

# Ann Sarah Walker

## List of Publications by Year in descending order

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Version: 2024-02-01

188  
papers

16,491  
citations

20759

60  
h-index

21474

114  
g-index

215  
all docs

215  
docs citations

215  
times ranked

20988  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	Oral versus Intravenous Antibiotics for Bone and Joint Infection. <i>New England Journal of Medicine</i> , 2019, 380, 425-436.	13.9	548
6	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
7	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
8	Multilocus Sequence Typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010, 48, 770-778.	1.8	399
9	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016, 14, 150-162.	13.6	373
10	Effect of Covid-19 Vaccination on Transmission of Alpha and Delta Variants. <i>New England Journal of Medicine</i> , 2022, 386, 744-756.	13.9	323
11	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
12	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
13	The challenge of antimicrobial resistance: What economics can contribute. <i>Science</i> , 2019, 364, .	6.0	292
14	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.	1.8	289
15	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
16	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. <i>Nature Medicine</i> , 2021, 27, 1370-1378.	15.2	260
17	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
18	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

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19	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	5.9	247
20	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
21	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
22	Characterisation of <i>Clostridium difficile</i> Hospital Ward-Based Transmission Using Extensive Epidemiological Data and Molecular Typing. <i>PLoS Medicine</i> , 2012, 9, e1001172.	3.9	202
23	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	13.9	199
24	The antibiotic course has had its day. <i>BMJ: British Medical Journal</i> , 2017, 358, j3418.	2.4	192
25	Relationship Between Bacterial Strain Type, Host Biomarkers, and Mortality in <i>Clostridium difficile</i> Infection. <i>Clinical Infectious Diseases</i> , 2013, 56, 1589-1600.	2.9	191
26	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
27	Evolutionary History of the <i>Clostridium difficile</i> Pathogenicity Locus. <i>Genome Biology and Evolution</i> , 2014, 6, 36-52.	1.1	190
28	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
29	Assessment of Second-Line Antiretroviral Regimens for HIV Therapy in Africa. <i>New England Journal of Medicine</i> , 2014, 371, 234-247.	13.9	178
30	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	171
31	WGS to predict antibiotic MICs for <i>Neisseria gonorrhoeae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1937-1947.	1.3	169
32	Enhanced Prophylaxis plus Antiretroviral Therapy for Advanced HIV Infection in Africa. <i>New England Journal of Medicine</i> , 2017, 377, 233-245.	13.9	156
33	Transmission of <i>Staphylococcus aureus</i> 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> , The, 2017, 17, 207-214.	4.6	155
34	Clinical <i>Clostridium difficile</i> : Clonality and Pathogenicity Locus Diversity. <i>PLoS ONE</i> , 2011, 6, e19993.	1.1	150
35	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
36	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

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37	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
38	Adjunctive rifampicin for <i>Staphylococcus aureus</i> bacteraemia (ARREST): a multicentre, randomised, double-blind, placebo-controlled trial. <i>Lancet</i> , The, 2018, 391, 668-678.	6.3	140
39	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	5.8	128
40	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
41	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	1.8	121
42	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
43	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
44	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
45	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018, 34, 1666-1671.	1.8	100
46	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.	2.8	100
47	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	2.8	93
48	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphismâ€“calling pipelines. <i>GigaScience</i> , 2020, 9, .	3.3	92
49	Maternal colonization with <i>Streptococcus agalactiae</i> and associated stillbirth and neonatal disease in coastal Kenya. <i>Nature Microbiology</i> , 2016, 1, 16067.	5.9	91
50	Ct threshold values, a proxy for viral load in community SARS-CoV-2 cases, demonstrate wide variation across populations and over time. <i>ELife</i> , 2021, 10, .	2.8	91
51	<i>Mycobacterial</i> 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
52	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
53	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021, 12, 6250.	5.8	88
54	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

