilm-Associated Genes and a Unique Composite of SCCmec. <i>Antibiotics</i> , 2022, 11, 861.	1.5	2
2865	Characteristics of <i>Mycoplasma hyopneumoniae</i> Strain ES-2 Isolated From Chinese Native Black Pig Lungs. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	3
2866	The Antibacterial Effect of Platelets on <i>Escherichia coli</i> Strains. <i>Biomedicines</i> , 2022, 10, 1533.	1.4	4
2867	<i>Acinetobacter baumannii</i> Sampled from Cattle and Pigs Represent Novel Clones. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	9
2868	Genomic Characterization of <i>Enterococcus hirae</i> From Beef Cattle Feedlots and Associated Environmental Continuum. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
2869	Stable antibiotic resistance and rapid human adaptation in livestock-associated MRSA. <i>ELife</i> , 0, 11, .	2.8	28
2870	The coral pathogen <i>Vibrio coralliilyticus</i> kills non-pathogenic holobiont competitors by triggering prophage induction. <i>Nature Ecology and Evolution</i> , 2022, 6, 1132-1144.	3.4	20
2871	CARB-ES-19 Multicenter Study of Carbapenemase-Producing <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> From All Spanish Provinces Reveals Interregional Spread of High-Risk Clones Such as ST307/OXA-48 and ST512/KPC-3. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	20
2874	Comparative Genomics and In Silico Evaluation of Genes Related to the Probiotic Potential of <i>Bifidobacterium breve</i> 1101A. , 2022, 1, 161-182.		5
2875	Molecular Characterization of <i>bla</i> <sub>NDM</sub> -Carrying IncX3 Plasmids: <i>bla</i> <sub>NDM-16b</sub> Likely Emerged from a Mutation of <i>bla</i> <sub>NDM-5</sub> on IncX3 Plasmid. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5

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2876	Genomic features of predominant non-PCV13 serotypes responsible for adult invasive pneumococcal disease in Spain. <i>Journal of Antimicrobial Chemotherapy</i> , 0, , .	1.3	1
2877	Comparative Genomic Analysis of the Human Pathogen <i>Wohlfahrtiimonas Chitiniclastica</i> Provides Insight Into the Identification of Antimicrobial Resistance Genotypes and Potential Virulence Traits. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
2879	Identification of a Putative CodY Regulon in the Gram-Negative Phylum Synergistetes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7911.	1.8	0
2880	Interspecies Transmission of CMY-2-Producing <i>Escherichia coli</i> Sequence Type 963 Isolates between Humans and Gulls in Australia. <i>MSphere</i> , 2022, 7, .	1.3	6
2881	Characterisation of Staphylococci species from neonatal blood cultures in low- and middle-income countries. <i>BMC Infectious Diseases</i> , 2022, 22, .	1.3	9
2882	<i>Brachybacterium kimchii</i> sp. nov. and <i>Brachybacterium halotolerans</i> subsp. <i>kimchii</i> subsp. nov., isolated from the Korean fermented vegetables, kimchi, and description of <i>Brachybacterium halotolerans</i> subsp. <i>halotolerans</i> subsp. nov.. <i>Journal of Microbiology</i> , 2022, 60, 678-688.	1.3	11
2883	Phenotypic and genotypic characterisation of thymine auxotrophy in <i>Escherichia coli</i> isolated from a patient with recurrent bloodstream infection. <i>PLoS ONE</i> , 2022, 17, e0270256.	1.1	2
2884	Core genes can have higher recombination rates than accessory genes within global microbial populations. <i>ELife</i> , 0, 11, .	2.8	9
2885	<i>Xylella fastidiosa</i> Outbreak in Israel: Population Genetics, Host Range, and Temporal and Spatial Distribution Analysis. <i>Phytopathology</i> , 2022, 112, 2296-2309.	1.1	6
2886	Whole-genome analyses of APEC carrying <i>mcr-1</i> in some coastal areas of China from 2019 to 2020. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 30, 370-376.	0.9	5
2887	The accurate identification and quantification of six <i>Enterococcus</i> species using quantitative polymerase chain reaction based novel DNA markers. <i>LWT - Food Science and Technology</i> , 2022, 166, 113769.	2.5	6
2888	Development of a Multi-Epitope Vaccine for <i>Mycoplasma hyopneumoniae</i> and Evaluation of Its Immune Responses in Mice and Piglets. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7899.	1.8	8
2889	Isolation of a novel <i>Lactiplantibacillus plantarum</i> strain resistant to nitrite stress and its transcriptome analysis. <i>Journal of Microbiology</i> , 2022, 60, 715-726.	1.3	0
2890	<i>Vibrio cholerae</i> O139 genomes provide a clue to why it may have failed to usher in the eighth cholera pandemic. <i>Nature Communications</i> , 2022, 13, .	5.8	8
2891	Comparative Genomics and Pan-Genome Driven Prediction of a Reduced Genome of <i>Akkermansia muciniphila</i> . <i>Microorganisms</i> , 2022, 10, 1350.	1.6	5
2892	Analysis of the Taxonomy, Synteny, and Virulence Factors for Soft Rot Pathogen <i>Pectobacterium aroidearum</i> in <i>Amorphophallus konjac</i> Using Comparative Genomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
2893	Within-host evolution of a gut pathobiont facilitates liver translocation. <i>Nature</i> , 2022, 607, 563-570.	13.7	65
2894	Genetic characterization of <i>Salmonella</i> <i>Infantis</i> from South Africa, 2004–2016. <i>Access Microbiology</i> , 2022, 4, .	0.2	1

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2895	Competitive Exclusion Bacterial Culture Derived from the Gut Microbiome of Nile Tilapia ( <i>Oreochromis niloticus</i> ) as a Resource to Efficiently Recover Probiotic Strains: Taxonomic, Genomic, and Functional Proof of Concept. <i>Microorganisms</i> , 2022, 10, 1376.	1.6	5
2896	Role of <i>Staphylococcus agnetis</i> and <i>Staphylococcus hyicus</i> in the Pathogenesis of Buffalo Fly Skin Lesions in Cattle. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
2898	Recovery of Lutacidiplasmatales archaeal order genomes suggests convergent evolution in Thermoplasmata. <i>Nature Communications</i> , 2022, 13, .	5.8	10
2899	Culture-Free Phylogenetic Analysis of <i>Legionella pneumophila</i> Using Targeted CRISPR/Cas9 Next-Generation Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
2900	Combining Immunoinformatics with Pangenome Analysis To Design a Multi-epitope Subunit Vaccine against <i>Klebsiella pneumoniae</i> K1, K2, K47, and K64. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
2902	Characterization and Comparative Genomic Analysis of a Highly Colistin-Resistant <i>Chryseobacterium gallinarum</i> : a Rare, Uncommon Pathogen. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
2903	High-quality pan-genome of <i>Escherichia coli</i> generated by excluding confounding and highly similar strains reveals an association between unique gene clusters and genomic islands. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
2904	<i>Pseudomonas boanensis</i> sp. nov., a bacterium isolated from river water used for household purposes in Boane District, Mozambique. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	9
2905	Selection of <i>Anabaena</i> sp. PCC 7938 as a Cyanobacterium Model for Biological ISRU on Mars. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	10
2906	Comparative Genomic Analysis of the Marine Cyanobacterium <i>Acaryochloris marina</i> MBIC10699 Reveals the Impact of Phycobiliprotein Reacquisition and the Diversity of <i>Acaryochloris</i> Plasmids. <i>Microorganisms</i> , 2022, 10, 1374.	1.6	2
2907	Genomic insights into bla <sub>NDM</sub> -carrying carbapenem-resistant <i>Klebsiella pneumoniae</i> clinical isolates from a university hospital in Thailand. <i>Microbiological Research</i> , 2022, 263, 127136.	2.5	8
2908	<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
2909	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> KJ, a Clinical Isolate from Taiwan. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
2910	Genomic diversity of genus <i>Limosilactobacillus</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
2911	Phylogenomic analysis of the genus <i>Leuconostoc</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
2912	Time Series Genomics of <i>Pseudomonas aeruginosa</i> Reveals the Emergence of a Hypermutator Phenotype and Within-Host Evolution in Clinical Inpatients. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
2913	Identification of <i>Streptococcus infantarius</i> subsp. <i>infantarius</i> as the species primarily responsible for acid production in Izmir Brined Tulum Cheese from the Aegean Region of Türkiye. <i>Food Research International</i> , 2022, 160, 111707.	2.9	6
2914	Increased Prevalence of <i>Salmonella infantis</i> Isolated from Raw Chicken and Turkey Products in the United States Is Due to a Single Clonal Lineage Carrying the pESI Plasmid. <i>Microorganisms</i> , 2022, 10, 1478.	1.6	13

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2915	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
2918	<i>Raoultibacter phocaeensis</i> sp. nov., A New Bacterium Isolated from a Patient with Recurrent <i>Clostridioides difficile</i> Infection. <i>Current Microbiology</i> , 2022, 79, .	1.0	0
2919	Genetic and Structural Variation in the O-Antigen of <i>Salmonella enterica</i> Serovar Typhimurium Isolates Causing Bloodstream Infections in the Democratic Republic of the Congo. <i>MBio</i> , 2022, 13, .	1.8	4
2920	Draft-genome analysis provides insights into the virulence properties and genome plasticity of <i>Vibrio fluvialis</i> organisms isolated from shrimp farms and Turag river in Bangladesh. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	0
2921	Molecular Characterization of pBOq-IncQ and pBOq-95LK Plasmids of <i>Escherichia coli</i> BOq 01, a New Isolated Strain from Poultry Farming, Involved in Antibiotic Resistance. <i>Microorganisms</i> , 2022, 10, 1509.	1.6	2
2922	Histamine production by the gut microbiota induces visceral hyperalgesia through histamine 4 receptor signaling in mice. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	41
2923	Phylogenomic analysis of <i>Salmonella</i> Indiana ST17, an emerging MDR clonal group in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 2937-2945.	1.3	7
2924	mOTUp: a robust Bayesian approach to leverage metagenome-assembled genomes for core-genome estimation. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	6
2925	Comparative Genomic Analysis of Seven <i>Vibrio alginolyticus</i> Strains Isolated From Shrimp Larviculture Water With Emphasis on Chitin Utilization. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
2926	Genomics of <i>Staphylococcus aureus</i> Strains Isolated from Infectious and Non-Infectious Ocular Conditions. <i>Antibiotics</i> , 2022, 11, 1011.	1.5	5
2927	Metagenomic Insights into Pathogenic Characterization of ST410 <i>Acinetobacter nosocomialis</i> Prevalent in China. <i>Pathogens</i> , 2022, 11, 838.	1.2	1
2928	<i>Rhodococcus pseudokoreensis</i> sp. nov. isolated from the rhizosphere of young M26 apple rootstocks. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3
2929	Comparative Genomic Analysis of Antarctic <i>Pseudomonas</i> Isolates with 2,4,6-Trinitrotoluene Transformation Capabilities Reveals Their Unique Features for Xenobiotics Degradation. <i>Genes</i> , 2022, 13, 1354.	1.0	12
2930	Comparative Genomics of <i>Escherichia coli</i> Serotype O55:H7 Using Complete Closed Genomes. <i>Microorganisms</i> , 2022, 10, 1545.	1.6	0
2931	Genome characteristics of clinical <i>Salmonella enterica</i> population from a state public health laboratory, New Hampshire, USA, 2017–2020. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
2932	Correlation of <i>Moraxella catarrhalis</i> macrolide susceptibility with the ability to adhere and invade human respiratory epithelial cells. <i>Emerging Microbes and Infections</i> , 2022, 11, 2055-2068.	3.0	7
2933	Pneumococcal genetic variability in age-dependent bacterial carriage. <i>ELife</i> , 0, 11, .	2.8	6
2934	Intra-species diversity of <i>Clostridium perfringens</i> : A diverse genetic repertoire reveals its pathogenic potential. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9

