Derrick W Crook

List of Publications by Year
in descending order

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	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. Clinical Infectious Diseases, 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. Clinical Infectious Diseases, 2022, 74, 1208-1219.	5.8	64
3	Whole-genome sequencing for surveillance of tuberculosis drug resistance and determination of resistance level in China. Clinical Microbiology and Infection, 2022, 28, 731.e9-731.e15.	6.0	25
4	Changes in paediatric respiratory infections at a UK teaching hospital 2016â€"2021; impact of the SARS-CoV-2 pandemic. Journal of Infection, 2022, 84, 40-47.	3.3	42
5	Symptoms and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Positivity in the General Population in the United Kingdom. Clinical Infectious Diseases, 2022, 75, e329-e337.	5.8	20
6	Time of Day of Vaccination Affects SARS-CoV-2 Antibody Responses in an Observational Study of Health Care Workers. Journal of Biological Rhythms, 2022, 37, 124-129.	2.6	42
7	Reduced neutralisation of SARS-CoV-2 omicron B.1.1.529 variant by post-immunisation serum. Lancet, The, 2022, 399, 234-236.	13.7	318
8	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. Cell, 2022, 185, 467-484.e15.	28.9	788
9	Antibody responses and correlates of protection in the general population after two doses of the ChAdOx1 or BNT162b2 vaccines. Nature Medicine, 2022, 28, 1072-1082.	30.7	147
10	Identifying Bacterial Airways Infection in Stable Severe Asthma Using Oxford Nanopore Sequencing Technologies. Microbiology Spectrum, 2022, 10, e0227921.	3.0	5
11	Clinical Metagenomic Sequencing for Species Identification and Antimicrobial Resistance Prediction in Orthopedic Device Infection. Journal of Clinical Microbiology, 2022, 60, e0215621.	3.9	18
12	The bacteriology of pleural infection (TORPIDS): an exploratory metagenomics analysis through next generation sequencing. Lancet Microbe, The, 2022, 3, e294-e302.	7.3	22
13	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. Lancet Microbe, The, 2022, 3, e265-e273.	7.3	114
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. ELife, 2022, 11, .	6.0	7
15	Potent cross-reactive antibodies following Omicron breakthrough in vaccinees. Cell, 2022, 185, 2116-2131.e18.	28.9	105
16	Whole genome sequencing reveals hidden transmission of carbapenemase-producing Enterobacterales. Nature Communications, 2022, 13, .	12.8	16
17	Antibody escape of SARS-CoV-2 Omicron BA.4 and BA.5 from vaccine and BA.1 serum. Cell, 2022, 185, 2422-2433.e13.	28.9	532
18	Catwalk: identifying closely related sequences in large microbial sequence databases. Microbial Genomics, 2022, 8, .	2.0	0

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19	SARS-CoV-2 antibody trajectories after a single COVID-19 vaccination with and without prior infection. Nature Communications, 2022, 13, .	12.8	6
20	Antibody Status and Incidence of SARS-CoV-2 Infection in Health Care Workers. New England Journal of Medicine, 2021, 384, 533-540.	27.0	803
21	Combining Charlson and Elixhauser scores with varying lookback predicated mortality better than using individual scores. Journal of Clinical Epidemiology, 2021, 130, 32-41.	5.0	3
22	Community prevalence of SARS-CoV-2 in England from April to November, 2020: results from the ONS Coronavirus Infection Survey. Lancet Public Health, The, 2021, 6, e30-e38.	10.0	147
23	Ten Years of Population-Level Genomic <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Serotype Surveillance Informs Vaccine Development for Invasive Infections. Clinical Infectious Diseases, 2021, 73, 2276-2282.	5.8	16
24	Stringent thresholds in SARS-CoV-2 IgG assays lead to under-detection of mild infections. BMC Infectious Diseases, 2021, 21, 187.	2.9	23
25	Preferences for Medical Consultations from Online Providers: Evidence from a Discrete Choice Experiment in the United Kingdom. Applied Health Economics and Health Policy, 2021, 19, 521-535.	2.1	12
26	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. Nature Communications, 2021, 12, 1951.	12.8	54
27	Genomic network analysis of environmental and livestock F-type plasmid populations. ISME Journal, 2021, 15, 2322-2335.	9.8	24
28	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. Cell, 2021, 184, 2348-2361.e6.	28.9	936
29	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. Science Advances, 2021, 7, .	10.3	47
30	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. Cell, 2021, 184, 2201-2211.e7.	28.9	442
31	Antibody evasion by the P.1 strain of SARS-CoV-2. Cell, 2021, 184, 2939-2954.e9.	28.9	519
32	Diagnosis of SARS-CoV-2 Infection with LamPORE, a High-Throughput Platform Combining Loop-Mediated Isothermal Amplification and Nanopore Sequencing. Journal of Clinical Microbiology, 2021, 59, .	3.9	30
33	Quantitative SARS-CoV-2 anti-spike responses to Pfizerâ€"BioNTech and Oxfordâ€"AstraZeneca vaccines by previous infection status. Clinical Microbiology and Infection, 2021, 27, 1516.e7-1516.e14.	6.0	100
34	Population-level faecal metagenomic profiling as a tool to predict antimicrobial resistance in Enterobacterales isolates causing invasive infections: An exploratory study across Cambodia, Kenya, and the UK. EClinicalMedicine, 2021, 36, 100910.	7.1	10
35	COVID-19: Rapid antigen detection for SARS-CoV-2 by lateral flow assay: A national systematic evaluation of sensitivity and specificity for mass-testing. EClinicalMedicine, 2021, 36, 100924.	7.1	162
36	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. Nature Medicine, 2021, 27, 1370-1378.	30.7	260