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55	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.	1.1	82
56	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998–2014. <i>Thorax</i> , 2016, 71, 535-542.	2.7	80
57	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
58	Prevalence of <i>Staphylococcus aureus</i> protein A ( <i>spa</i> ) mutants in the community and hospitals in Oxfordshire. <i>BMC Microbiology</i> , 2014, 14, 63.	1.3	72
59	Nucleoside reverse-transcriptase inhibitor cross-resistance and outcomes from second-line antiretroviral therapy in the public health approach: an observational analysis within the randomised, open-label, EARNEST trial. <i>Lancet HIV</i> , 2017, 4, e341-e348.	2.1	71
60	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	1.8	71
61	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
62	Mortality in the Year Following Antiretroviral Therapy Initiation in HIV-Infected Adults and Children in Uganda and Zimbabwe. <i>Clinical Infectious Diseases</i> , 2012, 55, 1707-1718.	2.9	68
63	High Rates of Human Fecal Carriage of <i>mcr-1</i> 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
64	Immediate Transfusion in African Children with Uncomplicated Severe Anemia. <i>New England Journal of Medicine</i> , 2019, 381, 407-419.	13.9	64
65	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
66	Predicting mortality in sick African children: the FEAST Paediatric Emergency Triage (PET) Score. <i>BMC Medicine</i> , 2015, 13, 174.	2.3	62
67	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
68	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
69	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
70	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
71	<i>Clostridium difficile</i> Mixed Infection and Reinfection. <i>Journal of Clinical Microbiology</i> , 2012, 50, 142-144.	1.8	55
72	<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

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73	Transfusion Volume for Children with Severe Anemia in Africa. <i>New England Journal of Medicine</i> , 2019, 381, 420-431.	13.9	49
74	Tracking the Emergence of SARS-CoV-2 Alpha Variant in the United Kingdom. <i>New England Journal of Medicine</i> , 2021, 385, 2582-2585.	13.9	49
75	Oral versus intravenous antibiotic treatment for bone and joint infections (OVIVA): study protocol for a randomised controlled trial. <i>Trials</i> , 2015, 16, 583.	0.7	48
76	Survival following <i>Staphylococcus aureus</i> bloodstream infection: A prospective multinational cohort study assessing the impact of place of care. <i>Journal of Infection</i> , 2018, 77, 516-525.	1.7	48
77	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	4.7	47
78	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
79	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
80	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
81	Contribution of behavioural science to antibiotic stewardship. <i>BMJ</i> , The, 2015, 350, h3413-h3413.	3.0	45
82	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
83	<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
84	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
85	Transfusion and Treatment of severe anaemia in African children (TRACT): a study protocol for a randomised controlled trial. <i>Trials</i> , 2015, 16, 593.	0.7	42
86	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
87	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
88	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
89	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	1.8	38
90	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

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91	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
92	<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
93	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
94	An efficient record linkage scheme using graphical analysis for identifier error detection. <i>BMC Medical Informatics and Decision Making</i> , 2011, 11, 7.	1.5	34
95	Antibiotic policies in acute English NHS trusts: implementation of "Start Smart" Then Focus™ and relationship with <i>Clostridium difficile</i> infection rates. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1230-1235.	1.3	34
96	Abacavir, zidovudine, or stavudine as paediatric tablets for African HIV-infected children (CHAPAS-3): an open-label, parallel-group, randomised controlled trial. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 169-179.	4.6	33
97	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
98	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
99	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
100	Acceptability of lopinavir/r pellets (minitabs), tablets and syrups in HIV-infected children. <i>Antiviral Therapy</i> , 2016, 21, 579-585.	0.6	32
101	Robust Prediction of Resistance to Trimethoprim in <i>Staphylococcus aureus</i> . <i>Cell Chemical Biology</i> , 2018, 25, 339-349.e4.	2.5	32
102	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
103	Adjunctive rifampicin to reduce early mortality from <i>Staphylococcus aureus</i> bacteraemia (ARREST): study protocol for a randomised controlled trial. <i>Trials</i> , 2012, 13, 241.	0.7	29
104	Raltegravir-intensified initial antiretroviral therapy in advanced HIV disease in Africa: A randomised controlled trial. <i>PLoS Medicine</i> , 2018, 15, e1002706.	3.9	28
105	Oral versus intravenous antibiotics for bone and joint infections: the OVIVA non-inferiority RCT. <i>Health Technology Assessment</i> , 2019, 23, 1-92.	1.3	27
106	Causes and Timing of Mortality and Morbidity Among Late Presenters Starting Antiretroviral Therapy in the REALITY Trial. <i>Clinical Infectious Diseases</i> , 2018, 66, S132-S139.	2.9	26
107	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne <i>bla</i> KPC in the United Kingdom from 2009 to 2014. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	26
108	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

