

Ashlee Earl

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

11,080
citations

236833

25
h-index

223716

46
g-index

51
all docs

51
docs citations

51
times ranked

19323
citing authors

#	ARTICLE	IF	CITATIONS
1	The interplay between community and hospital <i>Enterococcus faecium</i> clones within health-care settings: a genomic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e133-e141.	3.4	17
2	Establishing the role of the gut microbiota in susceptibility to recurrent urinary tract infections. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	17
3	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. <i>Genome Biology</i> , 2022, 23, 74.	3.8	35
4	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. <i>Genome Medicine</i> , 2022, 14, 37.	3.6	15
5	Drinking water chlorination has minor effects on the intestinal flora and resistomes of Bangladeshi children. <i>Nature Microbiology</i> , 2022, 7, 620-629.	5.9	9
6	Modulating the evolutionary trajectory of tolerance using antibiotics with different metabolic dependencies. <i>Nature Communications</i> , 2022, 13, 2525.	5.8	22
7	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. <i>Nature Microbiology</i> , 2022, 7, 630-639.	5.9	54
8	Clinically relevant mutations in core metabolic genes confer antibiotic resistance. <i>Science</i> , 2021, 371, .	6.0	187
9	Limited effects of long-term daily cranberry consumption on the gut microbiome in a placebo-controlled study of women with recurrent urinary tract infections. <i>BMC Microbiology</i> , 2021, 21, 53.	1.3	21
10	The global dissemination of hospital clones of <i>Enterococcus faecium</i> . <i>Genome Medicine</i> , 2021, 13, 52.	3.6	33
11	Genetic determinants facilitating the evolution of resistance to carbapenem antibiotics. <i>ELife</i> , 2021, 10, .	2.8	15
12	Global phylogenomic analyses of <i>Mycobacterium abscessus</i> provide context for non cystic fibrosis infections and the evolution of antibiotic resistance. <i>Nature Communications</i> , 2021, 12, 5145.	5.8	27
13	Genes Contributing to the Unique Biology and Intrinsic Antibiotic Resistance of <i>Enterococcus faecalis</i> . <i>MBio</i> , 2020, 11, .	1.8	19
14	Colon Cancer-Associated <i>Fusobacterium nucleatum</i> May Originate From the Oral Cavity and Reach Colon Tumors via the Circulatory System. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 400.	1.8	117
15	Computational Methods for Strain-Level Microbial Detection in Colony and Metagenome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 1925.	1.5	66
16	Spatially distinct physiology of <i>Bacteroides fragilis</i> within the proximal colon of gnotobiotic mice. <i>Nature Microbiology</i> , 2020, 5, 746-756.	5.9	57
17	QuantTB – a method to classify mixed <i>Mycobacterium tuberculosis</i> infections within whole genome sequencing data. <i>BMC Genomics</i> , 2020, 21, 80.	1.2	30
18	Adaptive evolution of virulence and persistence in carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Nature Medicine</i> , 2020, 26, 705-711.	15.2	148

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19	Acquisition and Long-term Carriage of Multidrug-Resistant Organisms in US International Travelers. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa543.	0.4	21
20	Deciphering drug resistance in <i>Mycobacterium tuberculosis</i> using whole-genome sequencing: progress, promise, and challenges. <i>Genome Medicine</i> , 2019, 11, 45.	3.6	88
21	ProphET, prophage estimation tool: A stand-alone prophage sequence prediction tool with self-updating reference database. <i>PLoS ONE</i> , 2019, 14, e0223364.	1.1	45
22	Chicken Meat-Associated Enterococci: Influence of Agricultural Antibiotic Use and Connection to the Clinic. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	34
23	Extensive global movement of multidrug-resistant <i>M. tuberculosis</i> strains revealed by whole-genome analysis. <i>Thorax</i> , 2019, 74, 882-889.	2.7	24
24	Impact of antibiotic treatment and host innate immune pressure on enterococcal adaptation in the human bloodstream. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	32
25	Simultaneous detection of genotype and phenotype enables rapid and accurate antibiotic susceptibility determination. <i>Nature Medicine</i> , 2019, 25, 1858-1864.	15.2	85
26	Whole Genome Sequencing detects Inter-Facility Transmission of Carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Journal of Infection</i> , 2019, 78, 187-199.	1.7	26
27	Key Transitions in the Evolution of Rapid and Slow Growing Mycobacteria Identified by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2019, 10, 3019.	1.5	37
28	Transferable vancomycin resistance in clade B commensal-type <i>Enterococcus faecium</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1479-1486.	1.3	20
29	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	6.0	447
30	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	1.0	18
31	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1135-1140.	3.3	158
32	Genomic analysis of globally diverse <i>Mycobacterium tuberculosis</i> strains provides insights into the emergence and spread of multidrug resistance. <i>Nature Genetics</i> , 2017, 49, 395-402.	9.4	258
33	<i>Mycobacterium tuberculosis</i> Whole Genome Sequences From Southern India Suggest Novel Resistance Mechanisms and the Need for Region-Specific Diagnostics. <i>Clinical Infectious Diseases</i> , 2017, 64, 1494-1501.	2.9	76
34	Tracing the Enterococci from Paleozoic Origins to the Hospital. <i>Cell</i> , 2017, 169, 849-861.e13.	13.5	209
35	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	139
36	Whole-Genome Sequencing of <i>Mycobacterium tuberculosis</i> Provides Insight into the Evolution and Genetic Composition of Drug-Resistant Tuberculosis in Belarus. <i>Journal of Clinical Microbiology</i> , 2017, 55, 457-469.	1.8	47

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37	Genomic and functional analyses of <i>Mycobacterium tuberculosis</i> strains implicate <i>ald</i> in D-cycloserine resistance. <i>Nature Genetics</i> , 2016, 48, 544-551.	9.4	145
38	Genomic Analysis of the Evolution of Fluoroquinolone Resistance in <i>Mycobacterium tuberculosis</i> Prior to Tuberculosis Diagnosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6600-6608.	1.4	19
39	Normalizing alternate representations of large sequence variants across multiple bacterial genomes. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	5
40	Individual intestinal symbionts induce a distinct population of ROR γ ³ regulatory T cells. <i>Science</i> , 2015, 349, 993-997.	6.0	707
41	Evolution of Extensively Drug-Resistant Tuberculosis over Four Decades: Whole Genome Sequencing and Dating Analysis of <i>Mycobacterium tuberculosis</i> Isolates from KwaZulu-Natal. <i>PLoS Medicine</i> , 2015, 12, e1001880.	3.9	236
42	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. <i>MBio</i> , 2014, 5, e01864.	1.8	82
43	Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. <i>PLoS ONE</i> , 2014, 9, e112963.	1.1	6,781
44	Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .	1.8	336
45	The "Most Wanted" Taxa from the Human Microbiome for Whole Genome Sequencing. <i>PLoS ONE</i> , 2012, 7, e41294.	1.1	104