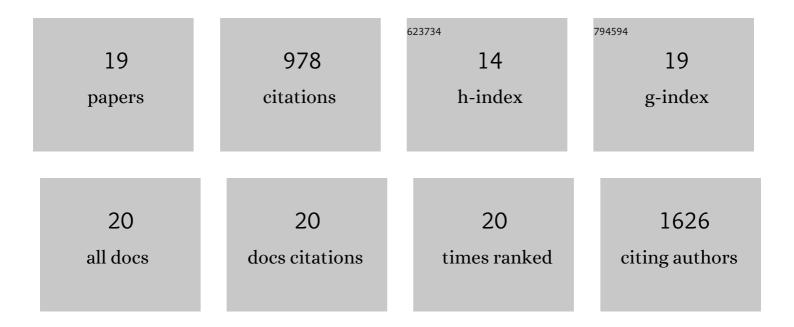
Christine J Boinett

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Risk factors for polymyxin-resistant carbapenemase-producing Enterobacteriaceae in critically ill patients: An epidemiological and clinical study. International Journal of Antimicrobial Agents, 2020, 55, 105882.	2.5	8
2	Molecular and epidemiological surveillance of polymyxin-resistant Klebsiella pneumoniae strains isolated from Brazil with multiple mgrB gene mutations. International Journal of Medical Microbiology, 2020, 310, 151448.	3.6	17
3	High-resolution sweep metagenomics using fast probabilistic inference. Wellcome Open Research, 2020, 5, 14.	1.8	13
4	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
5	Clinical and laboratory-induced colistin-resistance mechanisms in Acinetobacter baumannii. Microbial Genomics, 2019, 5, .	2.0	30
6	Clinical features, antimicrobial susceptibility patterns and genomics of bacteria causing neonatal sepsis in a children's hospital in Vietnam: protocol for a prospective observational study. BMJ Open, 2018, 8, e019611.	1.9	6
7	Morphological, genomic and transcriptomic responses of Klebsiella pneumoniae to the last-line antibiotic colistin. Scientific Reports, 2018, 8, 9868.	3.3	20
8	Transposon Insertion Sequencing Elucidates Novel Gene Involvement in Susceptibility and Resistance to Phages T4 and T7 in <i>Escherichia coli</i> O157. MBio, 2018, 9, .	4.1	23
9	Outbreaks of Serratia marcescens and Serratia rubidaea bacteremia in a central Kathmandu hospital following the 2015 earthquakes. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2018, 112, 467-472.	1.8	17
10	A global genomic approach uncovers novel components for twitching motility-mediated biofilm expansion in Pseudomonas aeruginosa. Microbial Genomics, 2018, 4, .	2.0	17
11	The secondary resistome of multidrug-resistant Klebsiella pneumoniae. Scientific Reports, 2017, 7, 42483.	3.3	69
12	Molecular epidemiology of Klebsiella pneumoniae invasive infections over a decade at Kilifi County Hospital in Kenya. International Journal of Medical Microbiology, 2017, 307, 422-429.	3.6	61
13	The essential genomic landscape of the commensal Bifidobacterium breve UCC2003. Scientific Reports, 2017, 7, 5648.	3.3	26
14	Phenotypic and genotypic characteristics of ESBL and AmpC producing organisms associated with bacteraemia in Ho Chi Minh City, Vietnam. Antimicrobial Resistance and Infection Control, 2017, 6, 105.	4.1	15
15	Recent independent emergence of multiple multidrug-resistant <i>Serratia marcescens</i> clones within the United Kingdom and Ireland. Genome Research, 2016, 26, 1101-1109.	5.5	74
16	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. Bioinformatics, 2016, 32, 1109-1111.	4.1	167
17	A highâ€resolution genomic analysis of multidrugâ€resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . EMBO Molecular Medicine, 2015, 7, 227-239.	6.9	104
18	High-Throughput Analysis of Gene Essentiality and Sporulation in Clostridium difficile. MBio, 2015, 6, e02383.	4.1	157

#	Article	IF	CITATIONS
19	Approaches to querying bacterial genomes with transposon-insertion sequencing. RNA Biology, 2013, 10, 1161-1169.	3.1	132