

Richard A Stabler

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

2,866
citations

279798
23
h-index

175258
52
g-index

56
all docs

56
docs citations

56
times ranked

3580
citing authors

#	ARTICLE	IF	CITATIONS
1	The multidrug-resistant human pathogen <i>Clostridium difficile</i> has a highly mobile, mosaic genome. <i>Nature Genetics</i> , 2006, 38, 779-786.	21.4	821
2	Comparative genome and phenotypic analysis of <i>Clostridium difficile</i> 027 strains provides insight into the evolution of a hypervirulent bacterium. <i>Genome Biology</i> , 2009, 10, R102.	9.6	431
3	Application of DNA Microarrays to Study the Evolutionary Genomics of <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> . <i>Genome Research</i> , 2003, 13, 2018-2029.	5.5	154
4	Macro and Micro Diversity of <i>Clostridium difficile</i> Isolates from Diverse Sources and Geographical Locations. <i>PLoS ONE</i> , 2012, 7, e31559.	2.5	114
5	Effects of <i>Eimeria tenella</i> infection on chicken caecal microbiome diversity, exploring variation associated with severity of pathology. <i>PLoS ONE</i> , 2017, 12, e0184890.	2.5	109
6	Microarray analysis of the transcriptional responses of <i>Clostridium difficile</i> to environmental and antibiotic stress. <i>Journal of Medical Microbiology</i> , 2008, 57, 757-764.	1.8	94
7	Emergence of new PCR ribotypes from the hypervirulent <i>Clostridium difficile</i> 027 lineage. <i>Journal of Medical Microbiology</i> , 2012, 61, 49-56.	1.8	81
8	Evidence for Community Transmission of Community-Associated but Not Health-Care-Associated Methicillin-Resistant <i>Staphylococcus Aureus</i> Strains Linked to Social and Material Deprivation: Spatial Analysis of Cross-sectional Data. <i>PLoS Medicine</i> , 2016, 13, e1001944.	8.4	76
9	The Genotoxin Colibactin Is a Determinant of Virulence in <i>Escherichia coli</i> K1 Experimental Neonatal Systemic Infection. <i>Infection and Immunity</i> , 2015, 83, 3704-3711.	2.2	69
10	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. <i>Microbial Genomics</i> , 2020, 6, .	2.0	69
11	Comparative analysis of BI/NAP1/027 hypervirulent strains reveals novel toxin B-encoding gene (<i>tcdB</i>) sequences. <i>Journal of Medical Microbiology</i> , 2008, 57, 771-775.	1.8	61
12	Assessing the role of p-cresol tolerance in <i>Clostridium difficile</i> . <i>Journal of Medical Microbiology</i> , 2008, 57, 745-749.	1.8	59
13	Comparative Genome Analysis and Global Phylogeny of the Toxin Variant <i>Clostridium difficile</i> PCR Ribotype 017 Reveals the Evolution of Two Independent Sublineages. <i>Journal of Clinical Microbiology</i> , 2017, 55, 865-876.	3.9	50
14	Role of Glycosyltransferases Modifying Type B Flagellin of Emerging Hypervirulent <i>Clostridium difficile</i> Lineages and Their Impact on Motility and Biofilm Formation. <i>Journal of Biological Chemistry</i> , 2016, 291, 25450-25461.	3.4	49
15	The Sudden Dominance of blaCTX β -M Harboring Plasmids in <i>Shigella</i> spp. Circulating in Southern Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e702.	3.0	48
16	Supporting surveillance capacity for antimicrobial resistance: Laboratory capacity strengthening for drug resistant infections in low and middle income countries. <i>Wellcome Open Research</i> , 2017, 2, 91.	1.8	48
17	The <i>In Vitro</i> and <i>In Vivo</i> Effect of Carvacrol in Preventing <i>Campylobacter</i> Infection, Colonization and in Improving Productivity of Chicken Broilers. <i>Foodborne Pathogens and Disease</i> , 2017, 14, 341-349.	1.8	42
18	Altered Innate Defenses in the Neonatal Gastrointestinal Tract in Response to Colonization by Neuropathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2013, 81, 3264-3275.	2.2	40

