**2025年第38周**

**中国大陆学者发表的结核病英文文章摘要**

**（20篇）**

**PubMed Publication date: 2025/9/15---2025/9/21**

**(tuberculosis[Title/Abstract]) AND (English[Language]) AND (China[Affiliation])**

**1. Nat Commun. 2025 Sep 17;16(1):8257. doi: 10.1038/s41467-025-63094-x.**

Sensitive pathogen DNA detection by a multi-guide RNA Cas12a assay favoring

trans- versus cis-cleavage.

Huang Z(1)(2)(3)(4), Song Z(5), Zeng J(5), Liu X(6), Fang M(5), Wu Z(7), Zhao

Y(5), Chen Y(7), Li D(5), Huang H(8)(6), Fu L(5), Xu P(5), Ning B(8)(9), Chen

J(10), Guan M(7), Sun L(11), Lyon CJ(8)(9), Fan XY(6), Lu S(12), Hu T(13)(14).

**Zhen Huang\*, Zhe Song, Jianfeng Zeng, Xuhui Liu, Mutong Fang, Zhiyuan Wu, Yao Zhao, Yanli Chen, Dan Li, Huan Huang, Liang Fu, Peng Xu, Bo Ning, Jun Chen, Ming Guan, Lin Sun, Christopher J Lyon, Xiao-Yong Fan, Shuihua Lu\*, Tony Hu\***

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Most CRISPR assays lack clinical utility due to their complex workflows and

limited validation. Here we present a streamlined "one-pot" asymmetric CRISPR

tuberculosis assay that attenuates amplicon degradation to achieve 5 copies/μL

sensitivity within 60 min and detect positive patient samples within 15 min.

This assay exhibited 93%, 83%, and 93% sensitivity with adult respiratory,

pediatric stool, and adult cerebral spinal fluid specimens, and detected 64% of

clinically diagnosed tuberculous meningitis cases, in a cohort of 603 clinical

samples. This assay achieves complete specificity and greater sensitivity (74%

vs. 56%) than the most sensitive reference test with prospectively collected

tongue swabs, and exhibits similar performance when adapted to a lateral flow

assay format and employed to analyze self-collected tongue swabs. These results

demonstrate the utility of this approach across diverse specimen types,

including those suitable for use in remote and resource-limited settings, to

improve access to molecular diagnostics.

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DOI: 10.1038/s41467-025-63094-x

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PMID: 40962795 [Indexed for MEDLINE]

**2. Microbiol Spectr. 2025 Sep 17:e0150025. doi: 10.1128/spectrum.01500-25. Online**

**ahead of print.**

Diagnostic accuracy of the ESAT6-CFP10 skin test for latent tuberculosis

infection among jail detainees.

Fei X(#)(1)(2), Wang S(#)(3), Wang Z(1)(2), Hu X(1)(2), Chen C(1)(2), Zhu

L(1)(2), Martinez L(4), Tang P(5), Liu Q(1)(2).

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As an alternative to the tuberculin skin test (TST) or QuantiFERON-TB Gold

In-Tube (QFT-GIT), ESAT6-CFP10 (EC) skin test is an emerging screening method;

however, its value in the diagnosis of latent tuberculosis infection (LTBI) in

detainees is still unclear in China. Newly admitted detainees meeting inclusion

criteria were enrolled, with demographic/clinical data collected via structured

questionnaires. TST, EC skin test, and QFT-GIT screenings were performed,

documenting the diameter of skin indurations and/or redness at injection sites

and blistering reactions at injection sites. In total, 1,038 detainees were

enrolled in this study from October 2022 to October 2023 with 236 LTBI (22.7%).

The positive rate of TST, EC skin test, and QFT-GIT was 18.1%, 10.6% and 11.9%.

The area under the curve for EC was 0.820, indicating a strong concordance with

QFT-GIT (κ = 0.673). Compared with QFT-GIT, the sensitivity of EC was 66.9%, and

the specificity was 97.0%. The mean induration diameter or redness of EC was

significantly larger than that of TST (P < 0.001). In the regression model, no

history of alcohol consumption (aOR = 0.433, 95% confidence interval [CI]:

0.200, 0.938), no history of surgical trauma (aOR = 0.731, 95% CI: 0.539,

0.991), and no drug use (aOR = 0.473, 95% CI: 0.233, 0.961) was identified as a

protective factor for LTBI. The EC demonstrated both high specificity and

sensitivity comparable to the QFT-GIT. When screening for LTBI among jail

detainees in this setting, particular attention should be given to individuals

with a history of alcohol consumption, surgical trauma, and drug use.