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2935	Phylogenetic and Multiple-Locus Variable number tandem repeat analysis of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> isolates from Argentina. <i>Veterinary Research Communications</i> , 2022, 46, 1121-1129.	0.6	2
2936	Two New <i>Rhizobiales</i> Species Isolated from Root Nodules of Common Sainfoin ( <i>Onobrychis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	6
2937	Intrinsic tet(L) sub-class in <i>Bacillus velezensis</i> and <i>Bacillus amyloliquefaciens</i> is associated with a reduced susceptibility toward tetracycline. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
2938	Antibiotic resistance genes in the gut microbiota of mothers and linked neonates with or without sepsis from low- and middle-income countries. <i>Nature Microbiology</i> , 2022, 7, 1337-1347.	5.9	23
2940	PanExplorer: a web-based tool for exploratory analysis and visualization of bacterial pan-genomes. <i>Bioinformatics</i> , 2022, 38, 4412-4414.	1.8	3
2941	Genetic Diversity of Virulent Polymyxin-Resistant <i>Klebsiella aerogenes</i> Isolated from Intensive Care Units. <i>Antibiotics</i> , 2022, 11, 1127.	1.5	4
2942	Genomic features of <i>Mycoplasma bovis</i> subtypes currently circulating in France. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
2943	First confirmed case of infant botulism caused by <i>Clostridium botulinum</i> type A(B) in a 10-month-old infant in Hanoi, Vietnam. <i>IJID Regions</i> , 2022, 5, 18-20.	0.5	3
2944	Bioinformatics and its role in the study of the evolution and probiotic potential of lactic acid bacteria. <i>Food Science and Biotechnology</i> , 2023, 32, 389-412.	1.2	4
2945	Genome-Scale Metabolic Modeling Combined with Transcriptome Profiling Provides Mechanistic Understanding of <i>Streptococcus thermophilus</i> CH8 Metabolism. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	6
2946	Co-occurrence of <i>mcr-2</i> and <i>mcr-3</i> genes on chromosome of multidrug-resistant <i>Escherichia coli</i> isolated from healthy individuals in Thailand. <i>International Journal of Antimicrobial Agents</i> , 2022, 60, 106662.	1.1	8
2947	Genomic surveillance of <i>Salmonella</i> spp. in the Philippines during 2013â€“2014. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2022, 116, 1202-1213.	0.7	3
2949	Evolution of longitudinal division in multicellular bacteria of the <i>Neisseriaceae</i> family. <i>Nature Communications</i> , 2022, 13, .	5.8	13
2950	First Report of <i>Bartonella</i> spp. in Marsupials from Brazil, with a Description of <i>Bartonella harrusi</i> sp. nov. and a New Proposal for the Taxonomic Reclassification of Species of the Genus <i>Bartonella</i> . <i>Microorganisms</i> , 2022, 10, 1609.	1.6	12
2951	Genetic determinants of antimicrobial resistance in three multi-drug resistant strains of <i>Cutibacterium acnes</i> isolated from patients with acne: a predictive in silico study. <i>Access Microbiology</i> , 2022, 4, .	0.2	3
2954	Enterobacterales high-risk clones and plasmids spreading <i>bla</i> ESBL/AmpC and <i>bla</i> OXA-48 genes within and between hospitalized dogs and their environment. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 2754-2762.	1.3	3
2955	Molecular Epidemiology of Penicillin-Susceptible <i>Staphylococcus aureus</i> Bacteremia in Australia and Reliability of Diagnostic Phenotypic Susceptibility Methods to Detect Penicillin Susceptibility. <i>Microorganisms</i> , 2022, 10, 1650.	1.6	1
2956	Emergence of uncommon KL38-OCL6-ST220 carbapenem-resistant <i>Acinetobacter pittii</i> strain, co-producing chromosomal NDM-1 and OXA-820 carbapenemases. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	5



#	ARTICLE	IF	CITATIONS
2957	Microbiota of the Pregnant Mouse: Characterization of the Bacterial Communities in the Oral Cavity, Lung, Intestine, and Vagina through Culture and DNA Sequencing. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
2958	Microbiological and Molecular Features Associated with Persistent and Relapsing <i>Staphylococcus aureus</i> Prosthetic Joint Infection. <i>Antibiotics</i> , 2022, 11, 1119.	1.5	5
2959	Mexican Strains of <i>Anaplasma marginale</i> : A First Comparative Genomics and Phylogeographic Analysis. <i>Pathogens</i> , 2022, 11, 873.	1.2	1
2960	Genomic Analysis of a Strain Collection Containing Multidrug-, Extensively Drug-, Pandrug-, and Carbapenem-Resistant Modern Clinical Isolates of <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	9
2961	<i>Shewanella</i> sp. T2.3D-1.1 a Novel Microorganism Sustaining the Iron Cycle in the Deep Subsurface of the Iberian Pyrite Belt. <i>Microorganisms</i> , 2022, 10, 1585.	1.6	6
2963	ESBL plasmids in <i>Klebsiella pneumoniae</i> : diversity, transmission and contribution to infection burden in the hospital setting. <i>Genome Medicine</i> , 2022, 14, .	3.6	23
2964	A tale of two plasmids: contributions of plasmid associated phenotypes to epidemiological success among <i>Shigella</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	7
2965	<i>Staphylococcus aureus</i> lineages associated with a free-ranging population of the fruit bat <i>Pteropus livingstonii</i> retained over 25 years in captivity. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
2966	Methicillin Resistant <i>Staphylococci</i> Isolated from Goats and Their Farm Environments in Saudi Arabia Genotypically Linked to Known Human Clinical Isolates: a Pilot Study. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
2967	Phylogenetic lineages of tuberculosis isolates and their association with patient demographics in Tanzania. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
2968	Combined comparative genomics and clinical modeling reveals plasmid-encoded genes are independently associated with <i>Klebsiella</i> infection. <i>Nature Communications</i> , 2022, 13, .	5.8	9
2969	Arm race among closely-related carbapenem-resistant <i>Klebsiella pneumoniae</i> clones. <i>ISME Communications</i> , 2022, 2, .	1.7	3
2970	A continental-scale survey of <i>Wolbachia</i> infections in blue butterflies reveals evidence of interspecific transfer and invasion dynamics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
2973	The Population Genomics of Increased Virulence and Antibiotic Resistance in Human Commensal <i>Escherichia coli</i> over 30 Years in France. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	23
2974	Open pangenome of <i>Lactococcus lactis</i> generated by a combination of metagenome-assembled genomes and isolate genomes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
2975	Genomic insights into the emergence and spread of NDM-1-producing <i>Vibrio</i> spp. isolates in China. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 3039-3049.	1.3	1
2976	Whole genome sequencing of mesorhizobia isolated from northern Canada. <i>Canadian Journal of Microbiology</i> , 2022, 68, 661-673.	0.8	2
2977	Complete genomic analysis of ST117 lineage extraintestinal pathogenic <i>Escherichia coli</i> (ExPEC) to reveal multiple genetic determinants to drive its global transmission: ST117 <i>E. coli</i> as an emerging multidrug-resistant foodborne ExPEC with zoonotic potential. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3256-3273.	1.3	10

#	ARTICLE	IF	CITATIONS
2978	Emergence and Transmission of Plasmid-Mediated Mobile Colistin Resistance Gene <i>mcr-10</i> in Humans and Companion Animals. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
2979	Machine learning algorithm to characterize antimicrobial resistance associated with the International Space Station surface microbiome. <i>Microbiome</i> , 2022, 10, .	4.9	14
2980	Comparative genome analysis of <i>Vagococcus fluvialis</i> reveals abundance of mobile genetic elements in sponge-isolated strains. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
2981	Co-Occurrence of $\beta$ -Lactam and Aminoglycoside Resistance Determinants among Clinical and Environmental Isolates of <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> : A Genomic Approach. <i>Pharmaceuticals</i> , 2022, 15, 1011.	1.7	6
2982	The human gut serves as a reservoir of hypervirulent <i>Klebsiella pneumoniae</i> . <i>Gut Microbes</i> , 2022, 14, .	4.3	4
2984	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
2985	Deep Population Genomics Reveals Systematic and Parallel Evolution at a Lipopolysaccharide Biosynthetic Locus in <i>Xanthomonas</i> Pathogens That Infect Rice and Sugarcane. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	1
2986	Genetic characterization of hypervirulent <i>Klebsiella pneumoniae</i> responsible for acute death in captive marmosets. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
2988	The effect of sequencing and assembly on the inference of horizontal gene transfer on chromosomal and plasmid phylogenies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, .	1.8	3
2989	Metagenomic data from cerebrospinal fluid permits tracing the origin and spread of <i>Neisseria meningitidis</i> CC4821 in China. <i>Communications Biology</i> , 2022, 5, .	2.0	1
2990	Comparative Genomics Reveal the High Conservation and Scarce Distribution of Nitrogen Fixation <i>nif</i> Genes in the Plant-Associated Genus <i>Herbaspirillum</i> . <i>Microbial Ecology</i> , 0, , .	1.4	0
2991	Comparative genomics of <i>Leuconostoc lactis</i> strains isolated from human gastrointestinal system and fermented foods microbiomes. <i>BMC Genomic Data</i> , 2022, 23, .	0.7	2
2992	Genomic dissection of the <i>Vibrio cholerae</i> O-serogroup global reference strains: reassessing our view of diversity and plasticity between two chromosomes. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
2993	A genome-led study on the pathogenesis of <i>Fusobacterium necrophorum</i> infections. <i>Gene</i> , 2022, 840, 146770.	1.0	2
2994	Molecular mechanisms and genomic basis of tigecycline-resistant Enterobacterales from swine slaughterhouses. <i>Microbiological Research</i> , 2022, 264, 127151.	2.5	1
2996	<i>Xanthomonas indica</i> sp. nov., a Novel Member of Non-Pathogenic <i>Xanthomonas</i> Community from Healthy Rice Seeds. <i>Current Microbiology</i> , 2022, 79, .	1.0	11
2997	Comparative Genomics of <i>Listeria</i> Species Recovered from Meat and Food Processing Facilities. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
2998	Significant compositional and functional variation reveals the patterns of gut microbiota evolution among the widespread Asian honeybee populations. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5

#	ARTICLE	IF	CITATIONS
2999	Molecular epidemiology and population genomics of tet(X4), blaNDM or mcr-1 positive Escherichia coli from migratory birds in southeast coast of China. <i>Ecotoxicology and Environmental Safety</i> , 2022, 244, 114032.	2.9	4
3000	Escherichia coli ST224 and IncF/blaCTX-M-55 plasmids drive resistance to extended-spectrum cephalosporins in poultry flocks in Parana, Brazil. <i>International Journal of Food Microbiology</i> , 2022, 380, 109885.	2.1	4
3001	Clostridium perfringens associated with dairy farm systems show diverse genotypes. <i>International Journal of Food Microbiology</i> , 2022, 382, 109933.	2.1	5
3002	Comparative genomic analysis of clinical Acinetobacter nosocomialis isolates from Terengganu, Malaysia led to the discovery of a novel tetracycline-resistant plasmid. <i>Journal of Global Antimicrobial Resistance</i> , 2022, 31, 104-109.	0.9	0
3003	Alternative nitrogenase of Paenibacillus sonchi genomovar Riograndensis: An insight in the origin of Fe-nitrogenase in the Paenibacillaceae family. <i>Molecular Phylogenetics and Evolution</i> , 2022, 177, 107624.	1.2	2
3004	Non-redundant nature of Lactiplantibacillus plantarum plasmidome revealed by comparative genomic analysis of 105 strains. <i>Food Microbiology</i> , 2023, 109, 104153.	2.1	5
3005	Phage PH826 Effectively Inhibits the Formation of Multidrug-Resistant Pseudomonas Aeruginosa Biofilm. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3006	<i>Prevotella merdae</i> sp. nov., a new bacterial species isolated from human faeces. <i>FEMS Microbiology Letters</i> , 2022, 369, .	0.7	1
3007	High prevalence and pathogenic potential of Shiga toxin-producing Escherichia coli strains in raw mutton and beef in Shandong, China. <i>Current Research in Food Science</i> , 2022, 5, 1596-1602.	2.7	3
3008	WGS-Based Lineage and Antimicrobial Resistance Pattern of Salmonella Typhimurium Isolated during 2000–2017 in Peru. <i>Antibiotics</i> , 2022, 11, 1170.	1.5	7
3009	Development and Evaluation of Duplex MIRA-qPCR Assay for Simultaneous Detection of Staphylococcus aureus and non-aureus Staphylococci. <i>Microorganisms</i> , 2022, 10, 1734.	1.6	4
3010	Epidemiology of Plasmid Lineages Mediating the Spread of Extended-Spectrum Beta-Lactamases among Clinical Escherichia coli. <i>MSystems</i> , 2022, 7, .	1.7	6
3012	Molecular epidemiology and antibiotic resistance profiles of invasive Haemophilus influenzae from Norway 2017–2021. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
3013	Complete Genome Sequence Analysis of Bacillus subtilis Bbv57, a Promising Biocontrol Agent against Phytopathogens. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9732.	1.8	13
3014	Genomic characterization of Staphylococcus aureus isolates causing osteoarticular infections in otherwise healthy children. <i>PLoS ONE</i> , 2022, 17, e0272425.	1.1	1
3016	Detection and characterisation of Bordetella hinzii in line-related bacteraemia and respiratory tract infection in Australia. <i>Pathology</i> , 2022, , .	0.3	0
3017	The genus Serratia revisited by genomics. <i>Nature Communications</i> , 2022, 13, .	5.8	21
3019	Identification of Leuconostoc species based on novel marker genes identified using real-time PCR via computational pangenome analysis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1

