

Derrick W Crook

List of Publications by Year in descending order

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Version: 2024-02-01

248
papers

27,886
citations

7096

78
h-index

8396

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.	28.9	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.	27.0	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.	28.9	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.	9.1	786
5	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	16.3	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.	9.1	644
7	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021, 184, 4220-4236.e13.	28.9	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.	27.0	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.	9.1	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.	28.9	532
11	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021, 184, 2939-2954.e9.	28.9	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.	12.8	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.	30.7	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.	28.9	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.	9.1	405
16	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
17	Multilocus Sequence Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 770-778.	3.9	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, .	3.9	378

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19	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016, 14, 150-162.	28.6	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.	9.1	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.	27.0	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.	13.7	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.	3.9	315
24	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.	4.1	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.	10.7	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.	6.7	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.	9.1	269
28	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. <i>Nature Medicine</i> , 2021, 27, 1370-1378.	30.7	260
29	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene <i>bla</i> _{KPC} . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3767-3778.	3.2	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, .	7.0	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.	13.3	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.	3.0	252
33	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	13.3	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.	7.1	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.	5.8	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.	5.8	235

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37	Fidaxomicin Versus Vancomycin for Clostridium difficile Infection: Meta-analysis of Pivotal Randomized Controlled Trials. <i>Clinical Infectious Diseases</i> , 2012, 55, S93-S103.	5.8	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.	1.9	228
39	Characterisation of Clostridium difficile Hospital Ward-Based Transmission Using Extensive Epidemiological Data and Molecular Typing. <i>PLoS Medicine</i> , 2012, 9, e1001172.	8.4	202
40	Microevolutionary analysis of Clostridium difficile genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	9.6	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.	10.7	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.	9.1	198
43	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020, 9, .	6.0	196
44	Within-Host Evolution of Staphylococcus aureus during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	2.5	194
45	Relationship Between Bacterial Strain Type, Host Biomarkers, and Mortality in Clostridium difficile Infection. <i>Clinical Infectious Diseases</i> , 2013, 56, 1589-1600.	5.8	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.	3.5	191
47	Evolutionary History of the Clostridium difficile Pathogenicity Locus. <i>Genome Biology and Evolution</i> , 2014, 6, 36-52.	2.5	190
48	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel. <i>Wellcome Open Research</i> , 2020, 5, 139.	1.8	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.	3.9	174
50	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	171
51	WGS to predict antibiotic MICs for Neisseria gonorrhoeae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1937-1947.	3.0	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.	7.1	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.	9.1	155
54	Clinical Clostridium difficile: Clonality and Pathogenicity Locus Diversity. <i>PLoS ONE</i> , 2011, 6, e19993.	2.5	150

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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.	9.1	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.	10.0	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.	30.7	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.	5.8	142
59	Improved workflows for high throughput library preparation using the transposome-based nextera system. <i>BMC Biotechnology</i> , 2013, 13, 104.	3.3	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.	3.2	140
61	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	12.8	128
62	Real-time analysis of nanopore-based metagenomic sequencing from infected orthopaedic devices. <i>BMC Genomics</i> , 2018, 19, 714.	2.8	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.	1.8	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.	2.3	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.	9.1	121
66	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	3.9	121
67	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	5.6	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, .	2.0	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.	9.1	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.	13.7	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.	7.3	114
72	Asymptomatic <i>Clostridium difficile</i> Colonisation and Onward Transmission. <i>PLoS ONE</i> , 2013, 8, e78445.	2.5	113

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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.	5.8	106
74	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	3.1	105
75	Potent cross-reactive antibodies following Omicron breakthrough in vaccinees. <i>Cell</i> , 2022, 185, 2116-2131.e18.	28.9	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.	7.1	103
77	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	1.8	103
78	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018, 34, 1666-1671.	4.1	100
79	Quantitative SARS-CoV-2 anti-spike responses to Pfizerâ€BioNTech and Oxfordâ€AstraZeneca vaccines by previous infection status. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1516.e7-1516.e14.	6.0	100
80	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	6.0	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.	7.3	92
82	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphismâ€calling pipelines. <i>GigaScience</i> , 2020, 9, .	6.4	92
83	Maternal colonization with <i>Streptococcus agalactiae</i> and associated stillbirth and neonatal disease in coastal Kenya. <i>Nature Microbiology</i> , 2016, 1, 16067.	13.3	91
84	<i>Mycobacterium</i> DNA Extraction for Whole-Genome Sequencing from Early Positive Liquid (MGIT) Cultures. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1137-1143.	3.9	90
85	The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2016, 7, e02039-15.	4.1	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.	1.4	89
87	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021, 12, 6250.	12.8	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.	4.0	83
89	Epidemiology of <i>Clostridium difficile</i> in infants in Oxfordshire, UK: Risk factors for colonization and carriage, and genetic overlap with regional <i>C. difficile</i> infection strains. <i>PLoS ONE</i> , 2017, 12, e0182307.	2.5	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.	1.8	81

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91	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998â€“2014. <i>Thorax</i> , 2016, 71, 535-542.	5.6	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.	3.2	75
93	Detection of Viral Pathogens With Multiplex Nanopore MinION Sequencing: Be Careful With Cross-Talk. <i>Frontiers in Microbiology</i> , 2018, 9, 2225.	3.5	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.	3.3	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.	2.0	74
96	Intensive Care Unit Wastewater Interventions to Prevent Transmission of Multispecies <i>Klebsiella pneumoniae</i> Carbapenemase-Producing Organisms. <i>Clinical Infectious Diseases</i> , 2018, 67, 171-178.	5.8	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.	3.0	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.	3.3	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, .	3.9	72
100	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	4.1	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.	5.0	69
102	High Rates of Human Fecal Carriage of mcr-1-Positive Multidrug-Resistant Enterobacteriaceae Emerge in China in Association With Successful Plasmid Families. <i>Clinical Infectious Diseases</i> , 2018, 66, 676-685.	5.8	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.	6.1	65
104	Enhanced <i>Klebsiella pneumoniae</i> Carbapenemase Expression from a Novel Tn 4401 Deletion. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	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.	4.3	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.	5.8	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.	3.0	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, .	3.2	62

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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, .	3.9	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.	5.8	60
111	A curated dataset of complete Enterobacteriaceae plasmids compiled from the NCBI nucleotide database. <i>Data in Brief</i> , 2017, 12, 423-426.	1.0	58
112	Pantonâ€“Valentine leucocidin is the key determinant of <i>Staphylococcus aureus</i> pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019, 8, .	6.0	56
113	Decline of meticillin-resistant <i>Staphylococcus aureus</i> in Oxfordshire hospitals is strain-specific and preceded infection-control intensification. <i>BMJ Open</i> , 2011, 1, e000160-e000160.	1.9	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.	5.8	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.	3.3	55
116	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 1951.	12.8	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.	3.3	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.	3.0	49
119	Tuberculosis is changing. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 359-361.	9.1	49
120	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	10.3	47
121	Chromosomal Integration of the <i>Klebsiella pneumoniae</i> Carbapenemase Gene, <i>bla</i> _{KPC} , in <i>Klebsiella</i> Species Is Elusive but Not Rare. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	46
122	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype O78. <i>MBio</i> , 2019, 10, .	4.1	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.	2.9	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.	1.8	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.	3.0	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.	5.8	45

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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, .	3.2	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.	3.3	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.	3.3	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.	2.6	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.	1.8	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.	5.8	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.	5.5	39
134	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	4.1	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.	1.8	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.	6.7	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.	1.4	36
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