

Resource Summary Report

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sistr

RRID:SCR_024342

Type: Tool

Proper Citation

sistr (RRID:SCR_024342)

Resource Information

URL: https://github.com/phac-nml/sistr_cmd

Proper Citation: sistr (RRID:SCR_024342)

Description: SISTR command-line tool. Open web accessible tool for rapidly typing and subtyping draft salmonella genome assemblies.

Abbreviations: SISTR

Synonyms: Salmonella In Silico Typing Resource

Resource Type: software application, software resource

Defining Citation: [PMID:26800248](#)

Keywords: rapidly typing and subtyping draft salmonella genome assemblies, salmonella genome assemblies,

Availability: Free, Available for download, Freely available,

Resource Name: sistr

Resource ID: SCR_024342

Alternate IDs: OMICS_12011

Old URLs: <https://sources.debian.org/src/sistr/>

License: Apache-2.0 license

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260810T040903+0000

Ratings and Alerts

No rating or validation information has been found for sistr.

No alerts have been found for sistr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Delgado-Suarez EJ, et al. (2026) Emergence of multidrug-resistant blaCTX-M-65/gyrA_D87Y clones among the circulating Salmonella Infantis population in Mexico. Microbial genomics, 12(2).

Duze ST, et al. (2026) Draft genome of extended-spectrum β -lactamase-producing multidrug-resistant Salmonella enterica serovar Brandearup strain DE0603 from an urban river in South Africa. Microbiology resource announcements, 15(3), e0095725.

Liao YS, et al. (2026) Emergence of azithromycin-resistant extensively drug-resistant Salmonella Kentucky ST314 in Taiwan. Frontiers in microbiology, 17, 1832575.

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

Hong Y-P, et al. (2026) Epidemiology and genomics of azithromycin-resistant extensively drug-resistant Salmonella enterica serovar Typhimurium in Taiwan. Antimicrobial agents and chemotherapy, 70(4), e0133425.

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

Habib I, et al. (2026) Genomic characterization and comparative analysis of multidrug-resistant Salmonella Indiana sequence type 17 carrying mcr-9.1 in retail eggs from the United Arab Emirates. Frontiers in veterinary science, 13, 1825641.

Jiang X, et al. (2025) Ecological prevalence and genomic characterization of Salmonella isolated from selected poultry farms in Jiangxi province, China. Poultry science, 104(7), 105197.

Wang Y, et al. (2025) A global atlas and drivers of antimicrobial resistance in Salmonella during 1900-2023. Nature communications, 16(1), 4611.

Huang D, et al. (2025) Plasmid-driven clonal expansion of multidrug-resistant monophasic Salmonella Typhimurium in a Global Food Trade Hub. Emerging microbes & infections, 14(1), 2542251.

- Ramachandran P, et al. (2025) Population structure analysis of *Salmonella* serovar Muenchen to redefine geno-serotyping using genome indexing approaches. *Frontiers in microbiology*, 16, 1681711.
- Liao YS, et al. (2025) Paratyphoid fever and the genomics of *Salmonella enterica* serovar Paratyphi A in Taiwan. *PLoS neglected tropical diseases*, 19(9), e0013048.
- Jia C, et al. (2025) Avian-specific *Salmonella* transition to endemicity is accompanied by localized resistome and mobilome interaction. *eLife*, 13.
- García-Álvarez MI, et al. (2025) Genomic characterization of antimicrobial-resistance and virulence factors in *Salmonella* isolates obtained from pig farms in Antioquia, Colombia. *PLoS neglected tropical diseases*, 19(1), e0012830.
- Sunmonu GT, et al. (2025) Genomic analysis of *Salmonella enterica* from cattle, beef and humans in the Greater Tamale Metropolis of Ghana. *PloS one*, 20(6), e0325048.
- Sunmonu GT, et al. (2025) Genomic characterization of foodborne *Salmonella enterica* and *Escherichia coli* isolates from Saboba district and Bolgatanga Municipality Ghana. *PloS one*, 20(2), e0315583.
- Bentum KE, et al. (2025) Comparative Genomic Profiles of *Salmonella* Typhimurium and *Salmonella* Dublin Bovine Isolates from the U.S. Indicate Possible Factors Associated with the Host Adaptation of *Salmonella* Dublin in the Region. *Microorganisms*, 13(4).
- Smith AM, et al. (2025) Whole-genome sequencing for surveillance of *Salmonella* at a public health institution in South Africa. *African journal of laboratory medicine*, 14(1), 2900.
- Lizarazo J, et al. (2025) Recurrent meningitis due to *Salmonella arizonae* in an adult with AIDS: case presentation and next-generation sequencing analysis. *ASM case reports*, 1(6).
- Dziegiel AH, et al. (2025) Metagenomic identification of disease-causing *Salmonella enterica* serovars and antimicrobial resistance genes from paediatric faecal samples. *Microbial genomics*, 11(10).