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3020	Reduced and Nonreduced Genomes in <i>Paraburkholderia</i> Symbionts of Social Amoebas. <i>MSystems</i> , 0, .	1.7	5
3021	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
3022	Meropenem plus Ceftaroline Is Active against <i>Enterococcus faecalis</i> in an <i>In Vitro</i> Pharmacodynamic Model Using Humanized Dosing Simulations. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, .	1.4	2
3024	VanA- <i>Enterococcus faecalis</i> in Poland: hospital population clonal structure and <i>vanA</i> mobilome. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 1245-1261.	1.3	5
3025	A functional selection reveals previously undetected anti-phage defence systems in the <i>E. coli</i> pangenome. <i>Nature Microbiology</i> , 2022, 7, 1568-1579.	5.9	108
3026	Limited Transmission of <i>Klebsiella pneumoniae</i> among Humans, Animals, and the Environment in a Caribbean Island, Guadeloupe (French West Indies). <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
3027	Extended genomic analyses of the broad-host-range phages $\nu$ B_KmiM-2Di and $\nu$ B_KmiM-4Dii reveal slopekviruses have highly conserved genomes. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	5
3028	Comprehensive Genome and Plasmidome Analysis of Antimicrobial Resistant Bacteria in Wastewater Treatment Plant Effluent of Tokyo. <i>Antibiotics</i> , 2022, 11, 1283.	1.5	8
3029	Temporo-spatial variations in resistance determinants and clonality of <i>Acinetobacter baumannii</i> and <i>Pseudomonas aeruginosa</i> strains from Romanian hospitals and wastewaters. <i>Antimicrobial Resistance and Infection Control</i> , 2022, 11, .	1.5	9
3030	PhaMMseqs: a new pipeline for constructing phage gene families using MMseqs2. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	14
3031	Late-Onset Sepsis in a Premature Infant Mediated by Breast Milk: Mother-to-Infant Transmission of Group B <i>Streptococcus</i> Detected by Whole-Genome Sequencing. <i>Infection and Drug Resistance</i> , 0, Volume 15, 5345-5352.	1.1	1
3032	New members of the family Eggerthellaceae isolated from <i>Marmota himalayana</i> : <i>Xiamenia xianingshaonis</i> gen. nov., sp. nov., from intestinal contents, and <i>Berryella wangjianwei</i> sp. nov., from trachea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	2
3033	Critical assessment of pan-genomic analysis of metagenome-assembled genomes. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
3034	Bioinformatics study of expression from genomes of epidemiologically related MRSA CC398 isolates from human and wild animal samples. <i>Journal of Proteomics</i> , 2022, 268, 104714.	1.2	3
3036	Changes in the genomes and methylomes of three <i>Salmonella enterica</i> serovars after long-term storage in ground black pepper. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3037	Using Genomes and Evolutionary Analyses to Screen for Host-Specificity and Positive Selection in the Plant Pathogen <i>Xylella fastidiosa</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	6
3038	Colonization dynamics of extended-spectrum beta-lactamase-producing Enterobacterales in the gut of Malawian adults. <i>Nature Microbiology</i> , 2022, 7, 1593-1604.	5.9	9
3039	Phenotypic and molecular characterization of IMP-producing Enterobacterales in Spain: Predominance of IMP-8 in <i>Klebsiella pneumoniae</i> and IMP-22 in <i>Enterobacter roggenkampii</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3

#	ARTICLE	IF	CITATIONS
3040	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
3042	Redox-Mediated Inactivation of the Transcriptional Repressor RcrR is Responsible for Uropathogenic <i>Escherichia coli</i> ™s Increased Resistance to Reactive Chlorine Species. <i>MBio</i> , 2022, 13, .	1.8	6
3043	Elevation of <i>Clavibacter michiganensis</i> subsp. <i>californiensis</i> to species level as <i>Clavibacter californiensis</i> sp. nov., merging and re-classification of <i>Clavibacter michiganensis</i> subsp. <i>chilensis</i> and <i>Clavibacter michiganensis</i> subsp. <i>phaseoli</i> as <i>Clavibacter phaseoli</i> sp. nov. based on complete genome in silico analyses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4
3044	Genome-Wide Association Study of <i>Listeria monocytogenes</i> Isolates Causing Three Different Clinical Outcomes. <i>Microorganisms</i> , 2022, 10, 1934.	1.6	4
3047	Widespread Dissemination of Plasmid-Mediated Tigecycline Resistance Gene <i>tet(X4)</i> in <i>Enterobacterales</i> of Porcine Origin. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
3048	How GBS Got Its Hump: Genomic Analysis of Group B <i>Streptococcus</i> from Camels Identifies Host Restriction as well as Mobile Genetic Elements Shared across Hosts and Pathogens. <i>Pathogens</i> , 2022, 11, 1025.	1.2	1
3049	Phylogenomic characterization and pangenomic insights into the surfactin-producing bacteria <i>Bacillus subtilis</i> strain RI4914. <i>Brazilian Journal of Microbiology</i> , 2022, 53, 2051-2063.	0.8	1
3050	IPGA: A handy integrated prokaryotes genome and pan-genome analysis web service. , 2022, 1, .		19
3051	Phylogenomic analysis of the genus <i>Delftia</i> reveals distinct major lineages with ecological specializations. <i>Microbial Genomics</i> , 2022, 8, .	1.0	6
3052	A compendium of 32,277 metagenome-assembled genomes and over 80 million genes from the early-life human gut microbiome. <i>Nature Communications</i> , 2022, 13, .	5.8	23
3053	Dissecting microbial communities and resistomes for interconnected humans, soil, and livestock. <i>ISME Journal</i> , 2023, 17, 21-35.	4.4	14
3054	Whole-Genome Sequencing and Comparative Genomic Analysis of <i>Enterococcus</i> spp. Isolated from Dairy Products: Genomic Diversity, Functional Characteristics, and Pathogenic Potential. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 9620.	1.3	2
3055	Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics. <i>Nature Genetics</i> , 2022, 54, 1553-1563.	9.4	46
3056	Investigating CRISPR spacer targets and their impact on genomic diversification of <i>Streptococcus mutans</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
3057	Drivers and determinants of strain dynamics following fecal microbiota transplantation. <i>Nature Medicine</i> , 2022, 28, 1902-1912.	15.2	54
3058	Comparative genomics of <i>Rothia</i> species reveals diversity in novel biosynthetic gene clusters and ecological adaptation to different eukaryotic hosts and host niches. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
3059	Fitness of evolving bacterial populations is contingent on deep and shallow history but only shallow history creates predictable patterns. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	2
3060	Prevalence and Population Diversity of <i>Listeria monocytogenes</i> Isolated from Dairy Cattle Farms in the Cantabria Region of Spain. <i>Animals</i> , 2022, 12, 2477.	1.0	8

#	ARTICLE	IF	CITATIONS
3061	Exploring the mobilome and resistome of <i>Enterococcus faecium</i> in a One Health context across two continents. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
3062	Comparative Genomic Analysis of Agarolytic <i>Flavobacterium faecale</i> WV33T. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10884.	1.8	2
3064	Genomic analysis of two <i>Bacillus safensis</i> isolated from Merzouga desert reveals desert adaptive and potential plant growth-promoting traits. <i>Functional and Integrative Genomics</i> , 2022, 22, 1173-1187.	1.4	1
3065	Polyphyly in widespread <i>Salmonella enterica</i> serovars and using genomic proximity to choose the best reference genome for bioinformatics analyses. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	2
3067	<i>Neisseria</i> species as pathobionts in bronchiectasis. <i>Cell Host and Microbe</i> , 2022, 30, 1311-1327.e8.	5.1	17
3071	ProPan: a comprehensive database for profiling prokaryotic pan-genome dynamics. <i>Nucleic Acids Research</i> , 2023, 51, D767-D776.	6.5	8
3072	Small wards in the ICU: a favorable measure for controlling the transmission of carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Intensive Care Medicine</i> , 2022, 48, 1573-1581.	3.9	5
3073	High genomic differentiation and limited gene flow indicate recent cryptic speciation within the genus <i>Laspinema</i> (cyanobacteria). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
3074	Global diversity and distribution of prophages are lineage-specific within the <i>Ralstonia solanacearum</i> species complex. <i>BMC Genomics</i> , 2022, 23, .	1.2	10
3075	Sugar Modification of Wall Teichoic Acids Determines Serotype-Dependent Strong Biofilm Production in <i>Listeria monocytogenes</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
3076	Lactic Acid Resistance and Population Structure of <i>Escherichia coli</i> from Meat Processing Environment. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
3077	Genome dynamics mediated by repetitive and mobile elements in <i>Xanthomonas citri</i> pv. <i>durantae</i> . <i>Access Microbiology</i> , 2022, 4, .	0.2	1
3078	Population genomics of emerging <i>Elizabethkingia anophelis</i> pathogens reveals potential outbreak and rapid global dissemination. <i>Emerging Microbes and Infections</i> , 2022, 11, 2590-2599.	3.0	5
3079	Whole genome sequence analysis of ESBL-producing <i>Escherichia coli</i> recovered from New Zealand freshwater sites. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
3080	First report of the whole genome of <i>Moraxella bovoculi</i> genotype 1 from India and comparative genomics of <i>Moraxella bovoculi</i> to identify genotype-specific markers. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	1
3081	Antigenic variability of <i>Vibrio anguillarum</i> serotype O2a: A hurdle for vaccine efficacy against vibriosis in rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Fish and Shellfish Immunology</i> , 2022, 131, 300-311.	1.6	1
3082	Transmission pathways of <i>Campylobacter</i> spp. at broiler farms and their environment in Brandenburg, Germany. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
3083	Discordant population structure among rhizobium divided genomes and their legume hosts. <i>Molecular Ecology</i> , 2023, 32, 2646-2659.	2.0	6

#	ARTICLE	IF	CITATIONS
3084	Characterization and Identification of Probiotic Features in <i>Lactiseibacillus Paracasei</i> Using a Comparative Genomic Analysis Approach. <i>Probiotics and Antimicrobial Proteins</i> , 2022, 14, 1211-1224.	1.9	5
3085	Population analysis of heavy metal and biocide resistance genes in <i>Salmonella enterica</i> from human clinical cases in New Hampshire, United States. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
3086	Characterization of <i>Mycobacterium salfingeri</i> sp. nov.: A novel nontuberculous mycobacteria isolated from a human wound infection. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
3087	Discovery and characterization of a new genotype of <i>Salmonella enterica</i> serovar Bareilly isolated from diarrhea patients of food-borne outbreaks. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3090	Maternal colonization and early-onset neonatal bacterial sepsis in the Gambia, West Africa: a genomic analysis of vertical transmission. <i>Clinical Microbiology and Infection</i> , 2023, 29, 386.e1-386.e9.	2.8	4
3091	Emergence of a Novel Lineage and Wide Spread of a blaCTX-M-15/IncHI2/ST1 Plasmid among Nosocomial <i>Enterobacter</i> in Guadeloupe. <i>Antibiotics</i> , 2022, 11, 1443.	1.5	1
3092	Comparative Genomic Analysis of Phytopathogenic <i>Xanthomonas</i> Species Suggests High Level of Genome Plasticity Related to Virulence and Host Adaptation. , 2022, 1, 218-241.		4
3093	Occurrence and Characterization of NDM-1-Producing <i>Shewanella</i> spp. and <i>Acinetobacter portensis</i> Co-Harboring tet(X3) in a Chinese Dairy Farm. <i>Antibiotics</i> , 2022, 11, 1422.	1.5	1
3094	Persistence of transferable oxazolidinone resistance genes in enterococcal isolates from a swine farm in China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
3095	Deciphering the role of non-Frankia nodular endophytes in alder through in vitro and genomic characterization. <i>Canadian Journal of Microbiology</i> , 0, , .	0.8	1
3096	Development of Genome-Driven, Lifestyle-Informed Markers for Identification of the Cereal-Infecting Pathogens <i>Xanthomonas translucens</i> Pathovars <i>undulosa</i> and <i>translucens</i> . <i>Phytopathology</i> , 2023, 113, 2110-2118.	1.1	6
3097	Genome-associations of extended-spectrum $\beta$ -lactamase producing (ESBL) or AmpC producing <i>E. coli</i> in small and medium pig farms from Khon Kaen province, Thailand. <i>BMC Microbiology</i> , 2022, 22, .	1.3	1
3098	A graph-based approach for the visualisation and analysis of bacterial pangenomes. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	7
3100	An update to the database for <i>Acinetobacter baumannii</i> capsular polysaccharide locus typing extends the extensive and diverse repertoire of genes found at and outside the K locus. <i>Microbial Genomics</i> , 2022, 8, .	1.0	13
3101	16S rRNA gene-based assessment of common broiler chicken sampling methods: Evaluating intra-flock sample size, cecal pair similarity, and cloacal swab similarity to other alimentary tract locations. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	5
3102	Genomic Characterization and Antimicrobial Susceptibility of Dromedary-Associated <i>Staphylococcaceae</i> from the Horn of Africa. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2
3103	Genomic Features of <i>Pseudomonas putida</i> PCL1760: A Biocontrol Agent Acting via Competition for Nutrient and Niche. <i>Applied Microbiology</i> , 2022, 2, 749-765.	0.7	1
3104	Metabolic genes on conjugative plasmids are highly prevalent in <i>Escherichia coli</i> and can protect against antibiotic treatment. <i>ISME Journal</i> , 2023, 17, 151-162.	4.4	16

