

# Benjamin P Howden

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7294145/publications.pdf>

Version: 2024-02-01

279  
papers

12,844  
citations

29994

54  
h-index

34900

98  
g-index

308  
all docs

308  
docs citations

308  
times ranked

13327  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reduced Vancomycin Susceptibility in <i>Staphylococcus aureus</i> , Including Vancomycin-Intermediate and Heterogeneous Vancomycin-Intermediate Strains: Resistance Mechanisms, Laboratory Detection, and Clinical Implications. <i>Clinical Microbiology Reviews</i> , 2010, 23, 99-139.	5.7	804
2	Treatment Outcomes for Serious Infections Caused by Methicillin-Resistant <i>Staphylococcus aureus</i> with Reduced Vancomycin Susceptibility. <i>Clinical Infectious Diseases</i> , 2004, 38, 521-528.	2.9	467
3	Clinical Features Associated with Bacteremia Due to Heterogeneous Vancomycin-Intermediate <i>Staphylococcus aureus</i> . <i>Clinical Infectious Diseases</i> , 2004, 38, 448-451.	2.9	368
4	Evolution of Multidrug Resistance during <i>Staphylococcus aureus</i> Infection Involves Mutation of the Essential Two Component Regulator WalKR. <i>PLoS Pathogens</i> , 2011, 7, e1002359.	2.1	315
5	Isolation and rapid sharing of the 2019 novel coronavirus (SARS-CoV-2) from the first patient diagnosed with COVID-19 in Australia. <i>Medical Journal of Australia</i> , 2020, 212, 459-462.	0.8	297
6	Current and Emerging Topical Antibacterials and Antiseptics: Agents, Action, and Resistance Patterns. <i>Clinical Microbiology Reviews</i> , 2017, 30, 827-860.	5.7	245
7	Prospective Whole-Genome Sequencing Enhances National Surveillance of <i>Listeria monocytogenes</i> . <i>Journal of Clinical Microbiology</i> , 2016, 54, 333-342.	1.8	239
8	Antibiotic Choice May Not Explain Poorer Outcomes in Patients With <i>Staphylococcus aureus</i> Bacteremia and High Vancomycin Minimum Inhibitory Concentrations. <i>Journal of Infectious Diseases</i> , 2011, 204, 340-347.	1.9	214
9	Global spread of three multidrug-resistant lineages of <i>Staphylococcus epidermidis</i> . <i>Nature Microbiology</i> , 2018, 3, 1175-1185.	5.9	206
10	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 913-921.	4.6	204
11	Isolates with Low-Level Vancomycin Resistance Associated with Persistent Methicillin-Resistant <i>Staphylococcus aureus</i> Bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 3039-3047.	1.4	199
12	Two Novel Point Mutations in Clinical <i>Staphylococcus aureus</i> Reduce Linezolid Susceptibility and Switch on the Stringent Response to Promote Persistent Infection. <i>PLoS Pathogens</i> , 2010, 6, e1000944.	2.1	191
13	<i>Staphylococcus aureus</i> bacteraemia: a major cause of mortality in Australia and New Zealand. <i>Medical Journal of Australia</i> , 2009, 191, 368-373.	0.8	184
14	Vancomycin AUC/MIC Ratio and 30-Day Mortality in Patients with <i>Staphylococcus aureus</i> Bacteremia. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1654-1663.	1.4	176
15	Effect of Vancomycin or Daptomycin With vs Without an Antistaphylococcal $\beta$ -Lactam on Mortality, Bacteremia, Relapse, or Treatment Failure in Patients With MRSA Bacteremia. <i>JAMA - Journal of the American Medical Association</i> , 2020, 323, 527.	3.8	169
16	Complete Bypass of Restriction Systems for Major <i>Staphylococcus aureus</i> Lineages. <i>MBio</i> , 2015, 6, e00308-15.	1.8	168
17	Not Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> (CA-MRSA)! A Clinician's Guide to Community MRSA - Its Evolving Antimicrobial Resistance and Implications for Therapy. <i>Clinical Infectious Diseases</i> , 2011, 52, 99-114.	2.9	166
18	Increasing tolerance of hospital <i>Enterococcus faecium</i> to handwash alcohols. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	165

#	ARTICLE	IF	CITATIONS
19	Dumb and Dumber–The Potential Waste of a Useful Antistaphylococcal Agent: Emerging Fusidic Acid Resistance in <i>Staphylococcus aureus</i> . <i>Clinical Infectious Diseases</i> , 2006, 42, 394-400.	2.9	156
20	Evolution of virulence in <i>Enterococcus faecium</i> , a hospital-adapted opportunistic pathogen. <i>Current Opinion in Microbiology</i> , 2018, 41, 76-82.	2.3	153
21	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020, 11, 4376.	5.8	152
22	In vitro pharmacodynamics of colistin against multidrug-resistant <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 62, 1311-1318.	1.3	150
23	Combination of Vancomycin and $\beta$ -Lactam Therapy for Methicillin-Resistant <i>Staphylococcus aureus</i> Bacteremia: A Pilot Multicenter Randomized Controlled Trial. <i>Clinical Infectious Diseases</i> , 2016, 62, 173-180.	2.9	149
24	Genomic Analysis Reveals a Point Mutation in the Two-Component Sensor Gene <i>graS</i> That Leads to Intermediate Vancomycin Resistance in Clinical <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 3755-3762.	1.4	137
25	Emergence and rapid global dissemination of CTX-M-15-associated <i>Klebsiella pneumoniae</i> strain ST307. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 577-581.	1.3	137
26	Genomic Insights to Control the Emergence of Vancomycin-Resistant Enterococci. <i>MBio</i> , 2013, 4, .	1.8	136
27	Comparative Analysis of the First Complete <i>Enterococcus faecium</i> Genome. <i>Journal of Bacteriology</i> , 2012, 194, 2334-2341.	1.0	133
28	Good Clinical Outcomes but High Rates of Adverse Reactions during Linezolid Therapy for Serious Infections: a Proposed Protocol for Monitoring Therapy in Complex Patients. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 1599-1602.	1.4	132
29	The evolution of vancomycin intermediate <i>Staphylococcus aureus</i> (VISA) and heterogenous-VISA. <i>Infection, Genetics and Evolution</i> , 2014, 21, 575-582.	1.0	115
30	Prospective Comparison of the Clinical Impacts of Heterogeneous Vancomycin-Intermediate Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) and Vancomycin-Susceptible MRSA. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3447-3452.	1.4	108
31	Different bacterial gene expression patterns and attenuated host immune responses are associated with the evolution of low-level vancomycin resistance during persistent methicillin-resistant <i>Staphylococcus aureus</i> bacteraemia. <i>BMC Microbiology</i> , 2008, 8, 39.	1.3	106
32	Enterococcal bacteraemia: factors influencing mortality, length of stay and costs of hospitalization. <i>Clinical Microbiology and Infection</i> , 2013, 19, E181-E189.	2.8	106
33	A Sustained Hospital Outbreak of Vancomycin-Resistant <i>Enterococcus faecium</i> Bacteremia due to Emergence of <i>vanB</i> E. <i>faecium</i> Sequence Type 203. <i>Journal of Infectious Diseases</i> , 2010, 202, 1278-1286.	1.9	98
34	Serine/Threonine Phosphatase Stp1 Contributes to Reduced Susceptibility to Vancomycin and Virulence in <i>Staphylococcus aureus</i> . <i>Journal of Infectious Diseases</i> , 2012, 205, 1677-1687.	1.9	98
35	The RpoB H481Y Rifampicin Resistance Mutation and an Active Stringent Response Reduce Virulence and Increase Resistance to Innate Immune Responses in <i>Staphylococcus aureus</i> . <i>Journal of Infectious Diseases</i> , 2013, 207, 929-939.	1.9	94
36	Daptomycin non-susceptibility in vancomycin-intermediate <i>Staphylococcus aureus</i> (VISA) and heterogeneous-VISA (hVISA): implications for therapy after vancomycin treatment failure. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1057-1060.	1.3	90

