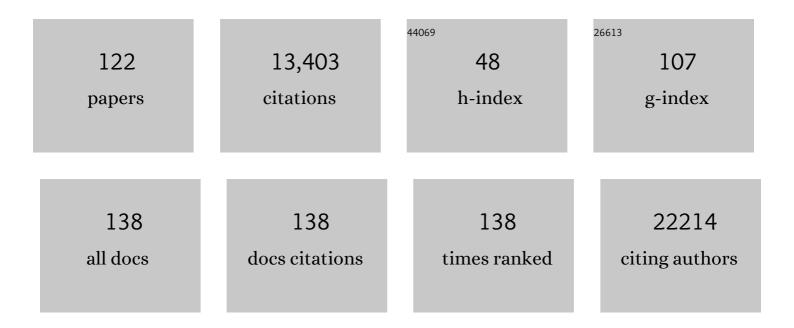
List of Publications by Year in descending order

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FSTEE TOPOK

#	Article	IF	CITATIONS
1	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. Lancet Microbe, The, 2022, 3, e151-e158.	7.3	25
2	A2B-COVID: A Tool for Rapidly Evaluating Potential SARS-CoV-2 Transmission Events. Molecular Biology and Evolution, 2022, 39, .	8.9	12
3	P48 The limited yield of cultures in the critically ill child. JAC-Antimicrobial Resistance, 2022, 4, .	2.1	0
4	Safety and efficacy of the ChAdOx1 nCoV-19 vaccine (AZD1222) against SARS-CoV-2: an interim analysis of four randomised controlled trials in Brazil, South Africa, and the UK. Lancet, The, 2021, 397, 99-111.	13.7	3,887
5	Quantifying acquisition and transmission of Enterococcus faecium using genomic surveillance. Nature Microbiology, 2021, 6, 103-111.	13.3	53
6	Genomic epidemiology of COVID-19 in care homes in the east of England. ELife, 2021, 10, .	6.0	20
7	Single-dose administration and the influence of the timing of the booster dose on immunogenicity and efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine: a pooled analysis of four randomised trials. Lancet, The, 2021, 397, 881-891.	13.7	979
8	Rapid Whole Genome Sequencing of Serotype K1 Hypervirulent Klebsiella pneumoniae from an Undocumented Chinese Migrant. Case Reports in Infectious Diseases, 2021, 2021, 1-5.	0.5	2
9	Low diagnostic yield and time to diagnostic confirmation results in prolonged use of antimicrobials in critically ill children. Wellcome Open Research, 2021, 6, 119.	1.8	5
10	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. Lancet Public Health, The, 2021, 6, e335-e345.	10.0	269
11	Challenges and opportunities for conducting a vaccine trial during the COVID-19 pandemic in the United Kingdom. Clinical Trials, 2021, 18, 615-621.	1.6	3
12	Applying prospective genomic surveillance to support investigation of hospital-onset COVID-19. Lancet Infectious Diseases, The, 2021, 21, 916-917.	9.1	14
13	Superspreaders drive the largest outbreaks of hospital onset COVID-19 infections. ELife, 2021, 10, .	6.0	34
14	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	6.0	110
15	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	12.6	111
16	Rapid Assay for Sick Children with Acute Lung infection Study (RASCALS): diagnostic cohort study protocol. BMJ Open, 2021, 11, e056197.	1.9	5
17	Population pharmacokinetics and pharmacogenetics of ritonavir-boosted darunavir in the presence of raltegravir or tenofovir disoproxil fumarate/emtricitabine in HIV-infected adults and the relationship with virological response: a sub-study of the NEAT001/ANRS143 randomized trial. Journal of Antimicrobial Chemotherapy, 2020, 75, 628-639.	3.0	7
18	Combined Point-of-Care Nucleic Acid and Antibody Testing for SARS-CoV-2 following Emergence of D614G Spike Variant. Cell Reports Medicine, 2020, 1, 100099.	6.5	61

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19	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. Lancet Infectious Diseases, The, 2020, 20, 1263-1271.	9.1	352
20	Defining persistent Staphylococcus aureus bacteraemia: secondary analysis of a prospective cohort study. Lancet Infectious Diseases, The, 2020, 20, 1409-1417.	9.1	84
21	How achievable are COVID-19 clinical trial recruitment targets? A UK observational cohort study and trials registry analysis. BMJ Open, 2020, 10, e044566.	1.9	11
22	Treatment of COVID-19 with remdesivir in the absence of humoral immunity: a case report. Nature Communications, 2020, 11, 6385.	12.8	103
23	Taking the right measures to control COVID-19. Lancet Infectious Diseases, The, 2020, 20, 523-524.	9.1	251
24	Screening of healthcare workers for SARS-CoV-2 highlights the role of asymptomatic carriage in COVID-19 transmission. ELife, 2020, 9, .	6.0	423
25	Effective control of SARS-CoV-2 transmission between healthcare workers during a period of diminished community prevalence of COVID-19. ELife, 2020, 9, .	6.0	40