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3107	Comparative genomics and pangenomics of vancomycin-resistant and susceptible <i>Enterococcus faecium</i> from Irish hospitals. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	4
3108	First Genome-Based Characterisation and Staphylococcal Enterotoxin Production Ability of Methicillin-Susceptible and Methicillin-Resistant <i>Staphylococcus aureus</i> Strains Isolated from Ready-to-Eat Foods in Algiers (Algeria). <i>Toxins</i> , 2022, 14, 731.	1.5	2
3109	A Novel High Discriminatory Protocol for the Detection of <i>Borrelia afzelii</i> , <i>Borrelia burgdorferi</i> Sensu Stricto and <i>Borrelia garinii</i> in Ticks. <i>Pathogens</i> , 2022, 11, 1234.	1.2	1
3110	Genome sequence of the entomopathogenic <i>Serratia entomophila</i> isolate 626 and characterisation of the species specific itaconate degradation pathway. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
3113	Molecular Epidemiology of mcr-1-Positive <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Isolates: Results from Russian Sentinel Surveillance (2013–2018). <i>Microorganisms</i> , 2022, 10, 2034.	1.6	2
3114	Comparative Genomics of <i>Listeria monocytogenes</i> Isolates from Ruminant Listeriosis Cases in the Midwest United States. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
3117	Quaternary Phosphonium Compound Unveiled as a Potent Disinfectant against Highly Resistant <i>Acinetobacter baumannii</i> Clinical Isolates. <i>ACS Infectious Diseases</i> , 2022, 8, 2307-2314.	1.8	6
3118	A truncated mutation of MucA in <i>Pseudomonas aeruginosa</i> from a bronchiectasis patient affects T3SS expression and inflammasome activation. <i>Acta Biochimica Et Biophysica Sinica</i> , 2022, 54, 1740-1747.	0.9	1
3119	Comparative Genomic Analysis of <i>Fusobacterium necrophorum</i> Provides Insights into Conserved Virulence Genes. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
3120	Pathogenome comparison and global phylogeny of <i>Escherichia coli</i> ST1485 strains. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
3121	Multimiomics characterization of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) isolates with heterogeneous intermediate resistance to vancomycin (hVISA) in Latin America. <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 122-132.	1.3	4
3123	Isolation and characterization of novel <i>Fusobacterium nucleatum</i> bacteriophages. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
3124	Comparative Genomics of <i>Streptococcus oralis</i> Identifies Large Scale Homologous Recombination and a Genetic Variant Associated with Infection. <i>MSphere</i> , 2022, 7, .	1.3	3
3125	Genome-Wide Association to Study the Host-Specificity Determinants of <i>Xanthomonas perforans</i> . <i>Phytopathology</i> , 2023, 113, 400-412.	1.1	4
3126	Sequence-Based Identification of Metronidazole-Resistant <i>Clostridioides difficile</i> Isolates. <i>Emerging Infectious Diseases</i> , 2022, 28, 2308-2311.	2.0	1
3127	Pan-Genome Analysis of <i>Staphylococcus aureus</i> Reveals Key Factors Influencing Genomic Plasticity. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
3128	Genome-wide association study of <i>Klebsiella pneumoniae</i> identifies variations linked to carbapenems resistance. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
3129	Genomic and Phenotypic Comparisons Reveal Distinct Variants of <i>Wolbachia</i> Strain <i>w</i> /AlbB. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	2



#	ARTICLE	IF	CITATIONS
3130	Genome-Wide Association Studies Identify an Association of Transferrin Binding Protein B Variation and Invasive Serogroup Y Meningococcal Disease in Older Adults. <i>Journal of Infectious Diseases</i> , 2022, 226, 2204-2214.	1.9	1
3131	In silico genomic analysis of <i>Rhodopseudomonas palustris</i> strains revealed potential biocontrol agents and crop yield enhancers. <i>Biological Control</i> , 2022, 176, 105085.	1.4	9
3132	Phage controlling method against novel freshwater-derived <i>Vibrio parahaemolyticus</i> in ready-to-eat crayfish ( <i>Procambarus clarkii</i> ). <i>Food Research International</i> , 2022, 162, 111986.	2.9	6
3134	Genetic Predictive Factors for Nonsusceptible Phenotypes and Multidrug Resistance in Expanded-Spectrum Cephalosporin-Resistant Uropathogenic <i>Escherichia coli</i> from a Multicenter Cohort: Insights into the Phenotypic and Genetic Basis of Coresistance. <i>MSphere</i> , 2022, 7, .	1.3	3
3135	Taxogenomic status of phylogenetically distant <i>Frankia</i> clusters warrants their elevation to the rank of genus: A description of <i>Protofrankia</i> gen. nov., <i>Parafrankia</i> gen. nov., and <i>Pseudofrankia</i> gen. nov. as three novel genera within the family <i>Frankiaceae</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
3136	Functional and Safety Characterization of <i>Weissella paramesenteroides</i> Strains Isolated from Dairy Products through Whole-Genome Sequencing and Comparative Genomics. <i>Dairy</i> , 2022, 3, 799-813.	0.7	9
3137	Multi-Epitope Vaccine for Monkeypox Using Pan-Genome and Reverse Vaccinology Approaches. <i>Viruses</i> , 2022, 14, 2504.	1.5	16
3138	The population structure and genetic diversity of <i>Listeria monocytogenes</i> ST9 strains based on genomic analysis. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
3139	Phylogenetic analyses of <i>Salmonella</i> detected along the broiler production chain in Trinidad and Tobago. <i>Poultry Science</i> , 2023, 102, 102322.	1.5	1
3140	Whole-Genome Sequencing-Based Species Classification, Multilocus Sequence Typing, and Antimicrobial Resistance Mechanism Analysis of the <i>Enterobacter cloacae</i> Complex in Southern China. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
3141	Comparative genomic analyses reveal genetic characteristics and pathogenic factors of <i>Bacillus pumilus</i> HM-7. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3142	Comparative genomics study of <i>Staphylococcus aureus</i> isolated from cattle and humans reveals virulence patterns exclusively associated with bovine clinical mastitis strains. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3143	Characterization of antibiotic-resistance traits in <i>Akkermansia muciniphila</i> strains of human origin. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
3145	Interruption of Capsular Polysaccharide Biosynthesis Gene <i>wbaZ</i> by Insertion Sequence IS <i>903B</i> Mediates Resistance to a Lytic Phage against ST11 K64 Carbapenem-Resistant <i>Klebsiella pneumoniae</i> . <i>MSphere</i> , 0, , .	1.3	0
3146	Exploring clade differentiation of the <i>Faecalibacterium prausnitzii</i> complex. <i>IScience</i> , 2022, 25, 105533.	1.9	0
3147	Role of the <i>fsr</i> Quorum-Sensing System in <i>Enterococcus faecalis</i> Bloodstream Infection. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	3
3149	Genomics of <i>Klebsiella pneumoniae</i> Species Complex Reveals the Circulation of High-Risk Multidrug-Resistant Pandemic Clones in Human, Animal, and Environmental Sources. <i>Microorganisms</i> , 2022, 10, 2281.	1.6	9
3150	<i>Helicobacter colisuis</i> sp. nov., isolated from caecal contents of domestic pigs ( <i>Sus scrofa</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	4

#	ARTICLE	IF	CITATIONS
3151	Genomic analysis of <i>Paenibacillus</i> sp. MDMC362 from the Merzouga desert leads to the identification of a potentially thermostable catalase. <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 21-38.	0.7	1
3152	Enterococci enhance <i>Clostridioides difficile</i> pathogenesis. <i>Nature</i> , 2022, 611, 780-786.	13.7	48
3153	<i>Pseudomonas aegrilactucaae</i> sp. nov. and <i>Pseudomonas morbosilactucaae</i> sp. nov., pathogens causing bacterial rot of lettuce in Japan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	1
3154	Genomic Diversity of <i>Campylobacter lari</i> Group Isolates from Europe and Australia in a One Health Context. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	6
3156	Taxonomic and genomic characterization of <i>Sporosarcina cyprini</i> sp. nov., moderately tolerant of Cr+6 and Cd+2 isolated from the gut of invasive fish <i>Cyprinus carpio</i> var. <i>communis</i> (Linn., 1758). <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 193-206.	0.7	0
3158	Analysis of the Features of the Genomic Organization of Plague Microbe Strains Suitable for the Creation of a New Attenuated Vaccine. <i>Epidemiologiya I Vaktsinoprofilaktika</i> , 2022, 21, 49-57.	0.2	0
3159	Emergence of tet(X4)-positive hypervirulent <i>Klebsiella pneumoniae</i> of food origin in China. <i>LWT - Food Science and Technology</i> , 2023, 173, 114280.	2.5	2
3160	Genomic characterization of tigeicycline-resistant tet(X4)-positive <i>E. coli</i> in slaughterhouses. <i>Veterinary Microbiology</i> , 2023, 276, 109606.	0.8	3
3161	Whole genome sequence data of a marine bacterium, <i>Marinobacter adhaerens</i> PBVC038, associated with toxic harmful algal bloom. <i>Data in Brief</i> , 2023, 46, 108768.	0.5	0
3162	Whole genome analysis of <i>Flavobacterium aziz-sancaraii</i> sp. nov., isolated from Ardley Island (Antarctica), revealed a rich resistome and bioremediation potential. <i>Chemosphere</i> , 2023, 313, 137511.	4.2	3
3163	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
3164	Development of two microbial source tracking markers for detection of wastewater-associated <i>Escherichia coli</i> isolates. <i>Science of the Total Environment</i> , 2023, 864, 160952.	3.9	4
3165	Comparative genomics and phylogenomics of the <i>Ralstonia solanacearum</i> Moko ecotype and its symptomatological variants. <i>Genetics and Molecular Biology</i> , 2022, 45, .	0.6	0
3166	Genomic Analysis of 13 Putative Active Prophages Located in the Genomes of Walnut Blight Pathogen <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> . <i>Microbiology and Biotechnology Letters</i> , 2022, 50, 563-573.	0.2	0
3167	A Comprehensive Genomic Analysis of the Emergent <i>Klebsiella pneumoniae</i> ST16 Lineage: Virulence, Antimicrobial Resistance and a Comparison with the Clinically Relevant ST11 Strain. <i>Pathogens</i> , 2022, 11, 1394.	1.2	4
3169	NOVEL AVIBACTERIUM SPECIES ASSOCIATED WITH SINUSITIS AND CONJUNCTIVITIS IN A MERRIAM'S WILD TURKEY (MELEAGRIS GALLOPAVO MERRIAM) FLOCK IN COLORADO, USA. <i>Journal of Wildlife Diseases</i> , 2022, 58, .	0.3	0
3170	Specialized Metabolism of <i>Gordonia</i> Genus: An Integrated Survey on Chemodiversity Combined with a Comparative Genomics-Based Analysis. <i>BioTech</i> , 2022, 11, 53.	1.3	0
3173	Tyroviruses are a new group of temperate phages that infect <i>Bacillus</i> species in soil environments worldwide. <i>BMC Genomics</i> , 2022, 23, .	1.2	5

