## Frequent Undetected Ward-Based Methicillin-Resistant Transmission Linked to Patient Sharing Between Hospi

Clinical Infectious Diseases 66, 840-848 DOI: 10.1093/cid/cix901

**Citation Report** 

#	Article	IF	CITATIONS
1	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of Staphylococcus aureus strains in a paediatric hospital. Genome Medicine, 2018, 10, 82.	3.6	54
2	Increased environmental sample area and recovery ofClostridium difficilespores from hospital surfaces by quantitative PCR and enrichment culture. Infection Control and Hospital Epidemiology, 2018, 39, 917-923.	1.0	8
3	Quantifying the transmission dynamics of MRSA in the community and healthcare settings in a low-prevalence country. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14599-14605.	3.3	26
4	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, .	1.8	9
5	Contribution of whole-genome sequencing to understanding of the epidemiology and control of meticillin-resistant Staphylococcus aureus. Journal of Hospital Infection, 2019, 102, 189-199.	1.4	40
6	What's new in the epidemiology of skin and soft tissue infections in 2018?. Current Opinion in Infectious Diseases, 2019, 32, 77-86.	1.3	27
7	MRSA dynamic circulation between the community and the hospital setting: New insights from a cohort study. Journal of Infection, 2020, 80, 24-37.	1.7	17
8	Longitudinal, strain-specific Staphylococcus aureus introduction and transmission events in households of children with community-associated meticillin-resistant S aureus skin and soft tissue infection: a prospective cohort study. Lancet Infectious Diseases, The, 2020, 20, 188-198.	4.6	51
9	Spread of Carbapenem-Resistant Klebsiella pneumoniae in Hub and Spoke Connected Health-Care Networks: A Case Study from Italy. Microorganisms, 2020, 8, 37.	1.6	7
10	Genomic Epidemiology of Invasive Methicillin-Resistant <i>Staphylococcus aureus</i> Infections Among Hospitalized Individuals in Ontario, Canada. Journal of Infectious Diseases, 2020, 222, 2071-2081.	1.9	8
11	Methicillin-Resistant Staphylococcus aureus ST80 Clone: A Systematic Review. Toxins, 2020, 12, 119.	1.5	25
12	Evaluation of a fully automated bioinformatics tool to predict antibiotic resistance from MRSA genomes. Journal of Antimicrobial Chemotherapy, 2020, 75, 1117-1122.	1.3	10
13	Polyclonality, Shared Strains, and Convergent Evolution in Chronic Cystic Fibrosis <i>Staphylococcus aureus</i> Airway Infection. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 1127-1137.	2.5	33
14	Defining metrics for whole-genome sequence analysis of MRSA in clinical practice. Microbial Genomics, 2020, 6, .	1.0	4
18	Genetic Diversity of norA, Coding for a Main Efflux Pump of Staphylococcus aureus. Frontiers in Genetics, 2018, 9, 710.	1.1	58
19	Prevalence and Sensitivity of Bacterial Urinary Tract Infection among Adult Diabetic Patients in Misan Province, Iraq. Journal of Pure and Applied Microbiology, 2019, 13, 993-1002.	0.3	0
20	Joint Healthcare Infection Society (HIS) and Infection Prevention Society (IPS) guidelines for the prevention and control of meticillin-resistant Staphylococcus aureus (MRSA) in healthcare facilities. Journal of Hospital Infection, 2021, 118, S1-S39.	1.4	14
23	Whole-genome sequencing surveillance and machine learning for healthcare outbreak detection and investigation: A systematic review and summary. Antimicrobial Stewardship & Healthcare Epidemiology, 2022, 2, .	0.2	9

#	Article	IF	CITATIONS
24	Threshold-free genomic cluster detection to track transmission pathways in health-care settings: a genomic epidemiology analysis. Lancet Microbe, The, 2022, , .	3.4	3
25	Molecular Epidemiology of Staphylococcus aureus in China Reveals the Key Gene Features Involved in Epidemic Transmission and Adaptive Evolution. Microbiology Spectrum, 2022, 10, .	1.2	4

CITATION REPORT