IMPORTANCE: Jail detainees represent a vulnerable population with an elevated

risk of tuberculosis. The EC skin test demonstrates promising potential as an

alternative to traditional diagnostic methods, such as the TST and QFT-GIT

assay, for LTBI screening. Targeted screening strategies can facilitate the

early detection, diagnosis, and management of LTBI.

DOI: 10.1128/spectrum.01500-25

PMID: 40960282

**3. Virulence. 2025 Dec;16(1):2552875. doi: 10.1080/21505594.2025.2552875. Epub 2025 Sep 16.**

Analyzing the distribution of virulence factors of Mycobacterium tuberculosis

and the impact of virulence gene mutations on treatment outcomes in different

lineages using whole-genome sequencing in Urumqi.

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This study centers on Urumqi, utilizing whole-genome sequencing and comparative

genomics, we explored virulence factor mutations in different Mycobacterium

tuberculosis lineages and their impact on tuberculosis patient prognosis. We

utilized routine national drug resistance surveillance data from Urumqi,

gathering demographic, epidemiological, and clinical data of patients with

tuberculosis between 1 January 2017 to 31 December 2021. Whole-genome sequencing

was employed, followed by bioinformatics analysis using various methods and

statistical models. A total of 457 patients with tuberculosis were analyzed.

Through whole-genome sequencing and bioinformatics analysis, we categorized

these strains into three lineages: Lineage2 (347), Lineage3 (37), and Lineage4

(73), identifying 71 virulence factor mutations. The mutation rates of virulence

factors in M. tuberculosis exhibited polarization. Significant differences in

virulence factor mutation rates were observed among different M. tuberculosis

lineages (all p values  < 0.05). Additionally, mutations in espE, fadE29, and

mbtI genes among Lineage2 patients were considered as risk factors influencing

treatment outcomes (all p values < 0.05), with odds ratios of 13.6200

(1.7285-107.3201), 7.1262 (1.3294-38.1997), and 14.8340 (1.1577-190.0784),

respectively. Varied virulence factor mutations and virulence factor-related

gene mutations exist across different M. tuberculosis lineages. Mutations in the

espE, fadE29, and mbtI genes are risk factors that significantly affect the

treatment outcome of Lineage2 patients. This finding serves as a reference for

investigating the future evolutionary direction, transmissibility, drug

resistance, and pathogenicity of M. tuberculosis virulence factors in regions

with diverse lineages and frequent population movements.

DOI: 10.1080/21505594.2025.2552875

PMCID: PMC12445446

PMID: 40958404 [Indexed for MEDLINE]

**4. JMIR Mhealth Uhealth. 2025 Sep 16;13:e75424. doi: 10.2196/75424.**

Comparative Effectiveness of Digital Health Technologies in Tuberculosis

Treatment: Systematic Review and Network Meta-Analysis of Randomized Controlled

Trials.

Cheng Q(#)(1)(2), Chen P(#)(3), Dai R(#)(1), Jia Q(1), Bai X(1), Cao Q(2), Li

Q(1), Wu Y(1), Huang Y(1).

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**BACKGROUND:** Tuberculosis (TB) treatment remains a critical global health

challenge, as traditional standard of care (SoC) approaches face limitations in

accessibility and efficacy. While digital health technologies (DHTs) offer

promising solutions to address these gaps, limited evidence exists on their

comparative effectiveness.

**OBJECTIVE:** This study systematically evaluates and compares the impact of

diverse DHTs on improving TB treatment outcomes and adherence, aiming to

identify optimal strategies across different patient populations.

**METHODS:** A systematic search was conducted across PubMed, Cochrane Library,

Embase, and Web of Science from database inception through February 28, 2025,

with no language restrictions. Eligible studies included randomized controlled

trials comparing DHTs with SoC for TB treatment. The primary outcome was

treatment success, defined as completion or cure. A random-effects network

meta-analysis was performed, calculating odds ratios (OR) and 95% credibility

intervals (CrI) to assess treatment effects. Surface under the cumulative

ranking curve (SUCRA) values were used to rank intervention effectiveness. This

study is registered with PROSPERO (International Prospective Register of

Systematic Reviews; CRD42025601199).