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19	Genome-Wide Identification by Transposon Insertion Sequencing of <i>Escherichia coli</i> K1 Genes Essential for <i>In Vitro</i> Growth, Gastrointestinal Colonizing Capacity, and Survival in Serum. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	32
20	The continually evolving <i>Clostridium difficile</i> species. <i>Future Microbiology</i> , 2012, 7, 945-957.	2.0	30
21	In-depth genetic analysis of <i>Clostridium difficile</i> PCR-ribotype 027 strains reveals high genome fluidity including point mutations and inversions. <i>Gut Microbes</i> , 2010, 1, 269-276.	9.8	29
22	Fabrication of a foldable all-in-one point-of-care molecular diagnostic microdevice for the facile identification of multiple pathogens. <i>Sensors and Actuators B: Chemical</i> , 2020, 314, 128057.	7.8	28
23	Genomic and Phenotypic Analyses of <i>Acinetobacter baumannii</i> Isolates From Three Tertiary Care Hospitals in Thailand. <i>Frontiers in Microbiology</i> , 2020, 11, 548.	3.5	26
24	Frequent Undetected Ward-Based Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission Linked to Patient Sharing Between Hospitals. <i>Clinical Infectious Diseases</i> , 2018, 66, 840-848.	5.8	25
25	Impact of <i>Eimeria tenella</i> Coinfection on <i>Campylobacter jejuni</i> Colonization of the Chicken. <i>Infection and Immunity</i> , 2019, 87, .	2.2	25
26	Staphylococcal Phenotypes Induced by Naturally Occurring and Synthetic Membrane-Interactive Polyphenolic β -Lactam Resistance Modifiers. <i>PLoS ONE</i> , 2014, 9, e93830.	2.5	23
27	Genome-Wide Evaluation of the Interplay between <i>Caenorhabditis elegans</i> and <i>Yersinia pseudotuberculosis</i> during <i>In Vivo</i> Biofilm Formation. <i>Infection and Immunity</i> , 2015, 83, 17-27.	2.2	19
28	The association between antimicrobial resistance and HIV infection: a systematic review and meta-analysis. <i>Clinical Microbiology and Infection</i> , 2021, 27, 846-853.	6.0	17
29	Impact of azithromycin mass drug administration on the antibiotic-resistant gut microbiome in children: a randomized, controlled trial. <i>Gut Pathogens</i> , 2022, 14, 5.	3.4	17
30	Characterization of water and wildlife strains as a subgroup of <i>Campylobacter jejuni</i> using DNA microarrays. <i>Environmental Microbiology</i> , 2013, 15, 2371-2383.	3.8	16
31	<i>In Vitro</i> Susceptibility to Closthiamide among Clinical and Reference Strains of <i>Neisseria gonorrhoeae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	15
32	Clonal variation in high- and low-level phenotypic and genotypic mupirocin resistance of MRSA isolates in south-east London. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, dkv248.	3.0	14
33	High-throughput analysis of <i>Yersinia pseudotuberculosis</i> gene essentiality in optimised <i>in vitro</i> conditions, and implications for the speciation of <i>Yersinia pestis</i> . <i>BMC Microbiology</i> , 2018, 18, 46.	3.3	13
34	Subscription model for antibiotic development. <i>BMJ: British Medical Journal</i> , 2019, 366, l5364.	2.3	13
35	Impact of the Mk VI SkinSuit on skin microbiota of terrestrial volunteers and an International Space Station-bound astronaut. <i>Npj Microgravity</i> , 2017, 3, 23.	3.7	11
36	Genetic and virulence characterization of colistin-resistant and colistin-sensitive <i>A. baumannii</i> clinical isolates. <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 95, 99-101.	1.8	10