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109	“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
110	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
111	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
112	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	4.4	24
113	Phase II trial of standard versus increased transfusion volume in Ugandan children with acute severe anemia. <i>BMC Medicine</i> , 2014, 12, 67.	2.3	23
114	Virological response and resistance among HIV-infected children receiving long-term antiretroviral therapy without virological monitoring in Uganda and Zimbabwe: Observational analyses within the randomised ARROW trial. <i>PLoS Medicine</i> , 2017, 14, e1002432.	3.9	22
115	Effect of ready-to-use supplementary food on mortality in severely immunocompromised HIV-infected individuals in Africa initiating antiretroviral therapy (REALITY): an open-label, parallel-group, randomised controlled trial. <i>Lancet HIV</i> , 2018, 5, e231-e240.	2.1	22
116	Multi-Label Random Forest Model for Tuberculosis Drug Resistance Classification and Mutation Ranking. <i>Frontiers in Microbiology</i> , 2020, 11, 667.	1.5	22
117	Complete Genome Sequence of KPC-Producing <i>Klebsiella pneumoniae</i> Strain CAV1193. <i>Genome Announcements</i> , 2016, 4, .	0.8	20
118	Epidemiology of <i>Mycobacterium abscessus</i> in England: an observational study. <i>Lancet Microbe</i> , 2021, 2, e498-e507.	3.4	20
119	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
120	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
121	Baseline Inflammatory Biomarkers Identify Subgroups of HIV-Infected African Children With Differing Responses to Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2016, 214, 226-236.	1.9	19
122	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
123	Overview of systematic reviews assessing the evidence for shorter versus longer duration antibiotic treatment for bacterial infections in secondary care. <i>PLoS ONE</i> , 2018, 13, e0194858.	1.1	18
124	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
125	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
126	Rapid antiretroviral therapy initiation in low- and middle-income countries: A resource-based approach. <i>PLoS Medicine</i> , 2019, 16, e1002723.	3.9	16



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127	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
128	Route and duration of antibiotic therapy in acute cellulitis: A systematic review and meta-analysis of the effectiveness and harms of antibiotic treatment. <i>Journal of Infection</i> , 2020, 81, 521-531.	1.7	15
129	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
130	Constructing a representative <i>in silico</i> population for paediatric simulations: Application to HIV-positive African children. <i>British Journal of Clinical Pharmacology</i> , 2021, 87, 2847-2854.	1.1	15
131	Transfusion management of severe anaemia in African children: a consensus algorithm. <i>British Journal of Haematology</i> , 2021, 193, 1247-1259.	1.2	15
132	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
133	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of <i>Mycobacteria</i> Direct from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	14
134	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. <i>Microbial Genomics</i> , 2020, 6, .	1.0	14
135	HIV-Related Arterial Stiffness in Malawian Adults Is Associated With the Proportion of PD-1-Expressing CD8+ T Cells and Reverses With Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2019, 219, 1948-1958.	1.9	13
136	Haematological quality and age of donor blood issued for paediatric transfusion to four hospitals in sub-Saharan Africa. <i>Vox Sanguinis</i> , 2019, 114, 340-348.	0.7	13
137	Evaluating Safety Reporting in Paediatric Antibiotic Trials, 2000-2016: A Systematic Review and Meta-Analysis. <i>Drugs</i> , 2018, 78, 231-244.	4.9	12
138	Flanker: a tool for comparative genomics of gene flanking regions. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12
139	Transient Viral Load Increases in HIV-Infected Children in the UK and Ireland: What do They Mean?. <i>Antiviral Therapy</i> , 2007, 12, 949-956.	0.6	12
140	Severity of illness and the weekend effect - Authors' reply. <i>Lancet</i> , The, 2017, 390, 1735.	6.3	11
141	Predictors of recurrence, early treatment failure and death from <i>Staphylococcus aureus</i> bacteraemia: Observational analyses within the ARREST trial. <i>Journal of Infection</i> , 2019, 79, 332-340.	1.7	11
142	An Analysis of <i>Clostridium difficile</i> Environmental Contamination During and After Treatment for <i>C difficile</i> Infection. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa362.	0.4	11
143	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
144	Personalised randomised controlled trial designs - a new paradigm to define optimal treatments for carbapenem-resistant infections. <i>Lancet Infectious Diseases</i> , The, 2021, 21, e175-e181.	4.6	11

