Resource Summary Report

Generated by ASWG on Aug 25, 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: consortium, data or information resource, data repository, disease-related portal, organization portal, portal, service resource, storage service resource, topical portal

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: 20260821T194107+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 20 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Mudzengi D, et al. (2026) panTB-HM: a multi-arm clinical trial of a pan-TB regimen targeting both host and microbe. Trials, 27(1).

Tang SN, et al. (2026) Differences in pulmonary cavity features among drug-sensitive pulmonary tuberculosis and multidrug/extensively-resistant pulmonary tuberculosis: a multi-national multi-center computed tomography-based study. Journal of thoracic disease, 18(2), 56.

Ding Z, et al. (2026) Refining weak supervision for robust lung cavity segmentation: A graph-affinity method with boundary constraints. PloS one, 21(2), e0341717.

Tang SN, et al. (2025) Differences in pulmonary nodular consolidation features among drug-sensitive pulmonary tuberculosis and multidrug/extensively-resistant pulmonary tuberculosis: a multi-national multi-center study. Journal of thoracic disease, 17(10), 7498.

Chimal-Muñoz 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.

Sethanan K, et al. (2023) Computer-aided diagnosis using embedded ensemble deep learning for multiclass drug-resistant tuberculosis classification. Frontiers in medicine, 10, 1122222.

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

Karki M, et al. (2022) Generalization Challenges in Drug-Resistant Tuberculosis Detection from Chest X-rays. Diagnostics (Basel, Switzerland), 12(1).

Tan H, et al. (2022) Discriminating TB lung nodules from early lung cancers using deep learning. BMC medical informatics and decision making, 22(1), 161.

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.

Bermudez-Hernández GA, et al. (2022) Whole genome sequencing analysis to evaluate the influence of T2DM on polymorphisms associated with drug resistance in M. tuberculosis. BMC genomics, 23(1), 465.

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).

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).

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.

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.