

# Glen P Carter

## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

3,915  
citations

230014

27  
h-index

145109

60  
g-index

65  
all docs

65  
docs citations

65  
times ranked

4756  
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of 1,2,4-Oxadiazole Antimicrobial Agents to Treat Enteric Pathogens within the Gastrointestinal Tract. <i>ACS Omega</i> , 2022, 7, 6737-6759.	1.6	3
2	Detection of Chimeric Cellular: HIV mRNAs Generated Through Aberrant Splicing in HIV-1 Latently Infected Resting CD4+ T Cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 855290.	1.8	3
3	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
4	Diarrhea in an infant due to <i>Shigella flexneri</i> 1 carrying multiple cephalosporinase-encoding genes. <i>Gut Pathogens</i> , 2021, 13, 18.	1.6	1
5	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
6	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
7	Structure-Activity Relationships of Daptomycin Lipopeptides. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 13266-13290.	2.9	30
8	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
9	Gut microbiome of native Arab Kuwaitis. <i>Gut Pathogens</i> , 2020, 12, 10.	1.6	7
10	Complete microbial genomes for public health in Australia and the Southwest Pacific. <i>Microbial Genomics</i> , 2020, 6, .	1.0	10
11	Reconstruction of the Genomes of Drug-Resistant Pathogens for Outbreak Investigation through Metagenomic Sequencing. <i>MSphere</i> , 2019, 4, .	1.3	15
12	Non-typhoidal <i>Salmonella</i> blood stream infection in Kuwait: Clinical and microbiological characteristics. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007293.	1.3	13
13	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
14	Mining the Methylome Reveals Extensive Diversity in <i>Staphylococcus epidermidis</i> Restriction Modification. <i>MBio</i> , 2019, 10, .	1.8	28
15	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
16	Genomic Analysis of Fluoroquinolone- and Tetracycline-Resistant <i>Campylobacter jejuni</i> Sequence Type 6964 in Humans and Poultry, New Zealand, 2014-2016. <i>Emerging Infectious Diseases</i> , 2019, 25, 2226-2234.	2.0	27
17	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
18	Genomics of vancomycin-resistant <i>Enterococcus faecium</i> . <i>Microbial Genomics</i> , 2019, 5, .	1.0	44

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19	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
20	Complete Genome Sequence of a New Zealand Isolate of the Bovine Pathogen <i>Streptococcus uberis</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	3
21	Genome-by-genome approach for fast bacterial genealogical relationship evaluation. <i>Bioinformatics</i> , 2018, 34, 3025-3027.	1.8	25
22	Incorporating Whole-Genome Sequencing into Public Health Surveillance: Lessons from Prospective Sequencing of <i>Salmonella</i> Typhimurium in Australia. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 161-167.	0.8	24
23	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
24	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
25	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
26	Genomic Analysis of Multiresistant <i>Staphylococcus capitis</i> Associated with Neonatal Sepsis. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	34
27	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
28	Increasing tolerance of hospital <i>Enterococcus faecium</i> to handwash alcohols. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	165
29	The First Isolation and Whole Genome Sequencing of Murray Valley Encephalitis Virus from Cerebrospinal Fluid of a Patient with Encephalitis. <i>Viruses</i> , 2018, 10, 319.	1.5	11
30	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
31	Current and Emerging Topical Antibacterials and Antiseptics: Agents, Action, and Resistance Patterns. <i>Clinical Microbiology Reviews</i> , 2017, 30, 827-860.	5.7	245
32	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
33	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
34	Draft Genome Sequences of Two Strains of a Newly Described Species, <i>Sphingobacterium cellulitidis</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	1
35	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
36	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

