

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 30, 2025

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

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: 20250430T060151+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 494 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Ofosu Appiah F, et al. (2025) Emergence of Carbapenem-Resistant blaPOM-1 Harboring *Pseudomonas otitidis* Isolated from River Water in Ghana. *Antibiotics* (Basel, Switzerland), 14(1).

Castillo G, et al. (2025) Genome Sequencing Reveals the Potential of *Enterobacter* sp. Strain UNJFSC003 for Hydrocarbon Bioremediation. *Genes*, 16(1).

Sivarajan V, et al. (2025) Prevalence and genomic insights of carbapenem resistant and ESBL producing Multidrug resistant *Escherichia coli* in urinary tract infections. *Scientific reports*, 15(1), 2541.

Hirabayashi A, et al. (2025) Emergence of the mobile RND-type efflux pump gene cluster *tmexCD1-toprJ1* in *Klebsiella pneumoniae* clinical isolates in Japan. *The Journal of antimicrobial chemotherapy*, 80(1), 192.

Li T, et al. (2025) Adaptive evolution of extensive drug resistance and persistence in epidemic ST11 KPC-producing *Klebsiella pneumoniae* during antimicrobial chemotherapy. *Antimicrobial agents and chemotherapy*, 69(1), e0123524.

González Ojeda I, et al. (2025) Linkage-based ortholog refinement in bacterial pangenomes with CLARC. *bioRxiv : the preprint server for biology*.

Gabor CE, et al. (2025) Characterization of *Shigella flexneri* serotype 6 strains from

geographically diverse low- and middle-income countries. *mBio*, 16(1), e0221024.

Hamed SM, et al. (2025) *Pseudocitrobacter cyperus*, a novel bacterial species recovered from *Cyperus alternifolius* in Egypt. *BMC microbiology*, 25(1), 20.

Magossi G, et al. (2025) Genomic and metabolic characterization of *Trueperella pyogenes* isolated from domestic and wild animals. *Applied and environmental microbiology*, 91(1), e0172524.

Selvaraj Anand S, et al. (2024) Identification of a novel CG307 sub-clade in third-generation-cephalosporin-resistant *Klebsiella pneumoniae* causing invasive infections in the USA. *Microbial genomics*, 10(2).

Pena-Fernández N, et al. (2024) Comparative pangenomic analysis of *Campylobacter fetus* isolated from Spanish bulls and other mammalian species. *Scientific reports*, 14(1), 4347.

Uesaka K, et al. (2024) Restoration of the Functional *nif* Gene Cluster by Complex Recombination Events during Heterocyst Development in the Nitrogen-Fixing *Cyanobacterium Calothrix* sp. NIES-4101. *Plant & cell physiology*, 65(6), 1050.

Rafiqullah IM, et al. (2024) Pneumococcal population genomics changes during the early time period of conjugate vaccine uptake in southern India. *Microbial genomics*, 10(2).

Mattioni Marchetti V, et al. (2024) *Enterobacter asburiae* ST229: an emerging carbapenemases producer. *Scientific reports*, 14(1), 6220.

Chen F, et al. (2024) Global genetic diversity and Asian clades evolution: a phylogeographic study of *Staphylococcus aureus* sequence type 5. *Antimicrobial agents and chemotherapy*, 68(3), e0117523.

Bouras N, et al. (2024) Whole genome-based reclassification of several species of the genus *Microbispora*. *PloS one*, 19(8), e0307299.

Thoraval L, et al. (2024) *Cutibacterium acnes* strains associated with bone prosthesis infections cannot evade the host immune system. *Frontiers in immunology*, 15, 1468709.

Kaur T, et al. (2024) Discovery of a novel *Wolbachia* in *Heterodera* expands nematode host distribution. *Frontiers in microbiology*, 15, 1446506.

Mazzamurro F, et al. (2024) Intragenomic conflicts with plasmids and chromosomal mobile genetic elements drive the evolution of natural transformation within species. *PLoS biology*, 22(10), e3002814.

Jia C, et al. (2024) A global genome dataset for *Salmonella Gallinarum* recovered between 1920 and 2024. *Scientific data*, 11(1), 1094.