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37	Nanopore metagenomic sequencing of influenza virus directly from respiratory samples: diagnosis, drug resistance and nosocomial transmission, United Kingdom, 2018/19 influenza season. Eurosurveillance, 2021, 26, .	7.0	17
38	Antibody responses to SARS-CoV-2 vaccines in 45,965 adults from the general population of the United Kingdom. Nature Microbiology, 2021, 6, 1140-1149.	13.3	254
39	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. Cell, 2021, 184, 4220-4236.e13.	28.9	630
40	An end-to-end heterogeneous graph attention network for <i>Mycobacterium tuberculosis</i> drug-resistance prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	7
41	Flanker: a tool for comparative genomics of gene flanking regions. Microbial Genomics, 2021, 7, .	2.0	12
42	Ten-year longitudinal molecular epidemiology study of Escherichia coli and Klebsiella species bloodstream infections in Oxfordshire, UK. Genome Medicine, 2021, 13, 144.	8.2	35
43	Human and Porcine Transmission of <i>Clostridioides difficile</i> Ribotype 078, Europe. Emerging Infectious Diseases, 2021, 27, 2294-2300.	4.3	12
44	Undetected carriage explains apparent Staphylococcus aureus acquisition in a non-outbreak healthcare setting. Journal of Infection, 2021, 83, 332-338.	3.3	2
45	Epidemiology of Mycobacterium abscessus in England: an observational study. Lancet Microbe, The, 2021, 2, e498-e507.	7.3	20
46	Antimicrobial resistance genes and clonal success in Escherichia coli isolates causing bloodstream infection. Lancet Microbe, The, 2021, 2, e492.	7.3	2
47	Viral detection and identification in 20 min by rapid single-particle fluorescence in-situ hybridization of viral RNA. Scientific Reports, 2021, 11, 19579.	3.3	16
48	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. Journal of Infection, 2021, 83, 473-482.	3.3	55
49	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. Clinical Infectious Diseases, 2021, 73, e699-e709.	5.8	235
50	A genomic epidemiological study shows that prevalence of antimicrobial resistance in Enterobacterales is associated with the livestock host, as well as antimicrobial usage. Microbial Genomics, 2021, 7, .	2.0	20
51	Effect of Delta variant on viral burden and vaccine effectiveness against new SARS-CoV-2 infections in the UK. Nature Medicine, 2021, 27, 2127-2135.	30.7	450
52	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. Nature Communications, 2021, 12, 6250.	12.8	88
53	Antimicrobial resistance determinants are associated with Staphylococcus aureus bacteraemia and adaptation to the healthcare environment: a bacterial genome-wide association study. Microbial Genomics, 2021, 7, .	2.0	15
54	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.	3.3	2

