

# Rapid antibiotic-resistance predictions from genome sequencing of *Staphylococcus aureus* and *Mycobacterium tuberculosis*

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Bacterial genomic epidemiology, from local outbreak characterization to species-history reconstruction. <i>Pathogens and Global Health</i> , 2015, 109, 319-327.	1.0	8
2	Whole-genome sequencing for prediction of <i>Mycobacterium tuberculosis</i> drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	4.6	553
3	The Challenge and Potential of Metagenomics in the Clinic. <i>Frontiers in Immunology</i> , 2016, 7, 29.	2.2	49
4	Pyrazinamide Resistance Is Caused by Two Distinct Mechanisms: Prevention of Coenzyme A Depletion and Loss of Virulence Factor Synthesis. <i>ACS Infectious Diseases</i> , 2016, 2, 616-626.	1.8	83
5	Mass spectrometry methods for predicting antibiotic resistance. <i>Proteomics - Clinical Applications</i> , 2016, 10, 964-981.	0.8	37
6	Predictive computational phenotyping and biomarker discovery using reference-free genome comparisons. <i>BMC Genomics</i> , 2016, 17, 754.	1.2	97
7	Diagnosing tuberculosis in the 21st century – Dawn of a genomics revolution?. <i>International Journal of Mycobacteriology</i> , 2016, 5, 384-391.	0.3	22
8	The variability and reproducibility of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. <i>Genome Medicine</i> , 2016, 8, 132.	3.6	44
9	Antimicrobial Resistance Prediction in PATRIC and RAST. <i>Scientific Reports</i> , 2016, 6, 27930.	1.6	179
11	Comparison of microbial DNA enrichment tools for metagenomic whole genome sequencing. <i>Journal of Microbiological Methods</i> , 2016, 127, 141-145.	0.7	141
12	Clinical use of whole genome sequencing for <i>Mycobacterium tuberculosis</i> . <i>BMC Medicine</i> , 2016, 14, 46.	2.3	91
13	Unveiling the molecular basis of antimicrobial resistance in <i>Staphylococcus aureus</i> from the Democratic Republic of the Congo using whole genome sequencing. <i>Clinical Microbiology and Infection</i> , 2016, 22, 644.e1-644.e5.	2.8	22
14	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
15	Oxford Nanopore MinION Sequencing and Genome Assembly. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 265-279.	3.0	638
16	Microbial bioinformatics 2020. <i>Microbial Biotechnology</i> , 2016, 9, 681-686.	2.0	16
17	Genomic Analysis of the Evolution of Fluoroquinolone Resistance in <i>Mycobacterium tuberculosis</i> Prior to Tuberculosis Diagnosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6600-6608.	1.4	19
18	Recent developments in genomics, bioinformatics and drug discovery to combat emerging drug-resistant tuberculosis. <i>Tuberculosis</i> , 2016, 101, 31-40.	0.8	19
19	Use of bacterial whole-genome sequencing to understand and improve the management of invasive <i>Staphylococcus aureus</i> infections. <i>Expert Review of Anti-Infective Therapy</i> , 2016, 14, 1023-1036.	2.0	16

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20	TwoPaCo: an efficient algorithm to build the compacted de Bruijn graph from many complete genomes. <i>Bioinformatics</i> , 2017, 33, 4024-4032.	1.8	64
21	Emergence and Spread of Antimicrobial Resistance: Recent Insights from Bacterial Population Genomics. <i>Current Topics in Microbiology and Immunology</i> , 2016, 398, 35-53.	0.7	6
22	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	5.9	247
23	Tuberculosis. <i>Nature Reviews Disease Primers</i> , 2016, 2, 16076.	18.1	830
24	Reply to Lesho. <i>Clinical Infectious Diseases</i> , 2016, 62, 1053.1-1053.	2.9	1
25	Hidden <i>Staphylococcus aureus</i> Carriage: Overrated or Underappreciated?. <i>MBio</i> , 2016, 7, e00079-16.	1.8	28
26	Multidrug evolutionary strategies to reverse antibiotic resistance. <i>Science</i> , 2016, 351, aad3292.	6.0	517
27	Microbial genomics and antimicrobial susceptibility testing. <i>Expert Review of Molecular Diagnostics</i> , 2017, 17, 257-269.	1.5	36
28	Rapid resistome mapping using nanopore sequencing. <i>Nucleic Acids Research</i> , 2017, 45, gkw1328.	6.5	62
29	Challenges and opportunities for whole-genome sequencing-based surveillance of antibiotic resistance. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 108-120.	1.8	87
30	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in <i>Mycobacterium tuberculosis</i> Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	29
31	The new frontier of diagnostics: Molecular assays and their role in infection prevention and control. <i>American Journal of Infection Control</i> , 2017, 45, 158-169.	1.1	13
32	Same-Day Diagnostic and Surveillance Data for Tuberculosis via Whole-Genome Sequencing of Direct Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1285-1298.	1.8	315
33	Enhanced understanding of the host-pathogen interaction in sepsis: new opportunities for omic approaches. <i>Lancet Respiratory Medicine</i> , 2017, 5, 212-223.	5.2	33
34	Infection control in the new age of genomic epidemiology. <i>American Journal of Infection Control</i> , 2017, 45, 170-179.	1.1	90
35	Whole-Genome Sequencing of Drug-Resistant <i>Salmonella enterica</i> Isolates from Dairy Cattle and Humans in New York and Washington States Reveals Source and Geographic Associations. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	89
36	<i>Mycobacterium tuberculosis</i> resistance prediction and lineage classification from genome sequencing: comparison of automated analysis tools. <i>Scientific Reports</i> , 2017, 7, 46327.	1.6	82
37	Re-emergence of methicillin susceptibility in a resistant lineage of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, dkw570.	1.3	22

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38	BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation. <i>Nucleic Acids Research</i> , 2017, 45, W171-W179.	6.5	84
39	Use of GeneXpert Remnants for Drug Resistance Profiling and Molecular Epidemiology of Tuberculosis in Libreville, Gabon. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2105-2115.	1.8	17
40	Cryptic Microheteroresistance Explains <i>Mycobacterium tuberculosis</i> Phenotypic Resistance. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 1191-1201.	2.5	37
41	A proposed analytic framework for determining the impact of an antimicrobial resistance intervention. <i>Animal Health Research Reviews</i> , 2017, 18, 1-25.	1.4	7
42	Pseudoalignment for metagenomic read assignment. <i>Bioinformatics</i> , 2017, 33, 2082-2088.	1.8	69
43	Correlation between phenotypic antibiotic susceptibility and the resistome in <i>Pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 210-218.	1.1	65
44	Next-generation approaches to understand and combat the antibiotic resistome. <i>Nature Reviews Microbiology</i> , 2017, 15, 422-434.	13.6	438
45	A Pan-Genomic Approach to Understand the Basis of Host Adaptation in <i>Achromobacter</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1030-1046.	1.1	40
46	Real-Time Sequencing of <i>Mycobacterium tuberculosis</i> : Are We There Yet?. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1249-1254.	1.8	38
47	A brief primer on genomic epidemiology: lessons learned from <i>Mycobacterium tuberculosis</i> . <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 59-77.	1.8	24
48	Removing the bottleneck in whole genome sequencing of <i>Mycobacterium tuberculosis</i> for rapid drug resistance analysis: a call to action. <i>International Journal of Infectious Diseases</i> , 2017, 56, 130-135.	1.5	49
49	Application of genomic technologies to measure and monitor antibiotic resistance in animals. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 121-135.	1.8	41
50	A world of opportunities with nanopore sequencing. <i>Journal of Experimental Botany</i> , 2017, 68, 5419-5429.	2.4	158
51	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. <i>Clinical Microbiology Reviews</i> , 2017, 30, 1015-1063.	5.7	310
52	Emerging Microtechnologies and Automated Systems for Rapid Bacterial Identification and Antibiotic Susceptibility Testing. <i>SLAS Technology</i> , 2017, 22, 585-608.	1.0	81
53	Machine learning: novel bioinformatics approaches for combating antimicrobial resistance. <i>Current Opinion in Infectious Diseases</i> , 2017, 30, 511-517.	1.3	55
54	Clinical metagenomics of bone and joint infections: a proof of concept study. <i>Scientific Reports</i> , 2017, 7, 7718.	1.6	97
55	Chemical genetics in drug discovery. <i>Current Opinion in Systems Biology</i> , 2017, 4, 35-42.	1.3	26