#	ARTICLE	IF	CITATIONS
37	Relationship between Vancomycin-Resistant <i>Staphylococcus aureus</i> , Vancomycin-Intermediate <i>S. aureus</i> , High Vancomycin MIC, and Outcome in Serious <i>S. aureus</i> Infections. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2548-2552.	1.8	86
38	Outbreak Investigation Using High-Throughput Genome Sequencing within a Diagnostic Microbiology Laboratory. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1396-1401.	1.8	86
39	Analysis of the Small RNA Transcriptional Response in Multidrug-Resistant <i>Staphylococcus aureus</i> after Antimicrobial Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3864-3874.	1.4	84
40	South Asia as a Reservoir for the Global Spread of Ciprofloxacin-Resistant <i>Shigella sonnei</i> : A Cross-Sectional Study. <i>PLoS Medicine</i> , 2016, 13, e1002055.	3.9	84
41	Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2015, 6, e00080.	1.8	81
42	The Dominant Australian Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> Clone ST93-IV [2B] Is Highly Virulent and Genetically Distinct. <i>PLoS ONE</i> , 2011, 6, e25887.	1.1	78
43	Co-circulation of Multidrug-resistant <i>Shigella</i> Among Men Who Have Sex With Men in Australia. <i>Clinical Infectious Diseases</i> , 2019, 69, 1535-1544.	2.9	77
44	The Interface Between Antibiotic Resistance and Virulence in <i>Staphylococcus aureus</i> and Its Impact Upon Clinical Outcomes. <i>Clinical Infectious Diseases</i> , 2011, 53, 576-582.	2.9	75
45	Complete Genome Sequence of <i>Staphylococcus aureus</i> Strain JKD6008, an ST239 Clone of Methicillin-Resistant <i>Staphylococcus aureus</i> with Intermediate-Level Vancomycin Resistance. <i>Journal of Bacteriology</i> , 2010, 192, 5848-5849.	1.0	71
46	Increased Detection of Pharyngeal and Rectal Gonorrhea in Men Who Have Sex With Men After Transition From Culture To Nucleic Acid Amplification Testing. <i>Sexually Transmitted Diseases</i> , 2017, 44, 114-117.	0.8	71
47	Molecular Epidemiology of Enterococcal Bacteremia in Australia. <i>Journal of Clinical Microbiology</i> , 2014, 52, 897-905.	1.8	70
48	<i>Mycobacterium chimaera</i> Spread from Heating and Cooling Units in Heart Surgery. <i>New England Journal of Medicine</i> , 2017, 376, 600-602.	13.9	70
49	Health Outcomes from Multidrug-Resistant <i>Salmonella</i> Infections in High-Income Countries: A Systematic Review and Meta-Analysis. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 428-436.	0.8	69
50	Bridging of <i>Neisseria gonorrhoeae</i> lineages across sexual networks in the HIV pre-exposure prophylaxis era. <i>Nature Communications</i> , 2019, 10, 3988.	5.8	69
51	Antibiotic resistance and host immune evasion in <i>Staphylococcus aureus</i> mediated by a metabolic adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3722-3727.	3.3	69
52	Unstable chromosome rearrangements in <i>Staphylococcus aureus</i> cause phenotype switching associated with persistent infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20135-20140.	3.3	69
53	Hyperexpression of $\hat{\pm}$ -hemolysin explains enhanced virulence of sequence type 93 community-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>BMC Microbiology</i> , 2014, 14, 31.	1.3	68
54	Translating genomics into practice for real-time surveillance and response to carbapenemase-producing Enterobacteriaceae: evidence from a complex multi-institutional KPC outbreak. <i>PeerJ</i> , 2018, 6, e4210.	0.9	66