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55	Relationship between microbiology of throat swab and clinical course among primary care patients with acute cough: a prospective cohort study. Family Practice, 2020, 37, 332-339.	1.9	10
56	Awareness of Appropriate Antibiotic Use in Primary Care for Influenza-Like Illness: Evidence of Improvement from UK Population-Based Surveys. Antibiotics, 2020, 9, 690.	3.7	3
57	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of Mycobacteria Direct from Clinical Samples. Journal of Clinical Microbiology, 2020, 58, .	3.9	14
58	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. Viruses, 2020, 12, 1164.	3.3	51
59	Evaluation of methods for detecting human reads in microbial sequencing datasets. Microbial Genomics, 2020, 6, .	2.0	11
60	High precision *Neisseria gonorrhoeae* variant and antimicrobial resistance calling from metagenomic Nanopore sequencing. Genome Research, 2020, 30, 1354-1363.	5.5	27
61	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. Lancet Infectious Diseases, The, 2020, 20, 1390-1400.	9.1	336
62	Assessing a novel, lab-free, point-of-care test for SARS-CoV-2 (CovidNudge): a diagnostic accuracy study. Lancet Microbe, The, 2020, 1, e300-e307.	7.3	92
63	Risk Factors Associated with Carbapenemase-Producing *Enterobacterales* (CPE) Positivity in the Hospital Wastewater Environment. Applied and Environmental Microbiology, 2020, 86, .	3.1	11
64	The importance of using whole genome sequencing and extended spectrum beta-lactamase selective media when monitoring antimicrobial resistance. Scientific Reports, 2020, 10, 19880.	3.3	27
65	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne *bla* $_{KPC}$ Carbapenemase in *Enterobacterales* in the United Kingdom from 2009 to 2014. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	26
66	GenomegaMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. Molecular Biology and Evolution, 2020, 37, 2450-2460.	8.9	25
67	Nanopore metagenomic sequencing to investigate nosocomial transmission of human metapneumovirus from a unique genetic group among haematology patients in the United Kingdom. Journal of Infection, 2020, 80, 571-577.	3.3	15
68	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphismâ€"calling pipelines. GigaScience, 2020, 9, .	6.4	92
69	Optimizing DNA Extraction Methods for Nanopore Sequencing of Neisseria gonorrhoeae Directly from Urine Samples. Journal of Clinical Microbiology, 2020, 58, .	3.9	33
70	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in *Escherichia coli*. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	33
71	Multi-Label Random Forest Model for Tuberculosis Drug Resistance Classification and Mutation Ranking. Frontiers in Microbiology, 2020, 11, 667.	3.5	22
72	Reducing expectations for antibiotics in primary care: a randomised experiment to test the response to fear-based messages about antimicrobial resistance. BMC Medicine, 2020, 18, 110.	5.5	24

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73	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. BMC Medicine, 2020, 18, 84.	5.5	39
74	NanoSPC: a scalable, portable, cloud compatible viral nanopore metagenomic data processing pipeline. Nucleic Acids Research, 2020, 48, W366-W371.	14.5	14
75	Genomic surveillance of Escherichia coli and Klebsiella spp. in hospital sink drains and patients. Microbial Genomics, 2020, 6, .	2.0	26
76	Dynamic linkage of COVID-19 test results between Public Health Englandâ€™s Second Generation Surveillance System and UK Biobank. Microbial Genomics, 2020, 6, .	2.0	120
77	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. Microbial Genomics, 2020, 6, .	2.0	14
78	Antibody testing for COVID-19: A report from theÂNational COVID Scientific Advisory Panel. Wellcome Open Research, 2020, 5, 139.	1.8	179
79	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	1.8	81
80	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. Wellcome Open Research, 2020, 5, 181.	1.8	122
81	SARS-CoV-2 antibody prevalence, titres and neutralising activity in an antenatal cohort, United Kingdom, 14 April to 15 June 2020. Eurosurveillance, 2020, 25, .	7.0	17
82	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. ELife, 2020, 9, .	6.0	196
83	Case Report: Disseminated, rifampicin resistant Mycobacterium bovis (BCG) infection in an immunocompromised child. Wellcome Open Research, 2020, 5, 242.	1.8	0
84	Comparative genomics of Clostridioides difficile toxinotypes identifies module-based toxin gene evolution. Microbial Genomics, 2020, 6, .	2.0	8
85	*Clostridium difficile*: Investigating Transmission Patterns Between Infected and Colonized Patients Using Whole Genome Sequencing. Clinical Infectious Diseases, 2019, 68, 204-209.	5.8	55
86	Antibiotic Review Kit for Hospitals (ARK-Hospital): study protocol for a stepped-wedge cluster-randomised controlled trial. Trials, 2019, 20, 421.	1.6	7
87	The Role of *fosA* in Challenges with Fosfomycin Susceptibility Testing of Multispecies Klebsiella pneumoniae Carbapenemase-Producing Clinical Isolates. Journal of Clinical Microbiology, 2019, 57, .	3.9	26
88	Using hospital network-based surveillance for antimicrobial resistance as a more robust alternative to self-reporting. PLoS ONE, 2019, 14, e0219994.	2.5	3
89	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.	2.5	6
90	â€˜Caveat emptorâ€™: the cautionary tale of endocarditis and the potential pitfalls of clinical coding dataâ€"an electronic health records study. BMC Medicine, 2019, 17, 169.	5.5	25