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37	Rapid Emergence and Evolution of <i>Staphylococcus aureus</i> Clones Harboring <i>stx2C</i> -Containing Staphylococcal Cassette Chromosome Elements. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2359-2365.	1.4	41
38	Genomic insights into a sustained national outbreak of <i>Yersinia pseudotuberculosis</i> . <i>Genome Biology and Evolution</i> , 2016, 8, eww285.	1.1	31
39	Defining the Roles of TcdA and TcdB in Localized Gastrointestinal Disease, Systemic Organ Damage, and the Host Response during <i>Clostridium difficile</i> Infections. <i>MBio</i> , 2015, 6, e00551.	1.8	228
40	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
41	<i>Clostridium difficile</i> virulence factors: Insights into an anaerobic spore-forming pathogen. <i>Gut Microbes</i> , 2014, 5, 579-593.	4.3	110
42	Regulation of toxin production in the pathogenic clostridia. <i>Molecular Microbiology</i> , 2014, 91, 221-231.	1.2	25
43	Utility of the Clostridial Site-Specific Recombinase TnpX To Clone Toxic-Product-Encoding Genes and Selectively Remove Genomic DNA Fragments. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3597-3603.	1.4	8
44	Emergence of a Ribotype 244 Strain of <i>Clostridium difficile</i> Associated With Severe Disease and Related to the Epidemic Ribotype 027 Strain. <i>Clinical Infectious Diseases</i> , 2014, 58, 1723-1730.	2.9	111
45	Expression of the large clostridial toxins is controlled by conserved regulatory mechanisms. <i>International Journal of Medical Microbiology</i> , 2014, 304, 1147-1159.	1.5	31
46	Novel Molecular Type of <i>Clostridium difficile</i> in Neonatal Pigs, Western Australia. <i>Emerging Infectious Diseases</i> , 2013, 19, 790-2.	2.0	39
47	Spo0A Differentially Regulates Toxin Production in Evolutionarily Diverse Strains of <i>Clostridium difficile</i> . <i>PLoS ONE</i> , 2013, 8, e79666.	1.1	79
48	The role of toxin A and toxin B in the virulence of <i>Clostridium difficile</i> . <i>Trends in Microbiology</i> , 2012, 20, 21-29.	3.5	138
49	Non-toxigenic <i>Clostridium sordellii</i> : Clinical and microbiological features of a case of cholangitis-associated bacteremia. <i>Anaerobe</i> , 2011, 17, 252-256.	1.0	16
50	TcdB or not TcdB: a tale of two <i>Clostridium difficile</i> toxins. <i>Future Microbiology</i> , 2011, 6, 121-123.	1.0	15
51	TcsL Is an Essential Virulence Factor in <i>Clostridium sordellii</i> ATCC 9714. <i>Infection and Immunity</i> , 2011, 79, 1025-1032.	1.0	51
52	The Anti-Sigma Factor TcdC Modulates Hypervirulence in an Epidemic BI/NAP1/027 Clinical Isolate of <i>Clostridium difficile</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002317.	2.1	139
53	The Cysteine Protease $\hat{\pm}$ -Clostripain is Not Essential for the Pathogenesis of <i>Clostridium perfringens</i> -Mediated Myonecrosis. <i>PLoS ONE</i> , 2011, 6, e22762.	1.1	15
54	The role of toxin A and toxin B in <i>Clostridium difficile</i> -associated disease. <i>Gut Microbes</i> , 2010, 1, 58-64.	4.3	90

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55	The VirSR Two-Component Signal Transduction System Regulates NetB Toxin Production in <i>Clostridium perfringens</i> . <i>Infection and Immunity</i> , 2010, 78, 3064-3072.	1.0	82
56	Methods for Gene Cloning and Targeted Mutagenesis. <i>Methods in Molecular Biology</i> , 2010, 646, 183-201.	0.4	1
57	Toxin B is essential for virulence of <i>Clostridium difficile</i> . <i>Nature</i> , 2009, 458, 1176-1179.	13.7	654
58	Binary Toxin Production in <i>Clostridium difficile</i> Is Regulated by CdtR, a LytTR Family Response Regulator. <i>Journal of Bacteriology</i> , 2007, 189, 7290-7301.	1.0	116
59	The Clostron: A universal gene knock-out system for the genus <i>Clostridium</i> . <i>Journal of Microbiological Methods</i> , 2007, 70, 452-464.	0.7	598
60	Quorum sensing in <i>Clostridium difficile</i> : analysis of a luxS-type signalling system. <i>Journal of Medical Microbiology</i> , 2005, 54, 119-127.	0.7	68
61	Gene Cloning in <i>Clostridia</i> . , 2005, , 37-52.		5
62	The development of <i>Clostridium difficile</i> genetic systems. <i>Anaerobe</i> , 2004, 10, 75-84.	1.0	14
63	Regulation of Toxin Production in <i>Clostridium difficile</i> . , 0, , 295-306.		0