

Derrick W Crook

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

284
papers

16,624
citations

67
h-index

123
g-index

333
ext. papers

23,887
ext. citations

12.7
avg, IF

6.43
L-index

#	Paper	IF	Citations
284	Whole-genome sequencing to delineate Mycobacterium tuberculosis outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases, The</i> , 2013 , 13, 137-46	25.5	615
283	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. <i>Cell</i> , 2021 , 184, 2348-2361.e6	56.2	549
282	Fidaxomicin versus vancomycin for infection with Clostridium difficile in Europe, Canada, and the USA: a double-blind, non-inferiority, randomised controlled trial. <i>Lancet Infectious Diseases, The</i> , 2012 , 12, 281-9	25.5	513
281	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012 , 13, 601-612	30.1	508
280	Antibody Status and Incidence of SARS-CoV-2 Infection in Health Care Workers. <i>New England Journal of Medicine</i> , 2021 , 384, 533-540	59.2	482
279	Diverse sources of C. difficile infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , 2013 , 369, 1195-205	59.2	471
278	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases, The</i> , 2015 , 15, 1193-1202	25.5	391
277	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , 2015 , 6, 10063	17.4	348
276	Differences in outcome according to Clostridium difficile testing method: a prospective multicentre diagnostic validation study of C difficile infection. <i>Lancet Infectious Diseases, The</i> , 2013 , 13, 936-45	25.5	320
275	Multilocus sequence typing of Clostridium difficile. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 770-8	9.7	310
274	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021 , 184, 4220-4236.e13	56.2	281
273	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021 , 184, 2939-2954.e9	56.2	281
272	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. <i>Cell</i> , 2021 , 184, 2201-2211.e7	56.2	269
271	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018 , 379, 1403-1415	59.2	243
270	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016 , 14, 150-62	22.2	239
269	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	9.7	221
268	Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study. <i>Lancet Respiratory Medicine, the</i> , 2016 , 4, 49-58	35.1	216

267	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	59.2	213
266	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. <i>Lancet Infectious Diseases</i> , 2020 , 20, 1390-1400	25.5	212
265	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , 2017 , 17, 411-421	25.5	202
264	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016 , 7, e02162	7.8	200
263	A standardised method for interpreting the association between mutations and phenotypic drug resistance in. <i>European Respiratory Journal</i> , 2017 , 50,	13.6	198
262	A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. <i>BMJ Open</i> , 2012 , 2,	3	197
261	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 4550-5	11.5	195
260	Fidaxomicin versus vancomycin for <i>Clostridium difficile</i> infection: meta-analysis of pivotal randomized controlled trials. <i>Clinical Infectious Diseases</i> , 2012 , 55 Suppl 2, S93-103	11.6	188
259	Characterisation of <i>Clostridium difficile</i> hospital ward-based transmission using extensive epidemiological data and molecular typing. <i>PLoS Medicine</i> , 2012 , 9, e1001172	11.6	172
258	Identification of Biomarkers for Differentiation of Hypervirulent <i>Klebsiella pneumoniae</i> from Classical <i>K. pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	170
257	Relationship between bacterial strain type, host biomarkers, and mortality in <i>Clostridium difficile</i> infection. <i>Clinical Infectious Diseases</i> , 2013 , 56, 1589-600	11.6	167
256	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene blaKPC. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 3767-78	5.9	166
255	Effect of Delta variant on viral burden and vaccine effectiveness against new SARS-CoV-2 infections in the UK. <i>Nature Medicine</i> , 2021 ,	50.5	162
254	Gonorrhoea treatment failure caused by a strain with combined ceftriaxone and high-level azithromycin resistance, England, February 2018. <i>Eurosurveillance</i> , 2018 , 23,	19.8	160
253	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses.. <i>Cell</i> , 2022 ,	56.2	154
252	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012 , 13, R118	18.3	151
251	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	11.6	149
250	Assessment of <i>Mycobacterium tuberculosis</i> transmission in Oxfordshire, UK, 2007-12, with whole pathogen genome sequences: an observational study. <i>Lancet Respiratory Medicine</i> , 2014 , 2, 285-292	35.1	149

