

Ann Sarah Walker

List of Publications by Year in descending order

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Version: 2024-02-01

188
papers

16,491
citations

20817

60
h-index

20961

115
g-index

215
all docs

215
docs citations

215
times ranked

20988
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Changes in paediatric respiratory infections at a UK teaching hospital 2016â€“2021; impact of the SARS-CoV-2 pandemic. <i>Journal of Infection</i> , 2022, 84, 40-47.	3.3	42
4	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.	5.8	20
5	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.	5.6	7
6	Effect of Covid-19 Vaccination on Transmission of Alpha and Delta Variants. <i>New England Journal of Medicine</i> , 2022, 386, 744-756.	27.0	323
7	A predictive algorithm for identifying children with sickle cell anemia among children admitted to hospital with severe anemia in Africa. <i>American Journal of Hematology</i> , 2022, 97, 527-536.	4.1	4
8	Eliciting risk preferences that predict risky health behavior: A comparison of two approaches. <i>Health Economics (United Kingdom)</i> , 2022, 31, 836-858.	1.7	10
9	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
10	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.	6.3	7
11	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.	3.3	7
12	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
13	K-mer based prediction of Clostridioides difficile relatedness and ribotypes. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
14	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, .	6.0	7
15	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
16	Constructing a representative inâ€silico population for paediatric simulations: Application to HIVâ€positive African children. <i>British Journal of Clinical Pharmacology</i> , 2021, 87, 2847-2854.	2.4	15
17	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.	5.0	3
18	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

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19	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.	3.2	9
20	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.	5.8	16
21	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	9.8	24
22	The impact of viraemia on inflammatory biomarkers and CD4+ cell subpopulations in HIV-infected children in sub-Saharan Africa. <i>Aids</i> , 2021, 35, 1537-1548.	2.2	5
23	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	10.3	47
24	Transfusion management of severe anaemia in African children: a consensus algorithm. <i>British Journal of Haematology</i> , 2021, 193, 1247-1259.	2.5	15
25	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
26	Personalised randomised controlled trial designsâ€a new paradigm to define optimal treatments for carbapenem-resistant infections. <i>Lancet Infectious Diseases</i> , The, 2021, 21, e175-e181.	9.1	11
27	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. <i>Nature Medicine</i> , 2021, 27, 1370-1378.	30.7	260
28	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, .	7.0	17
29	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, .	6.0	91
30	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
31	Public preferences for delayed or immediate antibiotic prescriptions in UK primary care: A choice experiment. <i>PLoS Medicine</i> , 2021, 18, e1003737.	8.4	3
32	Flanker: a tool for comparative genomics of gene flanking regions. <i>Microbial Genomics</i> , 2021, 7, .	2.0	12
33	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.	8.2	35
34	Epidemiology of <i>Mycobacterium abscessus</i> in England: an observational study. <i>Lancet Microbe</i> , The, 2021, 2, e498-e507.	7.3	20
35	Antimicrobial resistance genes and clonal success in <i>Escherichia coli</i> isolates causing bloodstream infection. <i>Lancet Microbe</i> , The, 2021, 2, e492.	7.3	2
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	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, .	2.0	20
38	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
39	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021, 12, 6250.	12.8	88
40	Variable short duration treatment versus standard treatment, with and without adjunctive ribavirin, for chronic hepatitis C: the STOP-HCV-1 non-inferiority, factorial RCT. <i>Efficacy and Mechanism Evaluation</i> , 2021, 8, 1-90.	0.7	0
41	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, .	2.0	15
42	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.	3.3	2
43	Tracking the Emergence of SARS-CoV-2 Alpha Variant in the United Kingdom. <i>New England Journal of Medicine</i> , 2021, 385, 2582-2585.	27.0	49
44	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of Mycobacteria Direct from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	14
45	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. <i>PLoS ONE</i> , 2020, 15, e0233877.	2.5	0
46	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.	3.3	15
47	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.	5.5	9
48	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.	0.9	11
49	Risk Factors Associated with Carbapenemase-Producing <i>Enterobacterales</i> (CPE) Positivity in the Hospital Wastewater Environment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	11
50	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, .	3.2	26
51	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.	3.3	15
52	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism calling pipelines. <i>GigaScience</i> , 2020, 9, .	6.4	92
53	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	33
54	Multi-Label Random Forest Model for Tuberculosis Drug Resistance Classification and Mutation Ranking. <i>Frontiers in Microbiology</i> , 2020, 11, 667.	3.5	22

