

Resource Summary Report

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SpoTyping

RRID:SCR_018466

Type: Tool

Proper Citation

SpoTyping (RRID:SCR_018466)

Resource Information

URL: <https://github.com/xiaeryu/SpoTyping-v2.0>

Proper Citation: SpoTyping (RRID:SCR_018466)

Description: Software tool for fast and accurate in silico Mycobacterium spoligotyping from sequence reads.

Synonyms: SpoTyping-v2.0, SpoTyping

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [DOI:10.1186/s13073-016-0270-7](https://doi.org/10.1186/s13073-016-0270-7)

Keywords: bio.tools

Funding: National University of Singapore ;
Singapore ;
Singapore

Availability: Free, Available for download, Freely available

Resource Name: SpoTyping

Resource ID: SCR_018466

Alternate IDs: biotools:spotyping

Alternate URLs: <https://bio.tools/spotyping>

License: GNU General Public License

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260905T132837+0000

Ratings and Alerts

No rating or validation information has been found for SpoTyping.

No alerts have been found for SpoTyping.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Couvin D, et al. (2025) Molecular typing of Mycobacterium tuberculosis: a review of current methods, databases, softwares, and analytical tools. FEMS microbiology reviews, 49.

Marcon DJ, et al. (2024) Comprehensive genomic surveillance reveals transmission profiles of extensively drug-resistant tuberculosis cases in Pará, Brazil. Frontiers in microbiology, 15, 1514862.

Martínez-Lirola M, et al. (2023) A One Health approach revealed the long-term role of Mycobacterium caprae as the hidden cause of human tuberculosis in a region of Spain, 2003 to 2022. Euro surveillance : bulletin Européen sur les maladies transmissibles = European communicable disease bulletin, 28(12).

Genestet C, et al. (2022) Development, Evaluation, and Implementation of a House-Made Targeted Next-Generation Sequencing Spoligotyping in a French Laboratory. International journal of molecular sciences, 23(19).

Valcheva V, et al. (2022) Mycobacterium bovis and M. caprae in Bulgaria: insight into transmission and phylogeography gained through whole-genome sequencing. BMC veterinary research, 18(1), 148.

Genestet C, et al. (2022) Consistency of Mycobacterium tuberculosis Complex Spoligotyping between the Membrane-Based Method and In Silico Approach. Microbiology spectrum, 10(3), e0022322.

Santos-Lazaro D, et al. (2021) Whole genome analysis of extensively drug resistant Mycobacterium tuberculosis strains in Peru. Scientific reports, 11(1), 9493.

Thawornwattana Y, et al. (2021) Revised nomenclature and SNP barcode for Mycobacterium tuberculosis lineage 2. Microbial genomics, 7(11).

Negrete-Paz AM, et al. (2021) Whole-genome comparative analysis at the lineage/sublineage level discloses relationships between Mycobacterium tuberculosis genotype and clinical phenotype. PeerJ, 9, e12128.

Almaw G, et al. (2021) Population structure and transmission of *Mycobacterium bovis* in Ethiopia. *Microbial genomics*, 7(5).

Li H, et al. (2021) Tuberculosis Outbreak in an Educational Institution in Henan Province, China. *Frontiers in public health*, 9, 737488.

Crispell J, et al. (2020) *Mycobacterium bovis* genomics reveals transmission of infection between cattle and deer in Ireland. *Microbial genomics*, 6(8).