#	ARTICLE	IF	CITATIONS
55	Staphylococcus aureus small colony variants impair host immunity by activating host cell glycolysis and inducing necroptosis. <i>Nature Microbiology</i> , 2020, 5, 141-153.	5.9	65
56	Antiseptic mouthwash against pharyngeal <i>Neisseria gonorrhoeae</i> : a randomised controlled trial and an in vitro study. <i>Sexually Transmitted Infections</i> , 2017, 93, 88-93.	0.8	64
57	Decreased Vancomycin Susceptibility in <i>Staphylococcus aureus</i> Caused by IS $\phi$ 256 Tempering of WalkR Expression. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3240-3249.	1.4	62
58	Emerging Gram negative resistance to last-line antimicrobial agents fosfomycin, colistin and ceftazidime-avibactam – epidemiology, laboratory detection and treatment implications. <i>Expert Review of Anti-Infective Therapy</i> , 2018, 16, 289-306.	2.0	62
59	CAMERA2 – combination antibiotic therapy for methicillin-resistant <i>Staphylococcus aureus</i> infection: study protocol for a randomised controlled trial. <i>Trials</i> , 2016, 17, 170.	0.7	61
60	Validation of a single-step, single-tube reverse transcription loop-mediated isothermal amplification assay for rapid detection of SARS-CoV-2 RNA. <i>Journal of Medical Microbiology</i> , 2020, 69, 1169-1178.	0.7	61
61	Vancomycin therapeutics and monitoring: a contemporary approach. <i>Internal Medicine Journal</i> , 2013, 43, 110-119.	0.5	57
62	Genomic epidemiology and antimicrobial resistance of <i>Neisseria gonorrhoeae</i> in New Zealand. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 353-364.	1.3	57
63	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing <i>Enterobacteriales</i> in Victoria, Australia, 2012 to 2016. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	56
64	Evaluation of Serological Tests for SARS-CoV-2: Implications for Serology Testing in a Low-Prevalence Setting. <i>Journal of Infectious Diseases</i> , 2020, 222, 1280-1288.	1.9	56
65	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant <i>Staphylococcus aureus</i> . <i>MSphere</i> , 2018, 3, .	1.3	55
66	Complete Genome Sequence of <i>Staphylococcus aureus</i> Strain JKD6159, a Unique Australian Clone of ST93-IV Community Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2010, 192, 5556-5557.	1.0	54
67	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health</i> , The, 2021, 6, e547-e556.	4.7	53
68	Detection of <i>Neisseria gonorrhoeae</i> in the pharynx and saliva: implications for gonorrhoea transmission: Table A1. <i>Sexually Transmitted Infections</i> , 2016, 92, 347-349.	0.8	51
69	Comparative analysis of the complete genome of an epidemic hospital sequence type 203 clone of vancomycin-resistant <i>Enterococcus faecium</i> . <i>BMC Genomics</i> , 2013, 14, 595.	1.2	50
70	Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent <i>Staphylococcus aureus</i> bacteraemia. <i>Genome Medicine</i> , 2018, 10, 65.	3.6	49
71	Comparison of the Xpert Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Assay, BD GeneOhm MRSA Assay, and Culture for Detection of Nasal and Cutaneous Groin Colonization by MRSA. <i>Journal of Clinical Microbiology</i> , 2009, 47, 3769-3772.	1.8	48
72	Genetic and Molecular Predictors of High Vancomycin MIC in <i>Staphylococcus aureus</i> Bacteremia Isolates. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3384-3393.	1.8	47

#	ARTICLE	IF	CITATIONS
73	Increasing Antimicrobial Resistance in Nontyphoidal Salmonella Isolates in Australia from 1979 to 2015. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	47
74	Kissing may be an important and neglected risk factor for oropharyngeal gonorrhoea: a cross-sectional study in men who have sex with men. <i>Sexually Transmitted Infections</i> , 2019, 95, 516-521.	0.8	47
75	Evolutionary origins of the emergent ST796 clone of vancomycin resistant <i>Enterococcus faecium</i> . <i>PeerJ</i> , 2017, 5, e2916.	0.9	46
76	<i>Neisseria gonorrhoeae</i> isolates with high-level resistance to azithromycin in Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1267-1268.	1.3	45
77	Inactivation of the Indigenous Methyltransferase RlmN in <i>Staphylococcus aureus</i> Increases Linezolid Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 2989-2991.	1.4	44
78	Emergence of endemic MLST non-typeable vancomycin-resistant <i>Enterococcus faecium</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3367-3371.	1.3	44
79	A multicentre double-blind randomised controlled trial evaluating the efficacy of daily use of antibacterial mouthwash against oropharyngeal gonorrhoea among men who have sex with men: the OMEGA (Oral Mouthwash use to Eradicate GonorrhoeA) study protocol. <i>BMC Infectious Diseases</i> , 2017, 17, 456.	1.3	44
80	Genomics of vancomycin-resistant <i>Enterococcus faecium</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	44
81	Whole-genome sequencing reveals transmission of gonococcal antibiotic resistance among men who have sex with men: an observational study. <i>Sexually Transmitted Infections</i> , 2018, 94, 151-157.	0.8	42
82	The Molecular Epidemiology of the Highly Virulent ST93 Australian Community <i>Staphylococcus aureus</i> Strain. <i>PLoS ONE</i> , 2012, 7, e43037.	1.1	42
83	The importance of regulatory RNAs in <i>Staphylococcus aureus</i> . <i>Infection, Genetics and Evolution</i> , 2014, 21, 616-626.	1.0	41
84	Rapid Emergence and Evolution of <i>Staphylococcus aureus</i> Clones Harboring <i>fusC</i> -Containing Staphylococcal Cassette Chromosome Elements. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2359-2365.	1.4	41
85	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	5.8	41
86	Solithromycin versus ceftriaxone plus azithromycin for the treatment of uncomplicated genital gonorrhoea (SOLITAIRE-U): a randomised phase 3 non-inferiority trial. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 833-842.	4.6	41
87	5: Hospitalâ€”theâ€”home treatment of infectious diseases. <i>Medical Journal of Australia</i> , 2002, 176, 440-445.	0.8	41
88	Adaptive Change Inferred from Genomic Population Analysis of the ST93 Epidemic Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 366-378.	1.1	40
89	Zinc-binding to the cytoplasmic PAS domain regulates the essential Walk histidine kinase of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2019, 10, 3067.	5.8	38
90	Mycolactone Gene Expression Is Controlled by Strong SigA-Like Promoters with Utility in Studies of <i>Mycobacterium ulcerans</i> and Buruli Ulcer. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e553.	1.3	37

#	ARTICLE	IF	CITATIONS
91	What's new in the treatment of serious MRSA infection?. <i>Current Opinion in Infectious Diseases</i> , 2014, 27, 471-478.	1.3	37
92	<i>Klebsiella pneumoniae</i> induces host metabolic stress that promotes tolerance to pulmonary infection. <i>Cell Metabolism</i> , 2022, 34, 761-774.e9.	7.2	36
93	Evolutionary dynamics of multidrug resistant <i>Salmonella enterica</i> serovar 4,[5],12:i:- in Australia. <i>Nature Communications</i> , 2021, 12, 4786.	5.8	35
94	Genomic Analysis of Multiresistant <i>Staphylococcus capitis</i> Associated with Neonatal Sepsis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	34
95	Prevalence of genital and oropharyngeal chlamydia and gonorrhoea among female sex workers in Melbourne, Australia, 2015–2017: need for oropharyngeal testing. <i>Sexually Transmitted Infections</i> , 2019, 95, 398-401.	0.8	33
96	The global dissemination of hospital clones of <i>Enterococcus faecium</i> . <i>Genome Medicine</i> , 2021, 13, 52.	3.6	33
97	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.	3.4	33
98	Treating Gram-positive infections: vancomycin update and the whys, wherefores and evidence base for continuous infusion of anti-Gram-positive antibiotics. <i>Current Opinion in Infectious Diseases</i> , 2009, 22, 525-534.	1.3	32
99	Population genetics and the evolution of virulence in <i>Staphylococcus aureus</i> . <i>Infection, Genetics and Evolution</i> , 2014, 21, 554-562.	1.0	32
100	Comparative Genomics Shows That <i>Mycobacterium ulcerans</i> Migration and Expansion Preceded the Rise of Buruli Ulcer in Southeastern Australia. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	32
101	Pandemic printing: a novel 3D-printed swab for detecting <scp>SARS</scp> –CoVâ€2. <i>Medical Journal of Australia</i> , 2020, 213, 276-279.	0.8	32
102	High-Resolution Melting Genotyping of <i>Enterococcus faecium</i> Based on Multilocus Sequence Typing Derived Single Nucleotide Polymorphisms. <i>PLoS ONE</i> , 2011, 6, e29189.	1.1	31
103	Outbreak of vanB vancomycin-resistant <i>Enterococcus faecium</i> colonization in a neonatal service. <i>American Journal of Infection Control</i> , 2015, 43, 1061-1065.	1.1	31
104	Heterogeneity of Genetic Pathways toward Daptomycin Nonsusceptibility in <i>Staphylococcus aureus</i> Determined by Adjunctive Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2799-2806.	1.4	31
105	Genomic insights into a sustained national outbreak of <i>Yersinia pseudotuberculosis</i>. <i>Genome Biology and Evolution</i> , 2016, 8, eww285.	1.1	31
106	NGMASTER: in silico multi-antigen sequence typing for <i>Neisseria gonorrhoeae</i> . <i>Microbial Genomics</i> , 2016, 2, e000076.	1.0	31
107	Comparative Study of Selective Chromogenic (chromID VRE) and Bile Esculin Agars for Isolation and Identification of <i>vanB</i>-Containing Vancomycin-Resistant Enterococci from Feces and Rectal Swabs. <i>Journal of Clinical Microbiology</i> , 2008, 46, 4034-4036.	1.8	30
108	Vancomycin-resistant <i>Enterococcus faecium</i> sequence type 796 - rapid international dissemination of a new epidemic clone. <i>Antimicrobial Resistance and Infection Control</i> , 2018, 7, 44.	1.5	30

