Benjamin P Howden

List of Publications by Year
in descending order

279	12,844	30047	34964
papers	citations	54 h-index	98 g-index

308	308	308	13327
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Reduced Vancomycin Susceptibility inStaphylococcus aureus, Including Vancomycin-Intermediate and Heterogeneous Vancomycin-Intermediate Strains: Resistance Mechanisms, Laboratory Detection, and Clinical Implications. Clinical Microbiology Reviews, 2010, 23, 99-139.	5.7	804
2	Treatment Outcomes for Serious Infections Caused by MethicillinâEResistantStaphylococcus aureuswith Reduced Vancomycin Susceptibility. Clinical Infectious Diseases, 2004, 38, 521-528.	2.9	467
3	Clinical Features Associated with Bacteremia Due to Heterogeneous VancomycinâEIntermediateStaphylococcus aureus. Clinical Infectious Diseases, 2004, 38, 448-451.	2.9	368
4	Evolution of Multidrug Resistance during Staphylococcus aureus Infection Involves Mutation of the Essential Two Component Regulator WalKR. PLoS Pathogens, 2011, 7, e1002359.	2.1	315
5	Isolation and rapid sharing of the 2019 novel coronavirus (<scp>SARS</scp> â€CoVâ€2) from the first patient diagnosed with <scp>COVID</scp> â€19 in Australia. Medical Journal of Australia, 2020, 212, 459-462.	0.8	297
6	Current and Emerging Topical Antibacterials and Antiseptics: Agents, Action, and Resistance Patterns. Clinical Microbiology Reviews, 2017, 30, 827-860.	5.7	245
7	Prospective Whole-Genome Sequencing Enhances National Surveillance of Listeria monocytogenes. Journal of Clinical Microbiology, 2016, 54, 333-342.	1.8	239
8	Antibiotic Choice May Not Explain Poorer Outcomes in Patients With Staphylococcus aureus Bacteremia and High Vancomycin Minimum Inhibitory Concentrations. Journal of Infectious Diseases, 2011, 204, 340-347.	1.9	214
9	Global spread of three multidrug-resistant lineages of Staphylococcus epidermidis. Nature Microbiology, 2018, 3, 1175-1185.	5.9	206
10	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. Lancet Infectious Diseases, The, 2015, 15, 913-921.	4.6	204
11	Isolates with Low-Level Vancomycin Resistance Associated with Persistent Methicillin-Resistant Staphylococcus aureus Bacteremia. Antimicrobial Agents and Chemotherapy, 2006, 50, 3039-3047.	1.4	199
12	Two Novel Point Mutations in Clinical Staphylococcus aureus Reduce Linezolid Susceptibility and Switch on the Stringent Response to Promote Persistent Infection. PLoS Pathogens, 2010, 6, e1000944.	2.1	191
13	Staphylococcus aureus bacteraemia: a major cause of mortality in Australia and New Zealand. Medical Journal of Australia, 2009, 191, 368-373.	0.8	184
14	Vancomycin AUC/MIC Ratio and 30-Day Mortality in Patients with Staphylococcus aureus Bacteremia. Antimicrobial Agents and Chemotherapy, 2013, 57, 1654-1663.	1.4	176
15	Effect of Vancomycin or Daptomycin With vs Without an Antistaphylococcal Î²-Lactam on Mortality, Bacteremia, Relapse, or Treatment Failure in Patients With MRSA Bacteremia. JAMA - Journal of the American Medical Association, 2020, 323, 527.	3.8	169
16	Complete Bypass of Restriction Systems for Major Staphylococcus aureus Lineages. MBio, 2015, 6, e00308-15.	1.8	168
17	Not Community-Associated Methicillin-Resistant Staphylococcus aureus (CA-MRSA)! A Clinician's Guide to Community MRSA - Its Evolving Antimicrobial Resistance and Implications for Therapy. Clinical Infectious Diseases, 2011, 52, 99-114.	2.9	166
18	Increasing tolerance of hospital Enterococcus faecium to handwash alcohols. Science Translational Medicine, 2018, 10, .	5.8	165

