

Resource Summary Report

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PubMLST

RRID:SCR_012955

Type: Tool

Proper Citation

PubMLST (RRID:SCR_012955)

Resource Information

URL: <http://pubmlst.org/>

Proper Citation: PubMLST (RRID:SCR_012955)

Description: Database for molecular typing and microbial genome diversity.

Resource Type: database, data or information resource

Keywords: FASEB list

Resource Name: PubMLST

Resource ID: SCR_012955

Alternate IDs: nlx_156844

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260803T040616+0000

Ratings and Alerts

No rating or validation information has been found for PubMLST.

No alerts have been found for PubMLST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2496 mentions in open access literature.

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

Stryko J, et al. (2026) Carbapenem-resistant *Acinetobacter baumannii* at a hospital in Botswana: detecting a protracted outbreak using whole genome sequencing. *Microbiology spectrum*, 14(1), e0176825.

Visser M, et al. (2026) *Neisseria gonorrhoeae* Sequence Types During an Increase of Gonorrhea Among Young Women in 2022 and 2023 in the Netherlands. *Open forum infectious diseases*, 13(1), ofaf767.

Zhang J, et al. (2026) Clonal dissemination of ST19 *Salmonella* Typhimurium within a Chinese poultry breeding pyramid and One-Health implications. *Poultry science*, 105(1), 106097.

Unitt A, et al. (2025) *Neisseria gonorrhoeae* LIN codes provide a robust, multi-resolution lineage nomenclature. *eLife*, 14.

Wei C, et al. (2025) Clinical characteristics, molecular epidemiology and mechanisms of colistin heteroresistance in *Enterobacter cloacae* complex. *Frontiers in cellular and infection microbiology*, 15, 1536058.

Bassiouny M, et al. (2025) Molecular Characterization of Presumptive *Klebsiella pneumoniae* Isolates from Companion and Farm Animals in Germany Reveals Novel Sequence Types. *Pathogens (Basel, Switzerland)*, 14(3).

Roca-Grande J, et al. (2025) Genomic characterization of invasive *Neisseria meningitidis* in Spain (2011/12-2022/23): expansion of clonal complex 213 and the potential threat to 4CMenB vaccine strain coverage. *Emerging microbes & infections*, 14(1), 2482696.

Tabatabaie Poya FS, et al. (2025) Unveiling the Genetic Landscape of *Staphylococcus aureus* Isolated From Hospital Wastewaters: Emergence of Hypervirulent CC8 Strains in Tehran, Iran. *International journal of microbiology*, 2025, 5458315.

Nila SS, et al. (2025) Epidemiological features of scrub typhus and molecular characteristics of *Orientia tsutsugamushi* in north-central Bangladesh. *IJID regions*, 14, 100571.

Mack AR, et al. (2025) β -Lactamase diversity in *Pseudomonas aeruginosa*. *Antimicrobial agents and chemotherapy*, 69(3), e0078524.

Kuang S, et al. (2025) Prevalence and genetic characteristics of *Campylobacter jejuni* from laying-hens in Hubei Province, China. *BMC veterinary research*, 21(1), 84.

Brodíková K, et al. (2025) Asymptomatic carriage and molecular characterization of *Staphylococcus aureus* in pre-clinical and clinical medical students. *Folia microbiologica*, 70(1), 241.

Guembe M, et al. (2025) Virulence profile of carbapenem-resistant *Klebsiella pneumoniae* strains by an in vivo model of *Galleria mellonella*. *Microbiology spectrum*, 13(2), e0221524.

Coll F, et al. (2025) The mutational landscape of *Staphylococcus aureus* during colonisation. *Nature communications*, 16(1), 302.

Zhang P, et al. (2025) Understanding the clinical and molecular epidemiological characteristics of carbapenem-resistant *Acinetobacter baumannii* infections within intensive care units of three teaching hospitals. *Annals of clinical microbiology and antimicrobials*, 24(1), 2.

Efrati Epchtien R, et al. (2025) Characterization of Enterobacterales growing on selective CPE screening plates with a focus on non-carbapenemase-producing strains. *Microbiology spectrum*, 13(2), e0207924.

Tristancho-Baró A, et al. (2025) Genomic Characterization of Carbapenemase-Producing Enterobacteriaceae from Clinical and Epidemiological Human Samples. *Antibiotics (Basel, Switzerland)*, 14(1).

Alam M, et al. (2025) A novel virulent core genome multilocus sequence type CT 11424 of *Listeria monocytogenes* isolate causing stillbirth in Bangladesh. *BMC microbiology*, 25(1), 61.

Sousa EG, et al. (2025) The research on the identification, taxonomy, and comparative genomics analysis of nine *Bacillus velezensis* strains significantly contributes to microbiology, genetics, bioinformatics, and biotechnology. *Frontiers in microbiology*, 16, 1544934.

Owiredu N, et al. (2025) Antimicrobial resistance and genomic characteristics of *Campylobacter* spp. From Australian meat chickens with A follow up investigation. *Scientific reports*, 15(1), 10780.