26	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7Âyears in a single center. Genome Biology, 2019, 20, 184.	8.8	22
27	An outbreak of meticillin-resistant Staphylococcus aureus colonization in a neonatal intensive care unit: use of a case–control study to investigate and control it and lessons learnt. Journal of Hospital Infection, 2019, 103, 35-43.	2.9	12
28	Dynamic Prediction of Death in Patients With Tuberculous Meningitis Using Time-updated Glasgow Coma Scale and Plasma Sodium Measurements. Clinical Infectious Diseases, 2019, 70, 827-834.	5.8	14
29	Multi-Compartment Profiling of Bacterial and Host Metabolites Identifies Intestinal Dysbiosis and Its Functional Consequences in the Critically III Child. Critical Care Medicine, 2019, 47, e727-e734.	0.9	19
30	Prospective genomic surveillance of methicillin-resistant Staphylococcus aureus (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. Eurosurveillance, 2019, 24, .	7.0	19
31	Absence of cerebrospinal fluid pleocytosis in tuberculous meningitis is a common occurrence in HIV co-infection and a predictor of poor outcomes. International Journal of Infectious Diseases, 2018, 68, 77-78.	3.3	13
32	Duration of exposure to multiple antibiotics is associated with increased risk of VRE bacteraemia: a nested case-control study. Journal of Antimicrobial Chemotherapy, 2018, 73, 1692-1699.	3.0	40
33	Suboptimal Exposure to Antiâ€₹B Drugs in a TBM/HIV+ Population Is Not Related to Antiretroviral Therapy. Clinical Pharmacology and Therapeutics, 2018, 103, 449-457.	4.7	13
34	Prognostic Models for 9-Month Mortality in Tuberculous Meningitis. Clinical Infectious Diseases, 2018, 66, 523-532.	5.8	65
35	Adjunctive rifampicin for Staphylococcus aureus bacteraemia (ARREST): a multicentre, randomised, double-blind, placebo-controlled trial. Lancet, The, 2018, 391, 668-678.	13.7	140
36	Extended-spectrum β-lactamase-producing and carbapenemase-producing Enterobacteriaceae. Microbial Genomics, 2018, 4, .	2.0	45

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37	Survival following Staphylococcus aureus bloodstream infection: A prospective multinational cohort study assessing the impact of place of care. Journal of Infection, 2018, 77, 516-525.	3.3	48
38	Point-prevalence survey of carbapenemase-producing Enterobacteriaceae and vancomycin-resistant enterococci in adult inpatients in a university teaching hospital in the UK. Journal of Hospital Infection, 2018, 100, 35-39.	2.9	21
39	Adjunctive rifampicin to reduce early mortality from Staphylococcus aureus bacteraemia: the ARREST RCT. Health Technology Assessment, 2018, 22, 1-148.	2.8	10
40	Complex Routes of Nosocomial Vancomycin-Resistant Enterococcus faecium Transmission Revealed by Genome Sequencing. Clinical Infectious Diseases, 2017, 64, 886-893.	5.8	93
41	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. Science Translational Medicine, 2017, 9, .	12.4	103
42	Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant Staphylococcus aureus Transmission in a Community Setting. Clinical Infectious Diseases, 2017, 65, 2069-2077.	5.8	11
43	Community outbreaks of group A Streptococcus revealed by genome sequencing. Scientific Reports, 2017, 7, 8554.	3.3	26
44	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant Staphylococcus aureus in the East of England. Scientific Reports, 2017, 7, 7406.	3.3	25
45	Clonal differences in Staphylococcus aureus bacteraemia-associated mortality. Nature Microbiology, 2017, 2, 1381-1388.	13.3	118
46	Antimicrobial resistance in human populations: challenges and opportunities. Global Health, Epidemiology and Genomics, 2017, 2, e4.	0.8	75
47	Evolution of mobile genetic element composition in an epidemic methicillin-resistant Staphylococcus aureus: temporal changes correlated with frequent loss and gain events. BMC Genomics, 2017, 18, 684.	2.8	43
48	Longitudinal genomic surveillance of multidrug-resistant Escherichia coli carriage in a long-term care facility in the United Kingdom. Genome Medicine, 2017, 9, 70.	8.2	44