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19	Dumb and Dumber--The Potential Waste of a Useful Antistaphylococcal Agent: Emerging Fusidic Acid Resistance in Staphylococcus aureus. Clinical Infectious Diseases, 2006, 42, 394-400.	2.9	156
20	Evolution of virulence in Enterococcus faecium, a hospital-adapted opportunistic pathogen. Current Opinion in Microbiology, 2018, 41, 76-82.	2.3	153
21	Tracking the COVID-19 pandemic in Australia using genomics. Nature Communications, 2020, 11, 4376.	5.8	152
22	In vitro pharmacodynamics of colistin against multidrug-resistant Klebsiella pneumoniae. Journal of Antimicrobial Chemotherapy, 2008, 62, 1311-1318.	1.3	150
23	Combination of Vancomycin and Î²-Lactam Therapy for Methicillin-ResistantStaphylococcus aureusBacteremia: A Pilot Multicenter Randomized Controlled Trial. Clinical Infectious Diseases, 2016, 62, 173-180.	2.9	149
24	Genomic Analysis Reveals a Point Mutation in the Two-Component Sensor Gene graS That Leads to Intermediate Vancomycin Resistance in Clinical Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2008, 52, 3755-3762.	1.4	137
25	Emergence and rapid global dissemination of CTX-M-15-associatedKlebsiella pneumoniaestrain ST307. Journal of Antimicrobial Chemotherapy, 2019, 74, 577-581.	1.3	137
26	Genomic Insights to Control the Emergence of Vancomycin-Resistant Enterococci. MBio, 2013, 4, .	1.8	136
27	Comparative Analysis of the First Complete Enterococcus faecium Genome. Journal of Bacteriology, 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. Antimicrobial Agents and Chemotherapy, 2006, 50, 1599-1602.	1.4	132
29	The evolution of vancomycin intermediate Staphylococcus aureus (VISA) and heterogenous-VISA. Infection, Genetics and Evolution, 2014, 21, 575-582.	1.0	115
30	Prospective Comparison of the Clinical Impacts of Heterogeneous Vancomycin-Intermediate Methicillin-Resistant Staphylococcus aureus (MRSA) and Vancomycin-Susceptible MRSA. Antimicrobial Agents and Chemotherapy, 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 Staphylococcus aureus bacteraemia. BMC Microbiology, 2008, 8, 39.	1.3	106
32	Enterococcal bacteraemia: factors influencing mortality, length of stay and costs of hospitalization. Clinical Microbiology and Infection, 2013, 19, E181-E189.	2.8	106
33	A Sustained Hospital Outbreak of Vancomycinâ€ResistantEnterococcus faeciumBacteremia due to Emergence ofvanB E. faeciumSequence Type 203. Journal of Infectious Diseases, 2010, 202, 1278-1286.	1.9	98
34	Serine/Threonine Phosphatase Stp1 Contributes to Reduced Susceptibility to Vancomycin and Virulence in Staphylococcus aureus. Journal of Infectious Diseases, 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 Staphylococcus aureus. Journal of Infectious Diseases, 2013, 207, 929-939.	1.9	94
36	Daptomycin non-susceptibility in vancomycin-intermediate Staphylococcus aureus (VISA) and heterogeneous-VISA (hVISA): implications for therapy after vancomycin treatment failure. Journal of Antimicrobial Chemotherapy, 2011, 66, 1057-1060.	1.3	90