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56	Comparative genomics of a drug-resistant <i>Pseudomonas aeruginosa</i> panel and the challenges of antimicrobial resistance prediction from genomes. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	40
57	PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2764-2768.	1.3	534
58	Molecular Methods for Detection of Antimicrobial Resistance. <i>Microbiology Spectrum</i> , 2017, 5, .	1.2	90
59	Genomic Epidemiology of Tuberculosis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 79-93.	0.8	21
60	Evolution of Phenotypic and Molecular Drug Susceptibility Testing. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 221-246.	0.8	28
61	The Evolution of Strain Typing in the <i>Mycobacterium tuberculosis</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 43-78.	0.8	43
62	Bacterial genome sequencing in clinical microbiology: a pathogen-oriented review. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2017, 36, 2007-2020.	1.3	122
63	Microfluidic Chip, a Lab-on-a-Chip Platform of Mono- and Polymicrobial Biofilms for High-Throughput Downstream Applications. <i>MSphere</i> , 2017, 2, .	1.3	16
64	Draft genome sequences of eight bacteria isolated from the indoor environment: <i>Staphylococcus capitis</i> strain H36, <i>S. capitis</i> strain H65, <i>S. cohnii</i> strain H62, <i>S. hominis</i> strain H69, <i>Mycobacterium</i> sp. strain H83, <i>Mycobacterium iranicum</i> strain H39, <i>Plantibacter</i> sp. strain H53, and <i>Pseudomonas oryzae</i> strain H72. <i>Standards in Genomic Sciences</i> , 2017, 12, 17.	1.5	9
65	Whole genome sequencing for M/XDR tuberculosis surveillance and for resistance testing. <i>Clinical Microbiology and Infection</i> , 2017, 23, 161-166.	2.8	61
66	MRSA and multidrug-resistant <i>Staphylococcus aureus</i> in U.S. retail meats, 2010–2011. <i>Food Microbiology</i> , 2017, 62, 289-297.	2.1	105
67	Identification of bacterial pathogens and antimicrobial resistance directly from clinical urines by nanopore-based metagenomic sequencing. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 104-114.	1.3	296
68	The role of whole genome sequencing in antimicrobial susceptibility testing of bacteria: report from the EUCAST Subcommittee. <i>Clinical Microbiology and Infection</i> , 2017, 23, 2-22.	2.8	428
69	Antimicrobial resistance surveillance in the genomic age. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 78-91.	1.8	71
70	<i>Mycobacterium tuberculosis</i> and whole genome sequencing: a practical guide and online tools available for the clinical microbiologist. <i>Clinical Microbiology and Infection</i> , 2017, 23, 69-72.	2.8	26
71	Bioinformatics in Microbiome Analysis. <i>Methods in Microbiology</i> , 2017, 44, 1-18.	0.4	4
72	Solution NMR Studies of <i>Mycobacterium tuberculosis</i> Proteins for Antibiotic Target Discovery. <i>Molecules</i> , 2017, 22, 1447.	1.7	2
73	Establishing Genotype-to-Phenotype Relationships in Bacteria Causing Hospital-Acquired Pneumonia: A Prelude to the Application of Clinical Metagenomics. <i>Antibiotics</i> , 2017, 6, 30.	1.5	54

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74	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
75	Horses in Denmark Are a Reservoir of Diverse Clones of Methicillin-Resistant and -Susceptible <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 543.	1.5	63
76	Sequence analysis of the rifampicin resistance determining region (RRDR) of <i>rpoB</i> gene in multidrug resistance confirmed and newly diagnosed tuberculosis patients of Punjab, Pakistan. <i>PLoS ONE</i> , 2017, 12, e0183363.	1.1	4
77	Application of whole genome sequence analysis to the study of <i>Mycobacterium tuberculosis</i> in Nunavut, Canada. <i>PLoS ONE</i> , 2017, 12, e0185656.	1.1	17
78	Prevalence and extent of heteroresistance by next generation sequencing of multidrug-resistant tuberculosis. <i>PLoS ONE</i> , 2017, 12, e0176522.	1.1	51
79	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , 2017, 18, 182.	3.8	260
80	Whole genome sequencing-based detection of antimicrobial resistance and virulence in non-typhoidal <i>Salmonella enterica</i> isolated from wildlife. <i>Gut Pathogens</i> , 2017, 9, 66.	1.6	54
81	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017, 3, e000131.	1.0	478
82	Emerging Technologies for Molecular Diagnosis of Sepsis. <i>Clinical Microbiology Reviews</i> , 2018, 31, .	5.7	210
83	Developing an in silico minimum inhibitory concentration panel test for <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2018, 8, 421.	1.6	136
84	Robust Prediction of Resistance to Trimethoprim in <i>Staphylococcus aureus</i> . <i>Cell Chemical Biology</i> , 2018, 25, 339-349.e4.	2.5	32
85	Use of whole genome sequencing in surveillance of drug resistant tuberculosis. <i>Expert Review of Anti-Infective Therapy</i> , 2018, 16, 433-442.	2.0	22
86	Population monitoring for drug-resistant tuberculosis: is genomics the answer?. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 592-594.	4.6	0
87	Dissecting whole-genome sequencing-based online tools for predicting resistance in <i>Mycobacterium tuberculosis</i> : can we use them for clinical decision guidance?. <i>Tuberculosis</i> , 2018, 110, 44-51.	0.8	25
88	Integrating long-range connectivity information into de Bruijn graphs. <i>Bioinformatics</i> , 2018, 34, 2556-2565.	1.8	61
89	Analysis of mutations in <i>pncA</i> reveals non-overlapping patterns among various lineages of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2018, 8, 4628.	1.6	5
90	Advances in Sequencing and Resequencing in Crop Plants. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 11-35.	0.6	4
91	New opportunities for managing acute and chronic lung infections. <i>Nature Reviews Microbiology</i> , 2018, 16, 111-120.	13.6	80

