

# Derrick W Crook

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2677249/publications.pdf>

Version: 2024-02-01

248  
papers

27,886  
citations

7069

78  
h-index

8370

147  
g-index

333  
all docs

333  
docs citations

333  
times ranked

30302  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. <i>Cell</i> , 2021, 184, 2348-2361.e6.	13.5	936
2	Antibody Status and Incidence of SARS-CoV-2 Infection in Health Care Workers. <i>New England Journal of Medicine</i> , 2021, 384, 533-540.	13.9	803
3	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. <i>Cell</i> , 2022, 185, 467-484.e15.	13.5	788
4	Whole-genome sequencing to delineate <i>Mycobacterium tuberculosis</i> outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 137-146.	4.6	786
5	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	7.7	684
6	Fidaxomicin versus vancomycin for infection with <i>Clostridium difficile</i> in Europe, Canada, and the USA: a double-blind, non-inferiority, randomised controlled trial. <i>Lancet Infectious Diseases</i> , The, 2012, 12, 281-289.	4.6	644
7	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021, 184, 4220-4236.e13.	13.5	630
8	Diverse Sources of <i>C. difficile</i> Infection Identified on Whole-Genome Sequencing. <i>New England Journal of Medicine</i> , 2013, 369, 1195-1205.	13.9	595
9	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
10	Antibody escape of SARS-CoV-2 Omicron BA.4 and BA.5 from vaccine and BA.1 serum. <i>Cell</i> , 2022, 185, 2422-2433.e13.	13.5	532
11	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021, 184, 2939-2954.e9.	13.5	519
12	Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 10063.	5.8	479
13	Effect of Delta variant on viral burden and vaccine effectiveness against new SARS-CoV-2 infections in the UK. <i>Nature Medicine</i> , 2021, 27, 2127-2135.	15.2	450
14	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. <i>Cell</i> , 2021, 184, 2201-2211.e7.	13.5	442
15	Differences in outcome according to <i>Clostridium difficile</i> testing method: a prospective multicentre diagnostic validation study of <i>C difficile</i> infection. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 936-945.	4.6	405
16	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	13.9	405
17	Multilocus Sequence Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 770-778.	1.8	399
18	Identification of Biomarkers for Differentiation of Hypervirulent <i>Klebsiella pneumoniae</i> from Classical <i>K. pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	378

#	ARTICLE	IF	CITATIONS
19	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016, 14, 150-162.	13.6	373
20	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1390-1400.	4.6	336
21	A <i>Candida auris</i> Outbreak and Its Control in an Intensive Care Setting. <i>New England Journal of Medicine</i> , 2018, 379, 1322-1331.	13.9	318
22	Reduced neutralisation of SARS-CoV-2 omicron B.1.1.529 variant by post-immunisation serum. <i>Lancet</i> , The, 2022, 399, 234-236.	6.3	318
23	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
24	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.	1.8	289
25	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. <i>Lancet Respiratory Medicine</i> , the, 2016, 4, 49-58.	5.2	282
26	A standardised method for interpreting the association between mutations and phenotypic drug resistance in <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2017, 50, 1701354.	3.1	273
27	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 411-421.	4.6	269
28	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. <i>Nature Medicine</i> , 2021, 27, 1370-1378.	15.2	260
29	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene <i>bla</i> <sub>KPC</sub> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3767-3778.	1.4	255
30	Gonorrhoea treatment failure caused by a <i>Neisseria gonorrhoeae</i> strain with combined ceftriaxone and high-level azithromycin resistance, England, February 2018. <i>Eurosurveillance</i> , 2018, 23, .	3.9	255
31	Antibody responses to SARS-CoV-2 vaccines in 45,965 adults from the general population of the United Kingdom. <i>Nature Microbiology</i> , 2021, 6, 1140-1149.	5.9	254
32	<i>mcr-1</i> and <i>mcr-2</i> ( <i>mcr-6.1</i> ) variant genes identified in <i>Moraxella</i> species isolated from pigs in Great Britain from 2014 to 2015. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2745-2749.	1.3	252
33	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	5.9	247
34	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555.	3.3	244
35	The Hospital Water Environment as a Reservoir for Carbapenem-Resistant Organisms Causing Hospital-Acquired Infections – A Systematic Review of the Literature. <i>Clinical Infectious Diseases</i> , 2017, 64, 1435-1444.	2.9	242
36	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021, 73, e699-e709.	2.9	235

