

Amy K Cain

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

2,442
citations

304743

22
h-index

233421

45
g-index

67
all docs

67
docs citations

67
times ranked

3261
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015, 47, 632-639.	21.4	403
2	A decade of advances in transposon-insertion sequencing. <i>Nature Reviews Genetics</i> , 2020, 21, 526-540.	16.3	228
3	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. <i>Bioinformatics</i> , 2016, 32, 1109-1111.	4.1	167
4	High-Throughput Analysis of Gene Essentiality and Sporulation in <i>Clostridium difficile</i> . <i>MBio</i> , 2015, 6, e02383.	4.1	157
5	Approaches to querying bacterial genomes with transposon-insertion sequencing. <i>RNA Biology</i> , 2013, 10, 1161-1169.	3.1	132
6	An amphipathic peptide with antibiotic activity against multidrug-resistant Gram-negative bacteria. <i>Nature Communications</i> , 2020, 11, 3184.	12.8	105
7	A high-resolution genomic analysis of multidrug-resistant hospital outbreaks of <i>Klebsiella pneumoniae</i> . <i>EMBO Molecular Medicine</i> , 2015, 7, 227-239.	6.9	104
8	Transposons Related to Tn ₁₆₉₆ in IncHI2 Plasmids in Multiply Antibiotic Resistant <i>Salmonella enterica</i> Serovar Typhimurium from Australian Animals. <i>Microbial Drug Resistance</i> , 2010, 16, 197-202.	2.0	102
9	Evolution of IncHI2 plasmids via acquisition of transposons carrying antibiotic resistance determinants. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1121-1127.	3.0	74
10	The secondary resistome of multidrug-resistant <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2017, 7, 42483.	3.3	69
11	Evolution of a multiple antibiotic resistance region in IncHI1 plasmids: reshaping resistance regions in situ. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 2848-2853.	3.0	57
12	Drug Resistance in <i>Salmonella enterica</i> ser. Typhimurium Bloodstream Infection, Malawi. <i>Emerging Infectious Diseases</i> , 2014, 20, 1957-1959.	4.3	56
13	Genomic landscape of extended-spectrum β -lactamase resistance in <i>Escherichia coli</i> from an urban African setting. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 1602-1609.	3.0	46
14	How antibiotics work together: molecular mechanisms behind combination therapy. <i>Current Opinion in Microbiology</i> , 2020, 57, 31-40.	5.1	45
15	The Murray collection of pre-antibiotic era Enterobacteriaceae: a unique research resource. <i>Genome Medicine</i> , 2015, 7, 97.	8.2	39
16	Genomic analysis of <i>Klebsiella pneumoniae</i> isolates from Malawi reveals acquisition of multiple ESBL determinants across diverse lineages. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1223-1232.	3.0	36
17	Transposon Tn ₅₃₉₃ Carrying the <i>aphA1</i> -Containing Transposon Tn ₆₀₂₃ Upstream of <i>strAB</i> Does Not Confer Resistance to Streptomycin. <i>Microbial Drug Resistance</i> , 2011, 17, 389-394.	2.0	34
18	A global data-driven census of <i>Salmonella</i> small proteins and their potential functions in bacterial virulence. <i>MicroLife</i> , 2020, 1, .	2.1	34