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92	Genomic characterization of a paediatric MRSA outbreak by next-generation sequencing. <i>Journal of Hospital Infection</i> , 2018, 98, 155-160.	1.4	8
93	MTBseq: a comprehensive pipeline for whole genome sequence analysis of <i>Mycobacterium tuberculosis</i> complex isolates. <i>PeerJ</i> , 2018, 6, e5895.	0.9	148
94	RiBoSOM. , 2018, , .		9
95	Advances in Clinical Sample Preparation for Identification and Characterization of Bacterial Pathogens Using Metagenomics. <i>Frontiers in Public Health</i> , 2018, 6, 363.	1.3	48
96	AIMMS suite: a web server dedicated for prediction of drug resistance on protein mutation. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	18
97	Analysis of antibiotics resistant genes in different strains of <i>Staphylococcus aureus</i> . <i>Bioinformatics</i> , 2018, 14, 113-122.	0.2	23
98	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. <i>F1000Research</i> , 2018, 7, 459.	0.8	31
99	Drivers and Dynamics of Methicillin-Resistant Livestock-Associated <i>Staphylococcus aureus</i> CC398 in Pigs and Humans in Denmark. <i>MBio</i> , 2018, 9, .	1.8	74
100	Nanoliter-Sized Microchamber/Microarray Microfluidic Platform for Antibiotic Susceptibility Testing. <i>Analytical Chemistry</i> , 2018, 90, 14137-14144.	3.2	51
101	Highlights on the Application of Genomics and Bioinformatics in the Fight Against Infectious Diseases: Challenges and Opportunities in Africa. <i>Frontiers in Genetics</i> , 2018, 9, 575.	1.1	23
102	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
103	DNA extraction from primary liquid blood cultures for bloodstream infection diagnosis using whole genome sequencing. <i>Journal of Medical Microbiology</i> , 2018, 67, 347-357.	0.7	40
104	First insights on the genetic diversity of MDR <i>Mycobacterium tuberculosis</i> in Lebanon. <i>BMC Infectious Diseases</i> , 2018, 18, 710.	1.3	7
105	Virulence of <i>Mycobacterium tuberculosis</i> Clinical Isolates Is Associated With Sputum Pre-treatment Bacterial Load, Lineage, Survival in Macrophages, and Cytokine Response. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 417.	1.8	21
106	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
107	Suspected transmission and subsequent spread of MRSA from farmer to dairy cows. <i>Veterinary Microbiology</i> , 2018, 225, 114-119.	0.8	12
108	An injectable dipeptide-“fullerene supramolecular hydrogel for photodynamic antibacterial therapy. <i>Journal of Materials Chemistry B</i> , 2018, 6, 7335-7342.	2.9	116
109	Defining antimicrobial resistance in cystic fibrosis. <i>Journal of Cystic Fibrosis</i> , 2018, 17, 696-704.	0.3	66

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110	Genomic evolution of <i>Staphylococcus aureus</i> isolates colonizing the nares and progressing to bacteremia. <i>PLoS ONE</i> , 2018, 13, e0195860.	1.1	17
111	Predicting bacterial resistance from whole-genome sequences using <i>k</i> -mers and stability selection. <i>BMC Bioinformatics</i> , 2018, 19, 383.	1.2	32
112	Phylogenomic Classification and the Evolution of Clonal Complex 5 Methicillin-Resistant <i>Staphylococcus aureus</i> in the Western Hemisphere. <i>Frontiers in Microbiology</i> , 2018, 9, 1901.	1.5	84
113	Identifying Mixed <i>Mycobacterium tuberculosis</i> Infection and Laboratory Cross-Contamination during Mycobacterial Sequencing Programs. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	16
114	From Theory to Practice: Translating Whole-Genome Sequencing (WGS) into the Clinic. <i>Trends in Microbiology</i> , 2018, 26, 1035-1048.	3.5	131
115	Molecular Methods for Detection of Antimicrobial Resistance. , 0, , 33-50.		8
116	Frequent transmission of the <i>Mycobacterium tuberculosis</i> Beijing lineage and positive selection for the <i>EsxW</i> Beijing variant in Vietnam. <i>Nature Genetics</i> , 2018, 50, 849-856.	9.4	167
117	Indexed variation graphs for efficient and accurate resistome profiling. <i>Bioinformatics</i> , 2018, 34, 3601-3608.	1.8	55
118	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
119	Lowering the Barriers to Routine Whole-Genome Sequencing of Bacteria in the Clinical Microbiology Laboratory. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	8
120	Linking minimum inhibitory concentrations to whole genome sequence-predicted drug resistance in <i>Mycobacterium tuberculosis</i> strains from Romania. <i>Scientific Reports</i> , 2018, 8, 9676.	1.6	27
121	Characterization of a community-acquired-MRSA USA300 isolate from a river sample in Austria and whole genome sequence based comparison to a diverse collection of USA300 isolates. <i>Scientific Reports</i> , 2018, 8, 9467.	1.6	22
122	Characterization of Mutations Conferring Resistance to Rifampin in <i>Mycobacterium tuberculosis</i> Clinical Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	29
123	Antimicrobial potential of <i>Chlorella</i> algae isolated from stacked waters of the Andean Region of Ecuador. <i>IOP Conference Series: Earth and Environmental Science</i> , 2018, 151, 012040.	0.2	6
124	Unexpected Genomic and Phenotypic Diversity of <i>Mycobacterium africanum</i> Lineage 5 Affects Drug Resistance, Protein Secretion, and Immunogenicity. <i>Genome Biology and Evolution</i> , 2018, 10, 1858-1874.	1.1	47
126	DeepARG: a deep learning approach for predicting antibiotic resistance genes from metagenomic data. <i>Microbiome</i> , 2018, 6, 23.	4.9	462
127	TB-EFI, a novel 18-Plex microbead-based method for prediction of second-line drugs and ethambutol resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Journal of Microbiological Methods</i> , 2018, 152, 10-17.	0.7	4
128	Validation of Novel <i>Mycobacterium tuberculosis</i> Isoniazid Resistance Mutations Not Detectable by Common Molecular Tests. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	33



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129	Tuning the Bandgap of Photo-Sensitive Polydopamine/Ag <sub>3</sub> PO <sub>4</sub> /Graphene Oxide Coating for Rapid, Noninvasive Disinfection of Implants. ACS Central Science, 2018, 4, 724-738.	5.3	227
130	Drug-resistant tuberculosis: challenges and opportunities for diagnosis and treatment. Current Opinion in Pharmacology, 2018, 42, 7-15.	1.7	121
131	Control of Artifacts in Reported Intersample Relatedness during Clinical Use of a Mycobacterium tuberculosis Sequencing Pipeline. Journal of Clinical Microbiology, 2018, 56, .	1.8	10
132	Applications of genomics to slow the spread of multidrug-resistant <i>Neisseria gonorrhoeae</i> . Annals of the New York Academy of Sciences, 2019, 1435, 93-109.	1.8	31
133	PATRIC as a unique resource for studying antimicrobial resistance. Briefings in Bioinformatics, 2019, 20, 1094-1102.	3.2	93
134	Using Genomics to Track Global Antimicrobial Resistance. Frontiers in Public Health, 2019, 7, 242.	1.3	263
135	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal Salmonella enterica Serovars by Using Machine Learning. MSystems, 2019, 4, .	1.7	21
136	Rapid phenotypic evolution in multidrug-resistant <i>Klebsiella pneumoniae</i> hospital outbreak strains. Microbial Genomics, 2019, 5, .	1.0	25
137	The Future of TB Resistance Diagnosis: The Essentials on Whole Genome Sequencing and Rapid Testing Methods. Archivos De Bronconeumologia, 2019, 55, 421-426.	0.4	0
138	Identification and Characterization of Genetic Determinants of Isoniazid and Rifampicin Resistance in Mycobacterium tuberculosis in Southern India. Scientific Reports, 2019, 9, 10283.	1.6	32
139	Using genomics to understand antimicrobial resistance and transmission in <i>Neisseria gonorrhoeae</i> . Microbial Genomics, 2019, 5, .	1.0	9
140	The Future of TB Resistance Diagnosis: The Essentials on Whole Genome Sequencing and Rapid Testing Methods. Archivos De Bronconeumologia, 2019, 55, 421-426.	0.4	7
141	Rapid metagenomics analysis of EMS vehicles for monitoring pathogen load using nanopore DNA sequencing. PLoS ONE, 2019, 14, e0219961.	1.1	9
142	Deciphering drug resistance in Mycobacterium tuberculosis using whole-genome sequencing: progress, promise, and challenges. Genome Medicine, 2019, 11, 45.	3.6	88
143	Integrating informatics tools and portable sequencing technology for rapid detection of resistance to anti-tuberculous drugs. Genome Medicine, 2019, 11, 41.	3.6	248
144	Personal clinical history predicts antibiotic resistance of urinary tract infections. Nature Medicine, 2019, 25, 1143-1152.	15.2	130
145	Determining antimicrobial susceptibility in <i>Salmonella enterica</i> serovar Typhimurium through whole genome sequencing: a comparison against multiple phenotypic susceptibility testing methods. BMC Microbiology, 2019, 19, 148.	1.3	20
146	Relative Performance of MinION (Oxford Nanopore Technologies) versus Sequel (Pacific Biosciences) Third-Generation Sequencing Instruments in Identification of Agricultural and Forest Fungal Pathogens. Applied and Environmental Microbiology, 2019, 85, .	1.4	68