#	ARTICLE	IF	CITATIONS
37	Fidaxomicin Versus Vancomycin for Clostridium difficile Infection: Meta-analysis of Pivotal Randomized Controlled Trials. <i>Clinical Infectious Diseases</i> , 2012, 55, S93-S103.	2.9	228
38	A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. <i>BMJ Open</i> , 2012, 2, e001124.	0.8	228
39	Characterisation of Clostridium difficile Hospital Ward-Based Transmission Using Extensive Epidemiological Data and Molecular Typing. <i>PLoS Medicine</i> , 2012, 9, e1001172.	3.9	202
40	Microevolutionary analysis of Clostridium difficile genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	13.9	199
41	Assessment of Mycobacterium tuberculosis transmission in Oxfordshire, UK, 2007-12, with whole pathogen genome sequences: an observational study. <i>Lancet Respiratory Medicine</i> , 2014, 2, 285-292.	5.2	199
42	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. <i>Lancet Infectious Diseases</i> , 2017, 17, 1033-1041.	4.6	198
43	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020, 9, .	2.8	196
44	Within-Host Evolution of Staphylococcus aureus during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	1.1	194
45	Relationship Between Bacterial Strain Type, Host Biomarkers, and Mortality in Clostridium difficile Infection. <i>Clinical Infectious Diseases</i> , 2013, 56, 1589-1600.	2.9	191
46	Plasmid Classification in an Era of Whole-Genome Sequencing: Application in Studies of Antibiotic Resistance Epidemiology. <i>Frontiers in Microbiology</i> , 2017, 8, 182.	1.5	191
47	Evolutionary History of the Clostridium difficile Pathogenicity Locus. <i>Genome Biology and Evolution</i> , 2014, 6, 36-52.	1.1	190
48	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel. <i>Wellcome Open Research</i> , 2020, 5, 139.	0.9	179
49	Molecular Diagnosis of Orthopedic-Device-Related Infection Directly from Sonication Fluid by Metagenomic Sequencing. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2334-2347.	1.8	174
50	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	171
51	WGS to predict antibiotic MICs for Neisseria gonorrhoeae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1937-1947.	1.3	169
52	COVID-19: Rapid antigen detection for SARS-CoV-2 by lateral flow assay: A national systematic evaluation of sensitivity and specificity for mass-testing. <i>EClinicalMedicine</i> , 2021, 36, 100924.	3.2	162
53	Transmission of Staphylococcus aureus between health-care workers, the environment, and patients in an intensive care unit: a longitudinal cohort study based on whole-genome sequencing. <i>Lancet Infectious Diseases</i> , 2017, 17, 207-214.	4.6	155
54	Clinical Clostridium difficile: Clonality and Pathogenicity Locus Diversity. <i>PLoS ONE</i> , 2011, 6, e19993.	1.1	150

#	ARTICLE	IF	CITATIONS
55	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1295-1303.	4.6	149
56	Community prevalence of SARS-CoV-2 in England from April to November, 2020: results from the ONS Coronavirus Infection Survey. <i>Lancet Public Health</i> , The, 2021, 6, e30-e38.	4.7	147
57	Antibody responses and correlates of protection in the general population after two doses of the ChAdOx1 or BNT162b2 vaccines. <i>Nature Medicine</i> , 2022, 28, 1072-1082.	15.2	147
58	Whole-Genome Sequencing Shows That Patient-to-Patient Transmission Rarely Accounts for Acquisition of <i>Staphylococcus aureus</i> in an Intensive Care Unit. <i>Clinical Infectious Diseases</i> , 2014, 58, 609-618.	2.9	142
59	Improved workflows for high throughput library preparation using the transposome-based nextera system. <i>BMC Biotechnology</i> , 2013, 13, 104.	1.7	141
60	<i>Klebsiella pneumoniae</i> Carbapenemase (KPC)-Producing <i>K. pneumoniae</i> at a Single Institution: Insights into Endemicity from Whole-Genome Sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1656-1663.	1.4	140
61	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	5.8	128
62	Real-time analysis of nanopore-based metagenomic sequencing from infected orthopaedic devices. <i>BMC Genomics</i> , 2018, 19, 714.	1.2	128
63	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. <i>Wellcome Open Research</i> , 2020, 5, 181.	0.9	122
64	Effect of antibiotic prescribing on antibiotic resistance in individual children in primary care: prospective cohort study. <i>BMJ: British Medical Journal</i> , 2007, 335, 429.	2.4	121
65	Trends over time in <i>Escherichia coli</i> bloodstream infections, urinary tract infections, and antibiotic susceptibilities in Oxfordshire, UK, 1998â€“2016: a study of electronic health records. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 1138-1149.	4.6	121
66	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	1.8	121
67	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	2.6	120
68	Dynamic linkage of COVID-19 test results between Public Health Englandâ€™s Second Generation Surveillance System and UK Biobank. <i>Microbial Genomics</i> , 2020, 6, .	1.0	120
69	Colistin resistance gene <i>mcr-1</i> and pHNSHP45 plasmid in human isolates of <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> . <i>Lancet Infectious Diseases</i> , The, 2016, 16, 285-286.	4.6	119
70	Mortality risks associated with emergency admissions during weekends and public holidays: an analysis of electronic health records. <i>Lancet</i> , The, 2017, 390, 62-72.	6.3	114
71	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	3.4	114
72	Asymptomatic <i>Clostridium difficile</i> Colonisation and Onward Transmission. <i>PLoS ONE</i> , 2013, 8, e78445.	1.1	113