#	ARTICLE	IF	CITATIONS
109	Structure-Activity Relationships of Daptomycin Lipopeptides. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 13266-13290.	2.9	30
110	Prolonged Outbreak of Multidrug-Resistant <i>Shigella sonnei</i> Harboring <i>bla</i> <sub>CTX-M-27</sub> in Victoria, Australia. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	29
111	Multi-site assessment of rapid, point-of-care antigen testing for the diagnosis of SARS-CoV-2 infection in a low-prevalence setting: A validation and implementation study. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 9, 100115.	1.3	29
112	Topical Antibiotic Use Coselects for the Carriage of Mobile Genetic Elements Conferring Resistance to Unrelated Antimicrobials in <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	28
113	Mining the Methylome Reveals Extensive Diversity in <i>Staphylococcus epidermidis</i> Restriction Modification. <i>MBio</i> , 2019, 10, .	1.8	28
114	Seven <i>Salmonella</i> Typhimurium Outbreaks in Australia Linked by Trace-Back and Whole Genome Sequencing. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 285-292.	0.8	27
115	The changing landscape of vancomycin-resistant <i>Enterococcus faecium</i> in Australia: a population-level genomic study. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3268-3278.	1.3	27
116	Extensively Drug-Resistant Shigellosis in Australia among Men Who Have Sex with Men. <i>New England Journal of Medicine</i> , 2019, 381, 2477-2479.	13.9	27
117	Comprehensive Genomic Investigation of Adaptive Mutations Driving the Low-Level Oxacillin Resistance Phenotype in <i>Staphylococcus aureus</i> . <i>MBio</i> , 2020, 11, .	1.8	27
118	The epidemiology of bacteriuria and candiduria in critically ill patients. <i>Epidemiology and Infection</i> , 2015, 143, 653-662.	1.0	26
119	A Phenotypically Silent <i>vanB2</i> Operon Carried on a Tn <sub>1549</sub> -Like Element in <i>Clostridium difficile</i> . <i>MSphere</i> , 2016, 1, .	1.3	26
120	Morbidity from in-hospital complications is greater than treatment failure in patients with <i>Staphylococcus aureus</i> bacteraemia. <i>BMC Infectious Diseases</i> , 2018, 18, 107.	1.3	26
121	Comprehensive antibiotic-linked mutation assessment by resistance mutation sequencing (RM-seq). <i>Genome Medicine</i> , 2018, 10, 63.	3.6	26
122	An implementation science approach to evaluating pathogen whole genome sequencing in public health. <i>Genome Medicine</i> , 2021, 13, 121.	3.6	26
123	Development of Phylodynamic Methods for Bacterial Pathogens. <i>Trends in Microbiology</i> , 2021, 29, 788-797.	3.5	26
124	Evidence for a new paradigm of gonorrhoea transmission: cross-sectional analysis of <i>Neisseria gonorrhoeae</i> infections by anatomical site in both partners in 60 male couples. <i>Sexually Transmitted Infections</i> , 2019, 95, 437-442.	0.8	25
125	Treatment and outcome of 104 hospitalized patients with legionnaires' disease. <i>Internal Medicine Journal</i> , 2003, 33, 484-488.	0.5	24
126	Phasevarion-Regulated Virulence in the Emerging Pediatric Pathogen <i>Kingella kingae</i> . <i>Infection and Immunity</i> , 2017, 85, .	1.0	24



