

Derrick W Crook

List of Publications by Year in Descending Order

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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	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses.. <i>Cell</i> , 2022 ,	56.2	154
283	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
282	Identifying Bacterial Airways Infection in Stable Severe Asthma Using Oxford Nanopore Sequencing Technologies.. <i>Microbiology Spectrum</i> , 2022 , e0227921	8.9	1
281	Clinical Metagenomic Sequencing for Species Identification and Antimicrobial Resistance Prediction in Orthopedic Device Infection.. <i>Journal of Clinical Microbiology</i> , 2022 , e0215621	9.7	3
280	The bacteriology of pleural infection (TORPIDS): an exploratory metagenomics analysis through next generation sequencing.. <i>Lancet Microbe, The</i> , 2022 , 3, e294-e302	22.2	3
279	The 2021 WHO catalogue of complex mutations associated with drug resistance: A genotypic analysis.. <i>Lancet Microbe, The</i> , 2022 , 3, e265-e273	22.2	3
278	Reduced neutralisation of SARS-CoV-2 omicron B.1.1.529 variant by post-immunisation serum.. <i>Lancet, The</i> , 2021 ,	40	115
277	Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. 2021 ,		25
276	Antimicrobial resistance determinants are associated with bacteraemia and adaptation to the healthcare environment: a bacterial genome-wide association study. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
275	Time of Day of Vaccination Affects SARS-CoV-2 Antibody Responses in an Observational Study of Health Care Workers. <i>Journal of Biological Rhythms</i> , 2021 , 7487304211059315	3.2	9
274	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	4.9	0
273	A genomic epidemiological study shows that prevalence of antimicrobial resistance in is associated with the livestock host, as well as antimicrobial usage. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
272	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
271	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021 , 12, 6250	17.4	13
270	Changes in paediatric respiratory infections at a UK teaching hospital 2016-2021; impact of the SARS-CoV-2 pandemic. <i>Journal of Infection</i> , 2021 ,	18.9	6
269	Symptoms and SARS-CoV-2 positivity in the general population in the UK. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	6
268	Preferences for Medical Consultations from Online Providers: Evidence from a Discrete Choice Experiment in the United Kingdom. <i>Applied Health Economics and Health Policy</i> , 2021 , 19, 521-535	3.4	2

267	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2. <i>Nature Communications</i> , 2021 , 12, 1951	17.4	25
266	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021 , 15, 2322-2335	11.9	4
265	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
264	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021 , 7,	14.3	12
263	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
262	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021 , 184, 2939-2954.e9	56.2	281
261	Diagnosis of SARS-CoV-2 Infection with LamPORE, a High-Throughput Platform Combining Loop-Mediated Isothermal Amplification and Nanopore Sequencing. <i>Journal of Clinical Microbiology</i> , 2021 , 59,	9.7	15
260	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
259	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
258	Population-level faecal metagenomic profiling as a tool to predict antimicrobial resistance in isolates causing invasive infections: An exploratory study across Cambodia, Kenya, and the UK. <i>EClinicalMedicine</i> , 2021 , 36, 100910	11.3	0
257	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
256	Impact of vaccination on new SARS-CoV-2 infections in the United Kingdom. <i>Nature Medicine</i> , 2021 , 27, 1370-1378	50.5	116
255	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
254	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
253	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	5.7	0
252	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> , <i>The</i> , 2021 , 6, e30-e38	22.4	64
251	Ten years of population-level genomic Escherichia coli and Klebsiella pneumoniae serotype surveillance informs vaccine development for invasive infections. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	5
250	Stringent thresholds in SARS-CoV-2 IgG assays lead to under-detection of mild infections. <i>BMC Infectious Diseases</i> , 2021 , 21, 187	4	12