#	ARTICLE	IF	CITATIONS
73	Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infectivity by Viral Load, S Gene Variants and Demographic Factors, and the Utility of Lateral Flow Devices to Prevent Transmission. <i>Clinical Infectious Diseases</i> , 2022, 74, 407-415.	2.9	106
74	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	1.4	105
75	Potent cross-reactive antibodies following Omicron breakthrough in vaccinees. <i>Cell</i> , 2022, 185, 2116-2131.e18.	13.5	105
76	Natural mutations in a <i>Staphylococcus aureus</i> virulence regulator attenuate cytotoxicity but permit bacteremia and abscess formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3101-10.	3.3	103
77	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	0.9	103
78	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018, 34, 1666-1671.	1.8	100
79	Quantitative SARS-CoV-2 anti-spike responses to Pfizer's BioNTech and Oxford's AstraZeneca vaccines by previous infection status. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1516.e7-1516.e14.	2.8	100
80	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	2.8	93
81	Assessing a novel, lab-free, point-of-care test for SARS-CoV-2 (CovidNudge): a diagnostic accuracy study. <i>Lancet Microbe</i> , The, 2020, 1, e300-e307.	3.4	92
82	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism calling pipelines. <i>GigaScience</i> , 2020, 9, .	3.3	92
83	Maternal colonization with Streptococcus agalactiae and associated stillbirth and neonatal disease in coastal Kenya. <i>Nature Microbiology</i> , 2016, 1, 16067.	5.9	91
84	Mycobacterial DNA Extraction for Whole-Genome Sequencing from Early Positive Liquid (MGIT) Cultures. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1137-1143.	1.8	90
85	The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant Staphylococcus aureus. <i>MBio</i> , 2016, 7, e02039-15.	1.8	90
86	Ordering the mob: Insights into replicon and MOB typing schemes from analysis of a curated dataset of publicly available plasmids. <i>Plasmid</i> , 2017, 91, 42-52.	0.4	89
87	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021, 12, 6250.	5.8	88
88	Reduction of Invasive Pneumococcal Disease 3 Years After the Introduction of the 13-Valent Conjugate Vaccine in the Oxfordshire Region of England. <i>Journal of Infectious Diseases</i> , 2014, 210, 1001-1011.	1.9	83
89	Epidemiology of Clostridium difficile in infants in Oxfordshire, UK: Risk factors for colonization and carriage, and genetic overlap with regional C. difficile infection strains. <i>PLoS ONE</i> , 2017, 12, e0182307.	1.1	82
90	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. <i>Wellcome Open Research</i> , 2020, 5, 181.	0.9	81

#	ARTICLE	IF	CITATIONS
91	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998â€“2014. <i>Thorax</i> , 2016, 71, 535-542.	2.7	80
92	Detection of Mixed Infection from Bacterial Whole Genome Sequence Data Allows Assessment of Its Role in <i>Clostridium difficile</i> Transmission. <i>PLoS Computational Biology</i> , 2013, 9, e1003059.	1.5	75
93	Detection of Viral Pathogens With Multiplex Nanopore MinION Sequencing: Be Careful With Cross-Talk. <i>Frontiers in Microbiology</i> , 2018, 9, 2225.	1.5	75
94	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	1.6	75
95	Resolving plasmid structures in Enterobacteriaceae using the MinION nanopore sequencer: assessment of MinION and MinION/Illumina hybrid data assembly approaches. <i>Microbial Genomics</i> , 2017, 3, e000118.	1.0	74
96	Intensive Care Unit Wastewater Interventions to Prevent Transmission of Multispecies <i>Klebsiella pneumoniae</i> Carbapenemaseâ€“Producing Organisms. <i>Clinical Infectious Diseases</i> , 2018, 67, 171-178.	2.9	74
97	Covert dissemination of carbapenemase-producing <i>Klebsiella pneumoniae</i> (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 3025-3034.	1.3	73
98	Prevalence of <i>Staphylococcus aureus</i> protein A (spa) mutants in the community and hospitals in Oxfordshire. <i>BMC Microbiology</i> , 2014, 14, 63.	1.3	72
99	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
100	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	1.8	71
101	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. <i>Environmental Microbiomes</i> , 2019, 14, 7.	2.2	69
102	High Rates of Human Fecal Carriage of mcr-1â€“Positive Multidrug-Resistant Enterobacteriaceae Emerge in China in Association With Successful Plasmid Families. <i>Clinical Infectious Diseases</i> , 2018, 66, 676-685.	2.9	68
103	A Quantitative Evaluation of MIRU-VNTR Typing Against Whole-Genome Sequencing for Identifying <i>Mycobacterium tuberculosis</i> Transmission: A Prospective Observational Cohort Study. <i>EBioMedicine</i> , 2018, 34, 122-130.	2.7	65
104	Enhanced <i>Klebsiella pneumoniae</i> Carbapenemase Expression from a Novel Tn <i>4401</i> Deletion. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	64
105	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
106	An Observational Cohort Study on the Incidence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection and B.1.1.7 Variant Infection in Healthcare Workers by Antibody and Vaccination Status. <i>Clinical Infectious Diseases</i> , 2022, 74, 1208-1219.	2.9	64
107	Colonization with Enterobacteriaceae producing ESBLs in children attending pre-school childcare facilities in the Lao People's Democratic Republic. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1893-1897.	1.3	62
108	Validating a 14-Drug Microtiter Plate Containing Bedaquiline and Delamanid for Large-Scale Research Susceptibility Testing of <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	62