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

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55	Staphylococcus aureus small colony variants impair host immunity by activating host cell glycolysis and inducing necroptosis. Nature Microbiology, 2020, 5, 141-153.	5.9	65
56	Antiseptic mouthwash against pharyngealNeisseria gonorrhoeae: a randomised controlled trial and an in vitro study. Sexually Transmitted Infections, 2017, 93, 88-93.	0.8	64
57	Decreased Vancomycin Susceptibility in Staphylococcus aureus Caused by IS 256 Tempering of WalKR Expression. Antimicrobial Agents and Chemotherapy, 2013, 57, 3240-3249.	1.4	62
58	Emerging Gram negative resistance to last-line antimicrobial agents fosfomycin, colistin and ceftazidime-avibactam â€“ epidemiology, laboratory detection and treatment implications. Expert Review of Anti-Infective Therapy, 2018, 16, 289-306.	2.0	62
59	CAMERA2 â€“ combination antibiotic therapy for methicillin-resistant Staphylococcus aureus infection: study protocol for a randomised controlled trial. Trials, 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. Journal of Medical Microbiology, 2020, 69, 1169-1178.	0.7	61
61	Vancomycin therapeutics and monitoring: a contemporary approach. Internal Medicine Journal, 2013, 43, 110-119.	0.5	57
62	Genomic epidemiology and antimicrobial resistance of Neisseria gonorrhoeae in New Zealand. Journal of Antimicrobial Chemotherapy, 2018, 73, 353-364.	1.3	57
63	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing Enterobacterales in Victoria, Australia, 2012 to 2016. Journal of Clinical Microbiology, 2019, 57, .	1.8	56
64	Evaluation of Serological Tests for SARS-CoV-2: Implications for Serology Testing in a Low-Prevalence Setting. Journal of Infectious Diseases, 2020, 222, 1280-1288.	1.9	56
65	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant Staphylococcus aureus. MSphere, 2018, 3, .	1.3	55
66	Complete Genome Sequence of Staphylococcus aureus Strain JKD6159, a Unique Australian Clone of ST93-IV Community Methicillin-Resistant Staphylococcus aureus. Journal of Bacteriology, 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. Lancet Public Health, The, 2021, 6, e547-e556.	4.7	53
68	Detection ofNeisseria gonorrhoeaein the pharynx and saliva: implications for gonorrhoea transmission: TableÂ1. Sexually Transmitted Infections, 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 Enterococcus faecium. BMC Genomics, 2013, 14, 595.	1.2	50
70	Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent Staphylococcus aureus bacteraemia. Genome Medicine, 2018, 10, 65.	3.6	49
71	Comparison of the Xpert Methicillin-Resistant Staphylococcus aureus (MRSA) Assay, BD GeneOhm MRSA Assay, and Culture for Detection of Nasal and Cutaneous Groin Colonization by MRSA. Journal of Clinical Microbiology, 2009, 47, 3769-3772.	1.8	48
72	Genetic and Molecular Predictors of High Vancomycin MIC in Staphylococcus aureus Bacteremia Isolates. Journal of Clinical Microbiology, 2014, 52, 3384-3393.	1.8	47

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73	Increasing Antimicrobial Resistance in Nontyphoidal Salmonella Isolates in Australia from 1979 to 2015. Antimicrobial Agents and Chemotherapy, 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. Sexually Transmitted Infections, 2019, 95, 516-521.	0.8	47
75	Evolutionary origins of the emergent ST796 clone of vancomycin resistantEnterococcus faecium. PeerJ, 2017, 5, e2916.	0.9	46
76	Neisseria gonorrhoeae isolates with high-level resistance to azithromycin in Australia. Journal of Antimicrobial Chemotherapy, 2015, 70, 1267-1268.	1.3	45
77	Inactivation of the Indigenous Methyltransferase RlmN in Staphylococcus aureus Increases Linezolid Resistance. Antimicrobial Agents and Chemotherapy, 2011, 55, 2989-2991.	1.4	44
78	Emergence of endemic MLST non-typeable vancomycin-resistant Enterococcus faecium. Journal of Antimicrobial Chemotherapy, 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. BMC Infectious Diseases, 2017, 17, 456.	1.3	44
80	Genomics of vancomycin-resistant Enterococcus faecium. Microbial Genomics, 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. Sexually Transmitted Infections, 2018, 94, 151-157.	0.8	42
82	The Molecular Epidemiology of the Highly Virulent ST93 Australian Community Staphylococcus aureus Strain. PLoS ONE, 2012, 7, e43037.	1.1	42
83	The importance of regulatory RNAs in Staphylococcus aureus. Infection, Genetics and Evolution, 2014, 21, 616-626.	1.0	41
84	Rapid Emergence and Evolution of Staphylococcus aureus Clones Harboring fusC -Containing Staphylococcal Cassette Chromosome Elements. Antimicrobial Agents and Chemotherapy, 2016, 60, 2359-2365.	1.4	41
85	Dissecting the molecular evolution of fluoroquinolone-resistant Shigella sonnei. Nature Communications, 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. Lancet Infectious Diseases, The, 2019, 19, 833-842.	4.6	41
87	5: Hospitalâ€inâ€theâ€home treatment of infectious diseases. Medical Journal of Australia, 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 Staphylococcus aureus. Genome Biology and Evolution, 2014, 6, 366-378.	1.1	40
89	Zinc-binding to the cytoplasmic PAS domain regulates the essential WalK histidine kinase of Staphylococcus aureus. Nature Communications, 2019, 10, 3067.	5.8	38
90	Mycolactone Gene Expression Is Controlled by Strong SigA-Like Promoters with Utility in Studies of Mycobacterium ulcerans and Buruli Ulcer. PLoS Neglected Tropical Diseases, 2009, 3, e553.	1.3	37