**RESULTS:** From 2420 screened studies, 27 randomized controlled trials involving

23,283 patients and eight DHT interventions were included. The network

meta-analysis revealed that digital health platforms showed marginal

improvements in treatment success (OR=3.44; 95% CrI 0.95-11.67; SUCRA=0.913;

P=.05). Compared with SoC, video directly observed treatment (VDOT)

significantly improved treatment success (OR=2.39; 95% CrI 1.18-4.75;

SUCRA=0.848; P=.01). Medication event reminder monitors significantly enhanced

treatment adherence (OR=3.13; 95% CrI 1.55-7.05; SUCRA=0.891; P=.003).

**CONCLUSIONS:** Results underscore the significant potential of DHTs to improve TB

treatment management. VDOT emerged as the most effective intervention for

enhancing treatment success, while medication event reminder monitors

demonstrated efficacy in sustaining adherence. Digital health platforms showed

promise but require additional validation. Caution is warranted due to potential

heterogeneity across studies, which may affect generalizability. This research

offers actionable insights for stakeholders aiming to optimize TB management

through strategic DHT integration.

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Qingchun Li, Yifei Wu, Yinyan Huang. Originally published in JMIR mHealth and

uHealth (https://mhealth.jmir.org).

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**5. Inflamm Res. 2025 Sep 16;74(1):126. doi: 10.1007/s00011-025-02096-3.**

Tuberculosis-infected macrophage exosomal miR-125b-5p induces osteoporosis by

targeting IGF2 through the PI3K/AKT pathway.

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**BACKGROUND:** Tuberculosis (TB) is a major infectious disease that can lead to

systemic complications, including osteoporosis, particularly in

immunocompromised individuals. Exosomal miRNAs derived from TB-infected

macrophages have been implicated in various pathophysiological processes,

including bone metabolism. This study investigates how exosomal miR-125b-5p from

TB-infected macrophages contributes to osteoporosis by targeting insulin-like

growth factor 2 (IGF2) and modulating the PI3K/AKT signaling pathway.

**METHODS:** We analyzed NHANES data to compare bone mineral density in TB patients

and healthy controls. In vitro experiments were conducted with Mycobacterium

tuberculosis-infected peritoneal macrophages from C57BL/6 mice, isolating

exosomes and using Western blot, flow cytometry, and bioinformatics tools to

assess the role of miR-125b-5p in regulating osteogenic markers. In vivo studies

in mouse models were performed to evaluate the impact of exosomal miR-125b-5p on

bone density and structure.

**RESULTS:** Exosomes from TB-infected macrophages were found to contain elevated

levels of miR-125b-5p, which targeted IGF2 and inhibited the PI3K/AKT pathway,

leading to impaired osteoblast function and reduced bone formation. Knockdown of

miR-125b-5p partially restored osteogenic markers and bone density. Furthermore,

IGF2 silencing exacerbated bone loss, confirming the critical role of IGF2 in

TB-induced osteoporosis.

**CONCLUSION:** This study demonstrates that miR-125b-5p from TB-infected

macrophages promotes osteoporosis by disrupting the IGF2/PI3K/AKT signaling

axis. Targeting this pathway could provide a potential therapeutic strategy for

managing TB-induced osteoporosis. Further clinical studies are necessary to

validate these findings and explore additional therapeutic options.

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PMID: 40956311 [Indexed for MEDLINE]

**6. J Infect Public Health. 2025 Sep 5;18(12):102952. doi:**

**10.1016/j.jiph.2025.102952. Online ahead of print.**

Clinical characteristics analysis of anti-interferon-γ autoantibodies-associated

adult-onset immunodeficiency with mycobacterium tuberculosis infection.

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Liang X(1), Chen N(1), Ning Y(1), Pang H(1), Zhang Z(1), Nong Y(1), Yan P(2), He

Z(3).

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**BACKGROUND:** Anti-interferon-γ autoantibodies (AIGAs) syndrome is a rare

adult-onset immunodeficiency (AOID) syndrome with multiple opportunistic

infections. However, its clinical characteristics in Mycobacterium tuberculosis

(MTB) infection remain unclear.

