

Resource Summary Report

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Short Read Sequence Typing for Bacterial Pathogens

RRID:SCR_015870

Type: Tool

Proper Citation

Short Read Sequence Typing for Bacterial Pathogens (RRID:SCR_015870)

Resource Information

URL: <https://github.com/katholt/srst2>

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Description: Software that is designed to take Illumina sequence data, a MLST database and/or a database of gene sequences (e.g. resistance genes, virulence genes, etc) and report the presence of STs and/or reference genes.

Abbreviations: SRST2

Synonyms: SRST2: Short Read Sequence Typing for Bacterial Pathogens, Short Read Sequence Typing v2

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, source code

Defining Citation: [PMID:25422674](#)

Keywords: genotype analysis, illumina sequence data, mlst database, gene sequence, st, reference gene, short read

Related Condition: infectious disease

Funding: NHMRC of Australia 1043830;
NHMRC of Australia 1061409;
NHMRC of Australia 1061435;
Victorian Life Sciences Computation Initiative (VLSCI) VR0082

Availability: Free, Available for download

Resource Name: Short Read Sequence Typing for Bacterial Pathogens

Resource ID: SCR_015870

Alternate IDs: OMICS_12777

Alternate URLs: <http://katholt.github.io/srst2/>, <https://sources.debian.org/src/srst2/>

Old URLs: <http://srst.sourceforge.net/>

License: New BSD 3-clause License

License URLs: <https://github.com/katholt/srst2/blob/master/LICENSE.txt>

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260821T194029+0000

Ratings and Alerts

No rating or validation information has been found for Short Read Sequence Typing for Bacterial Pathogens.

No alerts have been found for Short Read Sequence Typing for Bacterial Pathogens.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

de Lira DRP, et al. (2026) Genome on the move: emergence of hybrid atypical enteropathogenic/enteroaggregative Escherichia coli (aEPEC/EAEC) during a diarrheal outbreak in Brazil. Microbiology spectrum, 14(5), e0277425.

Gawor J, et al. (2025) ICESp1109, a Novel Hybrid Integrative Conjugative Element of Macrolide-Resistant Streptococcus pyogenes Serotype M77 Collected Between 2003 and 2017 in Poland. The Journal of infectious diseases, 231(3), e521.

Pillay A, et al. (2024) Molecular investigation of Treponema pallidum strains associated with ocular syphilis in the United States, 2016-2020. Microbiology spectrum, 12(10), e0058124.

Gong X, et al. (2024) Genomic insight into the diversity of Glaesserella parasuis isolates from 19 countries. mSphere, 9(9), e0023124.

Wei L, et al. (2023) Emergence of ST1193 Clone in Maternal and Neonatal ESBL-Producing E. coli Isolates. Infection and drug resistance, 16, 6681.

Lam MMC, et al. (2023) Detection and Typing of Plasmids in *Acinetobacter baumannii* Using rep Genes Encoding Replication Initiation Proteins. *Microbiology spectrum*, 11(1), e0247822.

Knight DR, et al. (2023) Genomic epidemiology and transmission dynamics of recurrent *Clostridioides difficile* infection in Western Australia. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 42(5), 607.

Afolayan AO, et al. (2022) An ST131 clade and a phylogroup A clade bearing an O101-like O-antigen cluster predominate among bloodstream *Escherichia coli* isolates from South-West Nigeria hospitals. *Microbial genomics*, 8(12).

Amin MB, et al. (2022) Identifying the Sources of Intestinal Colonization With Extended-Spectrum β -Lactamase-Producing *Escherichia coli* in Healthy Infants in the Community. *Frontiers in microbiology*, 13, 803043.

Ahn D, et al. (2021) An acquired acyltransferase promotes *Klebsiella pneumoniae* ST258 respiratory infection. *Cell reports*, 35(9), 109196.

Cornick J, et al. (2021) Genomic investigation of a suspected *Klebsiella pneumoniae* outbreak in a neonatal care unit in sub-Saharan Africa. *Microbial genomics*, 7(11).

Knight DR, et al. (2021) Major genetic discontinuity and novel toxigenic species in *Clostridioides difficile* taxonomy. *eLife*, 10.

Valdezate S, et al. (2021) Genomic Background and Phylogeny of *cfiA*-Positive *Bacteroides fragilis* Strains Resistant to Meropenem-EDTA. *Antibiotics (Basel, Switzerland)*, 10(3).

Cooper AL, et al. (2020) Systematic Evaluation of Whole Genome Sequence-Based Predictions of *Salmonella* Serotype and Antimicrobial Resistance. *Frontiers in microbiology*, 11, 549.

Hendriksen RS, et al. (2019) Using Genomics to Track Global Antimicrobial Resistance. *Frontiers in public health*, 7, 242.

, et al. (2019) Whole genome sequencing and metagenomics for outbreak investigation, source attribution and risk assessment of food-borne microorganisms. *EFSA journal. European Food Safety Authority*, 17(12), e05898.

Langelier C, et al. (2019) Microbiome and Antimicrobial Resistance Gene Dynamics in International Travelers. *Emerging infectious diseases*, 25(7), 1380.

Tang Y, et al. (2019) Identification of Genetic Features for Attenuation of Two *Salmonella* Enteritidis Vaccine Strains and Differentiation of These From Wildtype Isolates Using Whole Genome Sequencing. *Frontiers in veterinary science*, 6, 447.

Ingle DJ, et al. (2018) Dynamics of antimicrobial resistance in intestinal *Escherichia coli* from children in community settings in South Asia and sub-Saharan Africa. *Nature microbiology*, 3(9), 1063.

Lam MMC, et al. (2018) Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in *Klebsiella pneumoniae*. *Genome medicine*, 10(1), 77.