Timothy E A Peto

List of Publications by Year
in descending order

55 papers	3,639 citations	257450 24 h-index	182427 51 g-index
56 all docs	56 docs citations	56 times ranked	5330 citing authors

#	Article	IF	Citations
1	Cognitive behaviour therapy for the chronic fatigue syndrome: a randomised controlled trial. BMJ: British Medical Journal, 1996, 312, 22-26.	2.3	452
2	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	4.1	289
3	SARS-CoV-2 within-host diversity and transmission. Science, 2021, 372, .	12.6	278
4	Effects of control interventions on Clostridium difficile infection in England: an observational study. Lancet Infectious Diseases, The, 2017, 17, 411-421.	9.1	269
5	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
6	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
7	FAMILIAL POLYCYSTIC OVARIES: A GENETIC DISEASE?. Clinical Endocrinology, 1988, 29, 593-605.	2.4	165
8	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
9	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
10	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
11	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. Journal of Clinical Microbiology, 2019, 58, .	3.9	121
12	Rapid triage for COVID-19 using routine clinical data for patients attending hospital: development and prospective validation of an artificial intelligence screening test. The Lancet Digital Health, 2021, 3, e78-e87.	12.3	96
13	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
14	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998â€"2014. Thorax, 2016, 71, 535-542.	5.6	80
15	Application of machine learning techniques to tuberculosis drug resistance analysis. Bioinformatics, 2019, 35, 2276-2282.	4.1	71
16	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
17	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
18	A curated dataset of complete Enterobacteriaceae plasmids compiled from the NCBI nucleotide database. Data in Brief, 2017, 12, 423-426.	1.0	58

#	Article	IF	Citations
19	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. MBio, 2019, 10, .	4.1	46
20	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
21	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
22	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
23	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i>. Bioinformatics, 2019, 35, 3240-3249.	4.1	38
24	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
25	Whole-Genome Sequencing for Predicting Clarithromycin Resistance in <i>Mycobacterium abscessus</i>. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	34
26	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne <i>bla</i> _{KPC} Carbapenemase in <i>Enterobacterales</i> in the United Kingdom from 2009 to 2014. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	26
27	Genomic surveillance of Escherichia coli and Klebsiella spp. in hospital sink drains and patients. Microbial Genomics, 2020, 6, .	2.0	26
28	The evolutionary and clinical implications of the uneven distribution of the frequency of the inherited haemoglobin variants over short geographical distances. British Journal of Haematology, 2017, 176, 475-484.	2.5	25
29	Genomic network analysis of environmental and livestock F-type plasmid populations. ISME Journal, 2021, 15, 2322-2335.	9.8	24
30	Multi-Label Random Forest Model for Tuberculosis Drug Resistance Classification and Mutation Ranking. Frontiers in Microbiology, 2020, 11, 667.	3.5	22
31	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
32	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
33	BugMat and FindNeighbour: command line and server applications for investigating bacterial relatedness. BMC Bioinformatics, 2017, 18, 477.	2.6	16
34	Identifying Mixed Mycobacterium tuberculosis Infection and Laboratory Cross-Contamination during Mycobacterial Sequencing Programs. Journal of Clinical Microbiology, 2018, 56, .	3.9	16
35	Route and duration of antibiotic therapy in acute cellulitis: A systematic review and meta-analysis of the effectiveness and harms of antibiotic treatment. Journal of Infection, 2020, 81, 521-531.	3.3	15
36	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of Mycobacteria Direct from Clinical Samples. Journal of Clinical Microbiology, 2020, 58, .	3.9	14

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37	British HIV Association/British Association for Sexual Health and HIV/British Infection Association adult HIV testing guidelines 2020. HIV Medicine, 2020, 21, 1-26.	2.2	14
38	Flanker: a tool for comparative genomics of gene flanking regions. Microbial Genomics, 2021, 7, .	2.0	12
39	Absence of Atypical Pathogens in Pleural Infection. Chest, 2015, 148, e102-e103.	0.8	11
40	Severity of illness and the weekend effect â€" Authors' reply. Lancet, The, 2017, 390, 1735.	13.7	11
41	Predictors of recurrence, early treatment failure and death from Staphylococcus aureus bacteraemia: Observational analyses within the ARREST trial. Journal of Infection, 2019, 79, 332-340.	3.3	11
42	Risk Factors Associated with Carbapenemase-Producing *Enterobacterales* (CPE) Positivity in the Hospital Wastewater Environment. Applied and Environmental Microbiology, 2020, 86, .	3.1	11
43	Pneumococcal Carriage. , 0, , 136-147.		10
44	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
45	Why do hospital prescribers continue antibiotics when it is safe to stop? Results of a choice experiment survey. BMC Medicine, 2020, 18, 196.	5.5	9
46	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
47	Metalware-associated orthopaedic infections caused by Staphylococcus lugdunensis : An emerging pathogen. Journal of Infection, 2017, 75, 368-370.	3.3	8
48	Improved Performance Predicting Clarithromycin Resistance in *Mycobacterium abscessus* on an Independent Data Set. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	8
49	Antibiotic Review Kit for Hospitals (ARK-Hospital): study protocol for a stepped-wedge cluster-randomised controlled trial. Trials, 2019, 20, 421.	1.6	7
50	An end-to-end heterogeneous graph attention network for *Mycobacterium tuberculosis* drug-resistance prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	7
51	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
52	An Open-Source Azure Solution for Scalable Genomics Workflows. , 2018, , .		2
53	EFFECTS OF IRON AND DESFERRIOXAMINE ON THE GROWTH OF PLASMODIUM FALCIPARUM IN VITRO. British Journal of Haematology, 1987, 65, 257-257.	2.5	1
54	Reply to Mills and Linkin. Clinical Infectious Diseases, 2014, 59, 752-753.	5.8	0

#	ARTICLE	IF	CITATIONS
55	Staphylococcus aureus in critical care â€" Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 580-581.	9.1	0