#	ARTICLE	IF	CITATIONS
109	Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from <i>Staphylococcus aureus</i> Whole-Genome Sequences. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	61
110	Two Distinct Patterns of <i>Clostridium difficile</i> Diversity Across Europe Indicating Contrasting Routes of Spread. <i>Clinical Infectious Diseases</i> , 2018, 67, 1035-1044.	2.9	60
111	A curated dataset of complete Enterobacteriaceae plasmids compiled from the NCBI nucleotide database. <i>Data in Brief</i> , 2017, 12, 423-426.	0.5	58
112	Pantonâ€“Valentine leucocidin is the key determinant of <i>Staphylococcus aureus</i> pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019, 8, .	2.8	56
113	Decline of methicillin-resistant <i>Staphylococcus aureus</i> in Oxfordshire hospitals is strain-specific and preceded infection-control intensification. <i>BMJ Open</i> , 2011, 1, e000160-e000160.	0.8	55
114	<i>Clostridium difficile</i> : Investigating Transmission Patterns Between Infected and Colonized Patients Using Whole Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2019, 68, 204-209.	2.9	55
115	Epidemiological data and genome sequencing reveals that nosocomial transmission of SARS-CoV-2 is underestimated and mostly mediated by a small number of highly infectious individuals. <i>Journal of Infection</i> , 2021, 83, 473-482.	1.7	55
116	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 1951.	5.8	54
117	Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism. <i>Viruses</i> , 2020, 12, 1164.	1.5	51
118	Occurrence and characterization of mcr-1-harbouring <i>Escherichia coli</i> isolated from pigs in Great Britain from 2013 to 2015. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 72, dkw477.	1.3	49
119	Tuberculosis is changing. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 359-361.	4.6	49
120	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	4.7	47
121	Chromosomal Integration of the <i>Klebsiella pneumoniae</i> Carbapenemase Gene, <i>bla</i> <sub>KPC</sub> , in <i>Klebsiella</i> Species Is Elusive but Not Rare. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	46
122	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. <i>MBio</i> , 2019, 10, .	1.8	46
123	Carbapenem-resistant Enterobacteriaceae dispersal from sinks is linked to drain position and drainage rates in a laboratory model system. <i>Journal of Hospital Infection</i> , 2019, 102, 63-69.	1.4	46
124	Population structure of group B streptococcus from a low-incidence region for invasive neonatal disease. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1875-1881.	0.7	45
125	Increasing incidence of <i>Escherichia coli</i> bacteraemia is driven by an increase in antibiotic-resistant isolates: electronic database study in Oxfordshire 1999-2011. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1514-1524.	1.3	45
126	Contribution to <i>Clostridium Difficile</i> Transmission of Symptomatic Patients With Toxigenic Strains Who Are Fecal Toxin Negative. <i>Clinical Infectious Diseases</i> , 2017, 64, 1163-1170.	2.9	45