249	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
248	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
247	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021 , 184, 4220-4236.e13	42.6	13
246	Flanker: a tool for comparative genomics of gene flanking regions. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
245	Whole-genome sequencing for surveillance of tuberculosis drug resistance and determination of resistance level in China. <i>Clinical Microbiology and Infection</i> , 2021 ,	9.5	1
244	Ten-year longitudinal molecular epidemiology study of Escherichia coli and Klebsiella species bloodstream infections in Oxfordshire, UK. <i>Genome Medicine</i> , 2021 , 13, 144	14.4	4
243	Human and Porcine Transmission of Clostridioides difficile Ribotype 078, Europe. <i>Emerging Infectious Diseases</i> , 2021 , 27, 2294-2300	10.2	3
242	Undetected carriage explains apparent Staphylococcus aureus acquisition in a non-outbreak healthcare setting. <i>Journal of Infection</i> , 2021 , 83, 332-338	18.9	0
241	Epidemiology of in England: an observational study. <i>Lancet Microbe, The</i> , 2021 , 2, e498-e507	22.2	4
240	Antimicrobial resistance genes and clonal success in Escherichia coli isolates causing bloodstream infection.. <i>Lancet Microbe, The</i> , 2021 , 2, e492	22.2	1
239	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
238	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
237	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
236	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
235	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2450-2460	8.3	11
234	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	18.9	10
233	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism-calling pipelines. <i>GigaScience</i> , 2020 , 9,	7.6	42
232	Optimizing DNA Extraction Methods for Nanopore Sequencing of Neisseria gonorrhoeae Directly from Urine Samples. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	12

231	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64,	5.9	13
230	Multi-Label Random Forest Model for Tuberculosis Drug Resistance Classification and Mutation Ranking. <i>Frontiers in Microbiology</i> , 2020 , 11, 667	5.7	8
229	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
228	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
227	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
226	Case Report: Disseminated, rifampicin resistant (BCG) infection in an immunocompromised child. <i>Wellcome Open Research</i> , 2020 , 5, 242	4.8	
225	Comparative genomics of toxinotypes identifies module-based toxin gene evolution. <i>Microbial Genomics</i> , 2020 , 6,	4.4	3
224	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
223	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020 , 9,	8.9	122
222	Author response: Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study 2020 ,		4
221	NanoSPC: a scalable, portable, cloud compatible viral nanopore metagenomic data processing pipeline. <i>Nucleic Acids Research</i> , 2020 , 48, W366-W371	20.1	7
220	Genomic surveillance of and spp. in hospital sink drains and patients. <i>Microbial Genomics</i> , 2020 , 6,	4.4	6
219	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
218	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
217	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
216	Awareness of Appropriate Antibiotic Use in Primary Care for Influenza-Like Illness: Evidence of Improvement from UK Population-Based Surveys. <i>Antibiotics</i> , 2020 , 9,	4.9	1
215	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of Mycobacteria Direct from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	9
214	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

213	Evaluation of methods for detecting human reads in microbial sequencing datasets. <i>Microbial Genomics</i> , 2020 , 6,	4.4	2
212	High precision variant and antimicrobial resistance calling from metagenomic Nanopore sequencing. <i>Genome Research</i> , 2020 , 30, 1354-1363	9.7	10
211	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
210	Assessing a novel, lab-free, point-of-care test for SARS-CoV-2 (CovidNudge): a diagnostic accuracy study. <i>Lancet Microbe</i> , 2020 , 1, e300-e307	22.2	53
209	Risk Factors Associated with Carbapenemase-Producing (CPE) Positivity in the Hospital Wastewater Environment. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	3
208	The importance of using whole genome sequencing and extended spectrum beta-lactamase selective media when monitoring antimicrobial resistance. <i>Scientific Reports</i> , 2020 , 10, 19880	4.9	8
207	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
206	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
205	Revealing 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	11.4	12
204	Scalable Pathogen Pipeline Platform (SP ³): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing 2019 ,		1
203	Improved Performance Predicting Clarithromycin Resistance in on an Independent Data Set. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	6
202	<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	8.8	18
201	DeepAMR for predicting co-occurrent resistance of Mycobacterium tuberculosis. <i>Bioinformatics</i> , 2019 , 35, 3240-3249	7.2	10
200	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus <i>Rosenbach 1884</i> . <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
199	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
198	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated PCR Ribotype 078. <i>MBio</i> , 2019 , 10,	7.8	32
197	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
196	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

195	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
194	Antibiotic Review Kit for Hospitals (ARK-Hospital): study protocol for a stepped-wedge cluster-randomised controlled trial. <i>Trials</i> , 2019 , 20, 421	2.8	2
193	The Role of in Challenges with Fosfomycin Susceptibility Testing of Multispecies Klebsiella pneumoniae Carbapenemase-Producing Clinical Isolates. <i>Journal of Clinical Microbiology</i> , 2019 , 57,	9.7	15
192	Using hospital network-based surveillance for antimicrobial resistance as a more robust alternative to self-reporting. <i>PLoS ONE</i> , 2019 , 14, e0219994	3.7	2
191	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	3.7	2
190	Antibiotic resistance prediction for from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019 , 4, 191	4.8	34
189	Panton-Valentine leucocidin is the key determinant of pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019 , 8,	8.9	30
188	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019 , 5,	4.4	93
187	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
186	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019 , 58,	9.7	70
185	Hash-Based Core Genome Multilocus Sequence Typing for Clostridium difficile. <i>Journal of Clinical Microbiology</i> , 2019 , 58,	9.7	9
184	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
183	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
182	Whole-Genome Sequencing for Predicting Clarithromycin Resistance in. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	20
181	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019 , 35, 2276-2282	7.2	35
180	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant Enterobacteriaceae 2019 , 14, e0222831		
179	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant Enterobacteriaceae 2019 , 14, e0222831		
178	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant Enterobacteriaceae 2019 , 14, e0222831		

