

Resource Summary Report

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MentaLiST

RRID:SCR_016469

Type: Tool

Proper Citation

MentaLiST (RRID:SCR_016469)

Resource Information

URL: <https://github.com/WGS-TB/MentaLiST>

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Description: Software for a MLST (multi-locus sequence typing) caller, based on a k-mer counting algorithm and written in the Julia language. Designed and implemented to handle large typing schemes.

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

Defining Citation: [PMID:29319471](#)

Keywords: next, generation, sequencing, multi, locus, sequence, typing, pathogen, surveillance, gene, identify, strain, type, housekeeping, whole, genome, sequencing, data, bacteria, genotyping, bio.tools

Funding: Canadian Institute for Health Research ;
Genome BC ;
Genome Canada

Availability: Free, Available for download, Freely available

Resource Name: MentaLiST

Resource ID: SCR_016469

Alternate IDs: biotools:mentalist

Alternate URLs: <https://bio.tools/mentalist>

License: MIT License

Record Creation Time: 20220129T080330+0000

Ratings and Alerts

No rating or validation information has been found for MentaLiST.

No alerts have been found for MentaLiST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Mikhaylova Y, et al. (2026) Short-Term Within-Host Genomic Diversity and Clone Turnover of Carbapenem-Resistant *Klebsiella pneumoniae* in an Intensive Care Unit Patient. *Antibiotics* (Basel, Switzerland), 15(6).

Shelenkov A, et al. (2025) Genomic typing, antimicrobial resistance gene, virulence factor and plasmid replicon database for the important pathogenic bacteria *Staphylococcus aureus*. *BMC genomic data*, 26(1), 65.

Shelenkov A, et al. (2025) Genomic typing, antimicrobial resistance gene, virulence factor and plasmid replicon database for the important pathogenic bacteria *Klebsiella pneumoniae*. *BMC microbiology*, 25(1), 3.

Shelenkov A, et al. (2025) Study Protocol for Genomic Epidemiology Investigation of Intensive Care Unit Patient Colonization by Antimicrobial-Resistant ESKAPE Pathogens. *Methods and protocols*, 8(6).

Shelenkov A, et al. (2023) Whole-Genome Sequencing Revealed the Fusion Plasmids Capable of Transmission and Acquisition of Both Antimicrobial Resistance and Hypervirulence Determinants in Multidrug-Resistant *Klebsiella pneumoniae* Isolates. *Microorganisms*, 11(5).

Shelenkov A, et al. (2023) International Clones of High Risk of *Acinetobacter Baumannii*-Definitions, History, Properties and Perspectives. *Microorganisms*, 11(8).

Egorova A, et al. (2023) Plasmid Composition, Antimicrobial Resistance and Virulence Genes Profiles of Ciprofloxacin- and Third-Generation Cephalosporin-Resistant Foodborne *Salmonella enterica* Isolates from Russia. *Microorganisms*, 11(2).

Shelenkov A, et al. (2022) Long-Read Whole Genome Sequencing Elucidates the Mechanisms of Amikacin Resistance in Multidrug-Resistant *Klebsiella pneumoniae* Isolates Obtained from COVID-19 Patients. *Antibiotics* (Basel, Switzerland), 11(10).

Mikhaylova Y, et al. (2022) Whole-Genome Analysis of *Staphylococcus aureus* Isolates from Ready-to-Eat Food in Russia. *Foods* (Basel, Switzerland), 11(17).

Shelenkov A, et al. (2022) Genomic Characterization of Clinical *Acinetobacter baumannii* Isolates Obtained from COVID-19 Patients in Russia. *Antibiotics* (Basel, Switzerland), 11(3).

Shelenkov A, et al. (2021) Diversity of International High-Risk Clones of *Acinetobacter baumannii* Revealed in a Russian Multidisciplinary Medical Center during 2017-2019. *Antibiotics* (Basel, Switzerland), 10(8).

Tyumentseva M, et al. (2021) Genomic and Phenotypic Analysis of Multidrug-Resistant *Acinetobacter baumannii* Clinical Isolates Carrying Different Types of CRISPR/Cas Systems. *Pathogens* (Basel, Switzerland), 10(2).

Page AJ, et al. (2018) Rapid multi-locus sequence typing direct from uncorrected long reads using Krocus. *PeerJ*, 6, e5233.

Silva M, et al. (2018) chewBBACA: A complete suite for gene-by-gene schema creation and strain identification. *Microbial genomics*, 4(3).

Feijao P, et al. (2018) MentaLiST - A fast MLST caller for large MLST schemes. *Microbial genomics*, 4(2).