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91	Scalable Pathogen Pipeline Platform (SP^3): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing. , 2019, , .		1
92	Improved Performance Predicting Clarithromycin Resistance in *Mycobacterium abscessus* on an Independent Data Set. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	8
93	Clostridium difficile trehalose metabolism variants are common and not associated with adverse patient outcomes when variably present in the same lineage. EBioMedicine, 2019, 43, 347-355.	6.1	35
94	DeepAMR for predicting co-occurrent resistance of *Mycobacterium tuberculosis*. Bioinformatics, 2019, 35, 3240-3249.	4.1	38
95	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus Staphylococcus Rosenbach 1884. Microbiology Resource Announcements, 2019, 8, .	0.6	7
96	*Klebsiella quasipneumoniae* Provides a Window into Carbapenemase Gene Transfer, Plasmid Rearrangements, and Patient Interactions with the Hospital Environment. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	44
97	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated *Clostridium difficile* PCR Ribotype 078. MBio, 2019, 10, .	4.1	46
98	Don't overlook the little guy: An evaluation of the frequency of small plasmids co-conjugating with larger carbapenemase gene containing plasmids. Plasmid, 2019, 103, 1-8.	1.4	36
99	SNP-IT Tool for Identifying Subspecies and Associated Lineages of *Mycobacterium tuberculosis* Complex. Emerging Infectious Diseases, 2019, 25, 482-488.	4.3	64
100	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. Environmental Microbiomes, 2019, 14, 7.	5.0	69
101	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. Journal of Clinical Microbiology, 2019, 58, .	3.9	121
102	Hash-Based Core Genome Multilocus Sequence Typing for Clostridium difficile. Journal of Clinical Microbiology, 2019, 58, .	3.9	16
103	WGS to determine the extent of *Clostridioides difficile* transmission in a high incidence setting in North Wales in 2015. Journal of Antimicrobial Chemotherapy, 2019, 74, 1092-1100.	3.0	6
104	Carbapenem-resistant Enterobacteriaceae dispersal from sinks is linked to drain position and drainage ratesÂin a laboratory model system. Journal of Hospital Infection, 2019, 102, 63-69.	2.9	46
105	Whole-Genome Sequencing for Predicting Clarithromycin Resistance in *Mycobacterium abscessus*. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	34
106	Application of machine learning techniques to tuberculosis drug resistance analysis. Bioinformatics, 2019, 35, 2276-2282.	4.1	71
107	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. Microbial Genomics, 2019, 5, .	2.0	171
108	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	1.8	103

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109	Panton–Valentine leucocidin is the key determinant of Staphylococcus aureus pyomyositis in a bacterial GWAS. ELife, 2019, 8, .	6.0	56
110	Title is missing!. , 2019, 14, e0222831.		0
111	Title is missing!. , 2019, 14, e0222831.		0
112	Title is missing!. , 2019, 14, e0222831.		0
113	Title is missing!. , 2019, 14, e0222831.		0
114	Two Distinct Patterns of Clostridium difficile Diversity Across Europe Indicating Contrasting Routes of Spread. Clinical Infectious Diseases, 2018, 67, 1035-1044.	5.8	60
115	Patient and Strain Characteristics Associated With Clostridium difficile Transmission and Adverse Outcomes. Clinical Infectious Diseases, 2018, 67, 1379-1387.	5.8	24
116	Intensive Care Unit Wastewater Interventions to Prevent Transmission of Multispecies Klebsiella pneumoniae Carbapenemase–Producing Organisms. Clinical Infectious Diseases, 2018, 67, 171-178.	5.8	74
117	Robust Prediction of Resistance to Trimethoprim in Staphylococcus aureus. Cell Chemical Biology, 2018, 25, 339-349.e4.	5.2	32
118	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. Bioinformatics, 2018, 34, 1666-1671.	4.1	100
119	High Rates of Human Fecal Carriage of mcr-1–Positive Multidrug-Resistant Enterobacteriaceae Emerge in China in Association With Successful Plasmid Families. Clinical Infectious Diseases, 2018, 66, 676-685.	5.8	68
120	TETyper: a bioinformatic pipeline for classifying variation and genetic contexts of transposable elements from short-read whole-genome sequencing data. Microbial Genomics, 2018, 4, .	2.0	33
121	Gonorrhoea treatment failure caused by a Neisseria gonorrhoeae strain with combined ceftriaxone and high-level azithromycin resistance, England, February 2018. Eurosurveillance, 2018, 23, .	7.0	255
122	Using linked electronic health records to report healthcare-associated infections. PLoS ONE, 2018, 13, e0206860.	2.5	3
123	An Open-Source Azure Solution for Scalable Genomics Workflows. , 2018, , .		2
124	DNA extraction from primary liquid blood cultures for bloodstream infection diagnosis using whole genome sequencing. Journal of Medical Microbiology, 2018, 67, 347-357.	1.8	40
125	Detection of Viral Pathogens With Multiplex Nanopore MinION Sequencing: Be Careful With Cross-Talk. Frontiers in Microbiology, 2018, 9, 2225.	3.5	75
126	Real-time analysis of nanopore-based metagenomic sequencing from infected orthopaedic devices. BMC Genomics, 2018, 19, 714.	2.8	128