**METHODS:** A prospective cohort study of adult patients with opportunistic

infections was conducted from January 2021 to January 2025 in Guangxi, southern

China. MTB-infected patients were divided into AIGAs-positive and AIGAs-negative

groups, and their clinical and laboratory data were compared. Additionally, the

AIGAs-positive group was divided into subgroups (with or without nontuberculous

mycobacteria (NTM) or Talaromyces marneffei (TM) co-infection) for detailed

analysis.

**RESULTS:** Among over 400 patients recruited, 48 of the 86 with MTB infection were

AIGAs-positive (Group 1), and 38 were AIGAs-negative (Group 2). Group 1 patients

commonly show involvement of the lungs, lymph nodes, bones, and skin, with often

multi-organ involvement. Disseminated infections are more prevalent in Group 1,

often accompanied by TM/NTM infections. They also show elevated white blood cell

count, neutrophils, monocytes, C-reactive protein, erythrocyte sedimentation

rate, globulin, and immunoglobulin G levels (P < 0.05). During an average

follow-up of 19 months, 50.00 % of patients experienced acute exacerbations, of

which 82.61 % were caused by new pathogen infections. Multivariable Cox

regression analysis indicated that splenic involvement, elevated serum G test

levels, and NTM infection were risk factors for disease progression (P < 0.05).

The TM/NTM co-infected subgroup had higher acute exacerbation rates, AIGAs

titers, inflammatory/immune markers, and more organ involvement.

**CONCLUSIONS:** Patients with AIGAs-related AOID and MTB infection had high

infection markers, immune issues, and multi-organ involvement, which worsened

with TM/NTM co-infection.

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DOI: 10.1016/j.jiph.2025.102952

PMID: 40972369

**7. Front Microbiol. 2025 Sep 2;16:1663069. doi: 10.3389/fmicb.2025.1663069.**

**eCollection 2025.**

Drug selection based on pan-genomics genetic features of Mycobacterium

tuberculosis.

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Tuberculosis, caused by Mycobacterium tuberculosis, is a severe and persistent

global public health issue, particularly exacerbated by the emergence of

multidrug-resistant and extensively drug-resistant strains. This study employed

pan-genomic approaches to analyze different strains with various resistance

profiles, examining the diversity of bacterial genetic evolution in relation to

mutations in resistance-related genes. The findings indicate that

resistance-related genes are mostly core genes (94%), with a preference for base

mutations closely associated with nonsynonymous mutations at resistance sites.

Interestingly, while the majority of drugs induce positive selection in target

genes, the tlyA gene under the influence of amikacin (AMI) undergoes passive

selection. Cluster analysis of target genes suggests consistency between SNP

clusters and drug-resistant clusters, revealing a strong correlation between

bacterial evolutionary branches and resistance profiles. Consequently, based on

pan-genome evolutionary characteristics, we identified the drug-resistant

mutation pattern (DRMP) that can serve as a molecular fingerprint and indicator

for drug sensitivity, aiding in the assessment and guidance of drug selection

for treating different strains and the formulation of individualized treatment

plans. This research not only enhances our understanding of the mechanisms of

drug resistance in M. tuberculosis but also offers new perspectives for the

development of new drugs, which is crucial for global tuberculosis control.

Copyright © 2025 Sun, Xu, Shi, Wang and Li.

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PMCID: PMC12436377

PMID: 40964672

**8. Front Cell Infect Microbiol. 2025 Sep 2;15:1651920. doi:**

**10.3389/fcimb.2025.1651920. eCollection 2025.**

Epidemiological features of tuberculosis infection in a high-altitude

population: a population-based, cross-sectional survey in Tibet, China.

Wang J(#)(1), Pei S(#)(2)(3), Yang G(1), Qucuo N(1), Song Q(1), Liu X(4)(5), Li

X(4)(5), Chen W(4)(5), Li T(4)(5), Liu E(4)(5), Ou X(4)(5), Chen H(4)(5), Ni

N(4)(5), Ren J(4)(5), Zhao Y(4)(5), Gong H(1).