#	ARTICLE	IF	CITATIONS
127	<i>Klebsiella quasipneumoniae</i> Provides a Window into Carbapenemase Gene Transfer, Plasmid Rearrangements, and Patient Interactions with the Hospital Environment. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	44
128	Dynamics of acquisition and loss of carriage of <i>Staphylococcus aureus</i> strains in the community: The effect of clonal complex. <i>Journal of Infection</i> , 2014, 68, 426-439.	1.7	42
129	Changes in paediatric respiratory infections at a UK teaching hospital 2016–2021; impact of the SARS-CoV-2 pandemic. <i>Journal of Infection</i> , 2022, 84, 40-47.	1.7	42
130	Time of Day of Vaccination Affects SARS-CoV-2 Antibody Responses in an Observational Study of Health Care Workers. <i>Journal of Biological Rhythms</i> , 2022, 37, 124-129.	1.4	42
131	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
132	Comparison of Control of <i>Clostridium difficile</i> Infection in Six English Hospitals Using Whole-Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 65, 433-441.	2.9	40
133	Investigation of the impact of the NICE guidelines regarding antibiotic prophylaxis during invasive dental procedures on the incidence of infective endocarditis in England: an electronic health records study. <i>BMC Medicine</i> , 2020, 18, 84.	2.3	39
134	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	1.8	38
135	Reduction in invasive pneumococcal disease following implementation of the conjugate vaccine in the Oxfordshire region, England. <i>Journal of Medical Microbiology</i> , 2011, 60, 91-97.	0.7	36
136	The use of whole-genome sequencing in a cluster investigation of a multidrug-resistant tuberculosis outbreak. <i>European Respiratory Journal</i> , 2018, 51, 1702313.	3.1	36
137	Don't overlook the little guy: An evaluation of the frequency of small plasmids co-conjugating with larger carbapenemase gene containing plasmids. <i>Plasmid</i> , 2019, 103, 1-8.	0.4	36
138	Invasive pneumococcal disease: epidemiology in children and adults prior to implementation of the conjugate vaccine in the Oxfordshire region, England. <i>Journal of Medical Microbiology</i> , 2008, 57, 480-487.	0.7	35
139	Capsular Typing Method for <i>Streptococcus agalactiae</i> Using Whole-Genome Sequence Data. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1388-1390.	1.8	35
140	<i>Clostridium difficile</i> trehalose metabolism variants are common and not associated with adverse patient outcomes when variably present in the same lineage. <i>EBioMedicine</i> , 2019, 43, 347-355.	2.7	35
141	Ten-year longitudinal molecular epidemiology study of <i>Escherichia coli</i> and <i>Klebsiella</i> species bloodstream infections in Oxfordshire, UK. <i>Genome Medicine</i> , 2021, 13, 144.	3.6	35
142	Whole-Genome Sequencing for Predicting Clarithromycin Resistance in <i>Mycobacterium abscessus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	34
143	TETyper: a bioinformatic pipeline for classifying variation and genetic contexts of transposable elements from short-read whole-genome sequencing data. <i>Microbial Genomics</i> , 2018, 4, .	1.0	33
144	Optimizing DNA Extraction Methods for Nanopore Sequencing of <i>Neisseria gonorrhoeae</i> Directly from Urine Samples. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	33

#	ARTICLE	IF	CITATIONS
145	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	33
146	Reducing demand for antibiotic prescriptions: evidence from an online survey of the general public on the interaction between preferences, beliefs and information, United Kingdom, 2015. <i>Eurosurveillance</i> , 2018, 23, .	3.9	33
147	Molecular Epidemiology of <i>Clostridium difficile</i> Strains in Children Compared with That of Strains Circulating in Adults with <i>Clostridium difficile</i> -Associated Infection : Fig. 1.. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3994-3996.	1.8	32
148	Robust Prediction of Resistance to Trimethoprim in <i>Staphylococcus aureus</i> . <i>Cell Chemical Biology</i> , 2018, 25, 339-349.e4.	2.5	32
149	The Complexity and Diversity of the Pathogenicity Locus in <i>Clostridium difficile</i> Clade 5. <i>Genome Biology and Evolution</i> , 2014, 6, 3159-3170.	1.1	31
150	The relative importance of large problems far away versus small problems closer to home: insights into limiting the spread of antimicrobial resistance in England. <i>BMC Medicine</i> , 2017, 15, 86.	2.3	30
151	Diagnosis of SARS-CoV-2 Infection with LamPORE, a High-Throughput Platform Combining Loop-Mediated Isothermal Amplification and Nanopore Sequencing. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	30
152	Machine learning for the prediction of antibacterial susceptibility in <i>Mycobacterium tuberculosis</i> . , 2014, , .		29
153	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 <i>sls</i> Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	29
154	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
155	The importance of using whole genome sequencing and extended spectrum beta-lactamase selective media when monitoring antimicrobial resistance. <i>Scientific Reports</i> , 2020, 10, 19880.	1.6	27
156	The Role of <i>fosA</i> in Challenges with Fosfomycin Susceptibility Testing of Multispecies <i>Klebsiella pneumoniae</i> Carbapenemase-Producing Clinical Isolates. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	26
157	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne <i>bla</i> <sub>KPC</sub> Carbapenemase in <i>Enterobacteriales</i> in the United Kingdom from 2009 to 2014. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	26
158	Genomic surveillance of <i>Escherichia coli</i> and <i>Klebsiella</i> spp. in hospital sink drains and patients. <i>Microbial Genomics</i> , 2020, 6, .	1.0	26
159	Molecular Epidemiology of Unrelated Clusters of Multiresistant Strains of <i>Haemophilus influenzae</i> . <i>Journal of Infectious Diseases</i> , 1992, 165, 1069-1075.	1.9	25
160	“Caveat emptor”: the cautionary tale of endocarditis and the potential pitfalls of clinical coding data” an electronic health records study. <i>BMC Medicine</i> , 2019, 17, 169.	2.3	25
161	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	3.5	25
162	Whole-genome sequencing for surveillance of tuberculosis drug resistance and determination of resistance level in China. <i>Clinical Microbiology and Infection</i> , 2022, 28, 731.e9-731.e15.	2.8	25