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127	A *Candida auris* Outbreak and Its Control in an Intensive Care Setting. New England Journal of Medicine, 2018, 379, 1322-1331.	27.0	318
128	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. New England Journal of Medicine, 2018, 379, 1403-1415.	27.0	405
129	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. Scientific Reports, 2018, 8, 15382.	3.3	75
130	Identifying Mixed Mycobacterium tuberculosis Infection and Laboratory Cross-Contamination during Mycobacterial Sequencing Programs. Journal of Clinical Microbiology, 2018, 56, .	3.9	16
131	Validating a 14-Drug Microtiter Plate Containing Bedaquiline and Delamanid for Large-Scale Research Susceptibility Testing of Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	62
132	Identification of Biomarkers for Differentiation of Hypervirulent Klebsiella pneumoniae from Classical K. pneumoniae. Journal of Clinical Microbiology, 2018, 56, .	3.9	378
133	A Quantitative Evaluation of MIRU-VNTR Typing Against Whole-Genome Sequencing for Identifying Mycobacterium tuberculosis Transmission: A Prospective Observational Cohort Study. EBioMedicine, 2018, 34, 122-130.	6.1	65
134	The use of whole-genome sequencing inÂcluster investigation of a multidrug-resistant tuberculosis outbreak. European Respiratory Journal, 2018, 51, 1702313.	6.7	36
135	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
136	Control of Artifactual Variation in Reported Intersample Relatedness during Clinical Use of a Mycobacterium tuberculosis Sequencing Pipeline. Journal of Clinical Microbiology, 2018, 56, .	3.9	10
137	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis. Microbiology (United Kingdom), 2018, 164, 1522-1530.	1.8	21
138	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. Journal of Clinical Microbiology, 2018, 56, .	3.9	72
139	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
140	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
141	Some Synonymous and Nonsynonymous *gyrA* Mutations in Mycobacterium tuberculosis Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR *sl* Assays. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	29
142	Effects of control interventions on Clostridium difficile infection in England: an observational study. Lancet Infectious Diseases, The, 2017, 17, 411-421.	9.1	269
143	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
144	Tuberculosis is changing. Lancet Infectious Diseases, The, 2017, 17, 359-361.	9.1	49

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145	Re-emergence of methicillin susceptibility in a resistant lineage ofStaphylococcus aureus. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw570.	3.0	22
146	Molecular Diagnosis of Orthopedic-Device-Related Infection Directly from Sonication Fluid by Metagenomic Sequencing. Journal of Clinical Microbiology, 2017, 55, 2334-2347.	3.9	174
147	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
148	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
149	Clostridium difficile in England: can we stop washing our hands? â€" Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 478-479.	9.1	1
150	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
151	Staphylococcus aureus in critical care â€" Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 580-581.	9.1	0
152	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
153	WGS to predict antibiotic MICs for Neisseria gonorrhoeae. Journal of Antimicrobial Chemotherapy, 2017, 72, 1937-1947.	3.0	169
154	Enhanced Klebsiella pneumoniae Carbapenemase Expression from a Novel Tn *4401* Deletion. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	64
155	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
156	Chromosomal Integration of the Klebsiella pneumoniae Carbapenemase Gene, *bla*$_{KPC}$, in Klebsiella Species Is Elusive but Not Rare. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	46
157	Aiming for zero tuberculosis transmission in low-burden countries. Lancet Respiratory Medicine,the, 2017, 5, 846-848.	10.7	13
158	mcr-1 and mcr-2 (mcr-6.1) variant genes identified in Moraxella species isolated from pigs in Great Britain from 2014 to 2015. Journal of Antimicrobial Chemotherapy, 2017, 72, 2745-2749.	3.0	252
159	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. Lancet Infectious Diseases, The, 2017, 17, 1033-1041.	9.1	198
160	A curated dataset of complete Enterobacteriaceae plasmids compiled from the NCBI nucleotide database. Data in Brief, 2017, 12, 423-426.	1.0	58
161	Covert dissemination of carbapenemase-producing Klebsiella pneumoniae (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission. Journal of Antimicrobial Chemotherapy, 2017, 72, 3025-3034.	3.0	73
162	Developing an antimicrobial resistance reference laboratory and surveillance programme in Vietnam. The Lancet Global Health, 2017, 5, e1186-e1187.	6.3	19