#	ARTICLE	IF	CITATIONS
145	Control of Artfactual Variation in Reported Intersample Relatedness during Clinical Use of a Mycobacterium tuberculosis Sequencing Pipeline. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	1.8	10
146	Adjunctive rifampicin to reduce early mortality from <i>Staphylococcus aureus</i> bacteraemia: the ARREST RCT. <i>Health Technology Assessment</i> , 2018, 22, 1-148.	1.3	10
147	Eliciting risk preferences that predict risky health behavior: A comparison of two approaches. <i>Health Economics (United Kingdom)</i> , 2022, 31, 836-858.	0.8	10
148	Optimising trial designs to identify appropriate antibiotic treatment durations. <i>BMC Medicine</i> , 2019, 17, 115.	2.3	9
149	Why do hospital prescribers continue antibiotics when it is safe to stop? Results of a choice experiment survey. <i>BMC Medicine</i> , 2020, 18, 196.	2.3	9
150	Probabilistic transmission models incorporating sequencing data for healthcare-associated <i>Clostridioides difficile</i> outperform heuristic rules and identify strain-specific differences in transmission. <i>PLoS Computational Biology</i> , 2021, 17, e1008417.	1.5	9
151	Regarding "Clostridium Difficile Ribotype Does Not Predict Severe Infection". <i>Clinical Infectious Diseases</i> , 2013, 56, 1845-1846.	2.9	8
152	Once vs twice-daily abacavir and lamivudine in African children. <i>Aids</i> , 2016, 30, 1761-1770.	1.0	8
153	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
154	Measuring distance through dense weighted networks: The case of hospital-associated pathogens. <i>PLoS Computational Biology</i> , 2017, 13, e1005622.	1.5	8
155	Fecal-Free Toxin Detection Remains the Best Way to Detect <i>Clostridium difficile</i> Infection: Table 1.. <i>Clinical Infectious Diseases</i> , 2015, 61, 1210-1211.	2.9	7
156	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
157	Mapping the medical outcomes study HIV health survey (MOS-HIV) to the EuroQoL 5 Dimension (EQ-5D-3L) utility index. <i>Health and Quality of Life Outcomes</i> , 2019, 17, 83.	1.0	7
158	Fairness of financial penalties to improve control of <i>Clostridium difficile</i> . <i>BMJ: British Medical Journal</i> , 2008, 337, a2097-a2097.	2.4	7
159	Optimised versus standard dosing of vancomycin in infants with Gram-positive sepsis (NeoVanc): a multicentre, randomised, open-label, phase 2b, non-inferiority trial. <i>The Lancet Child and Adolescent Health</i> , 2022, 6, 49-59.	2.7	7
160	Whole blood versus red cell concentrates for children with severe anaemia: a secondary analysis of the Transfusion and Treatment of African Children (TRACT) trial. <i>The Lancet Global Health</i> , 2022, 10, e360-e368.	2.9	7
161	Impact of antibiotic use on patient-level risk of death in 36 million hospital admissions in England. <i>Journal of Infection</i> , 2022, 84, 311-320.	1.7	7
162	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

