

Timothy E A Peto

List of Publications by Year in descending order

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Version: 2024-02-01

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	Symptoms and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Positivity in the General Population in the United Kingdom. <i>Clinical Infectious Diseases</i> , 2022, 75, e329-e337.	5.8	20
2	A crowd of BashTheBug volunteers reproducibly and accurately measure the minimum inhibitory concentrations of 13 antitubercular drugs from photographs of 96-well broth microdilution plates. <i>ELife</i> , 2022, 11, .	6.0	7
3	Rapid triage for COVID-19 using routine clinical data for patients attending hospital: development and prospective validation of an artificial intelligence screening test. <i>The Lancet Digital Health</i> , 2021, 3, e78-e87.	12.3	96
4	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	9.8	24
5	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	12.6	278
6	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.	7.1	162
7	An end-to-end heterogeneous graph attention network for <i>Mycobacterium tuberculosis</i> drug-resistance prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
8	Flanker: a tool for comparative genomics of gene flanking regions. <i>Microbial Genomics</i> , 2021, 7, .	2.0	12
9	Ten-year longitudinal molecular epidemiology study of <i>Escherichia coli</i> and <i>Klebsiella</i> species bloodstream infections in Oxfordshire, UK. <i>Genome Medicine</i> , 2021, 13, 144.	8.2	35
10	DNA Thermo-Protection Facilitates Whole-Genome Sequencing of <i>Mycobacteria</i> Direct from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	14
11	Route and duration of antibiotic therapy in acute cellulitis: A systematic review and meta-analysis of the effectiveness and harms of antibiotic treatment. <i>Journal of Infection</i> , 2020, 81, 521-531.	3.3	15
12	Why do hospital prescribers continue antibiotics when it is safe to stop? Results of a choice experiment survey. <i>BMC Medicine</i> , 2020, 18, 196.	5.5	9
13	Risk Factors Associated with Carbapenemase-Producing <i>Enterobacterales</i> (CPE) Positivity in the Hospital Wastewater Environment. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	11
14	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne <i>bla</i> KPC in the United Kingdom from 2009 to 2014. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	26
15	Multi-Label Random Forest Model for Tuberculosis Drug Resistance Classification and Mutation Ranking. <i>Frontiers in Microbiology</i> , 2020, 11, 667.	3.5	22
16	Genomic surveillance of <i>Escherichia coli</i> and <i>Klebsiella</i> spp. in hospital sink drains and patients. <i>Microbial Genomics</i> , 2020, 6, .	2.0	26
17	British HIV Association/British Association for Sexual Health and HIV/British Infection Association adult HIV testing guidelines 2020. <i>HIV Medicine</i> , 2020, 21, 1-26.	2.2	14
18	Predictors of recurrence, early treatment failure and death from <i>Staphylococcus aureus</i> bacteraemia: Observational analyses within the ARREST trial. <i>Journal of Infection</i> , 2019, 79, 332-340.	3.3	11

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19	Antibiotic Review Kit for Hospitals (ARK-Hospital): study protocol for a stepped-wedge cluster-randomised controlled trial. <i>Trials</i> , 2019, 20, 421.	1.6	7
20	Improved Performance Predicting Clarithromycin Resistance in <i>Mycobacterium abscessus</i> on an Independent Data Set. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	8
21	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	4.1	38
22	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. <i>MBio</i> , 2019, 10, .	4.1	46
23	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	3.9	121
24	Whole-Genome Sequencing for Predicting Clarithromycin Resistance in <i>Mycobacterium abscessus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	34
25	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	4.1	71
26	An Open-Source Azure Solution for Scalable Genomics Workflows. , 2018, , .		2
27	Identifying Mixed <i>Mycobacterium tuberculosis</i> Infection and Laboratory Cross-Contamination during Mycobacterial Sequencing Programs. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	16
28	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, .	3.2	62
29	Control of Artfactual Variation in Reported Intersample Relatedness during Clinical Use of a <i>Mycobacterium tuberculosis</i> Sequencing Pipeline. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	10
30	Automated detection of bacterial growth on 96-well plates for high-throughput drug susceptibility testing of <i>Mycobacterium tuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 1522-1530.	1.8	21
31	Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from <i>Staphylococcus aureus</i> Whole-Genome Sequences. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	61
32	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 411-421.	9.1	269
33	The evolutionary and clinical implications of the uneven distribution of the frequency of the inherited haemoglobin variants over short geographical distances. <i>British Journal of Haematology</i> , 2017, 176, 475-484.	2.5	25
34	Contribution to <i>Clostridium Difficile</i> Transmission of Symptomatic Patients With Toxigenic Strains Who Are Fecal Toxin Negative. <i>Clinical Infectious Diseases</i> , 2017, 64, 1163-1170.	5.8	45
35	Metalware-associated orthopaedic infections caused by <i>Staphylococcus lugdunensis</i> : An emerging pathogen. <i>Journal of Infection</i> , 2017, 75, 368-370.	3.3	8
36	<i>Staphylococcus aureus</i> in critical care – Authors' reply. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 580-581.	9.1	0

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37	The Hospital Water Environment as a Reservoir for Carbapenem-Resistant Organisms Causing Hospital-Acquired Infectionsâ€”A Systematic Review of the Literature. <i>Clinical Infectious Diseases</i> , 2017, 64, 1435-1444.	5.8	242
38	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.	1.4	89
39	A curated dataset of complete Enterobacteriaceae plasmids compiled from the NCBI nucleotide database. <i>Data in Brief</i> , 2017, 12, 423-426.	1.0	58
40	Severity of illness and the weekend effect â€” Authors' reply. <i>Lancet</i> , The, 2017, 390, 1735.	13.7	11
41	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</i> , The, 2017, 17, 207-214.	9.1	155
42	Plasmid Classification in an Era of Whole-Genome Sequencing: Application in Studies of Antibiotic Resistance Epidemiology. <i>Frontiers in Microbiology</i> , 2017, 8, 182.	3.5	191
43	BugMat and FindNeighbour: command line and server applications for investigating bacterial relatedness. <i>BMC Bioinformatics</i> , 2017, 18, 477.	2.6	16
44	Antibiotic use and clinical outcomes in the acute setting under management by an infectious diseases acute physician versus other clinical teams: a cohort study. <i>BMJ Open</i> , 2016, 6, e010969.	1.9	8
45	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.	4.1	289
46	Increasing burden of community-acquired pneumonia leading to hospitalisation, 1998â€”2014. <i>Thorax</i> , 2016, 71, 535-542.	5.6	80
47	Absence of Atypical Pathogens in Pleural Infection. <i>Chest</i> , 2015, 148, e102-e103.	0.8	11
48	<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, 1656-1663.	3.2	140
49	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014, 59, 752-753.	5.8	0
50	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, 426-439.	3.3	42
51	Population structure of group B streptococcus from a low-incidence region for invasive neonatal disease. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1875-1881.	1.8	45
52	Cognitive behaviour therapy for the chronic fatigue syndrome: a randomised controlled trial. <i>BMJ: British Medical Journal</i> , 1996, 312, 22-26.	2.3	452
53	FAMILIAL POLYCYSTIC OVARIES: A GENETIC DISEASE?. <i>Clinical Endocrinology</i> , 1988, 29, 593-605.	2.4	165
54	EFFECTS OF IRON AND DESFERRIOXAMINE ON THE GROWTH OF <i>PLASMODIUM FALCIPARUM</i> IN VITRO. <i>British Journal of Haematology</i> , 1987, 65, 257-257.	2.5	1

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55	Pneumococcal Carriage. , 0, , 136-147.		10