

Resource Summary Report

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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 mobility 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: 20260819T044252+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 1242 mentions in open access literature.

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

Froschauer K, et al. (2025) Complementary Ribo-seq approaches map the translome and provide a small protein census in the foodborne pathogen *Campylobacter jejuni*. *Nature communications*, 16(1), 3078.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Chen J, et al. (2025) Exploring the clinical outcomes and molecular characteristics of *Acinetobacter baumannii* bloodstream infections: a study of sequence types, capsular types, and drug resistance in China. *Frontiers in cellular and infection microbiology*, 15, 1549940.

Mangroliya D, et al. (2025) Genomic insights into plasmid mediated AMR genes, virulence factors and mobile genetic elements in raw milk *Escherichia coli* from Gujarat, India. *Scientific reports*, 15(1), 6320.

Zhao C, et al. (2025) The type VI secretion system as a potential predictor of subsequent bloodstream infection of carbapenem-resistant *Klebsiella pneumoniae* strains on intestinal colonization. *Infection*, 53(2), 667.

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).

Nishihama S, et al. (2025) Oral colonization of antimicrobial-resistant bacteria in home health care participants and their association with oral and systemic status. *Scientific reports*, 15(1), 5776.

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.

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.

Mondol SM, et al. (2025) Comprehensive genomic insights into a highly pathogenic clone ST656 of mcr8.1 containing multidrug-resistant Klebsiella pneumoniae from Bangladesh. Scientific reports, 15(1), 5909.

Cadenas-Jimenez I, et al. (2025) Co-culture biofilm patterns among different Pseudomonas aeruginosa clones from cystic fibrosis patients. Biofilm, 9, 100257.

Hu F, et al. (2025) Study on the multidrug resistance and transmission factors of Staphylococcus aureus at the 'animal-environment-human' interface in the broiler feeding cycle. Frontiers in microbiology, 16, 1495676.

Li Y, et al. (2025) Potential links between human bloodstream infection by Salmonella enterica serovar Typhimurium and international transmission to Colombia. PLoS neglected tropical diseases, 19(1), e0012801.

Meng F, et al. (2025) Study on molecular characteristics of Staphylococcus from yak milk-Xizang. BMC microbiology, 25(1), 153.

Adhikari Y, et al. (2025) Genotypic and phenotypic characterization of antimicrobial resistance in Salmonella strains isolated from both No-Antibiotics-Ever (NAE) and conventional broiler complexes. Poultry science, 104(3), 104855.

Yaikhan T, et al. (2025) Genomic analysis of Enterobacter cloacae complex from Southern Thailand reveals insights into multidrug resistance genotypes and genetic diversity. Scientific reports, 15(1), 4670.

Fujii A, et al. (2025) Comprehensive analysis of bacteriocins produced by clinical enterococcal isolates and their antibacterial activity against Enterococci including VRE. Scientific reports, 15(1), 4846.

Fusco G, et al. (2025) Streptococcus suis-associated neonatal meningitis and sepsis: characterization, antimicrobial resistance, and public health implications. Frontiers in microbiology, 16, 1519247.

de Sevilla MF, et al. (2025) Clinical manifestations, serotype distribution, and incidence of pediatric invasive pneumococcal disease in Catalonia (Spain), 2018-2022. European journal of pediatrics, 184(5), 323.