#	ARTICLE	IF	CITATIONS
127	Incorporating Whole-Genome Sequencing into Public Health Surveillance: Lessons from Prospective Sequencing of Salmonella Typhimurium in Australia. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 161-167.	0.8	24
128	Detection of SARS-CoV-2 in saliva: implications for specimen transport and storage. <i>Journal of Medical Microbiology</i> , 2021, 70, .	0.7	24
129	Antiseptic mouthwash for gonorrhoea prevention (OMEGA): a randomised, double-blind, parallel-group, multicentre trial. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 647-656.	4.6	24
130	A phylogenomic framework for assessing the global emergence and evolution of clonal complex 398 methicillin-resistant <i>Staphylococcus aureus</i> . <i>Microbial Genomics</i> , 2017, 3, e000105.	1.0	24
131	Evaluation of the Xpert®, <sup>®</sup> MRSA/SA Blood Culture assay for the detection of <i>Staphylococcus aureus</i> including strains with reduced vancomycin susceptibility from blood culture specimens. <i>Diagnostic Microbiology and Infectious Disease</i> , 2011, 70, 404-407.	0.8	23
132	Oropharyngeal and Genital Gonorrhoea Infections Among Women and Heterosexual Men Reporting Sexual Contact With Partners With Gonorrhoea: Implication for Oropharyngeal Testing of Heterosexual Gonorrhoea Contacts. <i>Sexually Transmitted Diseases</i> , 2019, 46, 743-747.	0.8	23
133	Emergence and global spread of <i>Listeria monocytogenes</i> main clinical clonal complex. <i>Science Advances</i> , 2021, 7, eabj9805.	4.7	23
134	Vancomycin minimum inhibitory concentration, host comorbidities and mortality in <i>Staphylococcus aureus</i> bacteraemia. <i>Clinical Microbiology and Infection</i> , 2013, 19, 1163-1168.	2.8	22
135	Rifampicin resistance in <i>Staphylococcus epidermidis</i> : molecular characterisation and fitness cost of rpoB mutations. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 670-677.	1.1	22
136	Evolution of Daptomycin Resistance in Coagulase-Negative Staphylococci Involves Mutations of the Essential Two-Component Regulator WalkR. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	22
137	Failure of Vancomycin for Treatment of Methicillin-Resistant <i>Staphylococcus aureus</i> Infections. <i>Clinical Infectious Diseases</i> , 2004, 39, 1544-1544.	2.9	21
138	Polyclonal emergence of vancomycin-resistant <i>Enterococcus faecium</i> in Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 72, dkw539.	1.3	21
139	Daptomycin selects for genetic and phenotypic adaptations leading to antibiotic tolerance in MRSA. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2030-2033.	1.3	21
140	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.	1.5	21
141	Vancomycin Exposure and Acute Kidney Injury Outcome: A Snapshot From the CAMERA2 Study. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa538.	0.4	21
142	Australian Group on Antimicrobial Resistance Australian <i>Staphylococcus aureus</i> Sepsis Outcome Programme annual report, 2014. <i>Communicable Diseases Intelligence</i> , 2016, 40, E244-54.	0.5	21
143	Rise in invasive serogroup W meningococcal disease in Australia 2013-2015. <i>Communicable Diseases Intelligence</i> , 2016, 40, E454-E459.	0.5	21
144	Low mannose-binding lectin complement activation function is associated with predisposition to Legionnaires' disease. <i>Clinical and Experimental Immunology</i> , 2007, 149, 97-102.	1.1	20

#	ARTICLE	IF	CITATIONS
145	Emergence of multidrug resistance in locally-acquired human infections with <i>Salmonella</i> Typhimurium in Australia owing to a new clade harbouring bla CTX-M-9. <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 101-105.	1.1	20
146	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen <i>Mycobacterium kansasii</i> . <i>Nature Communications</i> , 2021, 12, 2491.	5.8	20
147	Genomic analysis of ST88 community-acquired methicillin resistant <i>Staphylococcus aureus</i> in Ghana. <i>PeerJ</i> , 2017, 5, e3047.	0.9	20
148	Optimising genomic approaches for identifying vancomycin-resistant <i>Enterococcus faecium</i> transmission in healthcare settings. <i>Nature Communications</i> , 2022, 13, 509.	5.8	20
149	Cutaneous zygomycosis caused by <i>Saksenea vasiformis</i> following water-related wound in a 24-year-old immunocompetent woman. <i>Mycoses</i> , 2009, 52, 547-549.	1.8	19
150	Genomic analysis of teicoplanin resistance emerging during treatment of vanB vancomycin-resistant <i>Enterococcus faecium</i> infections in solid organ transplant recipients including donor-derived cases. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2134-2139.	1.3	19
151	Trends and Risk Factors for Antimicrobial-Resistant <i>Neisseria gonorrhoeae</i> , Melbourne, Australia, 2007 to 2018. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	19
152	Increasing incidence of invasive nontyphoidal <i>Salmonella</i> infections in Queensland, Australia, 2007-2016. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007187.	1.3	19
153	Tenacious Endemic Typhoid Fever in Samoa. <i>Clinical Infectious Diseases</i> , 2020, 71, S120-S126.	2.9	19
154	Characterisation of <i>Treponema pallidum</i> lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. <i>Lancet Microbe</i> , The, 2022, 3, e417-e426.	3.4	19
155	Comparison of the bacterial isolates and antibiotic resistance patterns of elderly nursing home and general community patients. <i>Internal Medicine Journal</i> , 2012, 42, e157-64.	0.5	18
156	Case-case-control study on factors associated with vanB vancomycin-resistant and vancomycin-susceptible enterococcal bacteraemia. <i>BMC Infectious Diseases</i> , 2014, 14, 353.	1.3	18
157	Correspondence: Spontaneous secondary mutations confound analysis of the essential two-component system WalkR in <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2017, 8, 14403.	5.8	18
158	Remodeling of pSK1 Family Plasmids and Enhanced Chlorhexidine Tolerance in a Dominant Hospital Lineage of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	18
159	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.	1.0	18
160	Niche-specific genome degradation and convergent evolution shaping <i>Staphylococcus aureus</i> adaptation during severe infections. <i>ELife</i> , 0, 11, .	2.8	18
161	The growing burden of multidrug-resistant infections among returned Australian travellers. <i>Medical Journal of Australia</i> , 2014, 200, 116-118.	0.8	17
162	Target-Specific Assay for Rapid and Quantitative Detection of <i>Mycobacterium chimaera</i> DNA. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1847-1856.	1.8	17