177	Selective culture enrichment and sequencing of feces to enhance detection of antimicrobial resistance genes in third-generation cephalosporin resistant Enterobacteriaceae 2019 , 14, e0222831		
176	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
175	Patient and Strain Characteristics Associated With Clostridium difficile Transmission and Adverse Outcomes. <i>Clinical Infectious Diseases</i> , 2018 , 67, 1379-1387	11.6	13
174	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
173	Robust Prediction of Resistance to Trimethoprim in Staphylococcus aureus. <i>Cell Chemical Biology</i> , 2018 , 25, 339-349.e4	8.2	16
172	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018 , 34, 1666-1671	7.2	52
171	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
170	Identification of Biomarkers for Differentiation of Hypervirulent Klebsiella pneumoniae from Classical K. pneumoniae. <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	170
169	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
168	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
167	Trends over time in Escherichia coli 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
166	Control of Artifactual Variation in Reported Intersample Relatedness during Clinical Use of a Mycobacterium tuberculosis Sequencing Pipeline. <i>Journal of Clinical Microbiology</i> , 2018 , 56,	9.7	7
165	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
164	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
163	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
162	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis. <i>Microbiology (United Kingdom)</i> , 2018 , 164, 1522-1530	2.9	10
161	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,	4.4	14
160	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

159	Using linked electronic health records to report healthcare-associated infections. <i>PLoS ONE</i> , 2018 , 13, e0206860	3.7	2
158	An Open-Source Azure Solution for Scalable Genomics Workflows 2018 ,		2
157	DNA extraction from primary liquid blood cultures for bloodstream infection diagnosis using whole genome sequencing. <i>Journal of Medical Microbiology</i> , 2018 , 67, 347-357	3.2	15
156	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
155	Real-time analysis of nanopore-based metagenomic sequencing from infected orthopaedic devices. <i>BMC Genomics</i> , 2018 , 19, 714	4.5	67
154	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
153	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
152	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018 , 8, 15382	4.9	35
151	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,	9.7	15
150	Validating a 14-Drug Microtiter Plate Containing Bedaquiline and Delamanid for Large-Scale Research Susceptibility Testing of <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	31
149	Some Synonymous and Nonsynonymous Mutations in <i>Mycobacterium tuberculosis</i> 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
148	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 411-421	25.5	202
147	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
146	Tuberculosis is changing. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 359-361	25.5	35
145	Re-emergence of methicillin susceptibility in a resistant lineage of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1285-1288	5.1	13
144	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
143	Mortality risks associated with emergency admissions during weekends and public holidays: an analysis of electronic health records. <i>Lancet, The</i> , 2017 , 390, 62-72	4.0	75
142	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

141	Clostridium difficile in England: can we stop washing our hands? - AuthorsReply. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 478-479	25.5	1
140	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
139	Staphylococcus aureus in critical care - AuthorsReply. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 580-581	25.5	
138	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
137	WGS to predict antibiotic MICs for Neisseria gonorrhoeae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1937-1947	5.1	113
136	Enhanced Klebsiella pneumoniae Carbapenemase Expression from a Novel Tn Deletion. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	38
135	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
134	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
133	Aiming for zero tuberculosis transmission in low-burden countries. <i>Lancet Respiratory Medicine,the</i> , 2017 , 5, 846-848	35.1	9
132	BugMat and FindNeighbour: command line and server applications for investigating bacterial relatedness. <i>BMC Bioinformatics</i> , 2017 , 18, 477	3.6	11
131	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
130	mcr-1 and mcr-2 variant genes identified in Moraxella species isolated from pigs in Great Britain from 2014 to 2015. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 2745-2749	5.1	143
129	Global outbreak of severe Mycobacterium chimaera disease after cardiac surgery: a molecular epidemiological study. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 1033-1041	25.5	136
128	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
127	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
126	Developing an antimicrobial resistance reference laboratory and surveillance programme in Vietnam. <i>The Lancet Global Health</i> , 2017 , 5, e1186-e1187	13.6	12
125	Transmission of Staphylococcus aureus between health-care workers, the environment, and patients in an intensive care unit: a longitudinal cohort study based on whole-genome sequencing. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 207-214	25.5	113
124	A standardised method for interpreting the association between mutations and phenotypic drug resistance in. <i>European Respiratory Journal</i> , 2017 , 50,	13.6	198