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147	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data. <i>PLoS Computational Biology</i> , 2019, 15, e1007349.	1.5	64
148	Vertical capacitance aptasensors for real-time monitoring of bacterial growth and antibiotic susceptibility in blood. <i>Biosensors and Bioelectronics</i> , 2019, 143, 111623.	5.3	8
149	Whole-genome sequencing-based epidemiological analysis of anti-tuberculosis drug resistance genes in Japan in 2007: Application of the Genome Research for Asian Tuberculosis (GReAT) database. <i>Scientific Reports</i> , 2019, 9, 12823.	1.6	10
150	A Large-Scale Whole-Genome Comparison Shows that Experimental Evolution in Response to Antibiotics Predicts Changes in Naturally Evolved Clinical <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	31
151	Beyond the SNP Threshold: Identifying Outbreak Clusters Using Inferred Transmissions. <i>Molecular Biology and Evolution</i> , 2019, 36, 587-603.	3.5	121
152	Predicting Antibiotic Resistance in Gram-Negative Bacilli from Resistance Genes. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	18
153	Size-Transformable Metal-Organic Framework-Derived Nanocarbons for Localized Chemo-Photothermal Bacterial Ablation and Wound Disinfection. <i>Advanced Functional Materials</i> , 2019, 29, 1900143.	7.8	104
154	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	13.6	237
155	NanoARG: a web service for detecting and contextualizing antimicrobial resistance genes from nanopore-derived metagenomes. <i>Microbiome</i> , 2019, 7, 88.	4.9	72
156	Mechanisms and clinical relevance of bacterial heteroresistance. <i>Nature Reviews Microbiology</i> , 2019, 17, 479-496.	13.6	264
157	Genomic and Metagenomic Approaches for Predictive Surveillance of Emerging Pathogens and Antibiotic Resistance. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 512-524.	2.3	33
158	Core genome sequence analysis to characterize <i>Salmonella enterica</i> serovar Rissen ST469 from a swine production chain. <i>International Journal of Food Microbiology</i> , 2019, 304, 68-74.	2.1	15
159	Whole genome sequencing <i>Mycobacterium tuberculosis</i> directly from sputum identifies more genetic diversity than sequencing from culture. <i>BMC Genomics</i> , 2019, 20, 389.	1.2	56
160	Use of online tools for antimicrobial resistance prediction by whole-genome sequencing in methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) and vancomycin-resistant enterococci (VRE). <i>Journal of Global Antimicrobial Resistance</i> , 2019, 19, 136-143.	0.9	17
161	Beyond multidrug resistance: Leveraging rare variants with machine and statistical learning models in <i>Mycobacterium tuberculosis</i> resistance prediction. <i>EBioMedicine</i> , 2019, 43, 356-369.	2.7	66
162	Fulminant arterial vasculitis as an unusual complication of disseminated staphylococcal disease due to the emerging CC1 methicillin-susceptible <i>Staphylococcus aureus</i> clone: a case report. <i>BMC Infectious Diseases</i> , 2019, 19, 302.	1.3	3
163	Antibiotic Resistance and the MRSA Problem. <i>Microbiology Spectrum</i> , 2019, 7, .	1.2	208
164	Cryptic Resistance Mutations Associated With Misdiagnoses of Multidrug-Resistant Tuberculosis. <i>Journal of Infectious Diseases</i> , 2019, 220, 316-320.	1.9	19

#	ARTICLE	IF	CITATIONS
165	Sequencing-based methods and resources to study antimicrobial resistance. <i>Nature Reviews Genetics</i> , 2019, 20, 356-370.	7.7	263
166	Data-Driven Systems Level Approaches for Drug Repurposing: Combating Drug Resistance in Priority Pathogens. , 2019, , 229-253.		3
167	Overcoming the pitfalls of automatic interpretation of whole genome sequencing data by online tools for the prediction of pyrazinamide resistance in <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2019, 14, e0212798.	1.1	14
169	Rifampicin and rifabutin resistance in 1003 <i>Mycobacterium tuberculosis</i> clinical isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1477-1483.	1.3	39
170	Genomic prediction of tuberculosis drug-resistance: benchmarking existing databases and prediction algorithms. <i>BMC Bioinformatics</i> , 2019, 20, 68.	1.2	20
171	SNP-IT Tool for Identifying Subspecies and Associated Lineages of <i>Mycobacterium tuberculosis</i> Complex. <i>Emerging Infectious Diseases</i> , 2019, 25, 482-488.	2.0	64
172	Social network analysis and whole genome sequencing in a cohort study to investigate TB transmission in an educational setting. <i>BMC Infectious Diseases</i> , 2019, 19, 154.	1.3	15
173	Staphylococci: Evolving Genomes. , 2019, , 485-498.		1
174	Next-Generation Sequencing in Clinical Microbiology. <i>Clinics in Laboratory Medicine</i> , 2019, 39, 405-418.	0.7	83
175	Improved Resistance Prediction in <i>Mycobacterium tuberculosis</i> by Better Handling of Insertions and Deletions, Premature Stop Codons, and Filtering of Non-informative Sites. <i>Frontiers in Microbiology</i> , 2019, 10, 2464.	1.5	7
176	Approximate Computing Applied to Bacterial Genome Identification using Self-Organizing Maps. , 2019, , .		4
177	Antibiotic Resistance and the MRSA Problem. , 0, , 747-765.		11
178	Staphylococci: Evolving Genomes. <i>Microbiology Spectrum</i> , 2019, 7, .	1.2	19
179	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
180	LA-MRSA CC398 in Dairy Cattle and Veal Calf Farms Indicates Spillover From Pig Production. <i>Frontiers in Microbiology</i> , 2019, 10, 2733.	1.5	30
181	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
182	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
183	Evaluation of the CosmosID Bioinformatics Platform for Prosthetic Joint-Associated Sonicate Fluid Shotgun Metagenomic Data Analysis. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	59