#	ARTICLE	IF	CITATIONS
163	Functional analysis of the first complete genome sequence of a multidrug resistant sequence type 2 <i>Staphylococcus epidermidis</i> . <i>Microbial Genomics</i> , 2016, 2, e000077.	1.0	17
164	The interplay between community and hospital <i>Enterococcus faecium</i> clones within health-care settings: a genomic analysis. <i>Lancet Microbe, The</i> , 2022, 3, e133-e141.	3.4	17
165	AusTrakka: Fast-tracking nationalized genomics surveillance in response to the COVID-19 pandemic. <i>Nature Communications</i> , 2022, 13, 865.	5.8	17
166	Once bitten, twice shy: an unusual case report of a mycotic aortic aneurysm. <i>ANZ Journal of Surgery</i> , 2005, 75, 1024-1026.	0.3	16
167	Use of bacterial whole-genome sequencing to understand and improve the management of invasive <i>Staphylococcus aureus</i> infections. <i>Expert Review of Anti-Infective Therapy</i> , 2016, 14, 1023-1036.	2.0	16
168	A review of the public health management of shigellosis in Australia in the era of culture-independent diagnostic testing. <i>Australian and New Zealand Journal of Public Health</i> , 2016, 40, 588-591.	0.8	16
169	Bilateral osteomyelitis and liver abscess caused by hypervirulent <i>Klebsiella pneumoniae</i> - a rare clinical manifestation (case report). <i>BMC Infectious Diseases</i> , 2018, 18, 380.	1.3	16
170	Long-term Impact of Pneumococcal Conjugate Vaccines on Invasive Disease and Pneumonia Hospitalizations in Indigenous and Non-Indigenous Australians. <i>Clinical Infectious Diseases</i> , 2020, 70, 2607-2615.	2.9	16
171	Large tandem chromosome expansions facilitate niche adaptation during persistent infection with drug-resistant <i>Staphylococcus aureus</i> . <i>Microbial Genomics</i> , 2015, 1, e000026.	1.0	16
172	Gut microbiome signatures and host colonization with multidrug-resistant bacteria. <i>Trends in Microbiology</i> , 2022, 30, 853-865.	3.5	16
173	<i>Staphylococcal superantigen-like protein 5</i> induces thrombotic and bleeding complications in vivo: inhibition by an anti-SSL5 antibody and the glycan Bimosiamose. <i>Journal of Thrombosis and Haemostasis</i> , 2012, 10, 2607-2609.	1.9	15
174	Sharing Is Caring: International Sharing of Data Enhances Genomic Surveillance of <i>Listeria monocytogenes</i> . <i>Clinical Infectious Diseases</i> , 2016, 63, 846.1-848.	2.9	15
175	Reconstruction of the Genomes of Drug-Resistant Pathogens for Outbreak Investigation through Metagenomic Sequencing. <i>MSphere</i> , 2019, 4, .	1.3	15
176	RNase III-CLASH of multi-drug resistant <i>Staphylococcus aureus</i> reveals a regulatory mRNA 3'UTR required for intermediate vancomycin resistance. <i>Nature Communications</i> , 2022, 13, .	5.8	15
177	Chronic falciparum malaria causing massive splenomegaly 9 years after leaving an endemic area. <i>Medical Journal of Australia</i> , 2005, 182, 186-188.	0.8	14
178	New aspirations: the debate on aspiration pneumonia treatment guidelines. <i>Medical Journal of Australia</i> , 2011, 195, 380-381.	0.8	14
179	Ceftazidime/avibactam susceptibility by three different susceptibility testing methods in carbapenemase-producing Gram-negative bacteria from Australia. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 82-85.	1.1	14
180	Risk Factors for Asymptomatic Enteric Pathogen Detection Among Men Who Have Sex With Men. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz326.	0.4	14

#	ARTICLE	IF	CITATIONS
181	Genomic Epidemiology and Antimicrobial Resistance Mechanisms of Imported Typhoid in Australia. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0120021.	1.4	14
182	Use of emerging testing technologies and approaches for SARS-CoV-2: review of literature and global experience in an Australian context. <i>Pathology</i> , 2021, 53, 689-699.	0.3	14
183	Utilizing genomic analyses to investigate the first outbreak of van A vancomycin-resistant Enterococcus in Australia with emergence of daptomycin non-susceptibility. <i>Journal of Medical Microbiology</i> , 2019, 68, 303-308.	0.7	14
184	Community and health-care associated non-multiresistant methicillin-resistant <i>Staphylococcus aureus</i> in Victoria. <i>Medical Journal of Australia</i> , 2005, 183, 548-548.	0.8	13
185	Treatment of <i>Staphylococcus aureus</i> infections: new issues, emerging therapies and future directions. <i>Expert Opinion on Emerging Drugs</i> , 2007, 12, 1-22.	1.0	13
186	Continuous-infusion penicillin home-based therapy for serious infections due to penicillin-susceptible pathogens. <i>International Journal of Antimicrobial Agents</i> , 2007, 29, 544-548.	1.1	13
187	Biosynthesis and Ether Bridge Formation in Nargenicin Macrolides. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 3996-4001.	7.2	13
188	Reflex Detection of Ciprofloxacin Resistance in <i>Neisseria gonorrhoeae</i> by Use of the SpeDx ResistancePlus GC Assay. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	13
189	Rising incidence of invasive meningococcal disease caused by <i>Neisseria meningitidis</i> serogroup W in Victoria. <i>Medical Journal of Australia</i> , 2016, 204, 265-266.	0.8	12
190	1,2,4-Oxadiazole antimicrobials act synergistically with daptomycin and display rapid kill kinetics against MDR <i>Enterococcus faecium</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1562-1569.	1.3	12
191	Long-term Impact of Oral Azithromycin Taken by Gambian Women During Labor on Prevalence and Antibiotic Susceptibility of <i>Streptococcus pneumoniae</i> and <i>Staphylococcus aureus</i> in Their Infants: Follow-up of a Randomized Clinical Trial. <i>Clinical Infectious Diseases</i> , 2018, 67, 1191-1197.	2.9	12
192	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.	2.9	12
193	Diversity of bacteriophages encoding Panton-Valentine leukocidin in temporally and geographically related <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2020, 15, e0228676.	1.1	12
194	Sample pooling on the Cepheid Xpert® Xpress SARS-CoV-2 assay. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 99, 115238.	0.8	12
195	Elucidating the Pharmacokinetics/Pharmacodynamics of Aerosolized Colistin against Multidrug-Resistant <i>Acinetobacter baumannii</i> and <i>Klebsiella pneumoniae</i> in a Mouse Lung Infection Model. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	11
196	Implementation and evaluation of a novel real-time multiplex assay for SARS-CoV-2: in-field learnings from a clinical microbiology laboratory. <i>Pathology</i> , 2020, 52, 754-759.	0.3	11
197	Incursions of <i>Candida auris</i> into Australia, 2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 1326-1328.	2.0	11
198	Prolonged Exposure to $\beta$ -Lactam Antibiotics Reestablishes Susceptibility of Daptomycin-Nonsusceptible <i>Staphylococcus aureus</i> to Daptomycin. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	11