249	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016 , 1, 16041	26.6	143
248	mcr-1 and mcr-2 variant genes identified in <i>Moraxella</i> species isolated from pigs in Great Britain from 2014 to 2015. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 2745-2749	5.1	143
247	Within-host evolution of <i>Staphylococcus aureus</i> during asymptomatic carriage. <i>PLoS ONE</i> , 2013 , 8, e613197	3.7	141
246	Global outbreak of severe <i>Mycobacterium chimaera</i> disease after cardiac surgery: a molecular epidemiological study. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 1033-1041	25.5	136
245	Clinical <i>Clostridium difficile</i> : clonality and pathogenicity locus diversity. <i>PLoS ONE</i> , 2011 , 6, e19993	3.7	131
244	Evolutionary history of the <i>Clostridium difficile</i> pathogenicity locus. <i>Genome Biology and Evolution</i> , 2014 , 6, 36-52	3.9	123
243	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020 , 9,	8.9	122
242	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel. <i>Wellcome Open Research</i> , 2020 , 5, 139	4.8	120
241	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	11.6	120
240	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases, The</i> , 2016 , 16, 1295-1303	25.5	118
239	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. <i>Nature Medicine</i> , 2021 , 27, 1370-1378	50.5	116
238	Reduced neutralisation of SARS-CoV-2 omicron B.1.1.529 variant by post-immunisation serum.. <i>Lancet, The</i> , 2021 ,	40	115
237	WGS to predict antibiotic MICs for <i>Neisseria gonorrhoeae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1937-1947	5.1	113
236	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	25.5	113
235	Whole-genome sequencing shows that patient-to-patient transmission rarely accounts for acquisition of <i>Staphylococcus aureus</i> in an intensive care unit. <i>Clinical Infectious Diseases</i> , 2014 , 58, 609-18	11.6	112
234	<i>Klebsiella pneumoniae</i> carbapenemase (KPC)-producing <i>K. pneumoniae</i> at a single institution: insights into endemicity from whole-genome sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 1656-63	5.9	107
233	Improved workflows for high throughput library preparation using the transposome-based Nextera system. <i>BMC Biotechnology</i> , 2013 , 13, 104	3.5	106
232	Molecular Diagnosis of Orthopedic-Device-Related Infection Directly from Sonication Fluid by Metagenomic Sequencing. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 2334-2347	9.7	105

231	Plasmid Classification in an Era of Whole-Genome Sequencing: Application in Studies of Antibiotic Resistance Epidemiology. <i>Frontiers in Microbiology</i> , 2017 , 8, 182	5.7	102
230	Colistin resistance gene <i>mcr-1</i> and <i>pHNSHP45</i> plasmid in human isolates of <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> . <i>Lancet Infectious Diseases</i> , 2016 , 16, 285-6	25.5	95
229	Effect of antibiotic prescribing on antibiotic resistance in individual children in primary care: prospective cohort study. <i>BMJ</i> , 2007 , 335, 429	5.9	95
228	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019 , 5,	4.4	93
227	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014 , 5, 3956	17.4	90
226	Asymptomatic <i>Clostridium difficile</i> colonisation and onward transmission. <i>PLoS ONE</i> , 2013 , 8, e78445	3.7	90
225	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015 , 13, e1002229	9.7	76
224	Mortality risks associated with emergency admissions during weekends and public holidays: an analysis of electronic health records. <i>Lancet</i> , 2017 , 390, 62-72	4.0	75
223	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	26.6	74
222	Trends over time in <i>Escherichia coli</i> bloodstream infections, urinary tract infections, and antibiotic susceptibilities in Oxfordshire, UK, 1998-2016: a study of electronic health records. <i>Lancet Infectious Diseases</i> , 2018 , 18, 1138-1149	25.5	73
221	Dynamic linkage of COVID-19 test results between Public Health England's Second Generation Surveillance System and UK Biobank. <i>Microbial Genomics</i> , 2020 , 6,	4.4	73
220	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019 , 58,	9.7	70
219	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, 1001-11	7	69
218	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 2516-26	4.8	69
217	Real-time analysis of nanopore-based metagenomic sequencing from infected orthopaedic devices. <i>BMC Genomics</i> , 2018 , 19, 714	4.5	67
216	Detection of mixed infection from bacterial whole genome sequence data allows assessment of its role in <i>Clostridium difficile</i> transmission. <i>PLoS Computational Biology</i> , 2013 , 9, e1003059	5	65
215	COVID-19: Rapid antigen detection for SARS-CoV-2 by lateral flow assay: A national systematic evaluation of sensitivity and specificity for mass-testing. <i>EClinicalMedicine</i> , 2021 , 36, 100924	11.3	65
214	Maternal colonization with <i>Streptococcus agalactiae</i> and associated stillbirth and neonatal disease in coastal Kenya. <i>Nature Microbiology</i> , 2016 , 1, 16067	26.6	64

