

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/>

Proper Citation: Roary (RRID:SCR_018172)

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: 20260919T195517+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 [nidm-terms](#) .

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).

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.

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

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

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).

Zhou H, et al. (2026) One Health genomics reveals niche-specific lineage replacement in *Salmonella* Enteritidis. *National science review*, 13(11), nwag275.

Uruén C, et al. (2026) Clinically relevant genomic and phenotypic differences in virulence, antimicrobial resistance, and biofilm-associated tolerance between *Streptococcus suis* lineages ST1 and ST123. *Veterinary research*, 57(1).

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

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.

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.

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).

Mondéjar 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).

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.

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.

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.

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).

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.