#	ARTICLE	IF	CITATIONS
3174	A Practical Bioinformatics Workflow for Routine Analysis of Bacterial WGS Data. <i>Microorganisms</i> , 2022, 10, 2364.	1.6	6
3175	<i>Bacteroides vulgatus</i> attenuates experimental mice colitis through modulating gut microbiota and immune responses. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	12
3176	Multi-Omics of <i>Corynebacterium Pseudotuberculosis</i> 12CS0282 and an In Silico Reverse Vaccinology Approach Reveal Novel Vaccine and Drug Targets. <i>Proteomes</i> , 2022, 10, 39.	1.7	2
3177	Corekiburra: pan-genome post-processing using core gene synteny. <i>Journal of Open Source Software</i> , 2022, 7, 4910.	2.0	3
3179	Microscopy-based phenotypic profiling of infection by <i>Staphylococcus aureus</i> clinical isolates reveals intracellular lifestyle as a prevalent feature. <i>Nature Communications</i> , 2022, 13, .	5.8	8
3180	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
3181	Emergence of Colistin-Resistant <i>Acinetobacter junii</i> in China. <i>Antibiotics</i> , 2022, 11, 1693.	1.5	0
3182	<i>Streptococcus bouchesdurhonensis</i> sp. nov. isolated from a bronchoalveolar lavage of a patient with pneumonia. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	0
3183	Atypical enteropathogenic <i>E. coli</i> are associated with disease activity in ulcerative colitis. <i>Gut Microbes</i> , 2022, 14, .	4.3	6
3184	Comparative genomics and genomic diversity of <i>Pseudomonas syringae</i> clade 2b-a in Australia. <i>BMC Microbiology</i> , 2022, 22, .	1.3	1
3186	A <i>Shigella sonnei</i> clone with extensive drug resistance associated with waterborne outbreaks in China. <i>Nature Communications</i> , 2022, 13, .	5.8	7
3187	Pandemic <i>Vibrio cholerae</i> acquired competitive traits from an environmental <i>Vibrio</i> species. <i>Life Science Alliance</i> , 2023, 6, e202201437.	1.3	3
3188	Evolution and regulation of microbial secondary metabolism. <i>ELife</i> , 0, 11, .	2.8	11
3189	A large-scale genomic snapshot of <i>Klebsiella</i> spp. isolates in Northern Italy reveals limited transmission between clinical and non-clinical settings. <i>Nature Microbiology</i> , 2022, 7, 2054-2067.	5.9	34
3190	The Genomic Landscape Resource of <i>Pseudomonas syringae</i> pv. <i>syringae</i> Strains Isolated from Mango Trees. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 1109-1114.	1.4	0
3191	<i>Aeromonas</i> species isolated from aquatic organisms, insects, chicken, and humans in India show similar antimicrobial resistance profiles. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
3192	Dismantling and reorganizing <i>Pseudomonas marginalis</i> sensu lato. <i>Plant Pathology</i> , 2023, 72, 654-666.	1.2	1
3193	Large-scale comparative genomics to refine the organization of the global <i>Salmonella enterica</i> population structure. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1

#	ARTICLE	IF	CITATIONS
3195	Novel configurations of type I-E CRISPR-Cas system in <i>Corynebacterium striatum</i> clinical isolates. <i>Brazilian Journal of Microbiology</i> , 2023, 54, 69-80.	0.8	1
3196	Skin dysbiosis and <i>Cutibacterium acnes</i> biofilm in inflammatory acne lesions of adolescents. <i>Scientific Reports</i> , 2022, 12, .	1.6	16
3199	Comparative genomics of drug-resistant strains of <i>Mycobacterium tuberculosis</i> in Ecuador. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
3200	<i>Klebsiella</i> Species and <i>Enterobacter cloacae</i> Isolates Harboring <i>bla</i> <sub>OXA-181</sub> and <i>bla</i> <sub>OXA-48</sub> : Resistome, Fitness Cost, and Plasmid Stability. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
3202	<i>Staphylococcus aureus</i> populations from the gut and the blood are not distinguished by virulence traits—a critical role of host barrier integrity. <i>Microbiome</i> , 2022, 10, .	4.9	5
3203	Molecular Epidemiology, Antimicrobial Susceptibility, and Clinical Features of Methicillin-Resistant <i>Staphylococcus aureus</i> Bloodstream Infections over 30 Years in Barcelona, Spain (1990–2019). <i>Microorganisms</i> , 2022, 10, 2401.	1.6	4
3204	Phylogenomic diversity of <i>Vibrio</i> species and other Gammaproteobacteria isolated from Pacific oysters ( <i>Crassostrea gigas</i> ) during a summer mortality outbreak. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
3205	Multiplex PCR Assay for Clade Typing of <i>Salmonella enterica</i> Serovar Enteritidis. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
3206	Cyanobacterial Blooms Are Not a Result of Positive Selection by Freshwater Eutrophication. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
3207	The draft genome of Andean <i>Rhodospseudomonas</i> sp. strain AZUL predicts genome plasticity and adaptation to chemical homeostasis. <i>BMC Microbiology</i> , 2022, 22, .	1.3	0
3208	Impact of international travel and diarrhea on gut microbiome and resistome dynamics. <i>Nature Communications</i> , 2022, 13, .	5.8	9
3209	Horizontal transfer of the <i>rfb</i> cluster in <i>Leptospira</i> is a genetic determinant of serovar identity. <i>Life Science Alliance</i> , 2023, 6, e202201480.	1.3	6
3210	Emergence of <i>mcr-8.2</i> -harboring hypervirulent ST412 <i>Klebsiella pneumoniae</i> strain from pediatric sepsis: A comparative genomic survey. <i>Virulence</i> , 2023, 14, .	1.8	1
3211	Widespread formation of intracellular calcium carbonates by the bloom-forming cyanobacterium <i>Microcystis</i> . <i>Environmental Microbiology</i> , 2023, 25, 751-765.	1.8	1
3213	Dynamics of extended-spectrum cephalosporin resistance genes in <i>Escherichia coli</i> from Europe and North America. <i>Nature Communications</i> , 2022, 13, .	5.8	17
3216	Genomic Diversity and Chromosomal Rearrangements in <i>Neisseria gonorrhoeae</i> and <i>Neisseria meningitidis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 15644.	1.8	0
3217	A Complete Genome of <i>Nocardia terpenica</i> NC_YFY_NT001 and Pan-Genomic Analysis Based on Different Sources of <i>Nocardia</i> spp. Isolates Reveal Possibly Host-Related Virulence Factors. <i>Infection and Drug Resistance</i> , 0, Volume 15, 7259-7270.	1.1	1
3218	Draft Genome Sequence Resource of <i>Xylella fastidiosa</i> Strain Alm_Lz_1 Associated with a New Outbreak in Lazio, Italy. <i>Phytopathology</i> , 2023, 113, 108-111.	1.1	2

#	ARTICLE	IF	CITATIONS
3219	Two decades of association mapping: Insights on disease resistance in major crops. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3220	Genomics Analysis to Identify Multiple Genetic Determinants That Drive the Global Transmission of the Pandemic ST95 Lineage of Extraintestinal Pathogenic <i>Escherichia coli</i> (ExPEC). <i>Pathogens</i> , 2022, 11, 1489.	1.2	1
3222	Genetic and Phenotypic Characteristics of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Isolates from a Tertiary Hospital in Beijing. <i>Infection and Drug Resistance</i> , 0, Volume 15, 7503-7508.	1.1	0
3223	Outbreak of carbapenem-resistant enterobacteria in a thoracic-oncology unit through clonal and plasmid-mediated transmission of the blaOXA-48 gene in Southern France. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
3224	Genomic characterization of Japanese meningococcal strains isolated over a 17-year period between 2003 and 2020 in Japan. <i>Vaccine</i> , 2023, 41, 416-426.	1.7	3
3225	Antimicrobial Resistance and Genomic Epidemiology of tet(X4)-Bearing Bacteria of Pork Origin in Jiangsu, China. <i>Genes</i> , 2023, 14, 36.	1.0	4
3226	Crossing Bacterial Genomic Features and Methylation Patterns with MeStudio: An Epigenomic Analysis Tool. <i>International Journal of Molecular Sciences</i> , 2023, 24, 159.	1.8	0
3227	Distinction between <i>Enterococcus faecium</i> and <i>Enterococcus lactis</i> by a <i>gluP</i> PCR-Based Assay for Accurate Identification and Diagnostics. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	10
3228	Rapid identification of novel specific molecular targets for PCR detection of four <i>Enterococcus</i> species. <i>LWT - Food Science and Technology</i> , 2023, 173, 114356.	2.5	3
3229	Pharokka: a fast scalable bacteriophage annotation tool. <i>Bioinformatics</i> , 2023, 39, .	1.8	53
3230	Disentangling the lipid divide: Identification of key enzymes for the biosynthesis of membrane-spanning and ether lipids in Bacteria. <i>Science Advances</i> , 2022, 8, .	4.7	6
3231	Identification of Subunits for Novel Universal Vaccines against Three Predominant Serogroups and the Emerging O145 among Avian Pathogenic <i>Escherichia coli</i> by Pan-RV Pipeline. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	1
3232	Paratype: a genotyping tool for <i>Salmonella Paratyphi A</i> reveals its global genomic diversity. <i>Nature Communications</i> , 2022, 13, .	5.8	6
3233	Genomic landscape of prominent XDR <i>Acinetobacter</i> clonal complexes from Dhaka, Bangladesh. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
3234	Comparative Genomics of <i>Lentilactobacillus parabuchneri</i> isolated from dairy, KEM complex, Makgeolli, and Saliva Microbiomes. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
3235	Broad host range may be a key to long-term persistence of bacteriophages infecting intestinal Bacteroidaceae species. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
3236	Global Genomic Epidemiology of <i>Escherichia coli</i> (ExPEC) ST38 Lineage Revealed a Virulome Associated with Human Infections. <i>Microorganisms</i> , 2022, 10, 2482.	1.6	6
3237	Reclassification of eight <i>Akkermansia muciniphila</i> strains and description of <i>Akkermansia massiliensis</i> sp. nov. and <i>Candidatus Akkermansia timonensis</i> , isolated from human feces. <i>Scientific Reports</i> , 2022, 12, .	1.6	5

#	ARTICLE	IF	CITATIONS
3238	Genomic Shift in Population Dynamics of <i>mcr-1</i> -positive <i>Escherichia coli</i> in Human Carriage. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1168-1179.	3.0	1
3239	Diversity and Prevalence of <i>Clostridium innocuum</i> in the Human Gut Microbiota. <i>MSphere</i> , 2023, 8, .	1.3	6
3240	New perspectives on an old grouping: The genomic and phenotypic variability of <i>Oxalobacter formigenes</i> and the implications for calcium oxalate stone prevention. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3241	An Emerging Lineage of Uropathogenic Extended Spectrum $\beta$ -Lactamase <i>Escherichia coli</i> ST127. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
3242	Within-Host Genotypic and Phenotypic Diversity of Contemporaneous Carbapenem-Resistant <i>Klebsiella pneumoniae</i> from Blood Cultures of Patients with Bacteremia. <i>MBio</i> , 2022, 13, .	1.8	7
3243	Phenotypic and Genomic Comparison of <i>Staphylococcus aureus</i> Highlight Virulence and Host Adaptation Favoring the Success of Epidemic Clones. <i>MSystems</i> , 2022, 7, .	1.7	5
3244	Comparative genomics of trimethoprim-sulfamethoxazole-resistant <i>Achromobacter xylosoxidans</i> clinical isolates from Serbia reveals shortened variant of class 1 integron integrase gene. <i>Folia Microbiologica</i> , 2023, 68, 431-440.	1.1	2
3245	<i>Janthinobacterium</i> sp. Strain SLB01 as Pathogenic Bacteria for Sponge <i>Lubomirskia baikalensis</i> . <i>Pathogens</i> , 2023, 12, 8.	1.2	1
3246	Identification of Genetic Markers for the Detection of <i>Bacillus thuringiensis</i> Strains of Interest for Food Safety. <i>Foods</i> , 2022, 11, 3924.	1.9	1
3247	<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
3248	Draft genome sequence of <i>Joostella atrarenae</i> M1-2T with cellulolytic and hemicellulolytic ability. <i>3 Biotech</i> , 2023, 13, .	1.1	0
3249	All <i>Staphylococcus aureus</i> bacteraemia-inducing strains can cause infective endocarditis: Results of GWAS and experimental animal studies. <i>Journal of Infection</i> , 2023, 86, 123-133.	1.7	4
3250	Dissemination of Metallo- $\beta$ -Lactamase-Producing <i>Pseudomonas aeruginosa</i> in Serbian Hospital Settings: Expansion of ST235 and ST654 Clones. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1519.	1.8	5
3251	Emerging resistance in <i>Staphylococcus epidermidis</i> during dalbavancin exposure: a case report and <i>in vitro</i> analysis of isolates from prosthetic joint infections. <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 669-677.	1.3	6
3252	Genomic Characteristics and Comparative Genomic Analysis of a Probiotic Bacterial Strain, <i>Lactiplantibacillus plantarum</i> CKDB008. <i>Food Supplements and Biomaterials for Health</i> , 2022, 2, .	0.3	0
3253	Antimicrobial Susceptibility and Molecular Features of Colonizing Isolates of <i>Pseudomonas aeruginosa</i> and the Report of a Novel Sequence Type (ST) 3910 from Thailand. <i>Antibiotics</i> , 2023, 12, 165.	1.5	0
3254	Comparative Genomics and Phenotypic Characterization of <i>Gluconacetobacter entanii</i> , a Highly Acetic Acid-Tolerant Bacterium from Vinegars. <i>Foods</i> , 2023, 12, 214.	1.9	1
3255	Genetic characterization and virulence determinants of multidrug-resistant NDM-1-producing <i>Aeromonas caviae</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1

