

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 processing software, sequence analysis software, data analysis software, software resource, 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: 20260731T043026+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 602 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Strysko J, et al. (2026) Carbapenem-resistant *Acinetobacter baumannii* at a hospital in Botswana: detecting a protracted outbreak using whole genome sequencing. *Microbiology spectrum*, 14(1), e0176825.

Safari M, et al. (2026) Comprehensive genomic analysis of a novel *Bacillus cereus* decomposing toluene potentially applicable in bioremediation. *Microbiology spectrum*, 14(1), e0289224.

Wang X-Y, et al. (2026) Genomic epidemiology and plasmid characterization of antimicrobial resistance and virulence in cattle *Escherichia coli* from China. *Microbiology spectrum*, 14(1), e0325625.

Light-Maka I, et al. (2025) Bronze Age *Yersinia pestis* genome from sheep sheds light on hosts and evolution of a prehistoric plague lineage. *Cell*.

Ono M, et al. (2025) Identifying genetic variations in emm89 *Streptococcus pyogenes* associated with severe invasive infections. *eLife*, 14.

Liu Y, et al. (2025) Timescale and genetic linkage explain the variable impact of defense systems on horizontal gene transfer. *Genome research*, 35(2), 268.

González Ojeda I, et al. (2025) Linkage-based ortholog refinement in bacterial pangenomes with CLARC. *Nucleic acids research*, 53(12).

Zhang X, et al. (2025) *Streptococcus suis* serotype 5: Emerging zoonotic threat with distinct genomic heterogeneity. *Virulence*, 16(1), 2523882.

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).

Lu S, et al. (2025) Genomic characterization of an ESBL-producing *Klebsiella pneumoniae* ST37 recovered from a hospitalized patient in Armenia. *Microbiology spectrum*, 13(9), e0033225.

S?kowska A, et al. (2025) Whole-Genome Sequencing of *Klebsiella quasipneumoniae* subsp. *similipneumoniae* Isolated from a Patient with Pneumonia. *Current microbiology*, 82(9), 426.

Chen S, et al. (2025) Molecular characterization, comparative genome analysis and resistance determinants of three clinical *Elizabethkingia miricola* strains isolated from Michigan. *Frontiers in microbiology*, 16, 1582121.

Siddique N, et al. (2025) Probiotic potential and antimicrobial efficacy of a dairy isolate, *Enterococcus faecium* MBBL3. *Applied microbiology and biotechnology*, 109(1), 176.

Mills EG, et al. (2025) Bacteriocin production facilitates nosocomial emergence of vancomycin-resistant *Enterococcus faecium*. *Nature microbiology*, 10(4), 871.

Yang Y, et al. (2025) Genomic and phenotypic characterization of multidrug-resistant *Staphylococcus haemolyticus* isolated from burn patients in Chongqing, southwestern China. *Microbiology spectrum*, 13(6), e0257724.

Kim DD, et al. (2025) Contaminated drinking water facilitates *Escherichia coli* strain-sharing within households in urban informal settlements. *Nature microbiology*, 10(5), 1198.

Fernandez de Ullivarri M, et al. (2025) Cold induced expression of a novel levansucrase gene *sacB1* enhances exopolysaccharide production and stress resilience in *Leuconostoc mesenteroides*. *Scientific reports*, 15(1), 22980.

Sun S, et al. (2025) Identification of two KPC variants, KPC-204 and KPC-227, in ST11-K64 *Klebsiella pneumoniae* during prolonged hospitalization of a single patient. *Frontiers in microbiology*, 16, 1543470.

Halder G, et al. (2025) Antimicrobial resistance and phylogenetic lineages of KPC-2-producing blood-borne *Klebsiella pneumoniae* subsp. *pneumoniae* from Kolkata, India during 2015-2024: Emergence of *Klebsiella pneumoniae* subsp. *pneumoniae* with *bla*KPC-2, *bla*NDM, and *bla*OXA-48-like triple carbapenemases. *Microbiology spectrum*, 13(8), e0012625.