

Resource Summary Report

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Panaroo

RRID:SCR_021090

Type: Tool

Proper Citation

Panaroo (RRID:SCR_021090)

Resource Information

URL: <https://github.com/gtonkinhill/panaroo>

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Description: Software pipeline for pangenome investigation. Shares information between genomes to correct errors. Can call large structural variants. Fast and scalable to over 10k bacterial genomes.

Synonyms: Bacterial Pangenome Analysis Pipeline

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

Keywords: pangenome investigation, correct errors, genomes, large structural variants, bacterial genomes

Availability: Free, Available for download, Freely available

Resource Name: Panaroo

Resource ID: SCR_021090

Alternate URLs: <https://gtonkinhill.github.io/panaroo/#/gettingstarted/quickstart>

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260812T044401+0000

Ratings and Alerts

No rating or validation information has been found for Panaroo.

No alerts have been found for Panaroo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

de Larminat J, et al. (2026) Hemolytic Uremic Syndrome Outbreak in Adults and Shiga Toxin-Producing *Escherichia coli* Negative for Locus of Enterocyte Effacement, France, 2025. *Emerging infectious diseases*, 32(4), 592.

Garcia-Candela E, et al. (2026) Phylogenomic and comparative genomic analyses of *Aeromonas* spp. from South American aquatic systems reveal extensive genomic diversity, antimicrobial resistance, and predicted human pathogenicity. *Frontiers in microbiology*, 17, 1823138.

Meroni G, et al. (2026) Genomic Characterisation of Pyometra-Associated *Escherichia coli* in a Lombardy Veterinary Clinic: A Nanopore-Based Case Series. *Antibiotics (Basel, Switzerland)*, 15(2).

Jia C, et al. (2026) Distinct genomic trajectory among invasive *Salmonella* Typhimurium ST313 infections. *Nature communications*, 17(1).

De Allende CC, et al. (2026) Characterization of *Ornithobacterium hominis* colonization dynamics and interaction with the nasopharyngeal microbiome in a South African birth cohort. *Microbial genomics*, 12(5).

Al-Jardani A, et al. (2026) Genomic Characterization and Predictors of Mortality in Invasive *Streptococcus pneumoniae* Disease in Oman: A Four-Year National Genomic Study. *Vaccines*, 14(6).

Caballero F, et al. (2025) Genomic diversity of uropathogenic *Escherichia coli* in clinical isolates from six latin american countries, 2018-2023. *Revista peruana de medicina experimental y salud publica*, 42(2), 156.

Poudel S, et al. (2025) Interpreting roles of mutations associated with the emergence of *S. aureus* USA300 strains using transcriptional regulatory network reconstruction. *eLife*, 12.

Koong J, et al. (2025) Genomic characteristics of the multiresistant *Acinetobacter baumannii* global clone 1 reference strain A297/RUH875. *The Journal of antimicrobial chemotherapy*, 80(7), 1988.

Abu Sabah E, et al. (2025) Phylogenomics, evolution and origin of multidrug-resistant *Acinetobacter baumannii* ST15. *Microbial genomics*, 11(7).

Thye T, et al. (2025) Non-typhoidal Salmonella transmission reservoirs in Sub-Saharan Africa: a genomic assessment from a one health perspective. *Antimicrobial resistance and infection control*, 14(1), 46.

Ribas MR, et al. (2025) Emergence of Livestock-Associated Methicillin-Resistant *Staphylococcus aureus* ST398 in Wild Birds, Brazil. *MicrobiologyOpen*, 14(6), e70131.

De Allende CC, et al. (2025) Characterisation of *Ornithobacterium hominis* colonisation dynamics and interaction with the nasopharyngeal microbiome in a South African birth cohort. *bioRxiv : the preprint server for biology*.

Sibale LL, et al. (2025) Within-host genetic diversity of pneumococcal serotype 3 during one-year prolonged carriage in a healthy adult. *Nature communications*, 16(1), 8920.

Hu H, et al. (2025) Intestinal colonization of carbapenem-resistant gram-negative bacteria in pediatric hematology patients: risk factors and molecular characteristics, a multicenter case-control study. *BMC microbiology*, 25(1), 794.

Skaare D, et al. (2025) Genomic profiling of cefotaxime-resistant *Haemophilus influenzae* from Norway and Sweden reveals extensive expansion of virulent multidrug-resistant international clones. *Frontiers in microbiology*, 16, 1601390.

Zhou J, et al. (2025) Diverse modes of ceftazidime/avibactam resistance acquisition in carbapenem-resistant *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* from a Chinese intensive care unit. *Annals of clinical microbiology and antimicrobials*, 24(1), 35.

Thirumoorthy TP, et al. (2025) Recent emergence of cephalosporin-resistant *Salmonella* Typhi in India due to the endemic clone acquiring IncFIB(K) plasmid encoding blaCTX-M-15 gene. *Microbiology spectrum*, 13(5), e0087524.

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

Jacob JJ, et al. (2024) Limited Evidence of Spillover of Antimicrobial-Resistant *Klebsiella pneumoniae* from Animal/Environmental Reservoirs to Humans in Vellore, India. *Journal of epidemiology and global health*, 14(4), 1668.