#	ARTICLE	IF	CITATIONS
163	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant Enterobacteriaceae. PLoS ONE, 2019, 14, e0222831.	1.1	6
164	Mortality risk over time after early fluid resuscitation in African children. Critical Care, 2019, 23, 377.	2.5	6
165	WGS to determine the extent of <i>Clostridioides difficile</i> transmission in a high incidence setting in North Wales in 2015. Journal of Antimicrobial Chemotherapy, 2019, 74, 1092-1100.	1.3	6
166	Transient viral load increases in HIV-infected children in the U.K. and Ireland: what do they mean?. Antiviral Therapy, 2007, 12, 949-56.	0.6	6
167	The impact of viraemia on inflammatory biomarkers and CD4+ cell subpopulations in HIV-infected children in sub-Saharan Africa. Aids, 2021, 35, 1537-1548.	1.0	5
168	Standardising neonatal and paediatric antibiotic clinical trial design and conduct: the PENTA-ID network view. BMJ Open, 2019, 9, e032592.	0.8	4
169	Patient engagement with antibiotic messaging in secondary care: a qualitative feasibility study of the "review and revise" experience. Pilot and Feasibility Studies, 2020, 6, 43.	0.5	4
170	A predictive algorithm for identifying children with sickle cell anemia among children admitted to hospital with severe anemia in Africa. American Journal of Hematology, 2022, 97, 527-536.	2.0	4
171	Combining Charlson and Elixhauser scores with varying lookback predicated mortality better than using individual scores. Journal of Clinical Epidemiology, 2021, 130, 32-41.	2.4	3
172	Public preferences for delayed or immediate antibiotic prescriptions in UK primary care: A choice experiment. PLoS Medicine, 2021, 18, e1003737.	3.9	3
173	Mortality risks associated with empirical antibiotic activity in <i>Escherichia coli</i> bacteraemia: an analysis of electronic health records. Journal of Antimicrobial Chemotherapy, 0, , .	1.3	3
174	Antimicrobial resistance genes and clonal success in <i>Escherichia coli</i> isolates causing bloodstream infection. Lancet Microbe, The, 2021, 2, e492.	3.4	2
175	Antimicrobial resistance in commensal opportunistic pathogens isolated from non-sterile sites can be an effective proxy for surveillance in bloodstream infections. Scientific Reports, 2021, 11, 23359.	1.6	2
176	<i>Clostridium difficile</i> in England: can we stop washing our hands? " Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 478-479.	4.6	1
177	Rifampicin in treating <i>S aureus</i> bacteraemia " Authors' reply. Lancet, The, 2018, 392, 555-556.	6.3	1
178	Using metagenomics to investigate the impact of hospital stay and the ARK intervention on the human gut resistome. Access Microbiology, 2020, 2, .	0.2	1
179	Reply to Mills and Linkin. Clinical Infectious Diseases, 2014, 59, 752-753.	2.9	0
180	<i>Staphylococcus aureus</i> in critical care " Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 580-581.	4.6	0

#	ARTICLE	IF	CITATIONS
181	O03.5â€¦Utility of real-time whole genome sequencing in partner notification and control of neisseria gonorrhoeae infection. , 2019, , .		0
182	Marginal structural models for repeated measures where intercept and slope are correlated: An application exploring the benefit of nutritional supplements on weight gain in HIV-infected children initiating antiretroviral therapy. PLoS ONE, 2020, 15, e0233877.	1.1	0
183	Variable short duration treatment versus standard treatment, with and without adjunctive ribavirin, for chronic hepatitis C: the STOP-HCV-1 non-inferiority, factorial RCT. Efficacy and Mechanism Evaluation, 2021, 8, 1-90.	0.9	0
184	K-mer based prediction of Clostridioides difficile relatedness and ribotypes. Microbial Genomics, 2022, 8, .	1.0	0
185	Title is missing!. , 2019, 14, e0222831.		0
186	Title is missing!. , 2019, 14, e0222831.		0
187	Title is missing!. , 2019, 14, e0222831.		0
188	Title is missing!. , 2019, 14, e0222831.		0