

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

[Ariba](#)

RRID:SCR_015976

Type: Tool

Proper Citation

Ariba (RRID:SCR_015976)

Resource Information

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

Proper Citation: Ariba (RRID:SCR_015976)

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, data processing software, sequence analysis software, software application, software resource, software toolkit

Defining Citation: [PMID:29177089](#), [DOI:10.1099/mgen.0.000131](#)

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

Funding: Biotechnology and Biological Sciences Research Council BB/M014088/1; Wellcome Trust 206194

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: 20260905T132801+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 220 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Le Bastard Q, et al. (2026) Pre-existing β -lactamase gene diversity is associated with lower risk of ESBL-producing Enterobacterales colonization in patients exposed to ceftriaxone. *Gut microbes*, 18(1), 2627692.

Coldbeck-Shackley RC, et al. (2026) Increased Diversity and Introduction of Multidrug-Resistant Strains of *Neisseria gonorrhoeae* Following Cessation of COVID-19 Pandemic-Related Travel Restrictions: An Observational Genomic Epidemiologic Study. *The Journal of infectious diseases*, 233(5), e1130.

Moreno J, et al. (2026) Genetic structure of penicillin non-susceptible invasive *Streptococcus pneumoniae* in Colombia. *Microbial genomics*, 12(5).

Gonzales BE, et al. (2026) Genomic features of pneumococcal strains isolated from paediatric patients with invasive disease during pneumococcal conjugate vaccine introduction in Lima, Peru. *Microbial genomics*, 12(2).

McHugh MP, et al. (2026) Laboratory evaluation of the Allplex NG & DR assay for detection of *Neisseria gonorrhoeae* and associated azithromycin and ciprofloxacin resistance markers. *Sexually transmitted infections*, 102(3).

Ramirez de Arellano E, et al. (2026) Multidrug-resistant gram-negative bacteria in Spanish ICU patients: clinical and microbiological characterization (MURAN-UCI Project). *Microbiology spectrum*, 14(2), e0298725.

Hoang LH, et al. (2026) The emergence and spread of a novel sequence type of *Corynebacterium diphtheriae* in Vietnam. *Scientific reports*, 16(1).

Tinggaard M, et al. (2026) Periorbital infections caused by Group A streptococci: a case series. *BMC infectious diseases*, 26(1), 317.

Gallichan S, et al. (2026) A more complete picture: capturing single nucleotide variant diversity in extended-spectrum beta-lactamase producing *Escherichia coli* using post-enrichment metagenomics. *Microbial genomics*, 12(6).

Pilar V, et al. (2026) Sudden re-emergence of *Streptococcus pyogenes* subtype emm3.93 in Spain, 2023-2024. *New microbes and new infections*, 72, 101794.

da Silva AL, et al. (2026) Phenotypical-genetic virulence and resistance in atypical avian pathogenic *Escherichia coli*. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(5), 631.

Garzon A, et al. (2026) Characterizing the nasopharyngeal microbiome and resistome of dairy cattle with and without bovine respiratory disease. *Microbiology spectrum*, 14(5), e0264825.

Lebreton F, et al. (2026) Preferred evolutionary routes of convergence in *Klebsiella pneumoniae* favor siderophore acquisition over hypervirulence. *Research square*.

Akhtar M, et al. (2026) Clinical and environmental wastewater-based bacteriophage surveillance for high-impact diarrheal diseases, including cholera, in Bangladesh. *mBio*, 17(1), e0265425.

Derollez E, et al. (2026) Specific killing and resensitization of pathogenic *Escherichia coli* strains carrying blaCTX-M-15 β -lactamase using targeted-antibacterial-plasmids (TAPs). *Nucleic acids research*, 54(1).

Wittenbach JD, et al. (2026) Evaluation of a machine learning system for genomic antimicrobial susceptibility determination on a clinically representative test set. *Microbiology spectrum*, 14(3), e0056425.

Wilson HJ, et al. (2026) Whole-genome sequencing to investigate the prevalence and transmission of multidrug-resistant Gram-negative pathogens in an adult intensive care unit in the UK. *Microbial genomics*, 12(5).

Gottesdiener LS, et al. (2026) Resistance to novel β -lactam/ β -lactamase inhibitors among carbapenem-resistant *Pseudomonas aeruginosa* and clinical implications in the prospective observational *Pseudomonas* study. *Antimicrobial agents and chemotherapy*, 70(6), e0038825.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Edslev SM, et al. (2025) Antibiotic resistance and population structure of *Staphylococcus epidermidis* from prosthetic joint infections in Sweden and France. *The Journal of antimicrobial chemotherapy*, 80(7), 2007.