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91	WhatÊ¼s new in the treatment of serious MRSA infection?. Current Opinion in Infectious Diseases, 2014, 27, 471-478.	1.3	37
92	Klebsiella pneumoniae induces host metabolic stress that promotes tolerance to pulmonary infection. Cell Metabolism, 2022, 34, 761-774.e9.	7.2	36
93	Evolutionary dynamics of multidrug resistant Salmonella enterica serovar 4,[5],12:i:- in Australia. Nature Communications, 2021, 12, 4786.	5.8	35
94	Genomic Analysis of Multiresistant Staphylococcus capitis Associated with Neonatal Sepsis. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	34
95	Prevalence of genital and oropharyngeal chlamydia and gonorrhoea among female sex workers in Melbourne, Australia, 2015â€“2017: need for oropharyngeal testing. Sexually Transmitted Infections, 2019, 95, 398-401.	0.8	33
96	The global dissemination of hospital clones of Enterococcus faecium. Genome Medicine, 2021, 13, 52.	3.6	33
97	Key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria: a systematic analysis. Lancet Microbe, 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. Current Opinion in Infectious Diseases, 2009, 22, 525-534.	1.3	32
99	Population genetics and the evolution of virulence in Staphylococcus aureus. Infection, Genetics and Evolution, 2014, 21, 554-562.	1.0	32
100	Comparative Genomics Shows That Mycobacterium ulcerans Migration and Expansion Preceded the Rise of Buruli Ulcer in Southeastern Australia. Applied and Environmental Microbiology, 2018, 84, .	1.4	32
101	Pandemic printing: a novel 3Dâ€printed swab for detecting <scp>SARS</scp> â€CoVâ€2. Medical Journal of Australia, 2020, 213, 276-279.	0.8	32
102	High-Resolution Melting Genotyping of Enterococcus faecium Based on Multilocus Sequence Typing Derived Single Nucleotide Polymorphisms. PLoS ONE, 2011, 6, e29189.	1.1	31
103	Outbreak of vanB vancomycin-resistant Enterococcus faecium colonization in a neonatal service. American Journal of Infection Control, 2015, 43, 1061-1065.	1.1	31
104	Heterogeneity of Genetic Pathways toward Daptomycin Nonsusceptibility in Staphylococcus aureus Determined by Adjunctive Antibiotics. Antimicrobial Agents and Chemotherapy, 2015, 59, 2799-2806.	1.4	31
105	Genomic insights into a sustained national outbreak of Yersinia pseudotuberculosis. Genome Biology and Evolution, 2016, 8, evw285.	1.1	31
106	NGMASTER: in silico multi-antigen sequence typing for Neisseria gonorrhoeae. Microbial Genomics, 2016, 2, e000076.	1.0	31
107	Comparative Study of Selective Chromogenic (chromID VRE) and Bile Esculin Agars for Isolation and Identification of vanB -Containing Vancomycin-Resistant Enterococci from Feces and Rectal Swabs. Journal of Clinical Microbiology, 2008, 46, 4034-4036.	1.8	30
108	Vancomycin-resistant Enterococcus faecium sequence type 796 - rapid international dissemination of a new epidemic clone. Antimicrobial Resistance and Infection Control, 2018, 7, 44.	1.5	30

