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

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;
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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

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Record Last Update: 20250522T061013+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 17 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

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

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

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).

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.

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.

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

Jolley KA, et al. (2018) Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome open research, 3, 124.

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.

Hua X, et al. (2017) Evolution of Acinetobacter baumannii In Vivo: International Clone II, More Resistance to Ceftazidime, Mutation in ptk. Frontiers in microbiology, 8, 1256.

Kovac J, et al. (2016) Production of hemolysin BL by Bacillus cereus group isolates of dairy origin is associated with whole-genome phylogenetic clade. BMC genomics, 17, 581.

Ingle DJ, et al. (2016) In silico serotyping of E. coli from short read data identifies limited novel O-loci but extensive diversity of O:H serotype combinations within and between pathogenic lineages. Microbial genomics, 2(7), e000064.