#	ARTICLE	IF	CITATIONS
184	The use of next generation sequencing for improving food safety: Translation into practice. <i>Food Microbiology</i> , 2019, 79, 96-115.	2.1	225
185	Predicting Antimicrobial Resistance and Associated Genomic Features from Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	14
186	Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	221
187	Using Machine Learning To Predict Antimicrobial MICs and Associated Genomic Features for Nontyphoidal <i>Salmonella</i> . <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	181
188	Genome-wide discovery of epistatic loci affecting antibiotic resistance in <i>Neisseria gonorrhoeae</i> using evolutionary couplings. <i>Nature Microbiology</i> , 2019, 4, 328-338.	5.9	41
189	Evaluation of whole genome sequencing and software tools for drug susceptibility testing of <i>Mycobacterium tuberculosis</i> . <i>Clinical Microbiology and Infection</i> , 2019, 25, 82-86.	2.8	39
190	Genomic epidemiology of multidrug-resistant Gram-negative organisms. <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 39-56.	1.8	16
191	Genomics of antibiotic resistance prediction in <i>Pseudomonas aeruginosa</i> . <i>Annals of the New York Academy of Sciences</i> , 2019, 1435, 5-17.	1.8	51
192	Metagenomic insights into the changes in microbial community and antimicrobial resistance genes associated with different salt content of red pepper ( <i>Capsicum annuum</i> L.) sauce. <i>Food Microbiology</i> , 2020, 85, 103295.	2.1	27
193	New insights into the mycobacterial PE and PPE proteins provide a framework for future research. <i>Molecular Microbiology</i> , 2020, 113, 4-21.	1.2	59
194	From genotype to antibiotic susceptibility phenotype in the order Enterobacterales: a clinical perspective. <i>Clinical Microbiology and Infection</i> , 2020, 26, 643.e1-643.e7.	2.8	20
195	Interpreting k-mer-based signatures for antibiotic resistance prediction. <i>GigaScience</i> , 2020, 9, .	3.3	17
196	Prediction of rifampicin resistance beyond the RRDR using structure-based machine learning approaches. <i>Scientific Reports</i> , 2020, 10, 18120.	1.6	30
197	The Evolving Role of the Clinical Microbiology Laboratory in Identifying Resistance in Gram-Negative Bacteria. <i>Infectious Disease Clinics of North America</i> , 2020, 34, 659-676.	1.9	10
198	PARMAP: A Pan-Genome-Based Computational Framework for Predicting Antimicrobial Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 578795.	1.5	10
199	Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. <i>Frontiers in Genetics</i> , 2020, 11, 563975.	1.1	12
200	Antibiotic resistance surveillance systems: A review. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 23, 430-438.	0.9	69
201	Bacterial Isolation Microwell-Plug (1/4WELLplug) for Rapid Antibiotic Susceptibility Testing Using Morphology Analysis. <i>ACS Applied Bio Materials</i> , 2020, 3, 4798-4808.	2.3	4

#	ARTICLE	IF	CITATIONS
202	Genetic Identification and Drug-Resistance Characterization of Mycobacterium tuberculosis Using a Portable Sequencing Device. A Pilot Study. <i>Antibiotics</i> , 2020, 9, 548.	1.5	8
203	Analytical Performance Validation of Next-Generation Sequencing Based Clinical Microbiology Assays Using a K-mer Analysis Workflow. <i>Frontiers in Microbiology</i> , 2020, 11, 1883.	1.5	12
204	Genomic Prediction of Antimicrobial Resistance: Ready or Not, Here It Comes!. <i>Clinical Chemistry</i> , 2020, 66, 1278-1289.	1.5	25
205	Performance and Application of 16S rRNA Gene Cycle Sequencing for Routine Identification of Bacteria in the Clinical Microbiology Laboratory. <i>Clinical Microbiology Reviews</i> , 2020, 33, .	5.7	116
206	Comparative genomics in infectious disease. <i>Current Opinion in Microbiology</i> , 2020, 53, 61-70.	2.3	11
207	Dynamics of within-host Mycobacterium tuberculosis diversity and heteroresistance during treatment. <i>EBioMedicine</i> , 2020, 55, 102747.	2.7	52
208	Genomic profiling of antimicrobial resistance genes in clinical isolates of Salmonella Typhi from patients infected with Typhoid fever in India. <i>Scientific Reports</i> , 2020, 10, 8299.	1.6	41
209	Development of a rapid technique for extraction of viral DNA/RNA for whole genome sequencing directly from clinical liver tissues. <i>Journal of Virological Methods</i> , 2020, 283, 113907.	1.0	1
210	Detection of low-frequency resistance-mediating SNPs in next-generation sequencing data of Mycobacterium tuberculosis complex strains with binoSNP. <i>Scientific Reports</i> , 2020, 10, 7874.	1.6	14
211	Pangenome Graphs. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 139-162.	2.5	148
212	Spread of LA-MRSA CC398 in Danish mink (Neovison vison) and mink farm workers. <i>Veterinary Microbiology</i> , 2020, 245, 108705.	0.8	12
213	Parallel Evolution of Tobramycin Resistance across Species and Environments. <i>MBio</i> , 2020, 11, .	1.8	59
214	Prediction of Antimicrobial Resistance in Gram-Negative Bacteria From Whole-Genome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 1013.	1.5	40
215	The application of machine learning techniques to innovative antibacterial discovery and development. <i>Expert Opinion on Drug Discovery</i> , 2020, 15, 1165-1180.	2.5	30
216	Lean, mean, learning machines. <i>Nature Reviews Microbiology</i> , 2020, 18, 266-266.	13.6	1
217	Advances in diagnosis of Tuberculosis: an update into molecular diagnosis of Mycobacterium tuberculosis. <i>Molecular Biology Reports</i> , 2020, 47, 4065-4075.	1.0	109
218	Sources of Multidrug Resistance in Patients With Previous Isoniazid-Resistant Tuberculosis Identified Using Whole Genome Sequencing: A Longitudinal Cohort Study. <i>Clinical Infectious Diseases</i> , 2020, 71, e532-e539.	2.9	13
219	Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens. <i>PLoS Computational Biology</i> , 2020, 16, e1007608.	1.5	49

