# **Resource Summary Report**

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# **Ariba**

RRID:SCR\_015976

Type: Tool

### **Proper Citation**

Ariba (RRID:SCR\_015976)

#### **Resource Information**

URL: https://github.com/sanger-pathogens/ariba

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**Description:** Analysis software that identifies antibiotic resistance genes by running local assemblies. It can also be used for MLST calling.

**Resource Type:** data analysis software, sequence analysis software, software resource, data processing software, software toolkit, software application

**Defining Citation:** PMID:29177089, DOI:10.1099/mgen.0.000131

Keywords: software, analysis, tool, sequence, antibiotic, resistance, assembly, local, mlst

Funding: Wellcome Trust 206194;

Biotechnology and Biological Sciences Research Council BB/M014088/1

Availability: Free, Available for download, Freely available

Resource Name: Ariba

Resource ID: SCR\_015976

Alternate IDs: OMICS\_17327

Alternate URLs: https://sources.debian.org/src/artemis/

License: GPLv3

**Record Creation Time:** 20220129T080328+0000

**Record Last Update:** 20250430T060041+0000

## **Ratings and Alerts**

No rating or validation information has been found for Ariba.

No alerts have been found for Ariba.

#### Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 167 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Stepanskyi D, et al. (2024) Phenotypic and genomic analysis of bacteria from war wounds in Dnipro, Ukraine. JAC-antimicrobial resistance, 6(3), dlae090.

Klemm EJ, et al. (2024) Genomic analysis of clinical Aeromonas isolates reveals genetic diversity but little evidence of genetic determinants for diarrhoeal disease. Microbial genomics, 10(3).

Kean IRL, et al. (2024) Short-duration selective decontamination of the digestive tract infection control does not contribute to increased antimicrobial resistance burden in a pilot cluster randomised trial (the ARCTIC Study). Gut, 73(6), 910.

Mattock J, et al. (2024) A One Health Perspective on Salmonella enterica Serovar Infantis, an Emerging Human Multidrug-Resistant Pathogen. Emerging infectious diseases, 30(4), 701.

Habrun CA, et al. (2024) Multistate nontyphoidal Salmonella and Shiga toxin-producing Escherichia coli outbreaks linked to international travel-United States, 2017-2020. Epidemiology and infection, 152, e17.

Dziegiel AH, et al. (2024) High Campylobacter diversity in retail chicken: epidemiologically important strains may be missed with current sampling methods. Epidemiology and infection, 152, e101.

Dahdouh E, et al. (2024) Characterizing carbapenemase-producing Escherichia coli isolates from Spain: high genetic heterogeneity and wide geographical spread. Frontiers in cellular and infection microbiology, 14, 1390966.

Duckett M, et al. (2024) Parallel evolution of alternate morphotypes of Chryseobacterium

gleum during experimental evolution with Caenorhabditis elegans. FEMS microbiology ecology, 100(5).

Ackers-Johnson G, et al. (2024) Investigating the changing taxonomy and antimicrobial resistance of bacteria isolated from door handles in a new infectious disease ward pre- and post-patient admittance. Microbiology spectrum, 12(12), e0179724.

Snaith AE, et al. (2024) Longitudinal genomic surveillance of a UK intensive care unit shows a lack of patient colonisation by multi-drug-resistant Gram-negative bacterial pathogens. Microbial genomics, 10(11).

Ramírez de Arellano E, et al. (2024) Clinical, microbiological, and molecular characterization of pediatric invasive infections by Streptococcus pyogenes in Spain in a context of global outbreak. mSphere, 9(3), e0072923.

Zamudio R, et al. (2024) Global transmission of extended-spectrum cephalosporin resistance in Escherichia coli driven by epidemic plasmids. EBioMedicine, 103, 105097.

Thomas Iv JC, et al. (2024) Emergence and evolution of mosaic penA-60 and penA-237 alleles in a Neisseria gonorrhoeae core genogroup that was historically susceptible to extended spectrum cephalosporins. Frontiers in microbiology, 15, 1401303.

Reyes J, et al. (2023) Global epidemiology and clinical outcomes of carbapenem-resistant Pseudomonas aeruginosa and associated carbapenemases (POP): a prospective cohort study. The Lancet. Microbe, 4(3), e159.

Carroll LM, et al. (2023) A multidrug-resistant Salmonella enterica Typhimurium DT104 complex lineage circulating among humans and cattle in the USA lost the ability to produce pertussis-like toxin ArtAB. Microbial genomics, 9(7).

Hamilton WL, et al. (2023) The clinical, genomic, and microbiological profile of invasive multidrug resistant Escherichia coli in a major teaching hospital in the United Kingdom. Microbial genomics, 9(10).

Van Puyvelde S, et al. (2023) A genomic appraisal of invasive Salmonella Typhimurium and associated antibiotic resistance in sub-Saharan Africa. Nature communications, 14(1), 6392.

Hadjirin NF, et al. (2023) Dissemination of carbapenemase-producing Enterobacterales in Ireland from 2012 to 2017: a retrospective genomic surveillance study. Microbial genomics, 9(3).

Moran RA, et al. (2023) Extended-Spectrum ?-Lactamase Genes Traverse the Escherichia coli Populations of Intensive Care Unit Patients, Staff, and Environment. Microbiology spectrum, 11(2), e0507422.

David S, et al. (2023) Genomic surveillance of multidrug-resistant Klebsiella in Wales reveals persistent spread of Klebsiella pneumoniae ST307 and adaptive evolution of pOXA-48-like plasmids. Microbial genomics, 9(5).