123	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
122	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017 , 6,	8.9	55
121	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
120	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
119	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
118	First Report of blaIMP-14 on a Plasmid Harboring Multiple Drug Resistance Genes in Escherichia coli Sequence Type 131. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 5068-71	5.9	12
117	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016 , 1, 16041	26.6	143
116	Maternal colonization with Streptococcus agalactiae and associated stillbirth and neonatal disease in coastal Kenya. <i>Nature Microbiology</i> , 2016 , 1, 16067	26.6	64
115	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	3	4
114	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
113	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016 , 14, 150-62	22.2	239
112	Colistin resistance gene mcr-1 and pHNSHP45 plasmid in human isolates of Escherichia coli and Klebsiella pneumoniae. <i>Lancet Infectious Diseases, The</i> , 2016 , 16, 285-6	25.5	95
111	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
110	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. <i>MBio</i> , 2016 , 7, e02162	7.8	200
109	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998-2014. <i>Thorax</i> , 2016 , 71, 535-42	7.3	63
108	Complete Genome Sequence of KPC-Producing Klebsiella pneumoniae Strain CAV1193. <i>Genome Announcements</i> , 2016 , 4,		14
107	Capsular Typing Method for Streptococcus agalactiae Using Whole-Genome Sequence Data. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1388-90	9.7	24
106	Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae: an observational study. <i>Lancet Infectious Diseases, The</i> , 2016 , 16, 1295-1303	25.5	118

105	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
104	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
103	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 2516-26	4.8	69
102	Complete Sequencing of Plasmids Containing blaOXA-163 and blaOXA-48 in Escherichia coli Sequence Type 131. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 6948-6951	5.9	14
101	Colonization with Enterobacteriaceae producing ESBLs in children attending pre-school childcare facilities in the Lao People's Democratic Republic. <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 1893-1897	5.7	46
100	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , 2015 , 15, 1193-1202	25.5	391
99	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
98	Effects of proton pump inhibitors and histamine-2 receptor antagonists on response to fidaxomicin or vancomycin in patients with Clostridium difficile-associated diarrhoea. <i>BMJ Open Gastroenterology</i> , 2015 , 2, e000028	3.9	15
97	Rare variants in MYD88, IRAK4 and IKBKG and susceptibility to invasive pneumococcal disease: a population-based case-control study. <i>PLoS ONE</i> , 2015 , 10, e0123532	3.7	3
96	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. <i>PLoS Biology</i> , 2015 , 13, e1002229	9.7	76
95	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , 2015 , 6, 10063	17.4	348
94	Klebsiella pneumoniae carbapenemase (KPC)-producing K. pneumoniae at a single institution: insights into endemicity from whole-genome sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 1656-63	5.9	107
93	Machine learning for the prediction of antibacterial susceptibility in Mycobacterium tuberculosis 2014 ,		19
92	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
91	Pneumococcal Carriage 2014 , 136-147		10
90	Multidrug-resistant Escherichia coli soft tissue infection investigated with bacterial whole genome sequencing. <i>BMJ Case Reports</i> , 2014 , 2014,	0.9	2
89	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014 , 59, 752-3	11.6	
88	Reduction of invasive pneumococcal disease 3 years after the introduction of the 13-valent conjugate vaccine in the Oxfordshire region of England. <i>Journal of Infectious Diseases</i> , 2014 , 210, 1001-1007	11.7	69