#	ARTICLE	IF	CITATIONS
220	sraX: A Novel Comprehensive Resistome Analysis Tool. <i>Frontiers in Microbiology</i> , 2020, 11, 52.	1.5	15
221	Bioinformatics Approaches to the Understanding of Molecular Mechanisms in Antimicrobial Resistance. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1363.	1.8	39
222	β-cyclodextrin- soy soluble polysaccharide based core-shell bionanocomposites hydrogel for vitamin E swelling controlled delivery. <i>Food Hydrocolloids</i> , 2020, 104, 105751.	5.6	36
223	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism calling pipelines. <i>GigaScience</i> , 2020, 9, .	3.3	92
224	A snapshot of diversity: Intraclonal variation of <i>Escherichia coli</i> clones as commensals and pathogens. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151401.	1.5	7
225	Resistance Sniffer: An online tool for prediction of drug resistance patterns of <i>Mycobacterium tuberculosis</i> isolates using next generation sequencing data. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151399.	1.5	17
226	QuantTB – a method to classify mixed <i>Mycobacterium tuberculosis</i> infections within whole genome sequencing data. <i>BMC Genomics</i> , 2020, 21, 80.	1.2	30
227	Core genome MLST and resistome analysis of <i>Klebsiella pneumoniae</i> using a clinically amenable workflow. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 97, 114996.	0.8	6
228	Systematic Evaluation of Whole Genome Sequence-Based Predictions of <i>Salmonella</i> Serotype and Antimicrobial Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 549.	1.5	53
229	Prediction of Acquired Antimicrobial Resistance for Multiple Bacterial Species Using Neural Networks. <i>MSystems</i> , 2020, 5, .	1.7	36
230	In silico analysis of the antimicrobial activity of phytochemicals: towards a technological breakthrough. <i>Computer Methods and Programs in Biomedicine</i> , 2021, 200, 105820.	2.6	9
231	Rapid detection of <i>Mycobacterium tuberculosis</i> based on antigen 85B via real-time recombinase polymerase amplification. <i>Letters in Applied Microbiology</i> , 2021, 72, 106-112.	1.0	9
232	A review of artificial intelligence applications for antimicrobial resistance. <i>Biosafety and Health</i> , 2021, 3, 22-31.	1.2	65
233	Deep amplicon sequencing for culture-free prediction of susceptibility or resistance to 13 anti-tuberculous drugs. <i>European Respiratory Journal</i> , 2021, 57, 2002338.	3.1	58
234	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	15
235	WGS for Bacterial Identification and Susceptibility Testing in the Clinical Lab. , 2021, , 25-44.		1
236	Methicillin-Resistant <i>Staphylococcus epidermidis</i> Lineages in the Nasal and Skin Microbiota of Patients Planned for Arthroplasty Surgery. <i>Microorganisms</i> , 2021, 9, 265.	1.6	7
238	Geno-informatics for Prediction of Virulence and Drug Resistance in Bacterial Pathogens. , 2021, , 3-18.		0

#	ARTICLE	IF	CITATIONS
239	Antibiotic resistance: Time of synthesis in a post-genomic age. Computational and Structural Biotechnology Journal, 2021, 19, 3110-3124.	1.9	28
241	Comparative genomics of Staphylococcus epidermidis from prosthetic-joint infections and nares highlights genetic traits associated with antimicrobial resistance, not virulence. Microbial Genomics, 2021, 7, .	1.0	19
242	The role of artificial intelligence in the battle against antimicrobial-resistant bacteria. Current Genetics, 2021, 67, 421-429.	0.8	15
243	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. F1000Research, 0, 10, 80.	0.8	8
244	Prosthetic hip joint infection by Bacillus Calmette-Guerin therapy following intravesical instillation for bladder cancer identified using whole-genome sequencing: a case report. BMC Infectious Diseases, 2021, 21, 151.	1.3	2
245	Overview of bioinformatic methods for analysis of antibiotic resistome from genome and metagenome data. Journal of Microbiology, 2021, 59, 270-280.	1.3	16
246	Learning From Limited Data: Towards Best Practice Techniques for Antimicrobial Resistance Prediction From Whole Genome Sequencing Data. Frontiers in Cellular and Infection Microbiology, 2021, 11, 610348.	1.8	14
247	Value of routine whole genome sequencing for Mycobacterium tuberculosis drug resistance detection. International Journal of Infectious Diseases, 2021, 113, S48-S54.	1.5	31
248	Cross-Contamination versus Outbreak: Pre-XDR Mycobacterial Strains Confirmed by Whole-Genome Sequencing. Antibiotics, 2021, 10, 297.	1.5	1
249	Genomic investigation of clinically significant coagulase-negative staphylococci. Journal of Medical Microbiology, 2021, 70, .	0.7	2
250	Local and Travel-Associated Transmission of Tuberculosis at Central Western Border of Brazil, 2014â€“2017. Emerging Infectious Diseases, 2021, 27, 905-914.	2.0	4
251	Surveillance of antimicrobial resistance in low- and middle-income countries: a scattered picture. Antimicrobial Resistance and Infection Control, 2021, 10, 63.	1.5	137
252	Simplitigs as an efficient and scalable representation of de Bruijn graphs. Genome Biology, 2021, 22, 96.	3.8	22
253	A Bioinformatics Whole-Genome Sequencing Workflow for Clinical Mycobacterium tuberculosis Complex Isolate Analysis, Validated Using a Reference Collection Extensively Characterized with Conventional Methods and <i>In Silico</i> Approaches. Journal of Clinical Microbiology, 2021, 59, .	1.8	18
254	Applications of Machine Learning to the Problem of Antimicrobial Resistance: an Emerging Model for Translational Research. Journal of Clinical Microbiology, 2021, 59, e0126020.	1.8	70
255	Import and transmission of Mycobacterium orygis and Mycobacterium africanum, Norway. BMC Infectious Diseases, 2021, 21, 562.	1.3	9
257	Nanopore Sequencing for Mycobacterium tuberculosis: a Critical Review of the Literature, New Developments, and Future Opportunities. Journal of Clinical Microbiology, 2022, 60, JCM0064621.	1.8	21
258	Predictive Antibiotic Susceptibility Testing by Next-Generation Sequencing for Periprosthetic Joint Infections: Potential and Limitations. Biomedicines, 2021, 9, 910.	1.4	12

#	ARTICLE	IF	CITATIONS
259	MRSA strains with distinct accessory genes predominate at different ages in cystic fibrosis. <i>Pediatric Pulmonology</i> , 2021, 56, 2868-2878.	1.0	6
260	Whole-Genome Sequencing Analysis to Identify Infection with Multiple Species of Nontuberculous Mycobacteria. <i>Pathogens</i> , 2021, 10, 879.	1.2	7
261	Machine Learning Aids Classification and Discrimination of Noncanonical DNA Folding Motifs by an Arrayed Host:Guest Sensing System. <i>Journal of the American Chemical Society</i> , 2021, 143, 12791-12799.	6.6	31
262	INGOT-DR: an interpretable classifier for predicting drug resistance in <i>M. tuberculosis</i> . <i>Algorithms for Molecular Biology</i> , 2021, 16, 17.	0.3	9
263	Nanopore-Based Surveillance of Zoonotic Bacterial Pathogens in Farm-Dwelling Peridomestic Rodents. <i>Pathogens</i> , 2021, 10, 1183.	1.2	10
264	Computational resources in the management of antibiotic resistance: Speeding up drug discovery. <i>Drug Discovery Today</i> , 2021, 26, 2138-2151.	3.2	11
266	Bacterial evolution during human infection: Adapt and live or adapt and die. <i>PLoS Pathogens</i> , 2021, 17, e1009872.	2.1	33
267	Functionalized hollow mesoporous silica for detection of <i>Staphylococcus aureus</i> and sterilization. <i>Journal of Environmental Chemical Engineering</i> , 2021, 9, 105892.	3.3	5
268	Rapid detection and identification of bacteria directly from whole blood with light scattering spectroscopy based biosensor. <i>Sensors and Actuators B: Chemical</i> , 2021, 346, 130489.	4.0	1
269	Artificial intelligence and machine learning assisted drug delivery for effective treatment of infectious diseases. <i>Advanced Drug Delivery Reviews</i> , 2021, 178, 113922.	6.6	34
270	StLiter: A Novel Algorithm to Iteratively Build the Compacted de Bruijn Graph From Many Complete Genomes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2471-2483.	1.9	5
271	Curcumin-loaded high internal phase emulsions stabilized with lysine modified lignin: a biological agent with high photothermal protection and antibacterial properties. <i>Food and Function</i> , 2021, 12, 7469-7479.	2.1	14
272	Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159.	9.4	123
273	Comparison of bacterial genome assembly software for MinION data and their applicability to medical microbiology. <i>Microbial Genomics</i> , 2016, 2, e000085.	1.0	33
274	The resistomes of six carbapenem-resistant pathogens – a critical genotype–phenotype analysis. <i>Microbial Genomics</i> , 2018, 4, .	1.0	18
275	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	171
276	Using genomics to understand meticillin- and vancomycin-resistant <i>Staphylococcus aureus</i> infections. <i>Microbial Genomics</i> , 2020, 6, .	1.0	23
277	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