49	Within-host evolution of Enterococcus faecium during longitudinal carriage and transition to bloodstream infection in immunocompromised patients. Genome Medicine, 2017, 9, 119.	8.2	26
50	Prospective Surveillance and Rapid Whole-Genome Sequencing Detects Two Unsuspected Outbreaks of Carbapenemase-Producing Klebsiella pneumoniae in a UK Teaching Hospital. Open Forum Infectious Diseases, 2017, 4, S43-S44.	0.9	3
51	Population genetic structuring of methicillin-resistant Staphylococcus aureus clone EMRSA-15 within UK reflects patient referral patterns. Microbial Genomics, 2017, 3, e000113.	2.0	19
52	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. PLoS ONE, 2017, 12, e0189838.	2.5	19
53	Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011–2013. Emerging Infectious Diseases, 2016, 22, 1658-1659.	4.3	4
54	Methicillin-resistant Staphylococcus aureus multiple sites surveillance: a systemic review of the literature. Infection and Drug Resistance, 2016, 9, 35.	2.7	35

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55	Efavirenz and Metabolites in Cerebrospinal Fluid: Relationship with <i>CYP2B6</i> c.516G→T Genotype and Perturbed Blood-Brain Barrier Due to Tuberculous Meningitis. Antimicrobial Agents and Chemotherapy, 2016, 60, 4511-4518.	3.2	18
56	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. Genome Research, 2016, 26, 263-270.	5.5	63
57	<i>dfrA thyA</i> Double Deletion in <i>para</i> -Aminosalicylic Acid-Resistant Mycobacterium tuberculosis Beijing Strains. Antimicrobial Agents and Chemotherapy, 2016, 60, 3864-3867.	3.2	20
58	Transmission of methicillin-resistant Staphylococcus aureus in long-term care facilities and their related healthcare networks. Genome Medicine, 2016, 8, 102.	8.2	30
59	Genome-based characterization of hospital-adapted Enterococcus faecalis lineages. Nature Microbiology, 2016, 1, .	13.3	65
60	A decade of genomic history for healthcare-associated <i>Enterococcus faecium</i> in the United Kingdom and Ireland. Genome Research, 2016, 26, 1388-1396.	5.5	96
61	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 in the East of England. Journal of Infectious Diseases, 2016, 214, 447-453.	4.0	45
62	Comparison of two chromogenic media for the detection of vancomycin-resistant enterococcal carriage by nursing home residents. Diagnostic Microbiology and Infectious Disease, 2016, 85, 409-412.	1.8	7
63	Vaccination of chemotherapy patients—effect of guideline implementation. Supportive Care in Cancer, 2016, 24, 2317-2321.	2.2	17
64	Comparison of 2 chromogenic media for the detection of extended-spectrum β-lactamase producing Enterobacteriaceae stool carriage in nursing home residents. Diagnostic Microbiology and Infectious Disease, 2016, 84, 181-183.	1.8	16
65	Whole-genome sequencing reveals transmission of vancomycin-resistant Enterococcus faecium in a healthcare network. Genome Medicine, 2016, 8, 4.	8.2	58
66	Whole-genome sequencing for the diagnosis of drug-resistant tuberculosis. Lancet Infectious Diseases, The, 2016, 16, 17.	9.1	2
67	Indoor Air Pollution and Delayed Measles Vaccination Increase the Risk of Severe Pneumonia in Children: Results from a Case-Control Study in Mwanza, Tanzania. PLoS ONE, 2016, 11, e0160804.	2.5	14
68	Emergent and evolving antimicrobial resistance cassettes in community-associated fusidic acid and meticillin-resistant Staphylococcus aureus. International Journal of Antimicrobial Agents, 2015, 45, 477-484.	2.5	39
69	Drug-resistance mechanisms and tuberculosis drugs. Lancet, The, 2015, 385, 305-307.	13.7	22
70	Public perceptions of bacterial whole-genome sequencing for tuberculosis. Trends in Genetics, 2015, 31, 58-60.	6.7	5
71	Tuberculous meningitis: advances in diagnosis and treatment. British Medical Bulletin, 2015, 113, 117-131.	6.9	92
72	Impact of routine bedside infectious disease consultation on clinical management and outcome of Staphylococcus aureus bacteraemia in adults. Clinical Microbiology and Infection, 2015, 21, 779-785.	6.0	58