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163	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. Lancet Infectious Diseases, The, 2017, 17, 207-214.	9.1	155
164	A standardised method for interpreting the association between mutations and phenotypic drug resistance in *Mycobacterium tuberculosis*. European Respiratory Journal, 2017, 50, 1701354.	6.7	273
165	Plasmid Classification in an Era of Whole-Genome Sequencing: Application in Studies of Antibiotic Resistance Epidemiology. Frontiers in Microbiology, 2017, 8, 182.	3.5	191
166	Severe infections emerge from commensal bacteria by adaptive evolution. ELife, 2017, 6, .	6.0	93
167	BugMat and FindNeighbour: command line and server applications for investigating bacterial relatedness. BMC Bioinformatics, 2017, 18, 477.	2.6	16
168	Resolving plasmid structures in Enterobacteriaceae using the MinION nanopore sequencer: assessment of MinION and MinION/Illumina hybrid data assembly approaches. Microbial Genomics, 2017, 3, e000118.	2.0	74
169	Comparison of Control of Clostridium difficile Infection in Six English Hospitals Using Whole-Genome Sequencing. Clinical Infectious Diseases, 2017, 65, 433-441.	5.8	40
170	Epidemiology of Clostridium difficile in infants in Oxfordshire, UK: Risk factors for colonization and carriage, and genetic overlap with regional C. difficile infection strains. PLoS ONE, 2017, 12, e0182307.	2.5	82
171	Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae : an observational study. Lancet Infectious Diseases, The, 2016, 16, 1295-1303.	9.1	149
172	The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant Staphylococcus aureus. MBio, 2016, 7, e02039-15.	4.1	90
173	Occurrence and characterization of mcr-1-harbouring Escherichia coli isolated from pigs in Great Britain from 2013 to 2015. Journal of Antimicrobial Chemotherapy, 2016, 72, dkw477.	3.0	49
174	Natural mutations in a *Staphylococcus aureus* virulence regulator attenuate cytotoxicity but permit bacteremia and abscess formation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3101-10.	7.1	103
175	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. Applied and Environmental Microbiology, 2016, 82, 2516-2526.	3.1	105
176	Complete Sequencing of Plasmids Containing *bla*$_{OXA-163}$ and *bla*$_{OXA-48}$ in Escherichia coli Sequence Type 131. Antimicrobial Agents and Chemotherapy, 2016, 60, 6948-6951.	3.2	19
177	First Report of *bla*$_{IMP-14}$ on a Plasmid Harboring Multiple Drug Resistance Genes in Escherichia coli Sequence Type 131. Antimicrobial Agents and Chemotherapy, 2016, 60, 5068-5071.	3.2	15
178	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. Nature Microbiology, 2016, 1, 16041.	13.3	247
179	Maternal colonization with Streptococcus agalactiae and associated stillbirth and neonatal disease in coastal Kenya. Nature Microbiology, 2016, 1, 16067.	13.3	91
180	Antibiotic use and clinical outcomes in the acute setting under management by an infectious diseases acute physician versus other clinical teams: a cohort study. BMJ Open, 2016, 6, e010969.	1.9	8

#	Article	IF	Citations
181	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene *bla*~KPC~. Antimicrobial Agents and Chemotherapy, 2016, 60, 3767-3778.	3.2	255
182	Within-host evolution of bacterial pathogens. Nature Reviews Microbiology, 2016, 14, 150-162.	28.6	373
183	Colistin resistance gene mcr-1 and pHNSHP45 plasmid in human isolates of Escherichia coli and Klebsiella pneumoniae. Lancet Infectious Diseases, The, 2016, 16, 285-286.	9.1	119
184	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. Lancet Respiratory Medicine,the, 2016, 4, 49-58.	10.7	282
185	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	4.1	289
186	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998–2014. Thorax, 2016, 71, 535-542.	5.6	80
187	Complete Genome Sequence of KPC-Producing Klebsiella pneumoniae Strain CAV1193. Genome Announcements, 2016, 4, .	0.8	20
188	Capsular Typing Method for Streptococcus agalactiae Using Whole-Genome Sequence Data. Journal of Clinical Microbiology, 2016, 54, 1388-1390.	3.9	35
189	Effects of proton pump inhibitors and histamine-2 receptor antagonists on response to fidaxomicin or vancomycin in patients withClostridium difficile-associated diarrhoea. BMJ Open Gastroenterology, 2015, 2, e000028.	2.7	18
190	Rare Variants in MYD88, IRAK4 and IKBKG and Susceptibility to Invasive Pneumococcal Disease: A Population-Based Case-Control Study. PLoS ONE, 2015, 10, e0123532.	2.5	8
191	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. PLoS Biology, 2015, 13, e1002229.	5.6	120
192	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. Nature Communications, 2015, 6, 10063.	12.8	479
193	Klebsiella pneumoniae Carbapenemase (KPC)-Producing K. pneumoniae at a Single Institution: Insights into Endemicity from Whole-Genome Sequencing. Antimicrobial Agents and Chemotherapy, 2015, 59, 1656-1663.	3.2	140
194	Colonization with Enterobacteriaceae producing ESBLs in children attending pre-school childcare facilities in the Lao People's Democratic Republic. Journal of Antimicrobial Chemotherapy, 2015, 70, 1893-1897.	3.0	62
195	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 1193-1202.	9.1	553
196	Mycobacterial DNA Extraction for Whole-Genome Sequencing from Early Positive Liquid (MGIT) Cultures. Journal of Clinical Microbiology, 2015, 53, 1137-1143.	3.9	90
197	Multidrug-resistant Escherichia coli soft tissue infection investigated with bacterial whole genome sequencing. BMJ Case Reports, 2014, 2014, bcr2014207200-bcr2014207200.	0.5	4
198	Reply to Mills and Linkin. Clinical Infectious Diseases, 2014, 59, 752-753.	5.8	0

