

Resource Summary Report

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Roary

RRID:SCR_018172

Type: Tool

Proper Citation

Roary (RRID:SCR_018172)

Resource Information

URL: <https://sanger-pathogens.github.io/Roary/>

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Description: Software tool for rapid large scale prokaryote pan genome analysis. Builds large scale pan genomes, identifying core and accessory genes. Makes construction of pan genome of thousands of prokaryote samples on standard desktop without compromising on accuracy of results. Not intended for meta genomics or for comparing extremely diverse sets of genomes.

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

Defining Citation: [PMID:26198102](#)

Keywords: Genome analysis, prokaryote pan genome, pan genome, gene identification, analysis, bio.tools

Funding: Wellcome Trust

Availability: Free, Available for download, Freely available

Resource Name: Roary

Resource ID: SCR_018172

Alternate IDs: OMICS_09491, biotools:roary

Alternate URLs: <https://github.com/sanger-pathogens/Roary>, <https://bio.tools/roary>, <https://sources.debian.org/src/roary/>

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260905T133009+0000

Ratings and Alerts

No rating or validation information has been found for Roary.

No alerts have been found for Roary.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 710 mentions in open access literature.

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

Chen J, et al. (2026) Septic Shock Caused by Coinfection of Shewanella algae Bloodstream Infection and Epstein-Barr Virus: Clinical Characteristics and Genomic Analysis. MicrobiologyOpen, 15(1), e70221.

Anderson REV, et al. (2026) Characterization of extended-spectrum cephalosporin-resistant Klebsiella recovered from dairy manure in Southern Ontario, Canada. PloS one, 21(1), e0336012.

Zanon IP, et al. (2026) Salmonella Dublin outbreaks in Brazilian cattle: clinical-epidemiological aspects, antimicrobial resistance, and comparative genomic analysis. Microbiology spectrum, 14(4), e0266525.

Yuan B, et al. (2026) Rapid Detection of Vibrio vulnificus with Recombinase Polymerase Amplification Assays Based on Specific Sequence Tags of Core Genome. Microorganisms, 14(2).

Chukamnerd A, et al. (2026) Genomic Epidemiology of Carbapenem-Resistant Acinetobacter baumannii Isolated from Patients Admitted to Intensive Care Units in Network Hospitals in Southern Thailand. Antibiotics (Basel, Switzerland), 15(2).

Whealy RN, et al. (2026) Strain-level genomic variation of Streptococcus mutans and early childhood caries in preschool children from Northern Arizona and Hawaii. PeerJ, 14, e20808.

Mondjar L, et al. (2026) Characterizing Aeromonas spp. as a Potential Sentinel Organism for Antimicrobial Resistance Dissemination in Wastewater and Drinking Water Treatment Systems: A Case Study in the Barcelona Metropolitan Area, Spain. Antibiotics (Basel, Switzerland), 15(3).

Lajoinie DM, et al. (2026) Comparative genomics and biocontrol potential of five Bacillus strains isolated from grapevine rhizosphere. Scientific reports, 16(1).

Chen N, et al. (2026) Differential virulence potential of different clades of multidrug-resistant Klebsiella pneumoniae ST258. medRxiv : the preprint server for health sciences.

Akter NN, et al. (2026) Comprehensive genomic characterization and public health implications of multidrug-resistant *Escherichia coli* from poultry in Noakhali, Bangladesh. *BMC microbiology*, 26(1).

Chundru D, et al. (2026) In silico design of a multiepitope subunit vaccine targeting *Salmonella enterica* serovar Infantis: an immunoinformatics and reverse vaccinology approach. *Frontiers in immunology*, 17, 1717278.

Bahri S, et al. (2026) Spread of Multidrug-Resistant Enterobacterales Strains Isolated From the Hospital Environment and Clinical Specimens Within ICUs in Tunisia. *Cureus*, 18(1), e102231.

Thant EP, et al. (2026) Genomic characterization of clinical *Stenotrophomonas* strains from Thailand reveals five putative novel genospecies and extensive functional diversity. *Scientific reports*, 16(1).

Zhang L, et al. (2026) Genome and antimicrobial compounds analysis of *Bacillus subtilis* M51 as a potential biocontrol agent against *Fusarium oxysporum*. *BMC genomics*, 27(1).

Yin X, et al. (2026) Stepwise phage resistance and collateral phage susceptibility in *Klebsiella pneumoniae*. *Emerging microbes & infections*, 15(1), 2648890.

de Lira DRP, et al. (2026) Genome on the move: emergence of hybrid atypical enteropathogenic/enteroaggregative *Escherichia coli* (aEPEC/EAEC) during a diarrheal outbreak in Brazil. *Microbiology spectrum*, 14(5), e0277425.

Fang C, et al. (2026) Fourteen-year genomic surveillance of pediatric invasive *Streptococcus pneumoniae*: genomic and pan-genomic characterization. *BMC microbiology*, 26(1).

Sornsene P, et al. (2026) Probiotic Potential, Genomic Characterization, and In Silico Insights of Five *Lactiplantibacillus plantarum* Strains Isolated from Fermented Cacao Beans Against Multidrug-Resistant *Pseudomonas aeruginosa*. *Antibiotics (Basel, Switzerland)*, 15(4).

Kim J, et al. (2026) Complete genome and functional insights into *Microbacterium* sp. strain FBCC-B4120, a novel freshwater isolate with diverse biotechnological traits. *PloS one*, 21(5), e0347549.

Wu J, et al. (2026) Isolation, Identification, and Functional Characterization of a Rhizosphere Bacterium Promoting the Growth of *Alsophila spinulosa*. *Microorganisms*, 14(5).