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73	Characterization of Plasmids in Extensively Drug-Resistant Acinetobacter Strains Isolated in India and Pakistan. Antimicrobial Agents and Chemotherapy, 2015, 59, 923-929.	3.2	54
74	Impact of infectious diseases consultation on the management of Staphylococcus aureus bacteraemia in children. BMJ Open, 2014, 4, e004659-e004659.	1.9	18
75	Zero tolerance for healthcare-associated MRSA bacteraemia: is it realistic?. Journal of Antimicrobial Chemotherapy, 2014, 69, 2238-2245.	3.0	27
76	Staphylococcus aureus bloodstream infection: A pooled analysis of five prospective, observational studies. Journal of Infection, 2014, 68, 242-251.	3.3	207
77	Rapid single-colony whole-genome sequencing of bacterial pathogens. Journal of Antimicrobial Chemotherapy, 2014, 69, 1275-1281.	3.0	49
78	A Spaetzle-like role for nerve growth factor β in vertebrate immunity to <i>Staphylococcus aureus</i> . Science, 2014, 346, 641-646.	12.6	68
79	Prevalence and characterization of human mecC methicillin-resistant Staphylococcus aureus isolates in England. Journal of Antimicrobial Chemotherapy, 2014, 69, 907-910.	3.0	62
80	Read and assembly metrics inconsequential for clinical utility of whole-genome sequencing in mapping outbreaks. Nature Biotechnology, 2013, 31, 592-594.	17.5	26
81	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. JAMA Internal Medicine, 2013, 173, 1397.	5.1	181
82	Whole-Genome Sequencing for Rapid Susceptibility Testing of <i>M. tuberculosis</i> . New England Journal of Medicine, 2013, 369, 290-292.	27.0	195
83	Whole-genome sequencing for analysis of an outbreak of meticillin-resistant Staphylococcus aureus: a descriptive study. Lancet Infectious Diseases, The, 2013, 13, 130-136.	9.1	531
84	Rapid Whole-Genome Sequencing for Investigation of a Suspected Tuberculosis Outbreak. Journal of Clinical Microbiology, 2013, 51, 611-614.	3.9	80
85	A pilot study of rapid whole-genome sequencing for the investigation of a <i>Legionella</i> outbreak. BMJ Open, 2013, 3, e002175.	1.9	105
86	Use of Vitek 2 Antimicrobial Susceptibility Profile To Identify <i>mecC</i> in Methicillin-Resistant Staphylococcus aureus. Journal of Clinical Microbiology, 2013, 51, 2732-2734.	3.9	53
87	Initiation of antiretroviral therapy in <scp>HIV</scp> â€infected tuberculosis patients in rural <scp>K</scp> enya: an observational study. Tropical Medicine and International Health, 2013, 18, 907-914.	2.3	5
88	Incidence and Characterisation of Methicillin-Resistant Staphylococcus aureus (MRSA) from Nasal Colonisation in Participants Attending a Cattle Veterinary Conference in the UK. PLoS ONE, 2013, 8, e68463.	2.5	28
89	Influence of Antituberculosis Drug Resistance and Mycobacterium tuberculosis Lineage on Outcome in HIV-Associated Tuberculous Meningitis. Antimicrobial Agents and Chemotherapy, 2012, 56, 3074-3079.	3.2	44
90	Rapid whole-genome sequencing of bacterial pathogens in the clinical microbiology laboratorypipe dream or reality?. Journal of Antimicrobial Chemotherapy, 2012, 67, 2307-2308.	3.0	47

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91	Glucocorticoids plusN-Acetylcysteine in Alcoholic Hepatitis. New England Journal of Medicine, 2012, 366, 476-477.	27.0	2
92	Bacterial gene loss as a mechanism for gain of antimicrobial resistance. Current Opinion in Microbiology, 2012, 15, 583-587.	5.1	14
93	Adjunctive rifampicin to reduce early mortality from Staphylococcus aureus bacteraemia (ARREST): study protocol for a randomised controlled trial. Trials, 2012, 13, 241.	1.6	29
94	<i><scp>S</scp>trongyloides stercoralis</i> hyperinfection in a patient treated for multiple myeloma. British Journal of Haematology, 2012, 158, 2-2.	2.5	7
95	Timing of Initiation of Antiretroviral Therapy in Human Immunodeficiency Virus (HIV)-Associated Tuberculous Meningitis. Clinical Infectious Diseases, 2011, 52, 1374-1383.	5.8	286
96	Clinical management of Staphylococcus aureus bacteraemia. Lancet Infectious Diseases, The, 2011, 11, 208-222.	9.1	230