**Jian Wang, Shaojun Pei, Guofeng Yang, Nima Qucuo, Qifei Song, Xiaoqiu Liu, Xue Li, Wei Chen, Tao Li, Eryong Liu, Xichao Ou, Hui Chen, Ni Ni, Jingjuan Ren, Yanlin Zhao\*, Hongqiang Gong\***

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**BACKGROUND:** Targeted strategies for marginalized populations, including

high-altitude communities, are crucial for TB elimination. This study assessed

TB infection (TBI) prevalence across altitudinal gradients and evaluated

altitude-dependent risk factors in Tibet, China.

**METHODS:** A cross-sectional survey by multistage stratified random cluster

sampling was conducted using ESAT6-CFP10 skin test (C-TST), symptom screening,

chest X-rays, and bacteriological tests. The influencing factors of C-TST

positivity were analyzed via generalized linear mixed models (GLMMs) and Boruta

algorithm feature ranking. The TBI prevalence was estimated using

WHO-recommended methods. Causal mediation analysis was performed to explore

mediating variables contributing to association between altitude and TBI

prevalence.

**RESULTS:** The estimated TBI prevalence in Tibet was 20.7% (95% CI 14.3%-33.0%).

Residential altitude was the strongest predictor of C-TST positivity (aOR=0.53,

p<0.001). The interaction analyses revealed significant modification effects of

both smoking status (interaction p=0.0065) and BCG vaccination (interaction

p=0.028) on the altitude-C-TST positivity association. Mediation analysis

indicated that the observed inverse relationship between study site altitude and

crude TBI prevalence was mediated by per capita land space (IE= -6.29e-05,

p=0.04). The prevalence of TBI in very high-altitude (VHA) areas was 12.8%,

approximately one-third of that in high-altitude (HA) areas (35.0%). Stratified

analyses revealed distinct risk profiles - occupational exposures predominated

in HA regions, whereas physiological factors (age, BMI, smoking) drove

positivity in VHA areas.

**CONCLUSION:** Our results suggest that TB infection is significantly associated

with altitude, necessitating accelerated research into plateau-specific disease

mechanisms and the development of targeted public health strategies tailored to

local socio-medical conditions. This integrated biological and socio-economic

approach is essential to overcome the compounded vulnerabilities of

high-altitude populations and ensure that China equitably achieves its goal of

eliminating TB.

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Ni, Ren, Zhao and Gong.

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**9. Front Cell Infect Microbiol. 2025 Sep 2;15:1592296. doi:**

**10.3389/fcimb.2025.1592296. eCollection 2025.**

Depletion of Mycobacterium tuberculosis transmembrane protein Rv3737 reduces

pathogen survival and induces M1 macrophage polarization against tuberculosis.

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**OBJECTIVES:** Mycobacterium tuberculosis (Mtb) modulates macrophage polarization

to evade host immunity and enhance intracellular survival. Rv3737, a probable

conserved transmembrane protein in Mtb, has an unclear biological function. This

study investigates the role of Rv3737 in regulating macrophage polarization and

Mtb survival within host cells.

**METHODS:** The structure of Rv3737 was predicted using bioinformatics tools.

Macrophage polarization markers were assessed by real-time PCR for

M1/M2-associated cytokines, and flow cytometry for CD86+/CD206+ expression. RNA

sequencing, along with KEGG and GO analyses, was used to explore underlying

regulatory pathways. Western blotting evaluated the phosphorylation status of

NF-κB (P65, IκB) and MAPK (ERK, P38, JNK) signaling components. Colony-forming

units (CFUs) and inducible nitric oxide synthase (iNOS) levels were examined in

H37RvΔRv3737-infected macrophages pretreated with specific inhibitors (JSH-23,

U0126-EtOH, SB203580, SP600125).

**RESULTS:** Rv3737 is predicted to contain 10 transmembrane segments enriched in

aliphatic amino acids. Deletion of Rv3737 in H37Rv (H37RvΔRv3737) led to

upregulation of M1 markers (TNF-α, IL-1β, IL-6, iNOS, MCP-1, CD86) and

downregulation of M2 markers (Arg-1, IL-10, TGF-β, CD206). Conversely,

overexpression of Rv3737 (MS\_Rv3737) promoted M2 polarization. RNA sequencing

indicated NF-κB pathway activation in macrophages infected with H37RvΔRv3737,

along with increased phosphorylation of P65, IκB, ERK, and P38. Inhibition of

NF-κB (with JSH-23) and P38 MAPK (with SB203580) reduced iNOS levels and

partially restored Mtb survival, indicating that Rv3737 deletion enhances the

macrophage antimicrobial response.

