Resource Summary Report

Generated by dkNET on May 22, 2025

MLST

RRID:SCR_010245
Type: Tool

Proper Citation

MLST (RRID:SCR_010245)

Resource Information

URL: http://www.mlst.net/

Proper Citation: MLST (RRID:SCR_010245)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 17, 2022. A nucleotide sequence based approach for the unambiguous characterisation of isolates of bacteria and other organisms via the internet. The aim of MLST is to provide a portable, accurate, and highly discriminating typing system that can be used for most bacteria and some other organisms. It is envisaged that this approach will be particularly helpful for the typing of bacterial pathogens. To achieve this aim we have taken the proven concepts of multilocus enzyme electrophoresis (MLEE) and have adapted them so that alleles at each locus are defined directly, by nucleotide sequencing, rather than indirectly from the electrophoretic moblity of their gene products. MLST was developed in the laboratories of Martin Maiden, Dominique Caugant, Ian Feavers, Mark Achtman and Brian Spratt. This site is hosted at Imperial College with funding from the Wellcome Trust. The location of the subsites for the individual species are shown on their respective front pages.

Resource Type: database, data or information resource

Funding: Wellcome Trust

Availability: THIS RESOURCE IS NO LONGER IN SERVICE.

Resource Name: MLST

Resource ID: SCR_010245

Alternate IDs: nlx_156883

Record Creation Time: 20220129T080257+0000

Record Last Update: 20250522T060633+0000

Ratings and Alerts

No rating or validation information has been found for MLST.

No alerts have been found for MLST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1213 mentions in open access literature.

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

Ofosu Appiah F, et al. (2025) Emergence of Carbapenem-Resistant blaPOM-1 Harboring Pseudomonas otitidis Isolated from River Water in Ghana. Antibiotics (Basel, Switzerland), 14(1).

Horsman S, et al. (2025) Molecular Epidemiological Characteristics of Staphylococcus pseudintermedius, Staphylococcus coagulans, and Coagulase-Negative Staphylococci Cultured from Clinical Canine Skin and Ear Samples in Queensland. Antibiotics (Basel, Switzerland), 14(1).

do Amarante VS, et al. (2025) Dynamics of Salmonella Dublin infection and antimicrobial resistance in a dairy herd endemic to salmonellosis. PloS one, 20(1), e0318007.

Haenni M, et al. (2025) Distinct molecular epidemiology of resistances to extended-spectrum cephalosporins and carbapenems in Enterobacter hormaechei in cats and dogs versus horses in France. The Journal of antimicrobial chemotherapy, 80(2), 567.

An H, et al. (2025) Genomic and virulent characterization of a duck-associated Salmonella serovar Potsdam from China. Poultry science, 104(1), 104646.

Juma MA, et al. (2025) Genomic detection of Panton-Valentine Leucocidins encoding genes, virulence factors and distribution of antiseptic resistance determinants among Methicillin-resistant S. aureus isolates from patients attending regional referral hospitals in Tanzania. BMC medical genomics, 18(1), 14.

Tan J, et al. (2025) Molecular characterization of avian pathogenic Escherichia coli strains in Jiangxi Province, China, and development of polyvalent inactivated vaccines. Poultry

science, 104(2), 104766.

Vijayakumar S, et al. (2024) Genomic investigation unveils colistin resistance mechanism in carbapenem-resistant Acinetobacter baumannii clinical isolates. Microbiology spectrum, 12(2), e0251123.

Gencay YE, et al. (2024) Engineered phage with antibacterial CRISPR-Cas selectively reduce E. coli burden in mice. Nature biotechnology, 42(2), 265.

Hernández-García M, et al. (2024) Simultaneous clonal spread of NDM-1-producing Pseudomonas aeruginosa ST773 from Ukrainian patients in the Netherlands and Spain. IJID regions, 12, 100415.

Souza TGV, et al. (2024) Occurrence, genetic diversity, and antimicrobial resistance of methicillin-resistant Staphylococcus spp. in hospitalized and non-hospitalized cats in Brazil. PloS one, 19(10), e0309711.

Dziegiel AH, et al. (2024) High Campylobacter diversity in retail chicken: epidemiologically important strains may be missed with current sampling methods. Epidemiology and infection, 152, e101.

Zhou W, et al. (2024) Genotype Distribution and High-Risk Factors Analysis of Group B Streptococcus in Late-Stage Pregnant Women in the Linyi Region. International journal of microbiology, 2024, 9910073.

Jia C, et al. (2024) A global genome dataset for Salmonella Gallinarum recovered between 1920 and 2024. Scientific data, 11(1), 1094.

Zhang X, et al. (2024) WGS Analysis of Staphylococcus warneri Outbreak in a Neonatal Intensive Care Unit. Infection and drug resistance, 17, 4279.

Sabtcheva S, et al. (2024) Genomic Characterization of 16S rRNA Methyltransferase-Producing Enterobacterales Reveals the Emergence of Klebsiella pneumoniae ST6260 Harboring rmtF, rmtB, blaNDM-5, blaOXA-232 and blaSFO-1 Genes in a Cancer Hospital in Bulgaria. Antibiotics (Basel, Switzerland), 13(10).

Turton JF, et al. (2024) Klebsiella pneumoniae sequence type 147: a high-risk clone increasingly associated with plasmids carrying both resistance and virulence elements. Journal of medical microbiology, 73(4).

Liu C, et al. (2024) Characterization of linezolid- and methicillin-resistant coagulase-negative staphylococci in a tertiary hospital in China. BMC infectious diseases, 24(1), 486.

Yan W, et al. (2024) Antimicrobial resistance and genome characteristics of Salmonella enteritidis from Huzhou, China. PloS one, 19(6), e0304621.

Solis MN, et al. (2024) Detecting Class 1 Integrons and Their Variable Regions in Escherichia coli Whole-Genome Sequences Reported from Andean Community Countries. Antibiotics (Basel, Switzerland), 13(5).