

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 18, 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: 20260912T195833+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 [PRECISE-TBI](#) .

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.

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

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.

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.

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.