213	Community prevalence of SARS-CoV-2 in England from April to November, 2020: results from the ONS Coronavirus Infection Survey. <i>Lancet Public Health, The</i> , 2021 , 6, e30-e38	22.4	64
212	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998-2014. <i>Thorax</i> , 2016 , 71, 535-42	7.3	63
211	Natural mutations in a Staphylococcus aureus virulence regulator attenuate cytotoxicity but permit bacteremia and abscess formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3101-10	11.5	61
210	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. <i>Wellcome Open Research</i> , 2020 , 5, 181	4.8	60
209	Mycobacterial DNA extraction for whole-genome sequencing from early positive liquid (MGIT) cultures. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 1137-43	9.7	58
208	The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant Staphylococcus aureus. <i>MBio</i> , 2016 , 7, e02039-15	7.8	57
207	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017 , 6,	8.9	55
206	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel		55
205	Epidemiology of Clostridium difficile in infants in Oxfordshire, UK: Risk factors for colonization and carriage, and genetic overlap with regional C. difficile infection strains. <i>PLoS ONE</i> , 2017 , 12, e0182307	3.7	54
204	Assessing a novel, lab-free, point-of-care test for SARS-CoV-2 (CovidNudge): a diagnostic accuracy study. <i>Lancet Microbe, The</i> , 2020 , 1, e300-e307	22.2	53
203	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018 , 34, 1666-1671	7.2	52
202	Prevalence of Staphylococcus aureus protein A (spa) mutants in the community and hospitals in Oxfordshire. <i>BMC Microbiology</i> , 2014 , 14, 63	4.5	52
201	Impact of Delta on viral burden and vaccine effectiveness against new SARS-CoV-2 infections in the UK		52
200	Intensive Care Unit Wastewater Interventions to Prevent Transmission of Multispecies Klebsiella pneumoniae Carbapenemase-Producing Organisms. <i>Clinical Infectious Diseases</i> , 2018 , 67, 171-178	11.6	51
199	Resolving plasmid structures in using the MinION nanopore sequencer: assessment of MinION and MinION/Illumina hybrid data assembly approaches. <i>Microbial Genomics</i> , 2017 , 3, e000118	4.4	49
198	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. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 3025-3034	5.1	48
197	Colonization with Enterobacteriaceae producing ESBLs in children attending pre-school childcare facilities in the Lao People's Democratic Republic. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 1893-7	5.7	46
196	Decline of methicillin-resistant Staphylococcus aureus in Oxfordshire hospitals is strain-specific and preceded infection-control intensification. <i>BMJ Open</i> , 2011 , 1, e000160	3	46