**CONCLUSIONS:** Rv3737 suppresses M1 macrophage polarization to promote Mtb

survival. Its deletion enhances host antimicrobial activity by activating NF-κB

and MAPK signaling pathways. Targeting Rv3737 may represent a novel strategy for

tuberculosis therapy.

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**10. Front Pediatr. 2025 Sep 2;13:1616608. doi: 10.3389/fped.2025.1616608.**

**eCollection 2025.**

Clinical characteristics leading to misdiagnosis of abdominal tuberculosis in

children: a systematic review and meta-analysis.

Siddiqui MJ(1), Karmacharya A(2), Wan X(1), Zhu Y(1), Wan C(1), Luo S(1).

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**INTRODUCTION:** Abdominal tuberculosis (ATB) in children is an uncommon form of

extrapulmonary tuberculosis that often presents with non-specific symptoms.

These features frequently overlap with other abdominal conditions, increasing

the risk of misdiagnosis or delay in diagnosis. Although individual case series

have reported such diagnostic challenges, a pooled analysis of clinical

characteristics associated with misdiagnosis has not been previously conducted.

This study aimed to identify the clinical characteristics that contribute to the

misdiagnosis of ATB in children through a systematic review and meta-analysis.

**METHODS:** We conducted a systematic review and meta-analysis following PRISMA

2020 guidelines. A comprehensive literature search was carried out using PubMed,

Web of Science, and Google Scholar for studies published between 1900 and 2024.

Eligible studies were pediatric case series that included confirmed ATB cases

and provided information on initial misdiagnosis or diagnostic delays. Patients

who were misdiagnosed or delayed in diagnosis were categorized under the

"misdiagnosed" group. Data were extracted on presenting clinical features, and

odds ratios (ORs) with 95% confidence intervals (CIs) were calculated using

Review Manager (RevMan 5.4). Heterogeneity was assessed using the I 2 statistic,

and publication bias was evaluated using funnel plots.

**RESULT:** Seven studies met the inclusion criteria, comprising a total of 60

pediatric ATB cases. Among them, 24 were classified as misdiagnosed and 36 were

diagnosed without delay. No clinical characteristics were statistically

significantly associated with misdiagnosis. Although ascites and abdominal

distension were more frequently observed in misdiagnosed cases, overall

heterogeneity was low across most outcomes.

**CONCLUSIONS:** Clinical characteristics alone are not reliable indicators for

diagnosing ATB. Ascites and abdominal distension may increase the risk of

misdiagnosis, underscoring the importance of early suspicion and timely

diagnostic evaluation in TB-endemic regions.

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**eCollection 2025.**

Integrative Medicine Treatment Strategy for Tuberculosis of the Breast Combined

with Granulomatous Mastitis: A Case Report.

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**BACKGROUND:** Breast tuberculosis (BTB) is a clinically rare breast disease, and

cases of BTB combined with granulomatous mastitis are even rarer. This type of

disease is straightforward to misdiagnose or overlook during clinical diagnosis,

thereby delaying treatment.

**METHODS:** This case report describes a rare case of granulomatous mastitis

complicated by breast tuberculosis in an elderly female patient admitted to the

Breast Surgery Department of Beijing Traditional Chinese Medicine Hospital

affiliated with Capital Medical University. Through a retrospective analysis of

the integrated traditional Chinese and Western medicine treatment process, this

study compares the patient's condition after three follow-up visits following

the implementation of a traditional Chinese medicine (TCM) treatment regimen, as

well as the six-month post-operative follow-up outcomes. Additionally, by

referencing relevant prior literature, this study analyzes and summarizes the

current status of diagnostic and therapeutic research on BTB.

**RESULTS:** In this case, granulomatous mastitis was the first symptom in the early

stage, and traditional Chinese medicine soup was taken internally as well as

poultices applied externally, with a relatively obvious clinical effect. The

diagnosis was confirmed by ultrasound, CT, tissue biopsy, Mycobacterium

tuberculosis acid-fast stained smear, and other tests. The patient was treated

surgically, and the diagnosis was finally confirmed by molecular testing and

anti-tuberculosis treatment in a specialized hospital. The patient's condition

was stable on follow-up, and the prognosis was good.

