

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 toolkit, software resource, software library

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: 20260731T043137+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 74 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Quyen TLT, et al. (2025) Molecular epidemiology of carbapenem-resistant *Acinetobacter baumannii* group in Taiwan. *mSphere*, 10(1), e0079324.

Lurie-Weinberger MN, et al. (2025) Virulence factors are preserved within carbapenem-resistant *Acinetobacter baumannii* clades. *Virulence*, 16(1), 2542489.

Shoji K, et al. (2025) Skin Infections Caused by Panton-Valentine Leukocidin and Methicillin-Susceptible *Staphylococcus aureus* in Child, Japan. *Emerging infectious diseases*, 31(6), 1227.

Zhang X, et al. (2025) Developing genome typing strategies for the emerging zoonotic pathogen *Streptococcus parasuis*. *Journal of clinical microbiology*, 63(11), e0074125.

Križanac I, et al. (2025) Multigene Typing of Croatian 'Candidatus *Phytoplasma Mali*' Strains. *Pathogens (Basel, Switzerland)*, 14(10).

Sidor-Dzitkowska K, et al. (2025) Genotyping of *Acinetobacter baumannii* clinical isolates from Polish hospitals uncovers novel sequence types. *Scientific reports*, 15(1), 40171.

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.

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.

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.

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).

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.

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).

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

Lv C, et al. (2025) Genomic characterization of *Escherichia coli* with a polyketide synthase (pks) island isolated from ulcerative colitis patients. *BMC genomics*, 26(1), 19.

Lin S, et al. (2025) A molecular comparative study of intestinal colonization with *Staphylococcus aureus* between pediatric inpatients and outpatients of different age groups. *Microbiology spectrum*, 13(7), e0239424.

Ahmadi Y, et al. (2025) Genotyping of Clinical Samples of Methicillin-Resistant *Staphylococcus aureus* Isolates in Isfahan Using Multilocus Sequence Typing (MLST). *The Canadian journal of infectious diseases & medical microbiology = Journal canadien des maladies infectieuses et de la microbiologie medicale*, 2025, 7307394.

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.

Shi Q, et al. (2025) Molecular epidemiology and geographical variation of methicillin-resistant *Staphylococcus aureus*: a multicentre study across Xinjiang, China. *BMC microbiology*, 25(1), 769.

Ntozini B, et al. (2025) Molecular Epidemiology of Invasive Group B *Streptococcus* in South Africa, 2019-2020. *The Journal of infectious diseases*, 231(4), e697.

Chen T, et al. (2025) Emergence and molecular evolution of carbapenem-resistant hypervirulent ST23 *Klebsiella pneumoniae*: The superbug phenomenon in China. *Virulence*, 16(1), 2545556.