Resource Summary Report

Generated by nidm-terms on Jul 28, 2026

TB PORTALS

RRID:SCR_016594
Type: Tool

Proper Citation

TB PORTALS (RRID:SCR_016594)

Resource Information

URL: https://tbportals.niaid.nih.gov

Proper Citation: TB PORTALS (RRID:SCR_016594)

Description: Web based open access platform for global drug resistant tuberculosis data sharing and analysis. The NIAID TB Portals program and consortium of clinicians and scientists from countries with a heavy burden of TB, especially drug resistant TB, to collect TB data.

Resource Type: service resource, organization portal, topical portal, storage service resource, disease-related portal, portal, data repository, consortium, data or information resource

Defining Citation: DOI:10.1128/JCM.01013-17

Keywords: collect, data, sharing, analysis, tuberculosis, global, bio.tools

Related Condition: tuberculosis

Funding: NIH

Availability: Free, Freely available

Resource Name: TB PORTALS

Resource ID: SCR_016594

Alternate IDs: r3d100013925, biotools:TB_Portals

Alternate URLs: https://bio.tools/TB_Portals, https://doi.org/10.17616/R31NJN8L

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260728T043521+0000

Ratings and Alerts

No rating or validation information has been found for TB PORTALS.

No alerts have been found for TB PORTALS.

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 nidm-terms .

Chimal-Mu??oz M, et al. (2025) Whole-Genome Sequence Analysis to Assess Mutations in Efflux Pumps in Mycobacterium tuberculosis: The Influence in Drug Resistance. Microorganisms, 13(6).

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

Bassi PRAS, et al. (2024) Improving deep neural network generalization and robustness to background bias via layer-wise relevance propagation optimization. Nature communications, 15(1), 291.

Sambarey A, et al. (2024) Integrative analysis of multimodal patient data identifies personalized predictors of tuberculosis treatment prognosis. iScience, 27(2), 109025.

Bui VCB, et al. (2023) Combining Radiological and Genomic TB Portals Data for Drug Resistance Analysis. IEEE access : practical innovations, open solutions, 11, 84228.

Yan C, et al. (2022) A fully automatic artificial intelligence-based CT image analysis system for accurate detection, diagnosis, and quantitative severity evaluation of pulmonary tuberculosis. European radiology, 32(4), 2188.

Prasitpuriprecha C, et al. (2022) Drug-Resistant Tuberculosis Treatment Recommendation, and Multi-Class Tuberculosis Detection and Classification Using Ensemble Deep Learning-Based System. Pharmaceuticals (Basel, Switzerland), 16(1).

Long A, et al. (2021) The technology behind TB DEPOT: a novel public analytics platform integrating tuberculosis clinical, genomic, and radiological data for visual and statistical exploration. Journal of the American Medical Informatics Association : JAMIA, 28(1), 71.

Ejalonibu MA, et al. (2021) Drug Discovery for Mycobacterium tuberculosis Using Structure-Based Computer-Aided Drug Design Approach. International journal of molecular sciences, 22(24).

Zwyer M, et al. (2021) A new nomenclature for the livestock-associated Mycobacterium tuberculosis complex based on phylogenomics. Open research Europe, 1, 100.

Macalino SJY, et al. (2020) In Silico Strategies in Tuberculosis Drug Discovery. Molecules (Basel, Switzerland), 25(3).

Engle E, et al. (2020) Performance of Qure.ai automatic classifiers against a large annotated database of patients with diverse forms of tuberculosis. PloS one, 15(1), e0224445.