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19	Identification of Tse8 as a Type VI secretion system toxin from <i>Pseudomonas aeruginosa</i> that targets the bacterial transamidosome to inhibit protein synthesis in prey cells. <i>Nature Microbiology</i> , 2021, 6, 1199-1210.	13.3	30
20	Clinical and laboratory-induced colistin-resistance mechanisms in <i>Acinetobacter baumannii</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	30
21	Emergence and Evolution of Multiply Antibiotic-Resistant <i>Salmonella enterica</i> Serovar Paratyphi B <i>Δ</i> -Tartrate-Utilizing Strains Containing SGI1. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2319-2326.	3.2	29
22	Nontoxic Cobalt(III) Schiff Base Complexes with Broad-Spectrum Antifungal Activity. <i>Chemistry - A European Journal</i> , 2021, 27, 2021-2029.	3.3	28
23	Fluorescence-Based Flow Sorting in Parallel with Transposon Insertion Site Sequencing Identifies Multidrug Efflux Systems in <i>Acinetobacter baumannii</i> . <i>MBio</i> , 2016, 7, .	4.1	27
24	The essential genomic landscape of the commensal <i>Bifidobacterium breve</i> UCC2003. <i>Scientific Reports</i> , 2017, 7, 5648.	3.3	26
25	Complete Genome Sequence of <i>Pseudomonas aeruginosa</i> Reference Strain PAK. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	26
26	Defining the ABC of gene essentiality in streptococci. <i>BMC Genomics</i> , 2017, 18, 426.	2.8	25
27	O-Antigen-Dependent Colicin Insensitivity of Uropathogenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	24
28	Transposon Insertion Sequencing Elucidates Novel Gene Involvement in Susceptibility and Resistance to Phages T4 and T7 in <i>Escherichia coli</i> O157. <i>MBio</i> , 2018, 9, .	4.1	23
29	Platinum Cyclooctadiene Complexes with Activity against Gram-Positive Bacteria. <i>ChemMedChem</i> , 2021, 16, 3165-3171.	3.2	23
30	Microbiology's next top model: <i>Galleria</i> in the molecular age. <i>Pathogens and Disease</i> , 2021, 79, .	2.0	23
31	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7 years in a single center. <i>Genome Biology</i> , 2019, 20, 184.	8.8	22
32	The Role of Zinc Efflux during <i>Acinetobacter baumannii</i> Infection. <i>ACS Infectious Diseases</i> , 2020, 6, 150-158.	3.8	21
33	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018, 8, 9868.	3.3	20
34	Length-based separation of <i>Bacillus subtilis</i> bacterial populations by viscoelastic microfluidics. <i>Microsystems and Nanoengineering</i> , 2022, 8, 7.	7.0	18
35	A global genomic approach uncovers novel components for twitching motility-mediated biofilm expansion in <i>Pseudomonas aeruginosa</i> . <i>Microbial Genomics</i> , 2018, 4, .	2.0	17
36	Shape-based separation of drug-treated <i>Escherichia coli</i> using viscoelastic microfluidics. <i>Lab on A Chip</i> , 2022, 22, 2801-2809.	6.0	15

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37	Physical enrichment of transposon mutants from saturation mutant libraries using the TraDISort approach. <i>Mobile Genetic Elements</i> , 2017, 7, 1-7.	1.8	14
38	Evolution of IncHI1 plasmids: Two distinct lineages. <i>Plasmid</i> , 2013, 70, 201-208.	1.4	13
39	Elucidating Essential Genes in Plant-Associated <i>Pseudomonas protegens</i> Pf-5 Using Transposon Insertion Sequencing. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	11
40	Splicing factor proline and glutamine rich intron retention, reduced expression and aggregate formation are pathological features of amyotrophic lateral sclerosis. <i>Neuropathology and Applied Neurobiology</i> , 2021, 47, 990-1003.	3.2	11
41	The Transcriptomic Signature of Tigecycline in <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 565438.	3.5	10
42	<i>Acinetobacter baumannii</i> Fatty Acid Desaturases Facilitate Survival in Distinct Environments. <i>ACS Infectious Diseases</i> , 2021, 7, 2221-2228.	3.8	9
43	The Molecular Basis of <i>Acinetobacter baumannii</i> Cadmium Toxicity and Resistance. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0171821.	3.1	9
44	Genomic investigation of a suspected <i>Klebsiella pneumoniae</i> outbreak in a neonatal care unit in sub-Saharan Africa. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
45	A CRISPR view of genome sequences. <i>Nature Reviews Microbiology</i> , 2013, 11, 226-226.	28.6	7
46	Genomic and phenotypic analyses of diverse non-clinical <i>Acinetobacter baumannii</i> strains reveals strain-specific virulence and resistance capacity. <i>Microbial Genomics</i> , 2022, 8, .	2.0	7
47	Identification of genes required for the fitness of <i>Streptococcus equi</i> subsp. <i>equi</i> in whole equine blood and hydrogen peroxide. <i>Microbial Genomics</i> , 2020, 6, .	2.0	3
48	Inhibitors of bacterial RNA polymerase transcription complex. <i>Bioorganic Chemistry</i> , 2022, 118, 105481.	4.1	3
49	Comment on: Nucleotide sequence of the chromosomal region conferring multidrug resistance (R-type ASSuT) in <i>Salmonella</i> Typhimurium and monophasic <i>Salmonella</i> Typhimurium strains. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 785-785.	3.0	2
50	Recombination: genomic mix 'n' match. <i>Nature Reviews Microbiology</i> , 2014, 12, 795-795.	28.6	1
51	Editorial: Secondary Effects of Antibiotic Exposure. <i>Frontiers in Microbiology</i> , 2021, 12, 737958.	3.5	1
52	Whole genome sequence analysis of <i>Shigella</i> from Malawi identifies fluoroquinolone resistance. <i>Microbial Genomics</i> , 2021, 7, .	2.0	0
53	A Proposed Framework to Identify Dispensable and Essential Functions in Bifidobacteria: Case Study of <i>Bifidobacterium breve</i> UCC2003 as a Prototype of Its Genus. <i>Methods in Molecular Biology</i> , 2022, 2377, 273-302.	0.9	0