Resource Summary Report

Generated by NIF on May 3, 2025

Tuberculosis Database

RRID:SCR_006619
Type: Tool

Proper Citation

Tuberculosis Database (RRID:SCR_006619)

Resource Information

URL: http://tbdb.org

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Description: Database providing integrated access to genome sequence, expression data and literature curation for Tuberculosis (TB) that houses genome assemblies for numerous strains of Mycobacterium tuberculosis (MTB) as well assemblies for over 20 strains related to MTB and useful for comparative analysis. TBDB stores pre- and post-publication gene-expression data from M. tuberculosis and its close relatives, including over 3000 MTB microarrays, 95 RT-PCR datasets, 2700 microarrays for human and mouse TB related experiments, and 260 arrays for Streptomyces coelicolor. (July 2010) To enable wide use of these data, TBDB provides a suite of tools for searching, browsing, analyzing, and downloading the data.

Abbreviations: TBDB

Synonyms: TB Database, TBDatabase

Resource Type: database, data or information resource

Defining Citation: PMID:20488753, PMID:18835847

Keywords: genomic, protein, blast, genome, gene, systems biology, gene expression, microarray, comparative analysis, regulatory network, metabolic network, epitope, expression profile, rt-pcr, gene regulation, genome browser, FASEB list

Related Condition: Tuberculosis

Funding: Bill and Melinda Gates Foundation

Availability: Acknowledgement requested, Public, (Published data)

Resource Name: Tuberculosis Database

Resource ID: SCR_006619

Alternate IDs: nif-0000-03537

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250503T055833+0000

Ratings and Alerts

No rating or validation information has been found for Tuberculosis Database.

No alerts have been found for Tuberculosis Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 64 mentions in open access literature.

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

Davis NK, et al. (2024) Facile metabolic reprogramming distinguishes mycobacterial adaptation to hypoxia and starvation: ketosis drives starvation-induced persistence in M. bovis BCG. Communications biology, 7(1), 866.

Zhang X, et al. (2022) In silico Methods for Identification of Potential Therapeutic Targets. Interdisciplinary sciences, computational life sciences, 14(2), 285.

Liu Y, et al. (2021) Evaluation of the frequency of mutation genes in multidrug-resistant tuberculosis (MDR-TB) strains in Beijing, China. Epidemiology and infection, 149, e21.

Gample SP, et al. (2019) Evidence of nitrite acting as a stable and robust inducer of non-cultivability in Mycobacterium tuberculosis with physiological relevance. Scientific reports, 9(1), 9261.

Liu Y, et al. (2019) NapM enhances the survival of Mycobacterium tuberculosis under stress and in macrophages. Communications biology, 2, 65.

Xie L, et al. (2019) Comprehensive analysis of protein acetyltransferases of human pathogen

Mycobacterium tuberculosis. Bioscience reports, 39(12).

Krishnan G, et al. (2019) A New Functional Model for Prediction of Chaperone Activity of the Recombinant M. tb Acr (?-Crystallin) Using Insulin as Substrate. The Canadian journal of infectious diseases & medical microbiology = Journal canadien des maladies infectieuses et de la microbiologie medicale, 2019, 2532045.

Leung-Theung-Long S, et al. (2018) A multi-antigenic MVA vaccine increases efficacy of combination chemotherapy against Mycobacterium tuberculosis. PloS one, 13(5), e0196815.

Yang F, et al. (2018) Development and application of a recombination-based library versus library high- throughput yeast two-hybrid (RLL-Y2H) screening system. Nucleic acids research, 46(3), e17.

Bhat AH, et al. (2017) The alr-groEL1 operon in Mycobacterium tuberculosis: an interplay of multiple regulatory elements. Scientific reports, 7, 43772.

Michelsen SW, et al. (2017) The dynamics of immune responses to Mycobacterium tuberculosis during different stages of natural infection: A longitudinal study among Greenlanders. PloS one, 12(6), e0177906.

Otal I, et al. (2017) Detection of a Putative TetR-Like Gene Related to Mycobacterium bovis BCG Growth in Cholesterol Using a gfp-Transposon Mutagenesis System. Frontiers in microbiology, 8, 315.

Lee W, et al. (2017) Novel protein acetyltransferase, Rv2170, modulates carbon and energy metabolism in Mycobacterium tuberculosis. Scientific reports, 7(1), 72.

Liu Q, et al. (2016) Genetic features of Mycobacterium tuberculosis modern Beijing sublineage. Emerging microbes & infections, 5(2), e14.

Peters JS, et al. (2016) Identification of Quantitative Proteomic Differences between Mycobacterium tuberculosis Lineages with Altered Virulence. Frontiers in microbiology, 7, 813.

Boradia VM, et al. (2016) Mycobacterium tuberculosis H37Ra: a surrogate for the expression of conserved, multimeric proteins of M.tb H37Rv. Microbial cell factories, 15(1), 140.

Phelan JE, et al. (2016) Recombination in pe/ppe genes contributes to genetic variation in Mycobacterium tuberculosis lineages. BMC genomics, 17, 151.

Miranda-CasoLuengo AA, et al. (2016) Functional characterization of the Mycobacterium abscessus genome coupled with condition specific transcriptomics reveals conserved molecular strategies for host adaptation and persistence. BMC genomics, 17, 553.

Jaafar MM, et al. (2016) Genome Sequencing and Annotation of Mycobacterium tuberculosis PR08 strain. Genomics data, 7, 119.

Halim MZ, et al. (2016) Genome sequencing and annotation of multidrug resistant Mycobacterium tuberculosis (MDR-TB) PR10 strain. Genomics data, 7, 245.