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

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127	Incorporating Whole-Genome Sequencing into Public Health Surveillance: Lessons from Prospective Sequencing of Salmonella Typhimurium in Australia. Foodborne Pathogens and Disease, 2018, 15, 161-167.	0.8	24
128	Detection of SARS-CoV-2 in saliva: implications for specimen transport and storage. Journal of Medical Microbiology, 2021, 70, .	0.7	24
129	Antiseptic mouthwash for gonorrhoea prevention (OMEGA): a randomised, double-blind, parallel-group, multicentre trial. Lancet Infectious Diseases, 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 Staphylococcus aureus. Microbial Genomics, 2017, 3, e000105.	1.0	24
131	Evaluation of the Xpertâ„¢ MRSA/SA Blood Culture assay for the detection of Staphylococcus aureus including strains with reduced vancomycin susceptibility from blood culture specimens. Diagnostic Microbiology and Infectious Disease, 2011, 70, 404-407.	0.8	23
132	Oropharyngeal and Genital Gonorrhea Infections Among Women and Heterosexual Men Reporting Sexual Contact With Partners With Gonorrhea: Implication for Oropharyngeal Testing of Heterosexual Gonorrhea Contacts. Sexually Transmitted Diseases, 2019, 46, 743-747.	0.8	23
133	Emergence and global spread of Listeria monocytogenes main clinical clonal complex. Science Advances, 2021, 7, eabj9805.	4.7	23
134	Vancomycin minimum inhibitory concentration, host comorbidities and mortality in Staphylococcus aureus bacteraemia. Clinical Microbiology and Infection, 2013, 19, 1163-1168.	2.8	22
135	Rifampicin resistance in Staphylococcus epidermidis: molecular characterisation and fitness cost of rpoB mutations. International Journal of Antimicrobial Agents, 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. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	22
137	Failure of Vancomycin for Treatment of Methicillin-Resistant Staphylococcus aureus Infections. Clinical Infectious Diseases, 2004, 39, 1544-1544.	2.9	21
138	Polyclonal emergence ofvanAvancomycin-resistantEnterococcus faeciumin Australia. Journal of Antimicrobial Chemotherapy, 2016, 72, dkw539.	1.3	21
139	Daptomycin selects for genetic and phenotypic adaptations leading to antibiotic tolerance in MRSA. Journal of Antimicrobial Chemotherapy, 2018, 73, 2030-2033.	1.3	21
140	Genomic Insights Into Last-Line Antimicrobial Resistance in Multidrug-Resistant Staphylococcus and Vancomycin-Resistant Enterococcus. Frontiers in Microbiology, 2021, 12, 637656.	1.5	21
141	Vancomycin Exposure and Acute Kidney Injury Outcome: A Snapshot From the CAMERA2 Study. Open Forum Infectious Diseases, 2020, 7, ofaa538.	0.4	21
142	Australian Group on Antimicrobial Resistance Australian Staphylococcus aureus Sepsis Outcome Programme annual report, 2014. Communicable Diseases Intelligence, 2016, 40, E244-54.	0.5	21
143	Rise in invasive serogroup W meningococcal disease in Australia 2013-2015. Communicable Diseases Intelligence, 2016, 40, E454-E459.	0.5	21
144	Low mannose-binding lectin complement activation function is associated with predisposition to Legionnaires' disease. Clinical and Experimental Immunology, 2007, 149, 97-102.	1.1	20

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145	Emergence of multidrug resistance in locally-acquired human infections with Salmonella Typhimurium in Australia owing to a new clade harbouring bla CTX-M-9. International Journal of Antimicrobial Agents, 2017, 50, 101-105.	1.1	20
146	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen Mycobacterium kansasii. Nature Communications, 2021, 12, 2491.	5.8	20
147	Genomic analysis of ST88 community-acquired methicillin resistantStaphylococcus aureusin Ghana. PeerJ, 2017, 5, e3047.	0.9	20
148	Optimising genomic approaches for identifying vancomycin-resistant Enterococcus faecium transmission in healthcare settings. Nature Communications, 2022, 13, 509.	5.8	20
149	Cutaneous zygomycosis caused bySaksenaea vasiformisfollowing water-related wound in a 24-year-old immunocompetent woman. Mycoses, 2009, 52, 547-549.	1.8	19
150	Genomic analysis of teicoplanin resistance emerging during treatment of vanB vancomycin-resistant Enterococcus faecium infections in solid organ transplant recipients including donor-derived cases. Journal of Antimicrobial Chemotherapy, 2013, 68, 2134-2139.	1.3	19
151	Trends and Risk Factors for Antimicrobial-Resistant Neisseria gonorrhoeae , Melbourne, Australia, 2007 to 2018. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	19
152	Increasing incidence of invasive nontyphoidal Salmonella infections in Queensland, Australia, 2007-2016. PLoS Neglected Tropical Diseases, 2019, 13, e0007187.	1.3	19
153	Tenacious Endemic Typhoid Fever in Samoa. Clinical Infectious Diseases, 2020, 71, S120-S126.	2.9	19
154	Characterisation of Treponema pallidum lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. Lancet Microbe, 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. Internal Medicine Journal, 2012, 42, e157-64.	0.5	18
156	Case-case-control study on factors associated with vanB vancomycin-resistant and vancomycin-susceptible enterococcal bacteraemia. BMC Infectious Diseases, 2014, 14, 353.	1.3	18
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