#	ARTICLE	IF	CITATIONS
163	Patient and Strain Characteristics Associated With <i>Clostridium difficile</i> Transmission and Adverse Outcomes. <i>Clinical Infectious Diseases</i> , 2018, 67, 1379-1387.	2.9	24
164	Reducing expectations for antibiotics in primary care: a randomised experiment to test the response to fear-based messages about antimicrobial resistance. <i>BMC Medicine</i> , 2020, 18, 110.	2.3	24
165	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	4.4	24
166	Stringent thresholds in SARS-CoV-2 IgG assays lead to under-detection of mild infections. <i>BMC Infectious Diseases</i> , 2021, 21, 187.	1.3	23
167	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
168	Multi-Label Random Forest Model for Tuberculosis Drug Resistance Classification and Mutation Ranking. <i>Frontiers in Microbiology</i> , 2020, 11, 667.	1.5	22
169	The bacteriology of pleural infection (TORPIDS): an exploratory metagenomics analysis through next generation sequencing. <i>Lancet Microbe</i> , The, 2022, 3, e294-e302.	3.4	22
170	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of <i>Mycobacterium tuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 1522-1530.	0.7	21
171	Complete Genome Sequence of KPC-Producing <i>Klebsiella pneumoniae</i> Strain CAV1193. <i>Genome Announcements</i> , 2016, 4, .	0.8	20
172	Epidemiology of <i>Mycobacterium abscessus</i> in England: an observational study. <i>Lancet Microbe</i> , The, 2021, 2, e498-e507.	3.4	20
173	A genomic epidemiological study shows that prevalence of antimicrobial resistance in Enterobacterales is associated with the livestock host, as well as antimicrobial usage. <i>Microbial Genomics</i> , 2021, 7, .	1.0	20
174	Symptoms and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Positivity in the General Population in the United Kingdom. <i>Clinical Infectious Diseases</i> , 2022, 75, e329-e337.	2.9	20
175	Are There Better Methods of Monitoring MRSA Control than Bacteraemia Surveillance? An Observational Database Study. <i>PLoS ONE</i> , 2008, 3, e2378.	1.1	19
176	Complete Sequencing of Plasmids Containing <i>bla</i> <sub>OXA-163</sub> and <i>bla</i> <sub>OXA-48</sub> in <i>Escherichia coli</i> Sequence Type 131. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6948-6951.	1.4	19
177	Developing an antimicrobial resistance reference laboratory and surveillance programme in Vietnam. <i>The Lancet Global Health</i> , 2017, 5, e1186-e1187.	2.9	19
178	Can rapid integrated polymerase chain reaction-based diagnostics for gastrointestinal pathogens improve routine hospital infection control practice? A diagnostic study. <i>Health Technology Assessment</i> , 2014, 18, 1-167.	1.3	19
179	Effects of proton pump inhibitors and histamine-2 receptor antagonists on response to fidaxomicin or vancomycin in patients with <i>Clostridium difficile</i> -associated diarrhoea. <i>BMJ Open Gastroenterology</i> , 2015, 2, e000028.	1.1	18
180	Clinical Metagenomic Sequencing for Species Identification and Antimicrobial Resistance Prediction in Orthopedic Device Infection. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0215621.	1.8	18