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55	Patient engagement with antibiotic messaging in secondary care: a qualitative feasibility study of the "review and revise"™ experience. <i>Pilot and Feasibility Studies</i> , 2020, 6, 43.	1.2	4
56	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.	5.5	24
57	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
58	Using metagenomics to investigate the impact of hospital stay and the ARK intervention on the human gut resistome. <i>Access Microbiology</i> , 2020, 2, .	0.5	1
59	Genomic surveillance of <i>Escherichia coli</i> and <i>Klebsiella</i> spp. in hospital sink drains and patients. <i>Microbial Genomics</i> , 2020, 6, .	2.0	26
60	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. <i>Microbial Genomics</i> , 2020, 6, .	2.0	14
61	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
62	<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
63	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.	3.3	11
64	Antibiotic Review Kit for Hospitals (ARK-Hospital): study protocol for a stepped-wedge cluster-randomised controlled trial. <i>Trials</i> , 2019, 20, 421.	1.6	7
65	Transfusion Volume for Children with Severe Anemia in Africa. <i>New England Journal of Medicine</i> , 2019, 381, 420-431.	27.0	49
66	Immediate Transfusion in African Children with Uncomplicated Severe Anemia. <i>New England Journal of Medicine</i> , 2019, 381, 407-419.	27.0	64
67	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant Enterobacteriaceae. <i>PLoS ONE</i> , 2019, 14, e0222831.	2.5	6
68	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.	4.0	13
69	"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.	5.5	25
70	Oral versus Intravenous Antibiotics for Bone and Joint Infection. <i>New England Journal of Medicine</i> , 2019, 380, 425-436.	27.0	548
71	Optimising trial designs to identify appropriate antibiotic treatment durations. <i>BMC Medicine</i> , 2019, 17, 115.	5.5	9
72	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.	2.4	7

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73	<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.	6.1	35
74	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	4.1	38
75	<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
76	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.	1.5	13
77	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. <i>MBio</i> , 2019, 10, .	4.1	46
78	The challenge of antimicrobial resistance: What economics can contribute. <i>Science</i> , 2019, 364, .	12.6	292
79	Rapid antiretroviral therapy initiation in low- and middle-income countries: A resource-based approach. <i>PLoS Medicine</i> , 2019, 16, e1002723.	8.4	16
80	O03.5â€¦Utility of real-time whole genome sequencing in partner notification and control of <i>Neisseria gonorrhoeae</i> infection. , 2019, , .		0
81	Standardising neonatal and paediatric antibiotic clinical trial design and conduct: the PENTA-ID network view. <i>BMJ Open</i> , 2019, 9, e032592.	1.9	4
82	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
83	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	3.9	121
84	Mortality risk over time after early fluid resuscitation in African children. <i>Critical Care</i> , 2019, 23, 377.	5.8	6
85	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.	3.0	6
86	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
87	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	4.1	71
88	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	171
89	Oral versus intravenous antibiotics for bone and joint infections: the OVIVA non-inferiority RCT. <i>Health Technology Assessment</i> , 2019, 23, 1-92.	2.8	27
90	Title is missing!. , 2019, 14, e0222831.		0

#	ARTICLE	IF	CITATIONS
91	Title is missing!. , 2019, 14, e0222831.		0
92	Title is missing!. , 2019, 14, e0222831.		0
93	Title is missing!. , 2019, 14, e0222831.		0
94	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.	4.7	22
95	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
96	Patient and Strain Characteristics Associated With <i>Clostridium difficile</i> Transmission and Adverse Outcomes. <i>Clinical Infectious Diseases</i> , 2018, 67, 1379-1387.	5.8	24
97	Robust Prediction of Resistance to Trimethoprim in <i>Staphylococcus aureus</i> . <i>Cell Chemical Biology</i> , 2018, 25, 339-349.e4.	5.2	32
98	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018, 34, 1666-1671.	4.1	100
99	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.	5.8	68
100	Adjunctive rifampicin for <i>Staphylococcus aureus</i> bacteraemia (ARREST): a multicentre, randomised, double-blind, placebo-controlled trial. <i>Lancet</i> , 2018, 391, 668-678.	13.7	140
101	Evaluating Safety Reporting in Paediatric Antibiotic Trials, 2000-2016: A Systematic Review and Meta-Analysis. <i>Drugs</i> , 2018, 78, 231-244.	10.9	12
102	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, .	2.0	33
103	Raltegravir-intensified initial antiretroviral therapy in advanced HIV disease in Africa: A randomised controlled trial. <i>PLoS Medicine</i> , 2018, 15, e1002706.	8.4	28
104	Rifampicin in treating <i>S aureus</i> bacteraemia - Authors' reply. <i>Lancet</i> , 2018, 392, 555-556.	13.7	1
105	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
106	Identifying Mixed <i>Mycobacterium tuberculosis</i> Infection and Laboratory Cross-Contamination during <i>Mycobacterial</i> Sequencing Programs. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	16
107	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.	3.3	48
108	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.	5.8	26

