

# Ashlee Earl

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1368938/publications.pdf>

Version: 2024-02-01

45  
papers

11,080  
citations

236612

25  
h-index

223531

46  
g-index

51  
all docs

51  
docs citations

51  
times ranked

19323  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. PLoS ONE, 2014, 9, e112963.	1.1	6,781
2	Individual intestinal symbionts induce a distinct population of ROR $\gamma^3$ regulatory T cells. Science, 2015, 349, 993-997.	6.0	707
3	Gut microbiota utilize immunoglobulin A for mucosal colonization. Science, 2018, 360, 795-800.	6.0	447
4	Emergence of Epidemic Multidrug-Resistant Enterococcus faecium from Animal and Commensal Strains. MBio, 2013, 4, .	1.8	336
5	Genomic analysis of globally diverse Mycobacterium tuberculosis strains provides insights into the emergence and spread of multidrug resistance. Nature Genetics, 2017, 49, 395-402.	9.4	258
6	Evolution of Extensively Drug-Resistant Tuberculosis over Four Decades: Whole Genome Sequencing and Dating Analysis of Mycobacterium tuberculosis Isolates from KwaZulu-Natal. PLoS Medicine, 2015, 12, e1001880.	3.9	236
7	Tracing the Enterococci from Paleozoic Origins to the Hospital. Cell, 2017, 169, 849-861.e13.	13.5	209
8	Clinically relevant mutations in core metabolic genes confer antibiotic resistance. Science, 2021, 371, .	6.0	187
9	Multi-institute analysis of carbapenem resistance reveals remarkable diversity, unexplained mechanisms, and limited clonal outbreaks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1135-1140.	3.3	158
10	Adaptive evolution of virulence and persistence in carbapenem-resistant Klebsiella pneumoniae. Nature Medicine, 2020, 26, 705-711.	15.2	148
11	Genomic and functional analyses of Mycobacterium tuberculosis strains implicate ald in D-cycloserine resistance. Nature Genetics, 2016, 48, 544-551.	9.4	145
12	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. Science Translational Medicine, 2017, 9, .	5.8	139
13	Colon Cancer-Associated Fusobacterium nucleatum May Originate From the Oral Cavity and Reach Colon Tumors via the Circulatory System. Frontiers in Cellular and Infection Microbiology, 2020, 10, 400.	1.8	117
14	The "Most Wanted" Taxa from the Human Microbiome for Whole Genome Sequencing. PLoS ONE, 2012, 7, e41294.	1.1	104
15	Deciphering drug resistance in Mycobacterium tuberculosis using whole-genome sequencing: progress, promise, and challenges. Genome Medicine, 2019, 11, 45.	3.6	88
16	Simultaneous detection of genotype and phenotype enables rapid and accurate antibiotic susceptibility determination. Nature Medicine, 2019, 25, 1858-1864.	15.2	85
17	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. MBio, 2014, 5, e01864.	1.8	82
18	Mycobacterium tuberculosis Whole Genome Sequences From Southern India Suggest Novel Resistance Mechanisms and the Need for Region-Specific Diagnostics. Clinical Infectious Diseases, 2017, 64, 1494-1501.	2.9	76

#	ARTICLE	IF	CITATIONS
19	Computational Methods for Strain-Level Microbial Detection in Colony and Metagenome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 1925.	1.5	66
20	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
21	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
22	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
23	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
24	Key Transitions in the Evolution of Rapid and Slow Growing <i>Mycobacteria</i> Identified by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2019, 10, 3019.	1.5	37
25	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. <i>Genome Biology</i> , 2022, 23, 74.	3.8	35
26	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
27	The global dissemination of hospital clones of <i>Enterococcus faecium</i> . <i>Genome Medicine</i> , 2021, 13, 52.	3.6	33
28	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
29	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
30	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
31	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
32	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
33	Modulating the evolutionary trajectory of tolerance using antibiotics with different metabolic dependencies. <i>Nature Communications</i> , 2022, 13, 2525.	5.8	22
34	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
35	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
36	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

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37	Genomic Analysis of the Evolution of Fluoroquinolone Resistance in Mycobacterium tuberculosis Prior to Tuberculosis Diagnosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6600-6608.	1.4	19
38	Genes Contributing to the Unique Biology and Intrinsic Antibiotic Resistance of Enterococcus faecalis. <i>MBio</i> , 2020, 11, .	1.8	19
39	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	1.0	18
40	The interplay between community and hospital Enterococcus faecium clones within health-care settings: a genomic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e133-e141.	3.4	17
41	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
42	Genetic determinants facilitating the evolution of resistance to carbapenem antibiotics. <i>ELife</i> , 2021, 10, .	2.8	15
43	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
44	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
45	Normalizing alternate representations of large sequence variants across multiple bacterial genomes. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	5