#	ARTICLE	IF	CITATIONS
3256	CRISPR-Based Detection, Identification and Typing of Mycobacterium tuberculosis Complex Lineages. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3257	Genomic analysis of Mycobacterium brumae sustains its nonpathogenic and immunogenic phenotype. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3259	Infection and Persistence of Coxiella burnetii Clinical Isolate in the Placental Environment. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1209.	1.8	0
3260	Conjugation of plasmid harboring bla <sub>NDM-1</sub> in a clinical Providencia rettgeri strain through the formation of a fusion plasmid. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3261	Emergence of plasmid-mediated colistin resistance mcr-3.5 gene in Citrobacter amalonaticus and Citrobacter sedlakii isolated from healthy individual in Thailand. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
3262	Analyzing the genetic diversity and biotechnological potential of Leuconostoc pseudomesenteroides by comparative genomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
3265	Temperature-specific adaptations and genetic requirements in a biofilm formed by Pseudomonas aeruginosa. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
3266	The DNA Phosphorothioation Restriction-Modification System Influences the Antimicrobial Resistance of Pathogenic Bacteria. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3267	Clinical and genomic analysis of hypermucoviscous Klebsiella pneumoniae isolates: Identification of new hypermucoviscosity associated genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
3268	PPNet: Identifying Functional Association Networks by Phylogenetic Profiling of Prokaryotic Genomes. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3269	Whole-genome sequencing reveals genomic characterization of Listeria monocytogenes from food in China. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	10
3270	<i>Limosilactobacillus walteri</i> sp. nov., a novel probiotic antimicrobial lipopeptide-producing bacterium. <i>FEMS Microbiology Letters</i> , 2023, 370, .	0.7	4
3271	Escherichia coli O80 in Healthy Cattle: Absence of Shigatoxigenic and Enteropathogenic E. coli O80:H2 and (Phylo) Genomics of Non-Clonal Complex 165 E. coli O80. <i>Microorganisms</i> , 2023, 11, 230.	1.6	1
3272	Spread of the mcr-1 colistin-resistance gene in Escherichia coli through plasmid transmission and chromosomal transposition in French goats. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3273	Frequent Transmission of Streptococcus pneumoniae Serotype 35B and 35D, Clonal Complex 558 Lineage, across Continents and the Formation of Multiple Clades in Japan. <i>Antimicrobial Agents and Chemotherapy</i> , 2023, 67, .	1.4	2
3274	Diversity and prevalence of type VI secretion system effectors in clinical Pseudomonas aeruginosa isolates. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
3275	CanB is a metabolic mediator of antibiotic resistance in Neisseria gonorrhoeae. <i>Nature Microbiology</i> , 2023, 8, 28-39.	5.9	3
3276	Pathovar-Specific PCR Method for Detection and Identification of <i>Xanthomonas translucens</i> pv. <i>undulosa</i> . <i>Plant Disease</i> , 2023, 107, 2279-2287.	0.7	7

#	ARTICLE	IF	CITATIONS
3277	Comparative Genomics Revealed a Potential Threat of <i>Aeromonas</i> <i>Ä</i> rivipollensis G87 Strain and Its Antibiotic Resistance. <i>Antibiotics</i> , 2023, 12, 131.	1.5	1
3278	Molecular surveillance of multidrug-resistant Gram-negative bacteria in Ukrainian patients, Germany, March to June 2022. <i>Eurosurveillance</i> , 2023, 28, .	3.9	11
3279	Three Phages One Host: Isolation and Characterization of <i>Pantoea</i> agglomerans Phages from a Grasshopper Specimen. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1820.	1.8	1
3280	Comparative genomics and molecular epidemiology of colistin-resistant <i>Acinetobacter baumannii</i> . <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 574-585.	1.9	10
3283	Antioxidant prodigiosin-producing cold-adapted <i>Janthinobacterium</i> sp. ERMR3:09 from a glacier moraine: Genomic elucidation of cold adaptation and pigment biosynthesis. <i>Gene</i> , 2023, 857, 147178.	1.0	1
3284	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
3285	Genome sequence analysis and characterization of <i>Bacillus altitudinis</i> B12, a polylactic acid- and keratin-degrading bacterium. <i>Molecular Genetics and Genomics</i> , 0, , .	1.0	3
3286	Genomic Analysis Unveils the Pervasiveness and Diversity of Prophages Infecting <i>Erwinia</i> Species. <i>Pathogens</i> , 2023, 12, 44.	1.2	1
3287	PRAWNS: compact pan-genomic features for whole-genome population genomics. <i>Bioinformatics</i> , 2023, 39, .	1.8	0
3288	A <i>Salmonella enterica</i> Serovar Oranienburg Clone Caused a Cluster of Bacteremia Cases in Persons With No Recognizable Underlying Diseases in Japan. <i>Open Forum Infectious Diseases</i> , 2023, 10, .	0.4	0
3289	Design of a multi-epitope vaccine against <i>Haemophilus parasuis</i> based on pan-genome and immunoinformatics approaches. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	1
3290	Hybrid Genomic Analysis of <i>Salmonella enterica</i> Serovar Enteritidis SE3 Isolated from Polluted Soil in Brazil. <i>Microorganisms</i> , 2023, 11, 111.	1.6	2
3291	A one-year genomic investigation of <i>Escherichia coli</i> epidemiology and nosocomial spread at a large US healthcare network. <i>Genome Medicine</i> , 2022, 14, .	3.6	17
3292	Variability in Cold Tolerance of Food and Clinical <i>Listeria monocytogenes</i> Isolates. <i>Microorganisms</i> , 2023, 11, 65.	1.6	1
3295	Genomic Characterization of Three Novel <i>Bartonella</i> Strains in a Rodent and Two Bat Species from Mexico. <i>Microorganisms</i> , 2023, 11, 340.	1.6	2
3296	<i>Chrysochloridium ovalisporum</i> is synonymous with the true branching cyanobacterium <i>Umezakia natans</i> (Nostocales/Aphanizomenonaceae). <i>Journal of Phycology</i> , 2023, 59, 326-341.	1.0	1
3297	Genomic Analysis and In Vitro Investigation of the Hop Resistance Phenotype of Two Novel <i>Loigolactobacillus backii</i> Strains, Isolated from Spoiled Beer. <i>Microorganisms</i> , 2023, 11, 280.	1.6	2
3298	Split <i>k</i> -mer analysis compared to cgMLST and SNP-based core genome analysis for detecting transmission of vancomycin-resistant enterococci: results from routine outbreak analyses across different hospitals and hospitals networks in Berlin, Germany. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1



#	ARTICLE	IF	CITATIONS
3299	Characterization of <i>Escherichia coli</i> and Other Enterobacterales Resistant to Extended-Spectrum Cephalosporins Isolated from Dairy Manure in Ontario, Canada. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	2
3300	Genomic reconstruction and directed interventions in a multidrug-resistant Shigellosis outbreak in Seattle, WA, USA: a genomic surveillance study. <i>Lancet Infectious Diseases</i> , The, 2023, 23, 740-750.	4.6	10
3301	Draft Genome Sequence of Seven Pigmented Strains of <i>Xanthomonas citri</i> pv. <i>anacardii</i> , the Causal Agent of Cashew Angular Spot. <i>Phytopathology</i> , 0, .	1.1	0
3302	Phenotypic and Genomic Characterization of Nine String-Positive Carbapenem-Resistant <i>Acinetobacter baumannii</i> Isolates from Israel. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3303	Cryptic Diversity of Black Band Disease Cyanobacteria in <i>Siderastrea siderea</i> Corals Revealed by Chemical Ecology and Comparative Genome-Resolved Metagenomics. <i>Marine Drugs</i> , 2023, 21, 76.	2.2	4
3304	Retrospective Study of the Epidemiology of <i>Clostridioides difficile</i> Infection in the Neurosurgery Department of a Tertiary Hospital in China. <i>Infection and Drug Resistance</i> , 0, Volume 16, 545-554.	1.1	1
3305	Geography shapes the genomics and antimicrobial resistance of <i>Salmonella enterica</i> Serovar Enteritidis isolated from humans. <i>Scientific Reports</i> , 2023, 13, .	1.6	9
3306	Prevalence and genetic characteristics of <i>fosB</i> -positive <i>Staphylococcus aureus</i> in duck farms in Guangdong, China in 2020. <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 802-809.	1.3	2
3308	Avian strains of emerging pathogen <i>Escherichia fergusonii</i> are phylogenetically diverse and harbor the greatest AMR dissemination potential among different sources: Comparative genomic evidence. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3309	Pre-epidemic evolution of the MRSA USA300 clade and a molecular key for classification. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	1
3310	Exploring the Potential Molecular Mechanisms of Interactions between a Probiotic Consortium and Its Coral Host. <i>MSystems</i> , 2023, 8, .	1.7	4
3312	Robust analysis of prokaryotic pangenome gene gain and loss rates with Panstripe. <i>Genome Research</i> , 2023, 33, 129-140.	2.4	6
3313	Genome sequence and genomic analysis of liver abscess caused by hypervirulent <i>Klebsiella pneumoniae</i> . <i>3 Biotech</i> , 2023, 13, .	1.1	0
3314	Genomic relatedness and dissemination of <i>bla</i> <sub>NDM-5</sub> among <i>Acinetobacter baumannii</i> isolated from hospital environments and clinical specimens in Thailand. <i>PeerJ</i> , 0, 11, e14831.	0.9	1
3315	Description of <i>Defluviimonas salinarum</i> sp. nov. with the potential of benzene-degradation isolated from saltern in the Yellow Seacoast. <i>FEMS Microbiology Letters</i> , 2023, 370, .	0.7	1
3316	Identification of genes influencing the evolution of <i>Escherichia coli</i> ST372 in dogs and humans. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
3317	Emergence and clonal expansion of <i>Vibrio aestuarianus</i> lineages pathogenic for oysters in Europe. <i>Molecular Ecology</i> , 2023, 32, 2869-2883.	2.0	2
3318	Clonal outbreak of NDM-1-producing <i>Enterobacter hormaechei</i> belonging to high-risk international clone ST78 with the coexistence of <i>tmx</i> CD2-toprJ2 and <i>mcr</i> -9 in China. <i>International Journal of Antimicrobial Agents</i> , 2023, 61, 106790.	1.1	3

