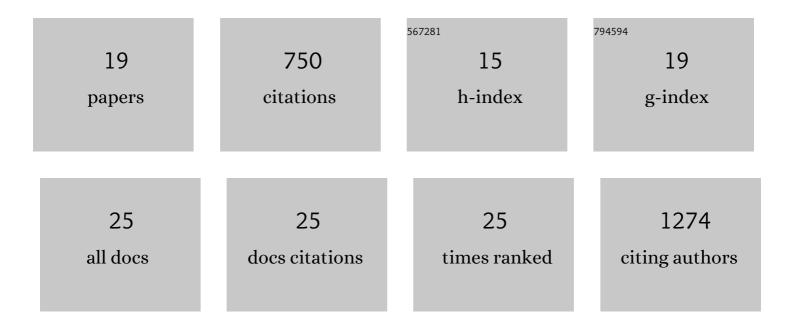
Catherine E Ludden

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Quantifying acquisition and transmission of Enterococcus faecium using genomic surveillance. Nature Microbiology, 2021, 6, 103-111.	13.3	53
2	Defining nosocomial transmission of Escherichia coli and antimicrobial resistance genes: a genomic surveillance study. Lancet Microbe, The, 2021, 2, e472-e480.	7.3	39
3	A One Health Study of the Genetic Relatedness of Klebsiella pneumoniae and Their Mobile Elements in the East of England. Clinical Infectious Diseases, 2020, 70, 219-226.	5.8	46
4	A novel therapeutic antibody screening method using bacterial high-content imaging reveals functional antibody binding phenotypes of Escherichia coli ST131. Scientific Reports, 2020, 10, 12414.	3.3	9
5	Genomic surveillance of Escherichia coli ST131 identifies local expansion and serial replacement of subclones. Microbial Genomics, 2020, 6, .	2.0	33
6	One Health Genomic Surveillance of Escherichia coli Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. MBio, 2019, 10, .	4.1	130
7	Detection of vancomycin-resistant <i>Enterococcus faecium</i> hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment. Genome Research, 2019, 29, 626-634.	5.5	40
8	Genomic surveillance of Escherichia coli in municipal wastewater treatment plants as an indicator of clinically relevant pathogens and their resistance genes. Microbial Genomics, 2019, 5, .	2.0	29
9	Genomic Surveillance of Enterococcus faecium Reveals Limited Sharing of Strains and Resistance Genes between Livestock and Humans in the United Kingdom. MBio, 2018, 9, .	4.1	63
10	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
11	Sharing of carbapenemase-encoding plasmids between Enterobacteriaceae in UK sewage uncovered by MinION sequencing. Microbial Genomics, 2017, 3, e000114.	2.0	33
12	Transmission of methicillin-resistant Staphylococcus aureus in long-term care facilities and their related healthcare networks. Genome Medicine, 2016, 8, 102.	8.2	30
13	Dissemination of clonally related multidrug-resistant <i>Klebsiella pneumoniae</i> in Ireland. Epidemiology and Infection, 2016, 144, 443-448.	2.1	16
14	Characterization of methicillin-resistant <i>Staphylococcus aureus</i> from residents and the environment in a long-term care facility. Epidemiology and Infection, 2015, 143, 2985-2988.	2.1	7
15	Colonisation with ESBL-producing and carbapenemase-producing Enterobacteriaceae, vancomycin-resistant enterococci, and meticillin-resistant Staphylococcus aureus in a long-term care facility over one year. BMC Infectious Diseases, 2015, 15, 168.	2.9	54
16	Rapid environmental contamination of a new nursing home with antimicrobial-resistant organisms preceding occupation by residents. Journal of Hospital Infection, 2013, 83, 327-329.	2.9	9
17	Detection of OXA-48 Carbapenemase in the Pandemic Clone Escherichia coli O25b:H4-ST131 in the Course of Investigation of an Outbreak of OXA-48-Producing Klebsiella pneumoniae. Antimicrobial Agents and Chemotherapy, 2012, 56, 4030-4031.	3.2	32
18	Production of KPC-2 Carbapenemase by an Escherichia coli Clinical Isolate Belonging to the International ST131 Clone. Antimicrobial Agents and Chemotherapy, 2011, 55, 4935-4936.	3.2	51

#	Article	IF	CITATIONS
19	Characterising the persistence of RT-PCR positivity and incidence in a community survey of SARS-CoV-2. Wellcome Open Research, 0, 7, 102.	1.8	7