195	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> , 2021 ,	11.6	45
194	A Quantitative Evaluation of MIRU-VNTR Typing Against Whole-Genome Sequencing for Identifying Mycobacterium tuberculosis Transmission: A Prospective Observational Cohort Study. <i>EBioMedicine</i> , 2018 , 34, 122-130	8.8	44
193	Evaluation of Whole-Genome Sequencing for Mycobacterial Species Identification and Drug Susceptibility Testing in a Clinical Setting: a Large-Scale Prospective Assessment of Performance against Line Probe Assays and Phenotyping. <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	43
192	Quantitative SARS-CoV-2 anti-spike responses to Pfizer-BioNTech and Oxford-AstraZeneca vaccines by previous infection status. <i>Clinical Microbiology and Infection</i> , 2021 , 27, 1516.e7-1516.e14	9.5	43
191	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	3.3	42
190	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism-calling pipelines. <i>GigaScience</i> , 2020 , 9,	7.6	42
189	Population structure of group B streptococcus from a low-incidence region for invasive neonatal disease. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 1875-1881	2.9	42
188	High Rates of Human Fecal Carriage of mcr-1-Positive Multidrug-Resistant Enterobacteriaceae Emerge in China in Association With Successful Plasmid Families. <i>Clinical Infectious Diseases</i> , 2018 , 66, 676-685	11.6	41
187	Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from Staphylococcus aureus Whole-Genome Sequences. <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	40
186	Enhanced Klebsiella pneumoniae Carbapenemase Expression from a Novel Tn Deletion. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	38
185	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. <i>Wellcome Open Research</i> , 2020 , 5, 181	4.8	38
184	Two Distinct Patterns of Clostridium difficile Diversity Across Europe Indicating Contrasting Routes of Spread. <i>Clinical Infectious Diseases</i> , 2018 , 67, 1035-1044	11.6	36
183	Dynamics of acquisition and loss of carriage of Staphylococcus aureus strains in the community: the effect of clonal complex. <i>Journal of Infection</i> , 2014 , 68, 426-39	18.9	36
182	Detection of Viral Pathogens With Multiplex Nanopore MinION Sequencing: Be Careful With Cross-Talk. <i>Frontiers in Microbiology</i> , 2018 , 9, 2225	5.7	36
181	Tuberculosis is changing. <i>Lancet Infectious Diseases</i> , 2017 , 17, 359-361	25.5	35
180	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019 , 35, 2276-2282	7.2	35
179	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018 , 8, 15382	4.9	35
178	Antibiotic resistance prediction for from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019 , 4, 191	4.8	34

177	Contribution to Clostridium Difficile Transmission of Symptomatic Patients With Toxigenic Strains Who Are Fecal Toxin Negative. <i>Clinical Infectious Diseases</i> , 2017 , 64, 1163-1170	11.6	33
176	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	3.2	33
175	Increasing incidence of Escherichia coli bacteraemia is driven by an increase in antibiotic-resistant isolates: electronic database study in Oxfordshire 1999-2011. <i>Journal of Antimicrobial Chemotherapy</i> , 2012 , 67, 1514-24	5.1	33
174	Invasive pneumococcal disease: epidemiology in children and adults prior to implementation of the conjugate vaccine in the Oxfordshire region, England. <i>Journal of Medical Microbiology</i> , 2008 , 57, 480-487 ^{3,2}	3.2	33
173	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated PCR Ribotype 078. <i>MBio</i> , 2019 , 10,	7.8	32
172	Chromosomal Integration of the Klebsiella pneumoniae Carbapenemase Gene, , in Klebsiella Species Is Elusive but Not Rare. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	31
171	SNP-IT Tool for Identifying Subspecies and Associated Lineages of Mycobacterium tuberculosis Complex. <i>Emerging Infectious Diseases</i> , 2019 , 25, 482-488	10.2	31
170	Increased infections, but not viral burden, with a new SARS-CoV-2 variant		31
169	Validating a 14-Drug Microtiter Plate Containing Bedaquiline and Delamanid for Large-Scale Research Susceptibility Testing of Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	31
168	An observational cohort study on the incidence of SARS-CoV-2 infection and B.1.1.7 variant infection in healthcare workers by antibody and vaccination status. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	31
167	Molecular epidemiology of Clostridium difficile strains in children compared with that of strains circulating in adults with Clostridium difficile-associated infection. <i>Journal of Clinical Microbiology</i> , 2011 , 49, 3994-6	9.7	30
166	Panton-Valentine leucocidin is the key determinant of pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019 , 8,	8.9	30
165	Occurrence and characterization of mcr-1-harboring Escherichia coli isolated from pigs in Great Britain from 2013 to 2015. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 691-695	5.1	30
164	A curated dataset of complete Enterobacteriaceae plasmids compiled from the NCBI nucleotide database. <i>Data in Brief</i> , 2017 , 12, 423-426	1.2	29
163	Clostridium difficile: Investigating Transmission Patterns Between Infected and Colonized Patients Using Whole Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2019 , 68, 204-209	11.6	27
162	The complexity and diversity of the Pathogenicity Locus in Clostridium difficile clade 5. <i>Genome Biology and Evolution</i> , 2014 , 6, 3159-70	3.9	27
161	Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. 2021 ,		25
160	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. <i>Nature Communications</i> , 2021 , 12, 1951	17.4	25