#	ARTICLE	IF	CITATIONS
199	Nonclassical Pathogens as Causative Agents of Proctitis in Men who Have Sex With Men. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab137.	0.4	11
200	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.	1.5	11
201	<i>Staphylococcus aureus</i> : a guide for the perplexed. <i>Medical Journal of Australia</i> , 2006, 184, 374-375.	0.8	10
202	Community-onset <i>Staphylococcus aureus</i> infections presenting to general practices in South-eastern Australia. <i>Epidemiology and Infection</i> , 2014, 142, 501-511.	1.0	10
203	The importance of public health genomics for ensuring health security for Australia. <i>Medical Journal of Australia</i> , 2019, 210, 295.	0.8	10
204	Bacterial Load of <i>Chlamydia trachomatis</i> in the Posterior Oropharynx, Tonsillar Fossae, and Saliva among Men Who Have Sex with Men with Untreated Oropharyngeal Chlamydia. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	1.8	10
205	An open-label, parallel-group, randomised controlled trial of antiseptic mouthwash versus Antibiotics for oropharyngeal gonorrhoea treatment (OMEGA2). <i>Scientific Reports</i> , 2020, 10, 19386.	1.6	10
206	<i>Staphylococcus aureus</i> induces cell-surface expression of immune stimulatory NKG2D ligands on human monocytes. <i>Journal of Biological Chemistry</i> , 2020, 295, 11803-11821.	1.6	10
207	Emergence and divergence of major lineages of Shiga-toxin-producing <i>Escherichia coli</i> in Australia. <i>Microbial Genomics</i> , 2019, 5, .	1.0	10
208	Complete microbial genomes for public health in Australia and the Southwest Pacific. <i>Microbial Genomics</i> , 2020, 6, .	1.0	10
209	Significant variability exists in the cytotoxicity of global methicillin-resistant <i>Staphylococcus aureus</i> lineages. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	10
210	Cytomegalovirus viral load monitoring after allogeneic bone marrow transplantation in patients receiving antiviral prophylaxis. <i>Bone Marrow Transplantation</i> , 2003, 32, 795-800.	1.3	9
211	Functional genomics of <i>Staphylococcus aureus</i> . <i>Briefings in Functional Genomics</i> , 2013, 12, 305-315.	1.3	9
212	Analysis of Hepatitis B Virus Haplotype Diversity Detects Striking Sequence Conservation Across Genotypes and Chronic Disease Phase. <i>Hepatology</i> , 2021, 73, 1652-1670.	3.6	9
213	Surveillance for SARS-CoV-2 variants of concern in the Australian context. <i>Medical Journal of Australia</i> , 2021, 214, 500.	0.8	9
214	Differences in the population structure of <i>Neisseria meningitidis</i> in two Australian states: Victoria and Western Australia. <i>PLoS ONE</i> , 2017, 12, e0186839.	1.1	9
215	Case Report: Confirmation by Metagenomic Sequencing of Visceral Leishmaniasis in an Immunosuppressed Returned Traveler. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 103, 1930-1933.	0.6	9
216	The rise of antimicrobial resistance: a clear and present danger. <i>Expert Review of Anti-Infective Therapy</i> , 2011, 9, 645-648.	2.0	8

#	ARTICLE	IF	CITATIONS
217	Molecular characterization and antimicrobial susceptibilities of <i>Clostridium difficile</i> clinical isolates from Victoria, Australia. <i>Anaerobe</i> , 2015, 34, 80-83.	1.0	8
218	A Supervised Statistical Learning Approach for Accurate <i>Legionella pneumophila</i> Source Attribution during Outbreaks. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	8
219	Improved Outcomes with Linezolid for Methicillin-Resistant <i>Staphylococcus aureus</i> Infections: Better Drug or Reduced Vancomycin Susceptibility?. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4816-4817.	1.4	7
220	Vancomycin in the treatment of methicillin-resistant <i>Staphylococcus aureus</i> – a clinician’s guide to the science informing current practice. <i>Expert Review of Anti-Infective Therapy</i> , 2015, 13, 855-869.	2.0	7
221	Serological tests for COVID –19. <i>Medical Journal of Australia</i> , 2020, 213, 397.	0.8	7
222	Comparative Transcriptomic and Functional Assessments of Linezolid-Responsive Small RNA Genes in <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2020, 5, .	1.7	7
223	<i>Coxiella burnetii</i> endocarditis after Q fever vaccination. <i>Journal of Medical Microbiology</i> , 2012, 61, 1775-1779.	0.7	6
224	Absence of high priority critically important antimicrobial resistance in <i>Salmonella</i> sp. isolated from Australian commercial egg layer environments. <i>International Journal of Food Microbiology</i> , 2021, 340, 109042.	2.1	6
225	Multi-site point of care assessment of Abbott ID NOW rapid molecular test for SARS-CoV-2 in a low-prevalence setting. <i>Pathology</i> , 2021, 53, 912-914.	0.3	6
226	Low-Cost, Open-Source Device for High-Performance Fluorescence Detection of Isothermal Nucleic Acid Amplification Reactions. <i>ACS Biomaterials Science and Engineering</i> , 2021, 7, 4982-4990.	2.6	6
227	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.	1.3	6
228	Genomic investigation of <i>Staphylococcus aureus</i> recovered from Gambian women and newborns following an oral dose of intra-partum azithromycin. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3170-3178.	1.3	5
229	The risk of resistance: what are the major antimicrobial resistance threats facing Australia?. <i>Medical Journal of Australia</i> , 2019, 211, 103.	0.8	5
230	Cell Membrane Adaptations Mediate Î²-Lactam-Induced Resensitization of Daptomycin-Resistant (DAP-R) <i>Staphylococcus aureus</i> In Vitro. <i>Microorganisms</i> , 2021, 9, 1028.	1.6	5
231	Defective Severe Acute Respiratory Syndrome Coronavirus 2 Immune Responses in an Immunocompromised Individual With Prolonged Viral Replication. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab359.	0.4	5
232	Impact of Intrapartum Oral Azithromycin on the Acquired Macrolide Resistome of Infants’s Nasopharynx: A Randomized Controlled Trial. <i>Clinical Infectious Diseases</i> , 2020, 71, 3222-3225.	2.9	5
233	Towards equitable access to public health pathogen genomics in the Western Pacific. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 18, 100321.	1.3	5
234	Australian Enterococcal Sepsis Outcome Programme annual report, 2013. <i>Communicable Diseases Intelligence</i> , 2014, 38, E320-6.	0.5	5