#	ARTICLE	IF	CITATIONS
199	Reduction of Invasive Pneumococcal Disease 3 Years After the Introduction of the 13-Valent Conjugate Vaccine in the Oxfordshire Region of England. Journal of Infectious Diseases, 2014, 210, 1001-1011.	4.0	83
200	Mobile elements drive recombination hotspots in the core genome of Staphylococcus aureus. Nature Communications, 2014, 5, 3956.	12.8	128
201	Whole-Genome Sequencing Shows That Patient-to-Patient Transmission Rarely Accounts for Acquisition of Staphylococcus aureus in an Intensive Care Unit. Clinical Infectious Diseases, 2014, 58, 609-618.	5.8	142
202	The Complexity and Diversity of the Pathogenicity Locus in Clostridium difficile Clade 5. Genome Biology and Evolution, 2014, 6, 3159-3170.	2.5	31
203	Evolutionary History of the Clostridium difficile Pathogenicity Locus. Genome Biology and Evolution, 2014, 6, 36-52.	2.5	190
204	Assessment of Mycobacterium tuberculosis transmission in Oxfordshire, UK, 2007â€"12, with whole pathogen genome sequences: an observational study. Lancet Respiratory Medicine,the, 2014, 2, 285-292.	10.7	199
205	Dynamics of acquisition and loss of carriage of Staphylococcus aureus strains in the community: The effect of clonal complex. Journal of Infection, 2014, 68, 426-439.	3.3	42
206	Machine learning for the prediction of antibacterial susceptibility in Mycobacterium tuberculosis. , 2014, , .		29
207	Prevalence of Staphylococcus aureus protein A (spa) mutants in the community and hospitals in Oxfordshire. BMC Microbiology, 2014, 14, 63.	3.3	72
208	Can rapid integrated polymerase chain reaction-based diagnostics for gastrointestinal pathogens improve routine hospital infection control practice? A diagnostic study. Health Technology Assessment, 2014, 18, 1-167.	2.8	19
209	Differences in outcome according to Clostridium difficile testing method: a prospective multicentre diagnostic validation study of C difficile infection. Lancet Infectious Diseases, The, 2013, 13, 936-945.	9.1	405
210	Diverse Sources of C. difficile Infection Identified on Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 1195-1205.	27.0	595
211	Whole-genome sequencing to delineate Mycobacterium tuberculosis outbreaks: a retrospective observational study. Lancet Infectious Diseases, The, 2013, 13, 137-146.	9.1	786
212	Improved workflows for high throughput library preparation using the transposome-based nextera system. BMC Biotechnology, 2013, 13, 104.	3.3	141
213	Relationship Between Bacterial Strain Type, Host Biomarkers, and Mortality in Clostridium difficile Infection. Clinical Infectious Diseases, 2013, 56, 1589-1600.	5.8	191
214	Detection of Mixed Infection from Bacterial Whole Genome Sequence Data Allows Assessment of Its Role in Clostridium difficile Transmission. PLoS Computational Biology, 2013, 9, e1003059.	3.2	75
215	Within-Host Evolution of Staphylococcus aureus during Asymptomatic Carriage. PLoS ONE, 2013, 8, e61319.	2.5	194
216	Short-Term Genome Stability of Serial Clostridium difficile Ribotype 027 Isolates in an Experimental Gut Model and Recurrent Human Disease. PLoS ONE, 2013, 8, e63540.	2.5	16