#	ARTICLE	IF	CITATIONS
181	Nanopore metagenomic sequencing of influenza virus directly from respiratory samples: diagnosis, drug resistance and nosocomial transmission, United Kingdom, 2018/19 influenza season. <i>Eurosurveillance</i> , 2021, 26, .	3.9	17
182	SARS-CoV-2 antibody prevalence, titres and neutralising activity in an antenatal cohort, United Kingdom, 14 April to 15 June 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	17
183	BugMat and FindNeighbour: command line and server applications for investigating bacterial relatedness. <i>BMC Bioinformatics</i> , 2017, 18, 477.	1.2	16
184	Identifying Mixed Mycobacterium tuberculosis Infection and Laboratory Cross-Contamination during Mycobacterial Sequencing Programs. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	16
185	Hash-Based Core Genome Multilocus Sequence Typing for <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2019, 58, .	1.8	16
186	Ten Years of Population-Level Genomic <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Serotype Surveillance Informs Vaccine Development for Invasive Infections. <i>Clinical Infectious Diseases</i> , 2021, 73, 2276-2282.	2.9	16
187	Viral detection and identification in 20Âmin by rapid single-particle fluorescence in-situ hybridization of viral RNA. <i>Scientific Reports</i> , 2021, 11, 19579.	1.6	16
188	Short-Term Genome Stability of Serial <i>Clostridium difficile</i> Ribotype 027 Isolates in an Experimental Gut Model and Recurrent Human Disease. <i>PLoS ONE</i> , 2013, 8, e63540.	1.1	16
189	Whole genome sequencing reveals hidden transmission of carbapenemase-producing Enterobacterales. <i>Nature Communications</i> , 2022, 13, .	5.8	16
190	Diversity of antibiotic resistance integrative and conjugative elements among haemophili. <i>Journal of Medical Microbiology</i> , 2007, 56, 838-846.	0.7	15
191	First Report of <i>bla</i> <sub>IMP-14</sub> on a Plasmid Harboring Multiple Drug Resistance Genes in <i>Escherichia coli</i> Sequence Type 131. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5068-5071.	1.4	15
192	Nanopore metagenomic sequencing to investigate nosocomial transmission of human metapneumovirus from a unique genetic group among haematology patients in the United Kingdom. <i>Journal of Infection</i> , 2020, 80, 571-577.	1.7	15
193	Antimicrobial resistance determinants are associated with <i>Staphylococcus aureus</i> bacteraemia and adaptation to the healthcare environment: a bacterial genome-wide association study. <i>Microbial Genomics</i> , 2021, 7, .	1.0	15
194	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of Mycobacteria Direct from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	14
195	NanoSPC: a scalable, portable, cloud compatible viral nanopore metagenomic data processing pipeline. <i>Nucleic Acids Research</i> , 2020, 48, W366-W371.	6.5	14
196	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. <i>Microbial Genomics</i> , 2020, 6, .	1.0	14
197	Aiming for zero tuberculosis transmission in low-burden countries. <i>Lancet Respiratory Medicine</i> , 2017, 5, 846-848.	5.2	13
198	Preferences for Medical Consultations from Online Providers: Evidence from a Discrete Choice Experiment in the United Kingdom. <i>Applied Health Economics and Health Policy</i> , 2021, 19, 521-535.	1.0	12

#	ARTICLE	IF	CITATIONS
199	Flanker: a tool for comparative genomics of gene flanking regions. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12
200	Human and Porcine Transmission of <i>Clostridioides difficile</i> Ribotype 078, Europe. <i>Emerging Infectious Diseases</i> , 2021, 27, 2294-2300.	2.0	12
201	Evaluation of methods for detecting human reads in microbial sequencing datasets. <i>Microbial Genomics</i> , 2020, 6, .	1.0	11
202	Risk Factors Associated with Carbapenemase-Producing <i>Enterobacterales</i> (CPE) Positivity in the Hospital Wastewater Environment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	11
203	Pneumococcal Carriage. , 0, , 136-147.		10
204	Control of Artfactual Variation in Reported Intersample Relatedness during Clinical Use of a <i>Mycobacterium tuberculosis</i> Sequencing Pipeline. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	10
205	Relationship between microbiology of throat swab and clinical course among primary care patients with acute cough: a prospective cohort study. <i>Family Practice</i> , 2020, 37, 332-339.	0.8	10
206	Population-level faecal metagenomic profiling as a tool to predict antimicrobial resistance in <i>Enterobacterales</i> isolates causing invasive infections: An exploratory study across Cambodia, Kenya, and the UK. <i>EClinicalMedicine</i> , 2021, 36, 100910.	3.2	10
207	Surveillance of Infection Severity: A Registry Study of Laboratory Diagnosed <i>Clostridium difficile</i> . <i>PLoS Medicine</i> , 2012, 9, e1001279.	3.9	8
208	Rare Variants in MYD88, IRAK4 and IKBKG and Susceptibility to Invasive Pneumococcal Disease: A Population-Based Case-Control Study. <i>PLoS ONE</i> , 2015, 10, e0123532.	1.1	8
209	Antibiotic use and clinical outcomes in the acute setting under management by an infectious diseases acute physician versus other clinical teams: a cohort study. <i>BMJ Open</i> , 2016, 6, e010969.	0.8	8
210	Improved Performance Predicting Clarithromycin Resistance in <i>Mycobacterium abscessus</i> on an Independent Data Set. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	8
211	Comparative genomics of <i>Clostridioides difficile</i> toxinotypes identifies module-based toxin gene evolution. <i>Microbial Genomics</i> , 2020, 6, .	1.0	8
212	Antibiotic Review Kit for Hospitals (ARK-Hospital): study protocol for a stepped-wedge cluster-randomised controlled trial. <i>Trials</i> , 2019, 20, 421.	0.7	7
213	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus <i>Staphylococcus</i> Rosenbach 1884. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
214	An end-to-end heterogeneous graph attention network for <i>Mycobacterium tuberculosis</i> drug-resistance prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
215	A crowd of BashTheBug volunteers reproducibly and accurately measure the minimum inhibitory concentrations of 13 antitubercular drugs from photographs of 96-well broth microdilution plates. <i>ELife</i> , 2022, 11, .	2.8	7
216	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant <i>Enterobacteriaceae</i> . <i>PLoS ONE</i> , 2019, 14, e0222831.	1.1	6

