Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 17, 2025

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 processing software, data analysis software, software resource, software application

Defining Citation: DOI: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

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250417T065632+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 8 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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 Europeen 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).

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.

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

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.

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

Santos-Lazaro D, et al. (2021) Whole genome analysis of extensively drug resistant

Mycobacterium tuberculosis strains in Peru. Scientific reports, 11(1), 9493.

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