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37	Host Immunity to <i>Clostridium difficile</i> PCR Ribotype 017 Strains. <i>Infection and Immunity</i> , 2014, 82, 4989-4996.	2.2	9
38	Pathoadaptive Mutations of <i>Escherichia coli</i> K1 in Experimental Neonatal Systemic Infection. <i>PLoS ONE</i> , 2016, 11, e0166793.	2.5	8
39	Development and application of the active surveillance of pathogens microarray to monitor bacterial gene flux.. <i>BMC Microbiology</i> , 2008, 8, 177.	3.3	7
40	Is there an association between long-term antibiotics for acne and subsequent infection sequelae and antimicrobial resistance? A systematic review protocol. <i>BMJ Open</i> , 2020, 10, e033662.	1.9	7
41	Prevalence of ESBL-producing <i>Escherichia coli</i> in adults with and without HIV presenting with urinary tract infections to primary care clinics in Zimbabwe. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab082.	2.1	7
42	Antimicrobial Resistance in Gram-negative bacteria from Urinary Specimens: a study of prevalence, risk factors and molecular mechanisms of resistance (ARGUS) in Zimbabwe – a study protocol. <i>Wellcome Open Research</i> , 2020, 5, 140.	1.8	7
43	Analysis of Antimicrobial Resistance in Non-typhoidal <i>Salmonella</i> Collected From Pork Retail Outlets and Slaughterhouses in Vietnam Using Whole Genome Sequencing. <i>Frontiers in Veterinary Science</i> , 2022, 9, 816279.	2.2	7
44	Draft Genome Sequences of <i>Pseudomonas fluorescens</i> BS2 and <i>Pseudomonas noertemannii</i> BS8, Soil Bacteria That Cooperate To Degrade the Poly- β -D-Glutamic Acid Anthrax Capsule. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
45	Genome-wide assessment of antimicrobial tolerance in <i>Yersinia pseudotuberculosis</i> under ciprofloxacin stress. <i>Microbial Genomics</i> , 2019, 5, .	2.0	6
46	Is there an association between long-term antibiotics for acne and subsequent infection sequelae and antimicrobial resistance? A systematic review. <i>BJGP Open</i> , 2021, 5, BJGPO.2020.0181.	1.8	4
47	Sequential Vaccination With Heterologous <i>Acinetobacter baumannii</i> Strains Induces Broadly Reactive Antibody Responses. <i>Frontiers in Immunology</i> , 2021, 12, 705533.	4.8	4
48	Comparative Genomics of <i>Campylobacter jejuni</i> . , 2014, , 63-71.		3
49	Draft Genome Sequence of <i>Campylobacter jejuni</i> 11168H. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
50	Ethnically diverse urban transmission networks of <i>Neisseria gonorrhoeae</i> without evidence of HIV serosorting. <i>Sexually Transmitted Infections</i> , 2020, 96, 106-109.	1.9	3
51	MdaB and NfrA, Two Novel Reductases Important in the Survival and Persistence of the Major Enteropathogen <i>Campylobacter jejuni</i> . <i>Journal of Bacteriology</i> , 2022, 204, JB0042121.	2.2	3
52	From FASTQ to Function: In Silico Methods for Processing Next-Generation Sequencing Data. <i>Methods in Molecular Biology</i> , 2016, 1476, 23-33.	0.9	1
53	Draft Genome Sequence of <i>Robinsoniella peoriensis</i> 6600698, a Confounder of <i>Clostridium difficile</i> Diagnosis. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
54	Comparative Genome Analysis of <i>Clostridium difficile</i> Using DNA Microarrays. <i>Methods in Molecular Biology</i> , 2010, 646, 149-162.	0.9	1

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55	β-Lactamase-Resistant <i>Streptococcus pneumoniae</i> Dynamics Following Treatment: A Dose-Response Meta-analysis. <i>Clinical Infectious Diseases</i> , 2022, 75, 1962-1970.	5.8	1
56	P17 Quality assurance in bacterial identification and antimicrobial susceptibility testing results: an essential component of antimicrobial resistance surveillance. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, .	2.1	0