

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>

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

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: 20260806T054631+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 197 mentions in open access literature.

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

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

Lebreton F, et al. (2025) High genetic relatedness between multidrug resistant bacteria before and after the 2022 invasion of Ukraine. *Genome medicine*, 17(1), 74.

Hernández-Villamizar S, et al. (2025) Improving health and productivity in laying hens with the phage cocktail SalmoFree®. *Poultry science*, 104(11), 105638.

Fraser AJ, et al. (2025) A 46-week outbreak of ertapenem-resistant, non-carbapenemase encoding *Klebsiella pneumoniae* ST45 in a paediatric cardiac unit involving shared equipment, United Kingdom, April 2022 to February 2023. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin*, 30(43).

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.

Buttler L, et al. (2025) Distinct clusters of bacterial and fungal microbiota in end-stage liver cirrhosis correlate with antibiotic treatment, intestinal barrier impairment, and systemic inflammation. *Gut microbes*, 17(1), 2487209.

Kondratiuk VM, et al. (2025) Phenotypic and genotypic analysis of *Acinetobacter baumannii* isolated from combat wounds in Ukraine during 2022 and 2023. *JAC-antimicrobial resistance*, 7(4), dlaf140.

Adetoye AA, et al. (2025) Assessing the Genomic Landscape of *Salmonella enterica* Isolated From Cattle Faeces on a Nigerian Farm. *MicrobiologyOpen*, 14(6), e70129.

Thiede SN, et al. (2025) Antibiotic-resistance plasmid amplified among MRSA cases in an urban jail and its connected communities. *medRxiv : the preprint server for health sciences*.

Wirth JS, et al. (2025) Genomic Characterization of *Escherichia coli* O157:H7 Associated with Multiple Sources, United States. *Emerging infectious diseases*, 31(13), 109.

Sagerfors S, et al. (2025) From colonizer to culprit: genomic and clinical insights into *S. epidermidis* from post-surgical endophthalmitis. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 44(10), 2409.

Rackov N, et al. (2025) Bacterial cellulose: Enhancing productivity and material properties through repeated harvest. *Biofilm*, 9, 100276.

Bui PH, et al. (2025) Identification of genetic determinants of antibiotic resistance in *Helicobacter pylori* isolates in Vietnam by high-throughput sequencing. *BMC microbiology*, 25(1), 264.

Oni FI, et al. (2025) Whole-genome sequencing reveals *Enterobacter hormaechei* as a key bloodstream pathogen in six tertiary care hospitals in southwestern Nigeria. *Microbial genomics*, 11(10).

Astorga G, et al. (2025) A multi-isolate genomic approach identifies diverse *Escherichia coli* contamination and antimicrobial resistance carriage on retail foods. *Microbial genomics*, 11(10).

Sunmonu GT, et al. (2025) Genomic characterization of foodborne *Salmonella enterica* and *Escherichia coli* isolates from Saboba district and Bolgatanga Municipality Ghana. *PloS one*, 20(2), e0315583.

Li Y, et al. (2025) Potential links between human bloodstream infection by *Salmonella enterica* serovar Typhimurium and international transmission to Colombia. *PLoS neglected tropical diseases*, 19(1), e0012801.

Nagaraj G, et al. (2025) Tracking the evolution of emerging serotypes and antibiotic resistance patterns in *Streptococcus pneumoniae* among Indian adults using high-throughput genome sequencing. *BMC infectious diseases*, 25(1), 1181.

Luo Q, et al. (2025) The dynamics of microbiome and virome in migratory birds of southwest China. *NPJ biofilms and microbiomes*, 11(1), 64.

Hung HCH, et al. (2025) GPS Pipeline: portable, scalable genomic pipeline for *Streptococcus pneumoniae* surveillance from Global Pneumococcal Sequencing Project. *Nature communications*, 16(1), 8345.