97	Optimum time to start antiretroviral therapy during HIV-associated opportunistic infections. Current Opinion in Infectious Diseases, 2011, 24, 34-42.	3.1	52
98	Randomized Pharmacokinetic and Pharmacodynamic Comparison of Fluoroquinolones for Tuberculous Meningitis. Antimicrobial Agents and Chemotherapy, 2011, 55, 3244-3253.	3.2	114
99	When to Start Antiretroviral Therapy in HIV-Associated Tuberculosis. New England Journal of Medicine, 2011, 365, 1538-1540.	27.0	41
100	Valacyclovir for Herpes Simplex Encephalitis. Antimicrobial Agents and Chemotherapy, 2011, 55, 3624-3626.	3.2	52
101	Human Immunodeficiency Virus-Associated Tuberculosis. Clinical and Developmental Immunology, 2011, 2011, 1-3.	3.3	1
102	Dexamethasone and Long-Term Outcome of Tuberculous Meningitis in Vietnamese Adults and Adolescents. PLoS ONE, 2011, 6, e27821.	2.5	77
103	HIV-associated tuberculous meningitis – diagnostic and therapeutic challenges. Tuberculosis, 2010, 90, 367-374.	1.9	60
104	First Report of <i>Salmonella enterica</i> Serotype Paratyphi A Azithromycin Resistance Leading to Treatment Failure. Journal of Clinical Microbiology, 2010, 48, 4655-4657.	3.9	62
105	Tuberculous meningitis: a uniform case definition for use in clinical research. Lancet Infectious Diseases, The, 2010, 10, 803-812.	9.1	659
106	Outpatient parenteral antimicrobial therapy: Recent developments and future prospects. Current Opinion in Investigational Drugs, 2010, 11, 929-39.	2.3	12
107	The Influence of Host and Bacterial Genotype on the Development of Disseminated Disease with Mycobacterium tuberculosis. PLoS Pathogens, 2008, 4, e1000034.	4.7	410
108	Relationship between <i>Mycobacterium tuberculosis</i> Genotype and the Clinical Phenotype of Pulmonary and Meningeal Tuberculosis. Journal of Clinical Microbiology, 2008, 46, 1363-1368.	3.9	134

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109	Immune reconstitution disease of the central nervous system. Current Opinion in HIV and AIDS, 2008, 3, 438-445.	3.8	28
110	Clinical and Microbiological Features of HIV-Associated Tuberculous Meningitis in Vietnamese Adults. PLoS ONE, 2008, 3, e1772.	2.5	82
111	Dexamethasone in Vietnamese Adolescents and Adults with Bacterial Meningitis. New England Journal of Medicine, 2007, 357, 2431-2440.	27.0	221
112	PCR-Restriction Fragment Length Polymorphism for Rapid, Low-Cost Identification of Isoniazid-Resistant Mycobacterium tuberculosis. Journal of Clinical Microbiology, 2007, 45, 1789-1793.	3.9	15
113	Neurological infections: clinical advances and emerging threats. Lancet Neurology, The, 2007, 6, 16-18.	10.2	5
114	Evaluation of the MODS Culture Technique for the Diagnosis of Tuberculous Meningitis. PLoS ONE, 2007, 2, e1173.	2.5	51
115	Validation of a Diagnostic Algorithm for Adult Tuberculous Meningitis. American Journal of Tropical Medicine and Hygiene, 2007, 77, 555-559.	1.4	42
116	Validation of a diagnostic algorithm for adult tuberculous meningitis. American Journal of Tropical Medicine and Hygiene, 2007, 77, 555-9.	1.4	16
117	Pretreatment Intracerebral and Peripheral Blood Immune Responses in Vietnamese Adults with Tuberculous Meningitis: Diagnostic Value and Relationship to Disease Severity and Outcome. Journal of Immunology, 2006, 176, 2007-2014.	0.8	87
118	Human immunodeficiency virus associated central nervous system infections. Practical Neurology, 2005, 5, 334-349.	1.1	3
119	Immediate or deferred antiretroviral therapy for central nervous system opportunistic infections?. Aids, 2005, 19, 535-536.	2.2	4
120	Hepatitis C virus infection is not associated with a marked increase in the prevalence of ophthalmic morbidity. Eye, 2000, 14, 889-891.	2.1	4
121	Hepatitis C virus dynamicsin vivoand the antiviral efficacy of interferon alfa therapy. Hepatology, 1999, 29, 1333-1334.	7.3	10
122	Association of hepatitis B surface antigen carriage with severe malaria in Gambian children. Nature Medicine, 1995, 1, 374-375.	30.7	62