159	Capsular Typing Method for Streptococcus agalactiae Using Whole-Genome Sequence Data. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1388-90	9.7	24
158	Amplicon based MinION sequencing of SARS-CoV-2 and metagenomic characterisation of nasopharyngeal swabs from patients with COVID-19		24
157	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. <i>Environmental Microbiomes</i> , 2019 , 14, 7	5.6	24
156	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	6.9	24
155	Comparison of Control of Clostridium difficile Infection in Six English Hospitals Using Whole-Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017 , 65, 433-441	11.6	23
154	Antibodies to SARS-CoV-2 are associated with protection against reinfection		23
153	Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism. <i>Viruses</i> , 2020 , 12,	6.2	23
152	Provides a Window into Carbapenemase Gene Transfer, Plasmid Rearrangements, and Patient Interactions with the Hospital Environment. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	22
151	Molecular epidemiology of unrelated clusters of multiresistant strains of Haemophilus influenzae. <i>Journal of Infectious Diseases</i> , 1992 , 165, 1069-75	7	22
150	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,	19.8	22
149	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	11.4	21
148	Impact of vaccination on new SARS-CoV-2 infections in the UK		20
147	Whole-Genome Sequencing for Predicting Clarithromycin Resistance in. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	20
146	Don't overlook the little guy: An evaluation of the frequency of small plasmids co-conjugating with larger carbapenemase gene containing plasmids. <i>Plasmid</i> , 2019 , 103, 1-8	3.3	19
145	The use of whole-genome sequencing in cluster investigation of a multidrug-resistant tuberculosis outbreak. <i>European Respiratory Journal</i> , 2018 , 51,	13.6	19
144	Machine learning for the prediction of antibacterial susceptibility in Mycobacterium tuberculosis 2014 ,		19
143	Some Synonymous and Nonsynonymous Mutations in Mycobacterium tuberculosis Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	18
142	Clostridium difficile 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	8.8	18

141	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	11.4	18
140	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	4.4	17
139	Robust Prediction of Resistance to Trimethoprim in <i>Staphylococcus aureus</i> . <i>Cell Chemical Biology</i> , 2018 , 25, 339-349.e4	8.2	16
138	Are there better methods of monitoring MRSA control than bacteraemia surveillance? An observational database study. <i>PLoS ONE</i> , 2008 , 3, e2378	3.7	16
137	An observational cohort study on the incidence of SARS-CoV-2 infection and B.1.1.7 variant infection in healthcare workers by antibody and vaccination status		16
136	Epidemiological data and genome sequencing reveals that nosocomial transmission of SARS-CoV-2 is underestimated and mostly mediated by a small number of highly infectious individuals. <i>Journal of Infection</i> , 2021 , 83, 473-482	18.9	16
135	The Role of in Challenges with Fosfomycin Susceptibility Testing of Multispecies <i>Klebsiella pneumoniae</i> Carbapenemase-Producing Clinical Isolates. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	15
134	Effects of proton pump inhibitors and histamine-2 receptor antagonists on response to fidaxomicin or vancomycin in patients with <i>Clostridium difficile</i> -associated diarrhoea. <i>BMJ Open Gastroenterology</i> , 2015 , 2, e000028	3.9	15
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110	Antibody responses and correlates of protection in the general population after two doses of the ChAdOx1 or BNT162b2 vaccines.. <i>Nature Medicine</i> , 2022 ,	50.5	11
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105	SARS-CoV-2 RNA detected in blood samples from patients with COVID-19 is not associated with infectious virus		10
104	Diagnosis of SARS-CoV-2 infection with LamPORE, a high-throughput platform combining loop-mediated isothermal amplification and nanopore sequencing		10
103	The duration, dynamics and determinants of SARS-CoV-2 antibody responses in individual healthcare workers		10
102	High precision variant and antimicrobial resistance calling from metagenomic Nanopore sequencing. <i>Genome Research</i> , 2020 , 30, 1354-1363	9.7	10
101	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	11.4	10
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99	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne Carbapenemase in in the United Kingdom from 2009 to 2014. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64,	5.9	9
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97	SARS-CoV-2 antibody prevalence, titres and neutralising activity in an antenatal cohort, United Kingdom, 14 April to 15 June 2020. <i>Eurosurveillance</i> , 2020 , 25,	19.8	9
96	Virus detection and identification in minutes using single-particle imaging and deep learning		9
95	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of Mycobacteria Direct from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	9
94	Hash-Based Core Genome Multilocus Sequence Typing for <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2019 , 58,	9.7	9
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88	Quantitative SARS-CoV-2 anti-spike responses to Pfizer-BioNTech and Oxford-AstraZeneca vaccines by previous infection status		7

