

# Beth Blane

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2872366/publications.pdf>

Version: 2024-02-01

41  
papers

2,041  
citations

331670

21  
h-index

276875

41  
g-index

45  
all docs

45  
docs citations

45  
times ranked

3910  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. Nature Communications, 2022, 13, 751.	12.8	27
2	Quantifying acquisition and transmission of Enterococcus faecium using genomic surveillance. Nature Microbiology, 2021, 6, 103-111.	13.3	53
3	A common protocol for the simultaneous processing of multiple clinically relevant bacterial species for whole genome sequencing. Scientific Reports, 2021, 11, 193.	3.3	3
4	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 variant of concern 202012/01 (B.1.1.7): an exploratory analysis of a randomised controlled trial. Lancet, The, 2021, 397, 1351-1362.	13.7	540
5	Applying prospective genomic surveillance to support investigation of hospital-onset COVID-19. Lancet Infectious Diseases, The, 2021, 21, 916-917.	9.1	14
6	Defining nosocomial transmission of Escherichia coli and antimicrobial resistance genes: a genomic surveillance study. Lancet Microbe, The, 2021, 2, e472-e480.	7.3	39
7	Significant variability exists in the cytotoxicity of global methicillin-resistant Staphylococcus aureus lineages. Microbiology (United Kingdom), 2021, 167, .	1.8	10
8	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
9	Evaluation of a fully automated bioinformatics tool to predict antibiotic resistance from MRSA genomes. Journal of Antimicrobial Chemotherapy, 2020, 75, 1117-1122.	3.0	10
10	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant Staphylococcus aureus: a genomic epidemiology analysis. Lancet Microbe, The, 2020, 1, e328-e335.	7.3	75
11	Defining metrics for whole-genome sequence analysis of MRSA in clinical practice. Microbial Genomics, 2020, 6, .	2.0	4
12	The composition and functional protein subsystems of the human nasal microbiome in granulomatosis with polyangiitis: a pilot study. Microbiome, 2019, 7, 137.	11.1	22
13	Pilot Evaluation of a Fully Automated Bioinformatics System for Analysis of Methicillin-Resistant Staphylococcus aureus Genomes and Detection of Outbreaks. Journal of Clinical Microbiology, 2019, 57, .	3.9	9
14	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
15	Genomic identification of cryptic susceptibility to penicillins and $\beta$ -lactamase inhibitors in methicillin-resistant Staphylococcus aureus. Nature Microbiology, 2019, 4, 1680-1691.	13.3	47
16	Rapid sequencing of MRSA direct from clinical plates in a routine microbiology laboratory. Journal of Antimicrobial Chemotherapy, 2019, 74, 2153-2156.	3.0	8
17	Methodology for Whole-Genome Sequencing of Methicillin-Resistant <i>Staphylococcus aureus</i> Isolates in a Routine Hospital Microbiology Laboratory. Journal of Clinical Microbiology, 2019, 57, .	3.9	22
18	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

#	ARTICLE	IF	CITATIONS
19	The Emergence of Successful <i>Streptococcus pyogenes</i> Lineages through Convergent Pathways of Capsule Loss and Recombination Directing High Toxin Expression. <i>MBio</i> , 2019, 10, .	4.1	22
20	Nasal carriage of <i>Staphylococcus pseudintermedius</i> in patients with granulomatosis with polyangiitis. <i>Rheumatology</i> , 2019, 58, 548-550.	1.9	8
21	Genomic surveillance of <i>Escherichia coli</i> in municipal wastewater treatment plants as an indicator of clinically relevant pathogens and their resistance genes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	29
22	Prospective genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , 2019, 24, .	7.0	19
23	Genomic Surveillance of <i>Enterococcus faecium</i> Reveals Limited Sharing of Strains and Resistance Genes between Livestock and Humans in the United Kingdom. <i>MBio</i> , 2018, 9, .	4.1	63
24	Are commercial providers a viable option for clinical bacterial sequencing?. <i>Microbial Genomics</i> , 2018, 4, .	2.0	5
25	Whole genome sequencing reveals high-resolution epidemiological links between clinical and environmental <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2017, 9, 6.	8.2	61
26	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	103
27	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in the East of England. <i>Scientific Reports</i> , 2017, 7, 7406.	3.3	25
28	Whole genome sequencing of ESBL-producing <i>Escherichia coli</i> isolated from patients, farm waste and canals in Thailand. <i>Genome Medicine</i> , 2017, 9, 81.	8.2	73
29	Clonal differences in <i>Staphylococcus aureus</i> bacteraemia-associated mortality. <i>Nature Microbiology</i> , 2017, 2, 1381-1388.	13.3	118
30	Evolution of the <i>Staphylococcus argenteus</i> ST2250 Clone in Northeastern Thailand Is Linked with the Acquisition of Livestock-Associated Staphylococcal Genes. <i>MBio</i> , 2017, 8, .	4.1	44
31	Longitudinal genomic surveillance of multidrug-resistant <i>Escherichia coli</i> carriage in a long-term care facility in the United Kingdom. <i>Genome Medicine</i> , 2017, 9, 70.	8.2	44
32	Within-host evolution of <i>Enterococcus faecium</i> during longitudinal carriage and transition to bloodstream infection in immunocompromised patients. <i>Genome Medicine</i> , 2017, 9, 119.	8.2	26
33	Prospective Surveillance and Rapid Whole-Genome Sequencing Detects Two Unsuspected Outbreaks of Carbapenemase-Producing <i>Klebsiella pneumoniae</i> in a UK Teaching Hospital. <i>Open Forum Infectious Diseases</i> , 2017, 4, S43-S44.	0.9	3
34	Sharing of carbapenemase-encoding plasmids between Enterobacteriaceae in UK sewage uncovered by MinION sequencing. <i>Microbial Genomics</i> , 2017, 3, e000114.	2.0	33
35	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. <i>Genome Research</i> , 2016, 26, 263-270.	5.5	63
36	Transmission of methicillin-resistant <i>Staphylococcus aureus</i> in long-term care facilities and their related healthcare networks. <i>Genome Medicine</i> , 2016, 8, 102.	8.2	30

#	ARTICLE	IF	CITATIONS
37	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 in the East of England. <i>Journal of Infectious Diseases</i> , 2016, 214, 447-453.	4.0	45
38	Comparison of two chromogenic media for the detection of vancomycin-resistant enterococcal carriage by nursing home residents. <i>Diagnostic Microbiology and Infectious Disease</i> , 2016, 85, 409-412.	1.8	7
39	PBP2a substitutions linked to ceftaroline resistance in MRSA isolates from the UK: Table 1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 268-269.	3.0	16
40	Comparison of 2 chromogenic media for the detection of extended-spectrum $\beta$ -lactamase producing Enterobacteriaceae stool carriage in nursing home residents. <i>Diagnostic Microbiology and Infectious Disease</i> , 2016, 84, 181-183.	1.8	16
41	Whole-genome sequencing reveals transmission of vancomycin-resistant <i>Enterococcus faecium</i> in a healthcare network. <i>Genome Medicine</i> , 2016, 8, 4.	8.2	58