

Resource Summary Report

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PHYLOViZ

RRID:SCR_024162

Type: Tool

Proper Citation

PHYLOViZ (RRID:SCR_024162)

Resource Information

URL: <http://www.phyloviz.net/>

Proper Citation: PHYLOViZ (RRID:SCR_024162)

Description: Platform independent JAVA software for analysis of sequence based typing methods that generate allelic profiles and their associated epidemiological data. Phylogenetic inference and data visualization for sequence based typing methods.

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:22568821](#)

Keywords: JAVA, phylogenetic inference, data visualization, sequence based typing methods, generate allelic profiles and their associated epidemiological data,

Availability: Free, Available for download, Freely available,

Resource Name: PHYLOViZ

Resource ID: SCR_024162

Old URLs: <https://sources.debian.org/src/phyloviz-core/>

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260821T194249+0000

Ratings and Alerts

No rating or validation information has been found for PHYLOViZ.

No alerts have been found for PHYLOViZ.

Data and Source Information

Usage and Citation Metrics

We found 109 mentions in open access literature.

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

Sun Q, et al. (2026) Whole genome sequencing analyses of Chinese *Glaesserella parasuis* isolates reveal insights into their genomic characterization, virulence genes and antibiotic resistance genes. *BMC genomics*, 27(1).

Akwetey SA, et al. (2026) Genomic surveillance of post-immunization pneumococcal carriage in Ghana. *Microbial genomics*, 12(6).

Xie S, et al. (2026) Toxin gene profiles, antibiotic resistance, and genetic diversity of *Clostridium perfringens* from food-producing animals: a whole-genome sequencing study with implications for food safety. *Current research in food science*, 12, 101460.

Chukamnerd A, et al. (2026) Genomic Epidemiology of Carbapenem-Resistant *Acinetobacter baumannii* Isolated from Patients Admitted to Intensive Care Units in Network Hospitals in Southern Thailand. *Antibiotics (Basel, Switzerland)*, 15(2).

Gonzales BE, et al. (2026) Genomic features of pneumococcal strains isolated from paediatric patients with invasive disease during pneumococcal conjugate vaccine introduction in Lima, Peru. *Microbial genomics*, 12(2).

He Y, et al. (2026) Prevalence and characterization of *Staphylococcus aureus* isolated from patients with aerobic vaginitis in Shenzhen, Southern China. *BMC microbiology*, 26(1).

González-Navarro MP, et al. (2026) Phenotypic and whole genome characterization of multidrug-resistant *Campylobacter coli* from chicken liver. *Poultry science*, 105(10), 107271.

Yang D, et al. (2026) Global genomic landscape of *Staphylococcus lugdunensis*: population structure, antimicrobial resistance, and virulence determinants. *Applied and environmental microbiology*, 92(3), e0189325.

Lin YT, et al. (2026) Re-examining cephalosporin activity against methicillin-susceptible *Staphylococcus aureus* among clinical isolates from southern Taiwan. *JAC-antimicrobial resistance*, 8(1), dlag029.

Kinoshita M, et al. (2026) Fc-free single-chain antibody mRNA therapy for airway infection of multidrug-resistant *Pseudomonas aeruginosa*. *Nature communications*, 17(1).

Zhong W, et al. (2025) Extended-spectrum β -lactamase-producing *Escherichia coli* isolated from captive primates: characteristics and horizontal gene transfer ability analysis. *PloS one*, 20(4), e0321514.

Chua TP, et al. (2025) Diversity of *Mycoplasma genitalium* strains in Australia: relationship with sexual networks and antimicrobial resistance. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 44(5), 1167.

Li CA, et al. (2025) Genetic and virulence analysis of carbapenem-resistant *Pseudomonas aeruginosa* in farm animals in Shandong province, China: implications for human health. *BMC microbiology*, 26(1), 50.

Steinke K, et al. (2025) RSYD-BASIC: a bioinformatic pipeline for routine sequence analysis and data processing of bacterial isolates for clinical microbiology. *Access microbiology*, 7(3).

Xu X, et al. (2025) Molecular epidemiology of *Nakaseomyces glabrata* associated with vulvovaginal candidiasis revealed high genetic variability and the presence of novel genotypes in China. *Virulence*, 16(1), 2543058.

Li X, et al. (2025) Molecular insights into the persistence and co-occurrence of two different carbapenem-resistant *Pseudomonas aeruginosa* lineages within a hospital setting. *Microbiology spectrum*, 13(10), e0043325.

Naing SY, et al. (2025) Molecular epidemiology and emergence of sequence type 25 hypervirulent *Klebsiella pneumoniae* in pigs in the Netherlands (2013-2020): a global comparative analysis with human and pig isolates. *Microbial genomics*, 11(4).

Manzanares-Pedrosa A, et al. (2025) Phenotypic and whole genome-based characterization of antibiotic resistance of *Campylobacter jejuni* isolates from chicken livers. *Poultry science*, 104(8), 105302.

Abdul Rahman NA, et al. (2025) Comparative Genotyping of Malaysian Clinical Isolates of *Streptococcus pneumoniae* by Multilocus Sequence Typing and Multilocus Variable-Number Tandem Repeat Analysis. *The Malaysian journal of medical sciences : MJMS*, 32(1), 69.

Tang Y, et al. (2025) Genomically defined hypervirulent *Klebsiella pneumoniae* contributed to early-onset increased mortality. *Nature communications*, 16(1), 2096.