87	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014 , 5, 3956	17.4	90
86	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
85	The complexity and diversity of the Pathogenicity Locus in <i>Clostridium difficile</i> clade 5. <i>Genome Biology and Evolution</i> , 2014 , 6, 3159-70	3.9	27
84	Evolutionary history of the <i>Clostridium difficile</i> pathogenicity locus. <i>Genome Biology and Evolution</i> , 2014 , 6, 36-52	3.9	123
83	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
82	Dynamics of acquisition and loss of carriage of <i>Staphylococcus aureus</i> strains in the community: the effect of clonal complex. <i>Journal of Infection</i> , 2014 , 68, 426-39	18.9	36
81	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
80	Differences in outcome according to <i>Clostridium difficile</i> testing method: a prospective multicentre diagnostic validation study of <i>C difficile</i> infection. <i>Lancet Infectious Diseases</i> , 2013 , 13, 936-45	25.5	320
79	Diverse sources of <i>C. difficile</i> infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , 2013 , 369, 1195-205	59.2	471
78	Whole-genome sequencing to delineate <i>Mycobacterium tuberculosis</i> outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , 2013 , 13, 137-46	25.5	615
77	Improved workflows for high throughput library preparation using the transposome-based Nextera system. <i>BMC Biotechnology</i> , 2013 , 13, 104	3.5	106
76	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
75	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
74	Within-host evolution of <i>Staphylococcus aureus</i> during asymptomatic carriage. <i>PLoS ONE</i> , 2013 , 8, e61319	3.7	141
73	Short-term genome stability of serial <i>Clostridium difficile</i> ribotype 027 isolates in an experimental gut model and recurrent human disease. <i>PLoS ONE</i> , 2013 , 8, e63540	3.7	14
72	Asymptomatic <i>Clostridium difficile</i> colonisation and onward transmission. <i>PLoS ONE</i> , 2013 , 8, e78445	3.7	90
71	Fidaxomicin versus vancomycin for infection with <i>Clostridium difficile</i> in Europe, Canada, and the USA: a double-blind, non-inferiority, randomised controlled trial. <i>Lancet Infectious Diseases</i> , 2012 , 12, 281-9	25.5	513
70	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012 , 13, 601-612	30.1	508

69	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
68	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012 , 13, R118	18.3	151
67	Surveillance of infection severity: a registry study of laboratory diagnosed <i>Clostridium difficile</i> . <i>PLoS Medicine</i> , 2012 , 9, e1001279	11.6	6
66	Increasing incidence of <i>Escherichia coli</i> bacteraemia is driven by an increase in antibiotic-resistant isolates: electronic database study in Oxfordshire 1999-2011. <i>Journal of Antimicrobial Chemotherapy</i> , 2012 , 67, 1514-24	5.1	33
65	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
64	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
63	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
62	Clinical <i>Clostridium difficile</i> : clonality and pathogenicity locus diversity. <i>PLoS ONE</i> , 2011 , 6, e19993	3.7	131
61	Decline of methicillin-resistant <i>Staphylococcus aureus</i> in Oxfordshire hospitals is strain-specific and preceded infection-control intensification. <i>BMJ Open</i> , 2011 , 1, e000160	3	46
60	Molecular epidemiology of <i>Clostridium difficile</i> strains in children compared with that of strains circulating in adults with <i>Clostridium difficile</i> -associated infection. <i>Journal of Clinical Microbiology</i> , 2011 , 49, 3994-6	9.7	30
59	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
58	Multilocus sequence typing of <i>Clostridium difficile</i> . <i>Journal of Clinical Microbiology</i> , 2010 , 48, 770-8	9.7	310
57	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
56	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
55	Diversity of antibiotic resistance integrative and conjugative elements among haemophili. <i>Journal of Medical Microbiology</i> , 2007 , 56, 838-846	3.2	11
54	Effect of antibiotic prescribing on antibiotic resistance in individual children in primary care: prospective cohort study. <i>BMJ, The</i> , 2007 , 335, 429	5.9	95
53	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
52	Molecular epidemiology of unrelated clusters of multiresistant strains of <i>Haemophilus influenzae</i> . <i>Journal of Infectious Diseases</i> , 1992 , 165, 1069-75	7	22