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83	Genomic surveillance of and spp. in hospital sink drains and patients. <i>Microbial Genomics</i> , 2020 , 6,	4.4	6
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81	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2		6
80	Genomic diversity affects the accuracy of bacterial SNP calling pipelines		6
79	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,	19.8	6
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74	Author response: Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study 2020 ,		4
73	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
72	Prediction of pyrazinamide resistance in Mycobacterium tuberculosis using structure-based machine learning approaches		4
71	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021 , 15, 2322-2335	11.9	4
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64	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae		3
63	MinION Nanopore Sequencing of Multiple Displacement Amplified Mycobacteria DNA Direct from Sputum		3
62	Nanopore metagenomic sequencing of full length human metapneumovirus (HMPV) within a unique sub-lineage		3
61	Relationship between microbiology of throat swab and clinical course among primary care patients with acute cough: a prospective cohort study. <i>Family Practice</i> , 2020 , 37, 332-339	1.9	3
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58	Symptoms and SARS-CoV-2 positivity in the general population in the UK		3
57	SARS-CoV-2 anti-spike IgG antibody responses after second dose of ChAdOx1 or BNT162b2 in the UK general population		3
56	Human and Porcine Transmission of <i>Clostridioides difficile</i> Ribotype 078, Europe. <i>Emerging Infectious Diseases</i> , 2021 , 27, 2294-2300	10.2	3
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51	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus Rosenbach 1884. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
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47	Multidrug-resistant Escherichia coli soft tissue infection investigated with bacterial whole genome sequencing. <i>BMJ Case Reports</i> , 2014 , 2014,	0.9	2
46	Reconciling the potentially irreconcilable? Genotypic and phenotypic amoxicillin-clavulanate resistance in Escherichia coli		2
45	M. tuberculosis microvariation is common and is associated with transmission: analysis of three years prospective universal sequencing in England		2
44	Optimizing DNA extraction methods for Nanopore sequencing of Neisseria gonorrhoeae direct from urine samples		2
43	Optimised use of Oxford Nanopore Flowcells for Hybrid Assemblies		2
42	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis		2
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35	Molecular epidemiology of Escherichia coli and Klebsiella species bloodstream infections in Oxfordshire (UK) 2008-2018		2
34	Clostridium difficile in England: can we stop washing our hands? - AuthorsPreply. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 478-479	25.5	1

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30	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples		1
29	Time of day of vaccination affects SARS-CoV-2 antibody responses in an observational study of healthcare workers		1
28	Metrics for Public Health Perspective Surveillance of Bacterial Antibiotic Resistance in Low- and Middle-Income Countries		1
27	Multi-omic surveillance of Escherichia coli and Klebsiella spp. in hospital sink drains and patients		1
26	DNA Thermo-Protection Facilitates Whole Genome Sequencing of Mycobacteria Direct from Clinical Samples by the Nanopore Platform		1
25	CovidNudge: diagnostic accuracy of a novel lab-free point-of-care diagnostic for SARS-CoV-2		1
24	Validating a 14-drug microtitre plate containing bedaquiline and delamanid for large-scale research susceptibility testing of Mycobacterium tuberculosis		1
23	Hash-based core genome multi-locus sequencing typing for Clostridium difficile		1
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20	WGS to determine the extent of Clostridioides difficile transmission in a high incidence setting in North Wales in 2015. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 1092-1100	5.1	1
19	Enhancing epidemiological investigation of nosocomial SARS-CoV-2 infection with whole genome sequencing: A retrospective cohort study across four hospitals in the UK.		1
18	Flanker: a tool for comparative genomics of gene flanking regions. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
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15	Antimicrobial resistance genes and clonal success in Escherichia coli isolates causing bloodstream infection.. <i>Lancet Microbe, The</i> , 2021 , 2, e492	22.2	1
14	Viral detection and identification in 20min by rapid single-particle fluorescence in-situ hybridization of viral RNA. <i>Scientific Reports</i> , 2021 , 11, 19579	4.9	1
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3	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant Enterobacteriaceae 2019 , 14, e0222831		
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