**CONCLUSION:** Early diagnosis and differentiation of breast tuberculosis is

difficult, and it is very easy to misdiagnose and delay the disease. In the

early stage of the disease, traditional Chinese medicine can be used in

combination, and in the stable stage of the disease, a reasonable choice of

surgical treatment can shorten the course of the disease. This also reveals the

important value of integrated Chinese and Western medicine treatment in the

clinical treatment of this type of patient.

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**eCollection 2025.**

Analysis of the trends and predictions of tuberculosis burden in China from 1990

to 2021 based on the GBD database.

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Hospital, Nanjing Medical University, Nanjing, Jiangsu, China.

**BACKGROUND:** Tuberculosis (TB) is a major public health concern in China,

exhibiting unique epidemiological traits and changing patterns. This study aims

to assess the burden of TB in China from 1990 to 2021 and forecast the future.

**METHODS:** Data on TB burden indicators in China from 1990 to 2021 were collected

from the Global Burden of Disease (GBD) database. The Joinpoint Regression (JPR)

model was employed to assess trends in disease burden, with calculations of the

annual percentage change (APC) and average annual percentage change (AAPC). The

Auto-Regressive Integrated Moving Average (ARIMA) model and the Bayesian

Age-Period-Cohort (BAPC) model were utilized to forecast trends in the

age-standardized incidence rate (ASIR) and age-standardized mortality rate

(ASMR) over the next 15 years.

**RESULTS:** From 1990 to 2021, the incidence, mortality, and disability-adjusted

life years (DALYs) of TB in China showed a declining trend, decreasing by 47.17,

78.14, and 81.25%, respectively, while the absolute number of TB cases increased

by 32.96%. In 2021, the ASIR, age-standardized prevalence rate (ASPR), ASMR, and

age-standardized DALY rate (ASDR) of TB in China were 36.28 per 100,000 (95% CI:

32.63-40.47), 30,557.45 per 100,000 (95% CI: 27,692.69-33,531.31), 1.91 per

100,000 (95% CI: 1.51-2.51), and 76.22 per 100,000 (95% CI: 62.59-94.45),

respectively, reflecting reductions of 66.60, 2.83, 90.72, and 89.53% from 1990

levels. The burden of TB exhibited disparities across gender and age groups,

with older males experiencing a higher burden than older females, and children

under 5 years old demonstrating the highest incidence rate among all age groups.

The JPR regression model indicated a significant decline in ASIR (AAPC = -3.49;

95% CI: -3.49 to -3.37; p < 0.001), ASMR (AAPC = -7.42; 95% CI: -7.78 to -7.07;

p < 0.001), and ASDR (AAPC = -7.01; 95% CI: -7.22 to -6.80; p < 0.001) from 1990

to 2021, whereas ASPR remained relatively stable (AAPC = -0.15; 95% CI: -0.37 to

-0.006; p = 0.17). Predictions from both the ARIMA and BAPC models were

consistent, suggesting a continued decline in ASIR and ASMR through 2036, with

the burden remaining higher among males than females.

**CONCLUSION:** From 1990 to 2021, TB incidence, mortality, and DALYs in China

demonstrated an overall downward trend, with similar declines observed in both

male and female populations. Projections indicate that ASIR and ASMR will

continue to decline from 2022 to 2036. These findings provide valuable insights

for the development of public health strategies aimed at reducing the TB burden

in China.

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**10.3389/fcimb.2025.1635486. eCollection 2025.**

Predicting tuberculosis progression in school contacts: novel host biomarkers

for early risk assessment.

Lu P(#)(1)(2), Tian M(#)(3), Lian Y(3), Wang R(4), Ding X(1), Pan J(1), Ding

H(1), Lu W(1), Zhu L(1), Liu Q(1).

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The low positive predictive value of tuberculin skin tests and interferon-γ

release assays often results in unnecessary prophylaxis. This study aimed to

identify antigen-specific biomarkers with high accuracy for predicting

progression to active tuberculosis (ATB). QuantiFERON supernatants from a school

tuberculosis outbreak cohort were analyzed, tracking students over two years to

identify ATB cases. We assessed 67 cytokines using the Luminex Multiplex Array

kit and applied LASSO and multivariate logistic regression to select predictors.