51	Omicron-associated changes in SARS-CoV-2 symptoms in the United Kingdom		4
50	Nanopore metagenomic sequencing of influenza virus directly from respiratory samples: diagnosis, drug resistance and nosocomial transmission		1
49	Prediction of Pyrazinamide Resistance in Mycobacterium Tuberculosis Using Structure-Based Machine Learning Approaches. <i>SSRN Electronic Journal</i> ,	1	5
48	Haemophilus spp.245-251		
47	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes		3
46	Reconciling the potentially irreconcilable? Genotypic and phenotypic amoxicillin-clavulanate resistance in Escherichia coli		2
45	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples		1
44	M. tuberculosis microvariation is common and is associated with transmission: analysis of three years prospective universal sequencing in England		2
43	Optimizing DNA extraction methods for Nanopore sequencing of Neisseria gonorrhoeae direct from urine samples		2
42	Time of day of vaccination affects SARS-CoV-2 antibody responses in an observational study of healthcare workers		1
41	Metrics for Public Health Perspective Surveillance of Bacterial Antibiotic Resistance in Low- and Middle-Income Countries		1
40	Multi-omic surveillance of Escherichia coli and Klebsiella spp. in hospital sink drains and patients		1
39	Amplicon based MinION sequencing of SARS-CoV-2 and metagenomic characterisation of nasopharyngeal swabs from patients with COVID-19		24
38	Optimised use of Oxford Nanopore Flowcells for Hybrid Assemblies		2
37	DNA Thermo-Protection Facilitates Whole Genome Sequencing of Mycobacteria Direct from Clinical Samples by the Nanopore Platform		1
36	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel		55
35	SARS-CoV-2 RNA detected in blood samples from patients with COVID-19 is not associated with infectious virus		10
34	Differential occupational risks to healthcare workers from SARS-CoV-2: A prospective observational study		6

33	Stringent thresholds for SARS-CoV-2 IgG assays result in under-detection of cases reporting loss of taste/smell?	
32	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae	3
31	CovidNudge: diagnostic accuracy of a novel lab-free point-of-care diagnostic for SARS-CoV-2	1
30	Diagnosis of SARS-CoV-2 infection with LamPORE, a high-throughput platform combining loop-mediated isothermal amplification and nanopore sequencing	10
29	A haemagglutination test for rapid detection of antibodies to SARS-CoV-2	6
28	Virus detection and identification in minutes using single-particle imaging and deep learning	9
27	The duration, dynamics and determinants of SARS-CoV-2 antibody responses in individual healthcare workers	10
26	Antibodies to SARS-CoV-2 are associated with protection against reinfection	23
25	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of Mycobacterium tuberculosis	2
24	Validating a 14-drug microtitre plate containing bedaquiline and delamanid for large-scale research susceptibility testing of Mycobacterium tuberculosis	1
23	MinION Nanopore Sequencing of Multiple Displacement Amplified Mycobacteria DNA Direct from Sputum	3
22	Nanopore metagenomic sequencing of full length human metapneumovirus (HMPV) within a unique sub-lineage	3
21	Prediction of pyrazinamide resistance in Mycobacterium tuberculosis using structure-based machine learning approaches	4
20	Genomic diversity affects the accuracy of bacterial SNP calling pipelines	6
19	Metagenomic Nanopore sequencing of influenza virus direct from clinical respiratory samples	2
18	Hash-based core genome multi-locus sequencing typing for Clostridium difficile	1
17	Antibody evasion by the Brazilian P.1 strain of SARS-CoV-2	14
16	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

15	Quantitative SARS-CoV-2 anti-spike responses to Pfizer-BioNTech and Oxford-AstraZeneca vaccines by previous infection status		7
14	The impact of SARS-CoV-2 vaccines on antibody responses in the general population in the United Kingdom		11
13	SARS-CoV-2 infectivity by viral load, S gene variants and demographic factors and the utility of lateral flow devices to prevent transmission		13
12	Impact of vaccination on new SARS-CoV-2 infections in the UK		20
11	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population		3
10	BashTheBug: a crowd of volunteers reproducibly and accurately measure the minimum inhibitory concentrations of 13 antitubercular drugs from photographs of 96-well broth microdilution plates		1
9	Reduced Neutralization of SARS-CoV-2 B.1.1.7 Variant from Naturally Acquired and Vaccine Induced Antibody Immunity. <i>SSRN Electronic Journal</i> ,	1	2
8	Increased infections, but not viral burden, with a new SARS-CoV-2 variant		31
7	Enhancing epidemiological investigation of nosocomial SARS-CoV-2 infection with whole genome sequencing: A retrospective cohort study across four hospitals in the UK.		1
6	Impact of Delta on viral burden and vaccine effectiveness against new SARS-CoV-2 infections in the UK		52
5	Symptoms and SARS-CoV-2 positivity in the general population in the UK		3
4	SARS-CoV-2 anti-spike IgG antibody responses after second dose of ChAdOx1 or BNT162b2 in the UK general population		3
3	Monitoring populations at increased risk for SARS-CoV-2 infection in the community		1
2	Molecular epidemiology of Escherichia coli and Klebsiella species bloodstream infections in Oxfordshire (UK) 2008-2018		2
1	Further antibody escape by Omicron BA.4 and BA.5 from vaccine and BA.1 serum		3