#	ARTICLE	IF	CITATIONS
278	Genomic variant-identification methods may alter Mycobacterium tuberculosis transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
305	Evaluation of Whole-Genome Sequencing for Mycobacterial Species Identification and Drug Susceptibility Testing in a Clinical Setting: a Large-Scale Prospective Assessment of Performance against Line Probe Assays and Phenotyping. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	72
306	Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from Staphylococcus aureus Whole-Genome Sequences. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	61
307	Laboratory diagnosis of tuberculosis. , 0, , 99-115.		1
308	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. <i>F1000Research</i> , 2018, 7, 459.	0.8	24
309	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	0.9	103
310	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
311	Diverse Distribution of Resistomes in the Human and Environmental Microbiomes. <i>Current Genomics</i> , 2018, 19, 701-711.	0.7	10
313	NGS-Based S. aureus Typing and Outbreak Analysis in Clinical Microbiology Laboratories: Lessons Learned From a Swiss-Wide Proficiency Test. <i>Frontiers in Microbiology</i> , 2020, 11, 591093.	1.5	9
314	StrainSeeker: fast identification of bacterial strains from raw sequencing reads using user-provided guide trees. <i>PeerJ</i> , 2017, 5, e3353.	0.9	46
315	Evidence-based design and evaluation of a whole genome sequencing clinical report for the reference microbiology laboratory. <i>PeerJ</i> , 2018, 6, e4218.	0.9	43
316	A large scale evaluation of TBProfiler and Mykrobe for antibiotic resistance prediction in <i>Mycobacterium tuberculosis</i> . <i>PeerJ</i> , 2019, 7, e6857.	0.9	18
317	Whole-genome characterisation of multidrug resistant monophasic variants of <i>Salmonella</i> Typhimurium from pig production in Thailand. <i>PeerJ</i> , 0, 8, e9700.	0.9	13
318	Bacteria-triggered Multifunctional Hydrogel for Localized Chemodynamic and Low-Temperature Photothermal Sterilization. <i>Small</i> , 2021, 17, e2103303.	5.2	69
334	A Review of Artificial Intelligence Applications in Bacterial Genomics. , 2020, , .		1
335	New technologies for the diagnosis of drug-resistant tuberculosis. <i>Vestnik Rossiiskoi Akademii Meditsinskikh Nauk</i> , 2019, 74, 413-422.	0.2	1
341	Evaluation of whole-genome sequence data analysis approaches for short- and long-read sequencing of Mycobacterium tuberculosis. <i>Microbial Genomics</i> , 2021, 7, .	1.0	13
342	Genome-Wide Mutation Scoring for Machine-Learning-Based Antimicrobial Resistance Prediction. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13049.	1.8	8

#	ARTICLE	IF	CITATIONS
343	SAM-TB: a whole genome sequencing data analysis website for detection of <i>Mycobacterium tuberculosis</i> drug resistance and transmission. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	26
344	Whole Genome Sequencing Assessing Impact of Diabetes Mellitus on Tuberculosis Mutations and Type of Recurrence in India. <i>Clinical Infectious Diseases</i> , 2022, 75, 768-776.	2.9	4
346	Drug susceptibility testing of <i>Mycobacterium tuberculosis</i> using next generation sequencing and Mykrobe software. <i>Zhurnal Mikrobiologii Epidemiologii I Immunobiologii</i> , 2022, 98, 697-705.	0.3	0
347	A multi-label learning framework for predicting antibiotic resistance genes via dual-view modeling. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
349	AIM and Evolutionary Theory. , 2022, , 341-350.		0
350	Tuberculosis drug resistance profiling based on machine learning: A literature review. <i>Brazilian Journal of Infectious Diseases</i> , 2022, 26, 102332.	0.3	7
351	Accurate and rapid prediction of tuberculosis drug resistance from genome sequence data using traditional machine learning algorithms and CNN. <i>Scientific Reports</i> , 2022, 12, 2427.	1.6	22
352	Characteristics Changes on Applications of Antibiotics and Current Approaches to Enhance Productivity with Soil Microbiome. <i>Journal of Pure and Applied Microbiology</i> , 2022, 16, 89-109.	0.3	0
353	Application of Next Generation Sequencing for Diagnosis and Clinical Management of Drug-Resistant Tuberculosis: Updates on Recent Developments in the Field. <i>Frontiers in Microbiology</i> , 2022, 13, 775030.	1.5	22
356	A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing. <i>F1000Research</i> , 0, 10, 80.	0.8	0
357	Gly, Encoded by <i>MAB_3167c</i> , Is Required for <i>In Vivo</i> Growth of <i>Mycobacteroides abscessus</i> and Exhibits Mild $\beta$ -Lactamase Activity. <i>Journal of Bacteriology</i> , 2022, , e0004622.	1.0	3
358	Recovering metagenome-assembled genomes from shotgun metagenomic sequencing data: Methods, applications, challenges, and opportunities. <i>Microbiological Research</i> , 2022, 260, 127023.	2.5	17
359	A system biology approach to determine therapeutic targets by identifying molecular mechanisms and key pathways for type 2 diabetes that are linked to the development of tuberculosis and rheumatoid arthritis. <i>Life Sciences</i> , 2022, 297, 120483.	2.0	10
360	Whole-Genome Sequencing to Identify Missed Rifampicin and Isoniazid Resistance Among Tuberculosis Isolates—Chennai, India, 2013–2016. <i>Frontiers in Microbiology</i> , 2021, 12, 720436.	1.5	3
361	Whole genome sequencing reveals large deletions and other loss of function mutations in <i>Mycobacterium tuberculosis</i> drug resistance genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
362	$\beta$ -Lactam Resistance in <i>Pseudomonas aeruginosa</i> : Current Status, Future Prospects. <i>Pathogens</i> , 2021, 10, 1638.	1.2	50
363	Whole Genome Sequencing of Drug Resistant and Drug Susceptible <i>Mycobacterium tuberculosis</i> Isolates From Tigray Region, Ethiopia. <i>Frontiers in Microbiology</i> , 2021, 12, 743198.	1.5	9
364	Triple-view Learning for Predicting Antibiotic Resistance Genes. , 2021, , .		0