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109	Trends over time in Escherichia coli bloodstream infections, urinary tract infections, and antibiotic susceptibilities in Oxfordshire, UK, 1998â€“2016: a study of electronic health records. Lancet Infectious Diseases, The, 2018, 18, 1138-1149.	9.1	121
110	Control of Artfactual Variation in Reported Intersample Relatedness during Clinical Use of a Mycobacterium tuberculosis Sequencing Pipeline. Journal of Clinical Microbiology, 2018, 56, .	3.9	10
111	Overview of systematic reviews assessing the evidence for shorter versus longer duration antibiotic treatment for bacterial infections in secondary care. PLoS ONE, 2018, 13, e0194858.	2.5	18
112	Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from Staphylococcus aureus Whole-Genome Sequences. Journal of Clinical Microbiology, 2018, 56, .	3.9	61
113	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. Eurosurveillance, 2018, 23, .	7.0	33
114	Adjunctive rifampicin to reduce early mortality from Staphylococcus aureus bacteraemia: the ARREST RCT. Health Technology Assessment, 2018, 22, 1-148.	2.8	10
115	Effects of control interventions on Clostridium difficile infection in England: an observational study. Lancet Infectious Diseases, The, 2017, 17, 411-421.	9.1	269
116	Same-Day Diagnostic and Surveillance Data for Tuberculosis via Whole-Genome Sequencing of Direct Respiratory Samples. Journal of Clinical Microbiology, 2017, 55, 1285-1298.	3.9	315
117	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. Lancet HIV,the, 2017, 4, e341-e348.	4.7	71
118	Mortality risks associated with emergency admissions during weekends and public holidays: an analysis of electronic health records. Lancet, The, 2017, 390, 62-72.	13.7	114
119	The relative importance of large problems far away versus small problems closer to home: insights into limiting the spread of antimicrobial resistance in England. BMC Medicine, 2017, 15, 86.	5.5	30
120	Clostridium difficile in England: can we stop washing our hands? â€œ Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 478-479.	9.1	1
121	Contribution to Clostridium Difficile Transmission of Symptomatic Patients With Toxigenic Strains Who Are Fecal Toxin Negative. Clinical Infectious Diseases, 2017, 64, 1163-1170.	5.8	45
122	Staphylococcus aureus in critical care â€œ Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 580-581.	9.1	0
123	The Hospital Water Environment as a Reservoir for Carbapenem-Resistant Organisms Causing Hospital-Acquired Infectionsâ€”A Systematic Review of the Literature. Clinical Infectious Diseases, 2017, 64, 1435-1444.	5.8	242
124	WGS to predict antibiotic MICs for Neisseria gonorrhoeae. Journal of Antimicrobial Chemotherapy, 2017, 72, 1937-1947.	3.0	169
125	Ordering the mob: Insights into replicon and MOB typing schemes from analysis of a curated dataset of publicly available plasmids. Plasmid, 2017, 91, 42-52.	1.4	89
126	Chromosomal Integration of the Klebsiella pneumoniae Carbapenemase Gene, <i>bla</i>_{KPC}, in Klebsiella Species Is Elusive but Not Rare. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	46

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127	Enhanced Prophylaxis plus Antiretroviral Therapy for Advanced HIV Infection in Africa. <i>New England Journal of Medicine</i> , 2017, 377, 233-245.	27.0	156
128	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
129	The antibiotic course has had its day. <i>BMJ: British Medical Journal</i> , 2017, 358, j3418.	2.3	192
130	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
131	Severity of illness and the weekend effect – Authors' reply. <i>Lancet, The</i> , 2017, 390, 1735.	13.7	11
132	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, The</i> , 2017, 17, 207-214.	9.1	155
133	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
134	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	6.0	93
135	Measuring distance through dense weighted networks: The case of hospital-associated pathogens. <i>PLoS Computational Biology</i> , 2017, 13, e1005622.	3.2	8
136	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.	8.4	22
137	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
138	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
139	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases, The</i> , 2016, 16, 1295-1303.	9.1	149
140	Once vs twice-daily abacavir and lamivudine in African children. <i>Aids</i> , 2016, 30, 1761-1770.	2.2	8
141	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	13.3	247
142	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
143	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.	1.9	8
144	Acceptability of lopinavir/r pellets (minitabs), tablets and syrups in HIV-infected children. <i>Antiviral Therapy</i> , 2016, 21, 579-585.	1.0	32

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145	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene <i>bla</i> _{KPC} . Antimicrobial Agents and Chemotherapy, 2016, 60, 3767-3778.	3.2	255
146	Abacavir, zidovudine, or stavudine as paediatric tablets for African HIV-infected children (CHAPAS-3): an open-label, parallel-group, randomised controlled trial. Lancet Infectious Diseases, The, 2016, 16, 169-179.	9.1	33
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