#	ARTICLE	IF	CITATIONS
235	Impact of <i>vanB</i> vancomycin-resistant enterococcal bacteraemia analysed as a time-varying covariate on length of hospital stay. <i>Epidemiology and Infection</i> , 2014, 142, 2667-2671.	1.0	4
236	A nonclonal outbreak of vancomycin-sensitive <i>Enterococcus faecalis</i> bacteremia in a neonatal intensive care unit. <i>Infection Control and Hospital Epidemiology</i> , 2019, 40, 1116-1122.	1.0	4
237	Clinical Relevance of Topical Antibiotic Use in Coselecting for Multidrug-Resistant <i>Staphylococcus aureus</i> : Insights from <i>In Vitro</i> and <i>Ex Vivo</i> Models. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	4
238	Analytical sensitivity and specificity of the Cepheid Xpert Xpress SARS-CoV-2/Flu/RSV assay. <i>Pathology</i> , 2022, 54, 120-122.	0.3	4
239	Lab-in-a-van: Rapid SARS-CoV-2 testing response with a mobile laboratory. <i>EBioMedicine</i> , 2022, 79, 103983.	2.7	4
240	A Potential "Blind Spot" in Vancomycin Treatment Studies. <i>Clinical Infectious Diseases</i> , 2012, 55, 165-165.	2.9	3
241	Antibiotics and <i>Staphylococcus aureus</i> —more than meets the MIC. <i>Journal of Molecular Medicine</i> , 2014, 92, 103-106.	1.7	3
242	Fulminant meningococcal sepsis due to non-groupable <i>Neisseria meningitidis</i> in a patient receiving eculizumab. <i>Medical Journal of Australia</i> , 2018, 208, 478-479.	0.8	3
243	Viral Genomics to Inform Infection-control Response in Occupational Coronavirus Disease 2019 (COVID-19) Transmission. <i>Clinical Infectious Diseases</i> , 2020, 73, e1881-e1884.	2.9	3
244	Microbe-Metabolite Associations Linked to the Rebounding Murine Gut Microbiome Postcolonization with Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>MSystems</i> , 2020, 5, .	1.7	3
245	Clinical manifestations of invasive meningococcal disease in Victoria with the emergence of serogroup W and serogroup Y <i>Neisseria meningitidis</i> . <i>Internal Medicine Journal</i> , 2021, 51, 390-397.	0.5	3
246	Accessible Platform for High-Throughput COVID-19 Molecular Diagnostics and Genome Sequencing Using a Repurposed 3D Printer for RNA Extraction. <i>ACS Biomaterials Science and Engineering</i> , 2021, 7, 4669-4676.	2.6	3
247	The $\beta$ 1 large serine recombinase catalyzes DNA integration at pseudo- <i>attB</i> sites in the genus <i>Nocardia</i> . <i>PeerJ</i> , 2018, 6, e4784.	0.9	3
248	Australian Enterococcal Sepsis Outcome Programme, 2011. <i>Communicable Diseases Intelligence</i> , 2014, 38, E247-52.	0.5	3
249	Recent trends in invasive group A <i>Streptococcus</i> disease in Victoria. <i>Communicable Diseases Intelligence</i> (2018), 2019, 43, .	0.3	3
250	State-wide genomic epidemiology investigations of COVID-19 in healthcare workers in 2020 Victoria, Australia: Qualitative thematic analysis to provide insights for future pandemic preparedness. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 25, 100487.	1.3	3
251	Assessment of the BD GeneOhm MRSA ACP assay using combined swabs for the detection of methicillin resistant <i>Staphylococcus aureus</i> (MRSA) colonisation. <i>Pathology</i> , 2013, 45, 612-614.	0.3	2
252	Biosynthesis and Ether Bridge Formation in Nargenicin Macrolides. <i>Angewandte Chemie</i> , 2019, 131, 4036-4041.	1.6	2

#	ARTICLE	IF	CITATIONS
253	Second SARS-CoV-2 infections twelve months after initial infections in Australia, confirmed by genomic analysis. Medical Journal of Australia, 2021, , .	0.8	2
254	Genomic diversity of antimicrobial resistance in non-typhoidal Salmonella in Victoria, Australia. Microbial Genomics, 2021, 7, .	1.0	2
255	Added Value of Genomic Surveillance of Virulence Factors in Shiga Toxin-Producing Escherichia coli in New South Wales, Australia. Frontiers in Microbiology, 2021, 12, 713724.	1.5	2
256	Accurate Assessment of Heterogeneous Vancomycin-Intermediate Staphylococcus aureus Nasal Carriage. Clinical Infectious Diseases, 2005, 41, 1071-1072.	2.9	1
257	Reply to De Angelis et al. Clinical Infectious Diseases, 2011, 52, 1472-1472.	2.9	1
258	Reporting practices for genomic epidemiology of tuberculosis: a systematic review of the literature using STROME-ID guidelines as a benchmark. Lancet Microbe, The, 2021, 2, e115-e129.	3.4	1
259	A multi-institutional outbreak of New Delhi metallo- $\beta$ -lactamase-producing <i>Escherichia coli</i> with subsequent acquisition of the <i>Klebsiella pneumoniae</i> carbapenemase gene. Infection Control and Hospital Epidemiology, 2021, 42, 1124-1127.	1.0	1
260	Search and Contain: Impact of an Integrated Genomic and Epidemiological Surveillance and Response Program for Control of Carbapenemase-Producing <i>Enterobacteriales</i> . SSRN Electronic Journal, 0, , .	0.4	1
261	Patient-focused pathogen genetic counselling "has the time come?. Genome Medicine, 2021, 13, 178.	3.6	1
262	Multi-Site Implementation of Whole Genome Sequencing for Hospital Infection Control: A Prospective Genomic-Epidemiological Analysis. SSRN Electronic Journal, 0, , .	0.4	1
263	Feasibility of a refurbished shipping container as a transportable laboratory for rapid SARS-CoV-2 diagnostics. Access Microbiology, 2022, 4, .	0.2	1
264	Reply to "Internet-Based Solutions for Analysis of Next-Generation Sequence Data". Journal of Clinical Microbiology, 2013, 51, 3163-3163.	1.8	0
265	O004...Inhibitory effect of an antiseptic mouthwash against <i>Neisseria gonorrhoeae</i> in the pharynx (GONE) among men who have sex with men: a randomised control trial. Sexually Transmitted Infections, 2016, 92, A2.1-A2.	0.8	0
266	The Critical Importance of Sampling Fraction to Inferences of <i>Mycobacterium tuberculosis</i> Transmission. Clinical Infectious Diseases, 2018, 66, 159-160.	2.9	0
267	P461...Bacterial load of chlamydia in the oropharynx and saliva among gay and bisexual men with untreated oropharyngeal chlamydia. , 2019, , .		0
268	O02.2...Oropharyngeal and genital gonorrhoea among heterosexuals who report sexual contact with partners with gonorrhoea. , 2019, , .		0
269	O07.1...Multiple lineages of multiresistant <i>Shigella</i> in Australia. , 2019, , .		0
270	Short-term increase in the carriage of azithromycin-resistant <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> in mothers and their newborns following intra-partum azithromycin: a post hoc analysis of a double-blind randomized trial. JAC-Antimicrobial Resistance, 2021, 3, dlaa128.	0.9	0



#	ARTICLE	IF	CITATIONS
271	Complete genome sequencing of <i>Staphylococcus aureus</i> : insights into virulence and antimicrobial resistance. <i>Microbiology Australia</i> , 2008, 29, 115.	0.1	0
272	A Simple Cleaning Intervention to Prevent Transmission of Carbapenemase-Producing Enterobacterales from Hospital Sinks. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, s103-s104.	1.0	0
273	Genomic Characterisation Reveals a Dominant Lineage of SARS-CoV-2 in Papua New Guinea. <i>Virus Evolution</i> , 0, , .	2.2	0
274	Title is missing!. , 2020, 15, e0228676.		0
275	Title is missing!. , 2020, 15, e0228676.		0
276	Title is missing!. , 2020, 15, e0228676.		0
277	Title is missing!. , 2020, 15, e0228676.		0
278	Title is missing!. , 2020, 15, e0228676.		0
279	Title is missing!. , 2020, 15, e0228676.		0