#	ARTICLE	IF	CITATIONS
217	Asymptomatic Clostridium difficile Colonisation and Onward Transmission. PLoS ONE, 2013, 8, e78445.	2.5	113
218	Surveillance of Infection Severity: A Registry Study of Laboratory Diagnosed Clostridium difficile. PLoS Medicine, 2012, 9, e1001279.	8.4	8
219	Increasing incidence of Escherichia coli bacteraemia is driven by an increase in antibiotic-resistant isolates: electronic database study in Oxfordshire 1999-2011. Journal of Antimicrobial Chemotherapy, 2012, 67, 1514-1524.	3.0	45
220	Fidaxomicin Versus Vancomycin for Clostridium difficile Infection: Meta-analysis of Pivotal Randomized Controlled Trials. Clinical Infectious Diseases, 2012, 55, S93-S103.	5.8	228
221	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4550-4555.	7.1	244
222	Fidaxomicin versus vancomycin for infection with Clostridium difficile in Europe, Canada, and the USA: a double-blind, non-inferiority, randomised controlled trial. Lancet Infectious Diseases, The, 2012, 12, 281-289.	9.1	644
223	Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics, 2012, 13, 601-612.	16.3	684
224	A pilot study of rapid benchtop sequencing of<i>Staphylococcus aureus</i>and<i>Clostridium difficile</i>for outbreak detection and surveillance. BMJ Open, 2012, 2, e001124.	1.9	228
225	Microevolutionary analysis of Clostridium difficile genomes to investigate transmission. Genome Biology, 2012, 13, R118.	9.6	199
226	Characterisation of Clostridium difficile Hospital Ward€"Based Transmission Using Extensive Epidemiological Data and Molecular Typing. PLoS Medicine, 2012, 9, e1001172.	8.4	202
227	Clinical Clostridium difficile: Clonality and Pathogenicity Locus Diversity. PLoS ONE, 2011, 6, e19993.	2.5	150
228	Decline of meticillin-resistant Staphylococcus aureus in Oxfordshire hospitals is strain-specific and preceded infection-control intensification. BMJ Open, 2011, 1, e000160-e000160.	1.9	55
229	Molecular Epidemiology of Clostridium difficile Strains in Children Compared with That of Strains Circulating in Adults with Clostridium difficile-Associated Infection : Fig. 1.. Journal of Clinical Microbiology, 2011, 49, 3994-3996.	3.9	32
230	Reduction in invasive pneumococcal disease following implementation of the conjugate vaccine in the Oxfordshire region, England. Journal of Medical Microbiology, 2011, 60, 91-97.	1.8	36
231	Multilocus Sequence Typing of <i>Clostridium difficile</i>. Journal of Clinical Microbiology, 2010, 48, 770-778.	3.9	399
232	Invasive pneumococcal disease: epidemiology in children and adults prior to implementation of the conjugate vaccine in the Oxfordshire region, England. Journal of Medical Microbiology, 2008, 57, 480-487.	1.8	35
233	Are There Better Methods of Monitoring MRSA Control than Bacteraemia Surveillance? An Observational Database Study. PLoS ONE, 2008, 3, e2378.	2.5	19
234	Diversity of antibiotic resistance integrative and conjugative elements among haemophili. Journal of Medical Microbiology, 2007, 56, 838-846.	1.8	15

#	ARTICLE	IF	CITATIONS
235	Effect of antibiotic prescribing on antibiotic resistance in individual children in primary care: prospective cohort study. BMJ: British Medical Journal, 2007, 335, 429.	2.3	121
236	Population structure of group B streptococcus from a low-incidence region for invasive neonatal disease. Microbiology (United Kingdom), 2005, 151, 1875-1881.	1.8	45
237	Molecular Epidemiology of Unrelated Clusters of Multiresistant Strains of Haemophilus influenzae. Journal of Infectious Diseases, 1992, 165, 1069-1075.	4.0	25
238	Pneumococcal Carriage. , 0, , 136-147.		10
239	Whole Genome Sequencing for Surveillance of Tuberculosis Drug Resistance in China: Based on a Cross-Sectional Surveillance Study. SSRN Electronic Journal, 0, , .	0.4	0
240	Reduced Neutralization of SARS-CoV-2 B.1.1.7 Variant from Naturally Acquired and Vaccine Induced Antibody Immunity. SSRN Electronic Journal, 0, , .	0.4	2
241	Transmission of pre-XDR and XDR-TB in the Mumbai Metropolitan Region, India. SSRN Electronic Journal, 0, , .	0.4	0
242	Prediction of Pyrazinamide Resistance in <i>Mycobacterium Tuberculosis</i> Using Structure-Based Machine Learning Approaches. SSRN Electronic Journal, 0, , .	0.4	5
243	<i>Mycobacterium abscessus</i> Genomic Clusters Span Geography and Patient Groups. SSRN Electronic Journal, 0, , .	0.4	2
244	Haemophilus spp.. , 0, , 245-251.		0
245	<i>M. tuberculosis</i> Microvariation Is Common and Is Associated with Transmission: Analysis of Three Years Prospective Universal Sequencing in England. SSRN Electronic Journal, 0, , .	0.4	0
246	Reducing Expectations for Antibiotics in Primary Care: A Randomised Experiment to Test the Response to Fear-Based Messages About Antimicrobial Resistance. SSRN Electronic Journal, 0, , .	0.4	0
247	Risk Factors Associated with Carbapenemase-Producing Enterobacterales (CPE) Positivity in the Hospital Wastewater Environment. SSRN Electronic Journal, 0, , .	0.4	0
248	Mortality risks associated with empirical antibiotic activity in <i>Escherichia coli</i> bacteraemia: an analysis of electronic health records. Journal of Antimicrobial Chemotherapy, 0, , .	3.0	3