

Claire L Gorrie

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

8,601
citations

516710

16
h-index

552781

26
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41
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docs citations

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times ranked

9404
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimising genomic approaches for identifying vancomycin-resistant <i>Enterococcus faecium</i> transmission in healthcare settings. <i>Nature Communications</i> , 2022, 13, 509.	12.8	20
2	<i>Klebsiella pneumoniae</i> induces host metabolic stress that promotes tolerance to pulmonary infection. <i>Cell Metabolism</i> , 2022, 34, 761-774.e9.	16.2	36
3	Multi-site implementation of whole genome sequencing for hospital infection control: A prospective genomic epidemiological analysis. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 23, 100446.	2.9	6
4	Genomic dissection of <i>Klebsiella pneumoniae</i> infections in hospital patients reveals insights into an opportunistic pathogen. <i>Nature Communications</i> , 2022, 13, .	12.8	51
5	Search and Contain: Impact of an Integrated Genomic and Epidemiological Surveillance and Response Program for Control of Carbapenemase-producing <i>Enterobacterales</i> . <i>Clinical Infectious Diseases</i> , 2021, 73, e3912-e3920.	5.8	12
6	Scabies and impetigo in Samoa: A school-based clinical and molecular epidemiological study. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 6, 100081.	2.9	8
7	Genomic Insights Into Last-Line Antimicrobial Resistance in Multidrug-Resistant <i>Staphylococcus</i> and Vancomycin-Resistant <i>Enterococcus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 637656.	3.5	21
8	Genomic surveillance of antimicrobial resistant bacterial colonisation and infection in intensive care patients. <i>BMC Infectious Diseases</i> , 2021, 21, 683.	2.9	18
9	Key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria: a systematic analysis. <i>Lancet Microbe</i> , The, 2021, 2, e575-e583.	7.3	33
10	Genomic sequencing of hypervirulent <i>Klebsiella pneumoniae</i> with novel patterns of virulence and global epidemiological linkage. <i>Pathology</i> , 2021, 53, 682-685.	0.6	1
11	Pilot study of a combined genomic and epidemiologic surveillance program for hospital-acquired multidrug-resistant pathogens across multiple hospital networks in Australia. <i>Infection Control and Hospital Epidemiology</i> , 2021, 42, 573-581.	1.8	18
12	Daptomycin Resistance Occurs Predominantly in vanA-Type Vancomycin-Resistant <i>Enterococcus faecium</i> in Australasia and Is Associated With Heterogeneous and Novel Mutations. <i>Frontiers in Microbiology</i> , 2021, 12, 749935.	3.5	11
13	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing <i>Enterobacterales</i> in Victoria, Australia, 2012 to 2016. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	56
14	Bridging of <i>Neisseria gonorrhoeae</i> lineages across sexual networks in the HIV pre-exposure prophylaxis era. <i>Nature Communications</i> , 2019, 10, 3988.	12.8	69
15	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of <i>Klebsiella pneumoniae</i> . <i>PLoS Genetics</i> , 2019, 15, e1008114.	3.5	228
16	Vancomycin-resistant <i>Enterococcus</i> (VRE) outbreak in a neonatal intensive care unit and special care nursery at a tertiary-care hospital in Australia—A retrospective case-control study. <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 551-558.	1.8	12
17	O19.2—Bridging of <i>neisseria gonorrhoeae</i> across diverse sexual networks in the HIV PrEP era. , 2019, , .		0
18	Genomics of vancomycin-resistant <i>Enterococcus faecium</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	44

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19	Antimicrobial-Resistant <i>Klebsiella pneumoniae</i> Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. <i>Clinical Infectious Diseases</i> , 2018, 67, 161-170.	5.8	108
20	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in <i>Klebsiella pneumoniae</i> populations. <i>Microbial Genomics</i> , 2018, 4, .	2.0	197
21	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. <i>Clinical Infectious Diseases</i> , 2017, 65, 208-215.	5.8	381
22	Completing bacterial genome assemblies with multiplex MinION sequencing. <i>Microbial Genomics</i> , 2017, 3, e000132.	2.0	559
23	Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. <i>PLoS Computational Biology</i> , 2017, 13, e1005595.	3.2	5,135
24	Hidden reservoirs of hospital-associated infections. <i>Microbiology Australia</i> , 2017, 38, 140.	0.4	0
25	Identification of <i>Klebsiella</i> capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , 2016, 2, e000102.	2.0	372
26	Differential host susceptibility and bacterial virulence factors driving <i>Klebsiella</i> liver abscess in an ethnically diverse population. <i>Scientific Reports</i> , 2016, 6, 29316.	3.3	87
27	Draft Genome Sequence of a Clinical Isolate of <i>Serratia marcescens</i> , Strain AH0650_Sm1. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
28	Extensive Capsule Locus Variation and Large-Scale Genomic Recombination within the <i>Klebsiella pneumoniae</i> Clonal Group 258. <i>Genome Biology and Evolution</i> , 2015, 7, 1267-1279.	2.5	99
29	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3574-81.	7.1	942
30	Search and Contain: Impact of an Integrated Genomic and Epidemiological Surveillance and Response Program for Control of Carbapenemase-Producing <i>Enterobacteriales</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	1