#	ARTICLE	IF	CITATIONS
217	WGS to determine the extent of <i>Clostridioides difficile</i> transmission in a high incidence setting in North Wales in 2015. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1092-1100.	1.3	6
218	SARS-CoV-2 antibody trajectories after a single COVID-19 vaccination with and without prior infection. <i>Nature Communications</i> , 2022, 13, .	5.8	6
219	Prediction of Pyrazinamide Resistance in <i>Mycobacterium Tuberculosis</i> Using Structure-Based Machine Learning Approaches. <i>SSRN Electronic Journal</i> , 0, , .	0.4	5
220	Identifying Bacterial Airways Infection in Stable Severe Asthma Using Oxford Nanopore Sequencing Technologies. <i>Microbiology Spectrum</i> , 2022, 10, e0227921.	1.2	5
221	Multidrug-resistant <i>Escherichia coli</i> soft tissue infection investigated with bacterial whole genome sequencing. <i>BMJ Case Reports</i> , 2014, 2014, bcr2014207200-bcr2014207200.	0.2	4
222	Using linked electronic health records to report healthcare-associated infections. <i>PLoS ONE</i> , 2018, 13, e0206860.	1.1	3
223	Using hospital network-based surveillance for antimicrobial resistance as a more robust alternative to self-reporting. <i>PLoS ONE</i> , 2019, 14, e0219994.	1.1	3
224	Awareness of Appropriate Antibiotic Use in Primary Care for Influenza-Like Illness: Evidence of Improvement from UK Population-Based Surveys. <i>Antibiotics</i> , 2020, 9, 690.	1.5	3
225	Combining Charlson and Elixhauser scores with varying lookback predicated mortality better than using individual scores. <i>Journal of Clinical Epidemiology</i> , 2021, 130, 32-41.	2.4	3
226	Mortality risks associated with empirical antibiotic activity in <i>Escherichia coli</i> bacteraemia: an analysis of electronic health records. <i>Journal of Antimicrobial Chemotherapy</i> , 0, , .	1.3	3
227	An Open-Source Azure Solution for Scalable Genomics Workflows. , 2018, , .		2
228	Reduced Neutralization of SARS-CoV-2 B.1.1.7 Variant from Naturally Acquired and Vaccine Induced Antibody Immunity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
229	Undetected carriage explains apparent <i>Staphylococcus aureus</i> acquisition in a non-outbreak healthcare setting. <i>Journal of Infection</i> , 2021, 83, 332-338.	1.7	2
230	Antimicrobial resistance genes and clonal success in <i>Escherichia coli</i> isolates causing bloodstream infection. <i>Lancet Microbe</i> , The, 2021, 2, e492.	3.4	2
231	<i>Mycobacterium abscessus</i> Genomic Clusters Span Geography and Patient Groups. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
232	Antimicrobial resistance in commensal opportunistic pathogens isolated from non-sterile sites can be an effective proxy for surveillance in bloodstream infections. <i>Scientific Reports</i> , 2021, 11, 23359.	1.6	2
233	<i>Clostridium difficile</i> in England: can we stop washing our hands? â€œ Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 478-479.	4.6	1
234	Scalable Pathogen Pipeline Platform (SP <sup>3</sup> ): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing. , 2019, , .		1

#	ARTICLE	IF	CITATIONS
235	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014, 59, 752-753.	2.9	0
236	<i>Staphylococcus aureus</i> in critical care – Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 580-581.	4.6	0
237	Whole Genome Sequencing for Surveillance of Tuberculosis Drug Resistance in China: Based on a Cross-Sectional Surveillance Study. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
238	Transmission of pre-XDR and XDR-TB in the Mumbai Metropolitan Region, India. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
239	<i>Haemophilus spp.</i> , 0, , 245-251.		0
240	<i>M. tuberculosis</i> Microvariation Is Common and Is Associated with Transmission: Analysis of Three Years Prospective Universal Sequencing in England. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
241	Reducing Expectations for Antibiotics in Primary Care: A Randomised Experiment to Test the Response to Fear-Based Messages About Antimicrobial Resistance. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
242	Risk Factors Associated with Carbapenemase-Producing Enterobacterales (CPE) Positivity in the Hospital Wastewater Environment. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
243	Case Report: Disseminated, rifampicin resistant <i>Mycobacterium bovis</i> (BCG) infection in an immunocompromised child. <i>Wellcome Open Research</i> , 2020, 5, 242.	0.9	0
244	Title is missing!. , 2019, 14, e0222831.		0
245	Title is missing!. , 2019, 14, e0222831.		0
246	Title is missing!. , 2019, 14, e0222831.		0
247	Title is missing!. , 2019, 14, e0222831.		0
248	Catwalk: identifying closely related sequences in large microbial sequence databases. <i>Microbial Genomics</i> , 2022, 8, .	1.0	0