#	ARTICLE	IF	CITATIONS
3319	Whole-Genome Sequencing and Comparative Genomics Analysis of a Newly Emerged Multidrug-Resistant <i>Klebsiella pneumoniae</i> Isolate of ST967. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
3321	Phylogeography of <i>Francisella tularensis</i> subspecies <i>holarctica</i> and epidemiology of tularemia in Switzerland. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
3322	A multiplex PCR assay for the differentiation of <i>Mycobacterium tuberculosis</i> complex reveals high rates of mixed-lineage tuberculosis infections among patients in Ghana. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	0
3323	Genomic Characterization of Carbapenem-Resistant <i>Acinetobacter baumannii</i> (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. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
3324	Pangenome Analysis of a <i>Salmonella Enteritidis</i> Population Links a Major Outbreak to a Gifsy-1-Like Prophage Containing Anti-Inflammatory Gene <i>gogB</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
3325	Genome-resolved metagenomics revealed metal-resistance, geochemical cycles in a Himalayan hot spring. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 3273-3289.	1.7	1
3326	Dissemination of <i>Pseudomonas aeruginosa bla</i> <sub>NDM-1</sub> -Positive ST308 Clone in Singapore. <i>Microbiology Spectrum</i> , 0, , .	1.2	2
3327	Genomic and functional analysis of high-level tigecycline resistant <i>Klebsiella michiganensis</i> co-carrying <i>tet(X4)</i> and <i>tmexCD2-toprj2</i> from pork. <i>International Journal of Food Microbiology</i> , 2023, 391-393, 110138.	2.1	2
3328	<i>Burkholderia semiarida</i> sp. nov. and <i>Burkholderia sola</i> sp. nov., two novel <i>B. cepacia</i> complex species causing onion sour skin. <i>Systematic and Applied Microbiology</i> , 2023, 46, 126415.	1.2	3
3329	Foremost report of the whole genome of <i>Spirabliibacterium mucosae</i> from India and comparative genomics of the novel genus <i>Spirabliibacterium</i> . <i>Gene</i> , 2023, 867, 147359.	1.0	0
3330	A novel lytic bacteriophage against colistin-resistant <i>Escherichia coli</i> isolated from different animals. <i>Virus Research</i> , 2023, 329, 199090.	1.1	0
3331	Genomic analysis of <i>Paenibacillus larvae</i> isolates from the Czech Republic and the neighbouring regions of Slovakia. <i>Research in Veterinary Science</i> , 2023, 158, 34-40.	0.9	1
3332	First reported detection of the mobile colistin resistance genes, <i>mcr-8</i> and <i>mcr-9</i> , in the Irish environment. <i>Science of the Total Environment</i> , 2023, 876, 162649.	3.9	2
3333	Determination of <i>Shigella</i> spp. via label-free SERS spectra coupled with deep learning. <i>Microchemical Journal</i> , 2023, 189, 108539.	2.3	6
3334	First report of enterotoxigenic <i>Staphylococcus argenteus</i> as a foodborne pathogen. <i>International Journal of Food Microbiology</i> , 2023, 394, 110182.	2.1	0
3335	One global disseminated 193Åkb high-risk hybrid plasmid harboring <i>tet(X4)</i> , <i>mcr</i> or <i>bla</i> <sub>NDM</sub> threatening public health. <i>Science of the Total Environment</i> , 2023, 876, 162807.	3.9	5
3336	Pan-genome analysis of the <i>Burkholderia gladioli</i> PV. <i>Cocovenenans</i> reveal the extent of variation in the toxigenic gene cluster. <i>Food Microbiology</i> , 2023, 113, 104249.	2.1	5
3337	Genomic diversity of antimicrobial-resistant and Shiga toxin gene-harboring non-O157 <i>Escherichia coli</i> from dairy calves. <i>Journal of Global Antimicrobial Resistance</i> , 2023, 33, 164-170.	0.9	1

#	ARTICLE	IF	CITATIONS
3339	Genomic characterization of endemic diarrheagenic <i>Escherichia coli</i> and <i>Escherichia albertii</i> from infants with diarrhea in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011259.	1.3	1
3342	MRSA lineage USA300 isolated from bloodstream infections exhibit altered virulence regulation. <i>Cell Host and Microbe</i> , 2023, 31, 228-242.e8.	5.1	8
3343	Genomic and phylogenetic characterization of <i>Elizabethkingia anophelis</i> strains: The first two cases of life-threatening infection in Japan. <i>Journal of Infection and Chemotherapy</i> , 2023, 29, 376-383.	0.8	2
3344	Rapid fluorescence visualization of <i>Yersinia enterocolitica</i> by CRISPR/Cas12a using novel specific target obtained by pan-genome analysis. <i>LWT - Food Science and Technology</i> , 2023, 175, 114500.	2.5	1
3345	Carbonyl Cyanide 3-Chloro Phenyl Hydrazone (CCCP) Restores the Colistin Sensitivity in <i>Brucella intermedia</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 2106.	1.8	1
3346	Genome sequencing and comparative genomic analysis of bovine mastitis-associated <i>Staphylococcus aureus</i> strains from India. <i>BMC Genomics</i> , 2023, 24, .	1.2	5
3347	Closed genomes uncover a saltwater species of <i>Candidatus</i> <i>Electronema</i> and shed new light on the boundary between marine and freshwater cable bacteria. <i>ISME Journal</i> , 2023, 17, 561-569.	4.4	10
3348	The persistence of time: the lifespan of <i>Bacillus anthracis</i> spores in environmental reservoirs. <i>Research in Microbiology</i> , 2023, 174, 104029.	1.0	8
3349	Comparative Genomic Analysis Reveals the Functional Traits and Safety Status of Lactic Acid Bacteria Retrieved from Artisanal Cheeses and Raw Sheep Milk. <i>Foods</i> , 2023, 12, 599.	1.9	5
3351	Whole-genome analysis of a <i>Vibrio cholerae</i> O1 biotype classical strain isolated in 1946 in Sasebo city, Nagasaki prefecture, from a returnee from the northeast part of China. <i>Tropical Medicine and Health</i> , 2023, 51, .	1.0	0
3352	Genome-wide association and dissociation studies in <i>Pantoea ananatis</i> reveal potential virulence factors affecting <i>Allium porrum</i> and <i>Allium fistulosum</i> × <i>Allium cepa</i> hybrid. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3353	<i>Proteus mirabilis</i> isolated from untreated hospital wastewater, Ibadan, Southwestern Nigeria showed low-level resistance to fluoroquinolone and carried <i>qnrD3</i> on Col3M plasmids. <i>Environmental Science and Pollution Research</i> , 2023, 30, 47158-47167.	2.7	0
3356	Insights into the genome of <i>Methylobacterium</i> sp. NMS14P, a novel bacterium for growth promotion of maize, chili, and sugarcane. <i>PLoS ONE</i> , 2023, 18, e0281505.	1.1	4
3358	<i>Corynebacterium megadyptis</i> sp. nov. with two subspecies, <i>Corynebacterium megadyptis</i> subsp. <i>megadyptis</i> subsp. nov. and <i>Corynebacterium megadyptis</i> subsp. <i>dunedinense</i> subsp. nov. isolated from yellow-eyed penguins. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	3
3359	Ceftazidime-avibactam resistance in <i>Klebsiella pneumoniae</i> sequence type 37: a decade of persistence and concealed evolution. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
3360	Adding context to the pneumococcal core genes using bioinformatic analysis of the intergenic pangenome of <i>Streptococcus pneumoniae</i> . <i>Frontiers in Bioinformatics</i> , 0, 3, .	1.0	2
3361	How Can Omics Inform Diabetic Foot Ulcer Clinical Management? A Whole Genome Comparison of Four Clinical Strains of <i>Staphylococcus aureus</i> . <i>OMICS A Journal of Integrative Biology</i> , 2023, 27, 51-61.	1.0	1
3362	Can non-typeable <i>Haemophilus influenzae</i> carriage surveillance data infer antimicrobial resistance associated with otitis media?. <i>Pediatric Investigation</i> , 2023, 7, 13-22.	0.6	2

#	ARTICLE	IF	CITATIONS
3367	Genomic insights into antibiotic resistance and mobilome of lactic acid bacteria and bifidobacteria. <i>Life Science Alliance</i> , 2023, 6, e202201637.	1.3	2
3368	Expansion of Kuravirus-like Phage Sequences within the Past Decade, including Escherichia Phage YF01 from Japan, Prompt the Creation of Three New Genera. <i>Viruses</i> , 2023, 15, 506.	1.5	4
3370	Transcriptome and Proteome of Methicillin-Resistant Staphylococcus aureus Small-Colony Variants Reveal Changed Metabolism and Increased Immune Evasion. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
3371	Streptococcus suis outbreak caused by an emerging zoonotic strain with acquired multi-drug resistance in Thailand. <i>Microbial Genomics</i> , 2023, 9, .	1.0	7
3372	Horizontal Gene Transfer, Fitness Costs and Mobility Shape the Spread of Antibiotic Resistance Genes into Experimental Populations of <i>Acinetobacter Baylyi</i> . <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	2
3373	Comparative genome identification of accessory genes associated with strong biofilm formation in <i>Vibrio parahaemolyticus</i> . <i>Food Research International</i> , 2023, 166, 112605.	2.9	4
3374	Comparative Genome Analysis of Enterococcus cecorum Reveals Intercontinental Spread of a Lineage of Clinical Poultry Isolates. <i>MSphere</i> , 2023, 8, .	1.3	5
3375	Emergence and Evolution of OXA-23-Producing ST46Pas-ST462Oxf-KL28-OCL1 Carbapenem-Resistant <i>Acinetobacter baumannii</i> Mediated by a Novel ISAbal1-Based Tn7534 Transposon. <i>Antibiotics</i> , 2023, 12, 396.	1.5	0
3376	Challenges and opportunities of strain diversity in gut microbiome research. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	4
3377	Computational Insight into Intraspecies Distinctions in <i>Pseudoalteromonas distincta</i> : Carotenoid-like Synthesis Traits and Genomic Heterogeneity. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4158.	1.8	2
3378	FrangiPANE, a tool for creating a panreference using left behind reads. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	3
3379	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. <i>Methods in Molecular Biology</i> , 2023, , 227-246.	0.4	0
3380	Genomic and clinical characteristics of carbapenem-resistant <i>Enterobacter cloacae</i> complex isolates collected in a Chinese tertiary hospital during 2013â€“2021. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
3381	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
3382	Genome-Based Analysis of the Potential Bioactivity of the Terrestrial <i>Streptomyces vinaceusdrappus</i> Strain AC-40. <i>Biology</i> , 2023, 12, 345.	1.3	3
3383	Improved Genomic Prediction of <i>Staphylococcus epidermidis</i> Isolation Sources with a Novel Polygenic Score. <i>Journal of Clinical Microbiology</i> , 2023, 61, .	1.8	0
3384	High-Throughput Mutagenesis Reveals a Role for Antimicrobial Resistance- and Virulence-Associated Mobile Genetic Elements in <i>Staphylococcus aureus</i> Host Adaptation. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
3385	Strain-level bacterial typing directly from patient samples using optical DNA mapping. <i>Communications Medicine</i> , 2023, 3, .	1.9	4

#	ARTICLE	IF	CITATIONS
3386	In Silico Evidence of the Multifunctional Features of <i>Lactiplantibacillus</i> <i>pentosus</i> LPG1, a Natural Fermenting Agent Isolated from Table Olive Biofilms. <i>Foods</i> , 2023, 12, 938.	1.9	4
3387	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlan 4. <i>Nature Biotechnology</i> , 2023, 41, 1633-1644.	9.4	132
3388	Revealing within-species diversity in uncultured human gut bacteria with single-cell long-read sequencing. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
3389	Genomic Comparative Analysis of Two Multi-Drug Resistance (MDR) <i>Acinetobacter baumannii</i> Clinical Strains Assigned to International Clonal Lineage II Recovered Pre- and Post-COVID-19 Pandemic. <i>Biology</i> , 2023, 12, 358.	1.3	2
3391	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
3393	Molecular Characterization and Clinical Relevance of Taxonomic Reassignment of <i>Staphylococcus schleiferi</i> Subspecies into Two Separate Species, <i>Staphylococcus schleiferi</i> and <i>Staphylococcus coagulans</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
3394	The Prevalence of Plasmid-Mediated Colistin Resistance Gene <i>mcr-1</i> and Different Transferability and Fitness of <i>mcr-1</i> -Bearing IncX4 Plasmids in <i>Escherichia coli</i> from Pigeons. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
3395	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
3396	Antimicrobial resistance in <i>Campylobacter fetus</i> : emergence and genomic evolution. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
3397	Association of ISVsa3 with Multidrug Resistance in <i>Salmonella enterica</i> Isolates from Cattle (Bos) Tj ETQq1 1 0.784314 rgBT (Overlock 1	1.6	3
3398	Comparative genomic analysis provides insights into taxonomy and temperature adaption of <i>Aeromonas salmonicida</i> . <i>Journal of Fish Diseases</i> , 2023, 46, 545-561.	0.9	4
3399	Identification and characterization of opportunistic pathogen <i>Pectobacterium polonicum</i> causing potato blackleg in China. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
3400	ProsmORF-pred: a machine learning-based method for the identification of small ORFs in prokaryotic genomes. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
3402	Spontaneous Genomic Variation as a Survival Strategy of Nosocomial <i>Staphylococcus haemolyticus</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3404	Core genome multilocus sequence typing scheme for <i>Bacillus cereus</i> group bacteria. <i>Research in Microbiology</i> , 2023, 174, 104050.	1.0	5
3407	A phylogenomic analysis of <i>Limosilactobacillus reuteri</i> reveals ancient and stable evolutionary relationships with rodents and birds and zoonotic transmission to humans. <i>BMC Biology</i> , 2023, 21, .	1.7	8
3408	Genome Analysis of Two <i>Pseudomonas syringae</i> pv. <i>aptata</i> Strains with Different Virulence Capacity Isolated from Sugar Beet: Features of Successful Pathogenicity in the Phyllosphere Microbiome. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
3409	Genomic and clinical case characterisation of <i>Staphylococcus haemolyticus</i> isolated from dogs and cats in the United States, including strains with high-level mupirocin tolerance. <i>Veterinary Dermatology</i> , 2023, 34, 298-309.	0.4	2