#	ARTICLE	IF	CITATIONS
365	Antibiotic Heteroresistance in <i>Klebsiella pneumoniae</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 449.	1.8	17
366	Spontaneous Phage Resistance in Avian Pathogenic <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 782757.	1.5	3
367	Enhancing predictions of antimicrobial resistance of pathogens by expanding the potential resistance gene repertoire using a pan-genome-based feature selection approach. <i>BMC Bioinformatics</i> , 2022, 23, 131.	1.2	5
369	Effective control of microbial spoilage in soybeans by water-soluble ZnO nanoparticles. <i>Food Chemistry</i> , 2022, 388, 132994.	4.2	5
392	Leveraging big data bioinformatics approaches to extract knowledge from <i>Staphylococcus aureus</i> public omics data. <i>Critical Reviews in Microbiology</i> , 2022, , 1-23.	2.7	1
394	Whole genome characterization, and geographical distribution of <i>M. tuberculosis</i> in central region of Veracruz, Mexico. <i>Brazilian Journal of Infectious Diseases</i> , 2022, 26, 102357.	0.3	1
395	Inferring antibiotic susceptibility from metagenomic data: dream or reality?. <i>Clinical Microbiology and Infection</i> , 2022, 28, 1225-1229.	2.8	3
396	MycoVarP: Mycobacterium Variant and Drug Resistance Prediction Pipeline for Whole-Genome Sequence Data Analysis. <i>Frontiers in Bioinformatics</i> , 0, 1, .	1.0	0
399	SeqScreen: accurate and sensitive functional screening of pathogenic sequences via ensemble learning. <i>Genome Biology</i> , 2022, 23, .	3.8	13
400	Genomics and pathotypes of the many faces of <i>Escherichia coli</i> . <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	36
401	Genomic analysis of diversity, biogeography, and drug resistance in <i>Mycobacterium bovis</i> . <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	2
402	Challenges of the practical applications of solid-state nanopore platforms for sensing biomolecules. <i>Applied Physics Express</i> , 2022, 15, 070101.	1.1	3
403	Machine Learning for Antimicrobial Resistance Research and Drug Development. , 0, , .		3
405	Sensing the Performance of Artificially Intelligent Nanopores Developed by Integrating Solid-State Nanopores with Machine Learning Methods. <i>Journal of Physical Chemistry C</i> , 2022, 126, 12197-12209.	1.5	10
406	Detection of <i>M. tuberculosis</i> in the environment as a tool for identifying high-risk locations for tuberculosis transmission. <i>Science of the Total Environment</i> , 2022, 843, 156970.	3.9	5
407	Next-generation sequencing and PCR technologies in monitoring the hospital microbiome and its drug resistance. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	9
408	Genome-wide association studies of global <i>Mycobacterium tuberculosis</i> resistance to 13 antimicrobials in 10,228 genomes identify new resistance mechanisms. <i>PLoS Biology</i> , 2022, 20, e3001755.	2.6	27
409	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

#	ARTICLE	IF	CITATIONS
410	Scalable, ultra-fast, and low-memory construction of compacted de Bruijn graphs with Cuttlefish 2. <i>Genome Biology</i> , 2022, 23, .	3.8	15
412	Relationships between Efflux Pumps and Emergence of Heteroresistance: A Comprehensive Study on the Current Findings. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2022, 2022, 1-11.	0.7	0
413	New concepts in antimicrobial resistance in cystic fibrosis respiratory infections. <i>Journal of Cystic Fibrosis</i> , 2022, 21, 937-945.	0.3	9
414	Role of Nature-Inspired Intelligence in Genomic Diagnosis of Antimicrobial Resistance. <i>Studies in Computational Intelligence</i> , 2023, , 223-245.	0.7	2
415	Role of gene sequencing for the diagnosis, tracking and prevention of bacterial infections. <i>Journal of the Academy of Clinical Microbiologists</i> , 2022, 24, 8.	0.2	0
416	Use of Whole-Genome Sequencing for Detection of Antimicrobial Resistance: <i>Mycobacterium tuberculosis</i> , a Model Organism. <i>Clinical Laboratory Science: Journal of the American Society for Medical Technology</i> , 2019, 32, ascls.2019001784.	0.1	0
417	Application of Decision-Tree-Based Machine Learning Algorithms for Prediction of Antimicrobial Resistance. <i>Antibiotics</i> , 2022, 11, 1593.	1.5	11
418	Web-based prediction of antimicrobial resistance in enterococcal clinical isolates by whole-genome sequencing. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2023, 42, 67-76.	1.3	3
419	eMIC-AntiKP: Estimating minimum inhibitory concentrations of antibiotics towards <i>Klebsiella pneumoniae</i> using deep learning. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 751-757.	1.9	2
420	Computational biology: Role and scope in taming antimicrobial resistance. <i>Indian Journal of Medical Microbiology</i> , 2023, 41, 33-38.	0.3	2
421	A Cross-Validated Feature Selection (CVFS) approach for extracting the most parsimonious feature sets and discovering potential antimicrobial resistance (AMR) biomarkers. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 769-779.	1.9	3
422	Using a combination of short- and long-read sequencing to investigate the diversity in plasmid- and chromosomally encoded extended-spectrum beta-lactamases (ESBLs) in clinical <i>Shigella</i> and <i>Salmonella</i> isolates in Belgium. <i>Microbial Genomics</i> , 2023, 9, .	1.0	1
424	Benchmarking of two bioinformatic workflows for the analysis of whole-genome sequenced <i>Staphylococcus aureus</i> collected from patients with suspected sepsis. <i>BMC Infectious Diseases</i> , 2023, 23, .	1.3	0
425	Bioinformatics toolbox for exploring target mutation-induced drug resistance. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	4
427	Metagenomic Antimicrobial Susceptibility Testing from Simulated Native Patient Samples. <i>Antibiotics</i> , 2023, 12, 366.	1.5	2
428	Performances of bioinformatics tools for the analysis of sequencing data of <i>Mycobacterium tuberculosis</i> complex strains. <i>Tuberculosis</i> , 2023, 139, 102324.	0.8	0
429	From the basics to emerging diagnostic technologies: What is on the horizon for tilapia disease diagnostics?. <i>Reviews in Aquaculture</i> , 2023, 15, 186-212.	4.6	6
430	Artificial Intelligence for Antimicrobial Resistance Prediction: Challenges and Opportunities towards Practical Implementation. <i>Antibiotics</i> , 2023, 12, 523.	1.5	13

#	ARTICLE	IF	CITATIONS
431	The evolution and international spread of extensively drug resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	11
432	Molecular detection and characterization of foodborne bacteria: Recent progresses and remaining challenges. <i>Comprehensive Reviews in Food Science and Food Safety</i> , 2023, 22, 2433-2464.	5.9	3
433	Exploration of the diversity of multi-drug resistant <i>Mycobacterium tuberculosis</i> complex in Lagos, Nigeria using WGS: Distribution of lineages, drug resistance patterns and genetic mutations. <i>Tuberculosis</i> , 2023, 140, 102343.	0.8	0
434	Clinical Diagnostics of Bacterial Infections and Their Resistance to Antibioticsâ€”Current State and Whole Genome Sequencing Implementation Perspectives. <i>Antibiotics</i> , 2023, 12, 781.	1.5	9
437	Metagenomic next generation sequencing for studying antibiotic resistance genes in the environment. <i>Advances in Applied Microbiology</i> , 2023, , .	1.3	0
442	Genomic surveillance of bacterial pathogens. , 2023, , 71-117.		1
448	Genomic approaches to tuberculosis management and control. , 2023, , 178-190.		0
449	Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Livestock Diseases and Management</i> , 2023, , 215-230.	0.5	0
450	Genomics Innovations and Advanced Technologies. <i>Livestock Diseases and Management</i> , 2023, , 151-169.	0.5	0
452	The <i>Pseudomonas aeruginosa</i> Resistome: Permanent and Transient Antibiotic Resistance, an Overview. <i>Methods in Molecular Biology</i> , 2024, , 85-102.	0.4	0
466	Whole Genome Sequencing for Food Safety, Clinical and Public Health Microbiology. <i>IFMBE Proceedings</i> , 2024, , 865-873.	0.2	0