#	ARTICLE	IF	CITATIONS
3410	Insight into phylogenomic bias of bla <sub>OR</sub> or bla dissemination amongst carbapenem-resistant <i>Pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2023, 61, 106788.	1.1	6
3413	Unlocking the microbial studies through computational approaches: how far have we reached?. <i>Environmental Science and Pollution Research</i> , 2023, 30, 48929-48947.	2.7	4
3414	Genomic Characterization of <i>Staphylococcus aureus</i> in Wildlife. <i>Animals</i> , 2023, 13, 1064.	1.0	6
3415	Phylogenomic analysis of the genus <i>Rosenbergiella</i> and description of <i>Rosenbergiella gaditana</i> sp. nov., <i>Rosenbergiella metrosideri</i> sp. nov., <i>Rosenbergiella epipactidis</i> subsp. nov., <i>Rosenbergiella epipactidis</i> subsp. californiensis subsp. nov., <i>Rosenbergiella epipactidis</i> subsp. japonicus subsp. nov., <i>Rosenbergiella nectarea</i> subsp. nov. and <i>Rosenbergiella nectarea</i> subsp. apis subsp. nov., isolated from floral nectar and insects. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	2
3416	A pangenome approach-based loop-mediated isothermal amplification assay for the specific and early detection of <i>Bordetella pertussis</i> . <i>Scientific Reports</i> , 2023, 13, .	1.6	0
3417	Emergence of KPC-3- and OXA-181-producing ST13 and ST17 <i>Klebsiella pneumoniae</i> in Portugal: genomic insights on national and international dissemination. <i>Journal of Antimicrobial Chemotherapy</i> , 2023, 78, 1300-1308.	1.3	1
3418	<i>Helicobacter kumamotonensis</i> sp. nov., isolated from human clinical specimens. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
3419	Monitoring Longitudinal Trends and Assessment of the Health Risk of <i>Shigella flexneri</i> Antimicrobial Resistance. <i>Environmental Science &amp; Technology</i> , 2023, 57, 4971-4983.	4.6	6
3420	A food poisoning caused by ST7 <i>Staphylococcus aureus</i> harboring sea gene in Hainan province, China. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
3421	Adaptation Strategies to High Hydrostatic Pressures in <i>Pseudothromotoga</i> species Revealed by Transcriptional Analyses. <i>Microorganisms</i> , 2023, 11, 773.	1.6	1
3422	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
3423	Vancomycin Resistance in <i>Enterococcus faecium</i> from the Dallas, Texas, Area Is Conferred Predominantly on pRUM-Like Plasmids. <i>MSphere</i> , 2023, 8, .	1.3	2
3424	Sifting through the core-genome to identify putative cross-protective antigens against <i>Riemerella anatipestifer</i> . <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 3085-3098.	1.7	0
3425	Development and Clinical Application of a Multilocus Sequence Typing Scheme for <i>Bacteroides fragilis</i> Based on Whole-Genome Sequencing Data. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3427	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
3428	The risk of pig and chicken farming for carriage and transmission of <i>Escherichia coli</i> containing extended-spectrum beta-lactamase (ESBL) and mobile colistin resistance (mcr) genes in Thailand. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
3429	Global population structure, genomic diversity and carbohydrate fermentation characteristics of clonal complex 119 (CC119), an understudied Shiga toxin-producing <i>E. coli</i> (STEC) lineage including O165:H25 and O172:H25. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
3430	Analysis of bacterial pangenomes reduces CRISPR dark matter and reveals strong association between membranome and CRISPR-Cas systems. <i>Science Advances</i> , 2023, 9, .	4.7	1

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3431	Global scenario of the RmtE pan-aminoglycoside-resistance mechanism: emergence of the rmtE4 gene in South America associated with a hospital-related IncL plasmid. <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
3433	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
3434	Genomic analysis of <i>Vibrio harveyi</i> strain PH1009, a potential multi-drug resistant pathogen due to acquisition of toxin genes. <i>Heliyon</i> , 2023, 9, e14926.	1.4	1
3435	Draft genome sequence of <i>Enterobacter chengduensis</i> ECC445, isolated from fresh water in the West Indies. <i>BMC Genomic Data</i> , 2023, 24, .	0.7	1
3436	The genomics of linkage drag in inbred lines of sunflower. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	14
3437	Emergence of hypervirulent <i>Pseudomonas aeruginosa</i> pathotypically armed with co-expressed T3SS effectors ExoS and ExoU. , 2023, 1, 44-56.		1
3438	Enterococcal Linear Plasmids Adapt to <i>Enterococcus faecium</i> and Spread within Multidrug-Resistant Clades. <i>Antimicrobial Agents and Chemotherapy</i> , 2023, 67, .	1.4	3
3439	Genomics of Invasive <i>Cutibacterium acnes</i> Isolates from Deep-Seated Infections. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	1
3440	Parallel host shifts in a bacterial plant pathogen suggest independent genetic solutions. <i>Molecular Plant Pathology</i> , 2023, 24, 527-535.	2.0	5
3441	Phylogenic position and low genomic diversity of <i>Candidatus Rickettsia kotlanii</i> inferred by complete genome sequences of two Japanese isolates. <i>Microbiology and Immunology</i> , 2023, 67, 275-280.	0.7	1
3442	Comparative genomics of 40 <i>Weissella paramesenteroides</i> strains. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
3443	Assessment of plasmids for relating the 2020 <i>Salmonella enterica</i> serovar Newport onion outbreak to farms implicated by the outbreak investigation. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
3444	Characterization and Association of Rips Repertoire to Host Range of Novel <i>Ralstonia solanacearum</i> Strains by In Silico Approaches. <i>Microorganisms</i> , 2023, 11, 954.	1.6	0
3445	Description of <i>Agathobaculum massiliense</i> sp. nov., a new bacterial species prevalent in the human gut and predicted to produce indole and tryptophan based on genomic analysis. <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	1
3446	Genome-wide association reveals host-specific genomic traits in <i>Escherichia coli</i> . <i>BMC Biology</i> , 2023, 21, .	1.7	7
3447	Comparative Genomics Analysis of Habitat Adaptation by <i>Lactobacillus kefirifaciens</i> . <i>Foods</i> , 2023, 12, 1606.	1.9	0
3448	Monkeypox virus: phylogenomics, host-pathogen interactome and mutational cascade. <i>Microbial Genomics</i> , 2023, 9, .	1.0	2
3449	Prevalence and Genomic Characteristics of <i>mcr</i> -Positive <i>Escherichia coli</i> Strains Isolated from Humans, Pigs, and Foods in China. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4

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3450	Whole-Genome Sequencing of <i>Lactobacillus johnsonii</i> MT4, a Novel Strain Isolated from the Oral Cavity of C57BL/6 Mice. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	2
3451	Infection of Endothelial Cells with <i>Acinetobacter baumannii</i> Reveals Remodelling of Mitochondrial Protein Complexes. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	2
3452	<i>Escherichia cryptic</i> clade I is an emerging source of human intestinal pathogens. <i>BMC Biology</i> , 2023, 21, .	1.7	0
3453	Design and validation of <i>Dolosigranulum pigrum</i> specific PCR primers using the bacterial core genome. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
3454	Species-Level Taxonomic Characterization of Uncultured Core Gut Microbiota of Plateau Pika. <i>Microbiology Spectrum</i> , 0, , .	1.2	1
3455	Core-Genome Multilocus Sequence Typing for Epidemiological and Evolutionary Analyses of Phytopathogenic <i>Xanthomonas citri</i> . <i>Applied and Environmental Microbiology</i> , 0, , .	1.4	0
3456	<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
3457	Variation in <i>Sphingomonas</i> traits across habitats and phylogenetic clades. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
3458	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
3459	Genome profiling of uropathogenic <i>E. coli</i> from strictly defined community-acquired UTI in paediatric patients: a multicentric study. <i>Antimicrobial Resistance and Infection Control</i> , 2023, 12, .	1.5	0
3460	Virotyping and genetic antimicrobial susceptibility testing of porcine ETEC/STEC strains and associated plasmid types. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
3461	Genomic features, antimicrobial susceptibility, and epidemiological insights into <i>Burkholderia cenocepacia</i> clonal complex 31 isolates from bloodstream infections in India. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	0
3462	<i>E. coli</i> ST11 (O157:H7) does not encode a functional AcrF efflux pump. <i>Microbiology (United Kingdom)</i> , 2023, 169, .	0.7	3
3463	Comparative genomic insights into habitat adaptation of coral-associated <i>Prosthecochloris</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
3464	Extensive genome analysis identifies novel plasmid families in <i>Clostridium perfringens</i> . <i>Microbial Genomics</i> , 2023, 9, .	1.0	0
3465	Genomic analysis of the population structure of <i>Paenibacillus larvae</i> in New Zealand. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
3466	Epidemiological and Genetic Characteristics of Clinical Carbapenem-Resistant <i>Pseudomonas aeruginosa</i> Strains in Guangdong Province, China. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	4
3467	Genomic epidemiology and transmission characteristics of <i>mcr1</i> -positive colistin-resistant <i>Escherichia coli</i> strains circulating at natural environment. <i>Science of the Total Environment</i> , 2023, 882, 163600.	3.9	3



#	ARTICLE	IF	CITATIONS
3468	Metapangenomics of wild and cultivated banana microbiome reveals a plethora of host-associated protective functions. <i>Environmental Microbiomes</i> , 2023, 18, .	2.2	3
3469	Comparative genomic analyses of the clinically-derived <i>Winkia</i> strain NY0527: the reassignment of <i>W. neuui</i> subsp. <i>neuui</i> and <i>W. neuui</i> subsp. <i>antitratus</i> into two separate species and insights into their virulence characteristics. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
3470	Identification of novel <i>Carnobacterium maltaromaticum</i> strains in bone marrow samples of patients with acute myeloid leukemia using a metagenomic binning approach. <i>International Microbiology</i> , 2023, 26, 1033-1040.	1.1	1
3632	Genomic surveillance of bacterial pathogens. , 2023, , 71-117.		1
3696	Comparison of the relative impacts of acute consumption of an inulin-enriched diet, milk kefir or a commercial probiotic product on the human gut microbiome and metabolome. <i>Npj Science of Food</i> , 2023, 7, .	2.5	1
3778	BacWGSpire: A Snakemake Workflow for a Complete Analysis of Bacterial Whole-Genome Sequencing Data. , 2023, , .		0
3896	Detection and Analysis of <i>Wolbachia</i> in Plant-Parasitic Nematodes and Insights into <i>Wolbachia</i> Evolution. <i>Methods in Molecular Biology</i> , 2024, , 115-134.	0.4	0
3909	Bacteriophage Taxonomy: A Continually Evolving Discipline. <i>Methods in Molecular Biology</i> , 2024, , 27-45.	0.4	0
3932	Short communication: first case of bacteraemia caused by <i>Dielma fastidiosa</i> in a patient hospitalized with diverticulitis. <i>Apmis</i> , 0, , .	0.9	0
3959	Bacterial whole-genome determination and applications. , 2024, , 511-525.		0
3996	Bioinformatics in the study of microbial infections. , 2024, , 1975-1992.		0
4002	Description of <i>Mycolicibacterium arenosum</i> sp. nov. Isolated from Coastal Sand on the Yellow Sea Coast. <i>Current Microbiology</i> , 2024, 81, .	1.0	0