A nomogram was developed from the coefficients of top predictors. Model

performance was evaluated by AUC, C-index, and AIC. The levels of FGFbasic,

GM-CSF, MPIF-1/CCL23, as well as the combinations of ratios of FGFbasic/GM-CSF

and FGFbasic/MPIF-1/CCL23 were significantly associated with the risk of ATB.

AUC values for the prediction models based on individual cytokines ranged from

0.607 to 0.713, notably lower than those of the fixed models based on the

logistic regression (0.932) and LASSO regression (0.939). The LASSO regression

model exhibited the best predictive performance, with a higher sensitivity

(0.858 vs. 0.818) and specificity (0.949 vs.0.923), lower AIC (36.323 vs.

38.232), and equivalent C-index (0.939) compared to the traditional logistic

regression model. The biomarkers identified in this study offer valuable

insights for developing a more precise tool to identify individuals at high risk

for rapid progression to ATB disease, enabling targeted interventions. The

combination of multiple immune indicators shows significant promise in improving

diagnostic accuracy.

Copyright © 2025 Lu, Tian, Lian, Wang, Ding, Pan, Ding, Lu, Zhu and Liu.

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**14. Int J Mycobacteriol. 2025 Jul 1;14(3):261-267. doi: 10.4103/ijmy.ijmy\_106\_25.**

**Epub 2025 Sep 15.**

Risk Factors Analysis of Nontuberculous Mycobacterial Pulmonary Infection in

Hospitalized Patients in Yulin, China.

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University, Nanning, China.

**BACKGROUND:** Nontuberculous mycobacterial lung disease (NTM-LD) is an

increasingly serious chronic lung infection, especially in people with low

immune function.

**METHODS:** This study collected clinical inpatient data from January 2020 to

December 2024 at the First People's Hospital of Yulin, aiming to evaluate the

risk factors for nontuberculous mycobacterial (NTM) infection.

**RESULTS:** A study involving 199 patients found that 143 (71.86%) were infected

with Mycobacterium tuberculosis (MTB), whereas 56 (28.14%) were infected with

NTM. The most common NTM species were Mycobacteroides abscessus, accounting for

53.57% (30/56), followed by Mycobacterium intracellulare at 10.71% (6/56). The

NTM separation department mainly focuses on respiratory medicine, accounting for

80.36% (45/56) of cases. The median age of the patients is 60 years. The risk

factors associated with NTM infection include age (45-65), autoimmune diseases,

chronic obstructive pulmonary disease, bronchiectasis, concomitant pulmonary

aspergillosis, and immunosuppressant use. Among these, bronchiectasis is an

independent risk factor for infection (odds ratio [OR]: 7.357, 95% confidence

interval [CI] 3.080-17.574). In addition, expectoration is a significant risk

factor for rapidly growing mycobacteria (RGM) infection in NTM-LD (OR: 4.278,

95% CI 1.314-13.928).

**CONCLUSIONS:** Over one-third of patients suspected of having tuberculosis are

actually infected with NTM, and those with bronchiectasis have a higher risk of

NTM infection. The most common NTM-LD strain is M. abscessus, which is

clinically associated with expectoration as a risk factor for RGM infection.

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**eCollection 2025.**

Computed tomography in the diagnosis of bilateral renal tuberculosis: diagnostic

value, limitations, and future directions.

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As equipment improves and technology advances, the application of Computed

Tomography (CT) in clinical disease diagnosis has become increasingly

widespread, particularly demonstrating significant advantages in diagnosing

solid lesions. However, CT scans still face challenges, including insufficient

sensitivity and an inability to assess renal function when diagnosing bilateral

renal tuberculosis (BRTB). By reviewing relevant high-quality literature, we

compared the sensitivity, specificity, advantages, and limitations of USG, KUB,

IVU, MRI, PET-CT, and CT in the diagnosis of BRTB. CT offers higher clinical

detection rates and reduces the economic burden on patients compared to other

imaging methods, making it the preferred modality for imaging in patients with

BRTB. AI-assisted diagnosis and the integration of CT with PET may represent

promising future directions for CT imaging.

© 2025 Tian, Zhu, Zhang, Yu and Fu.

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**eCollection 2025.**

Hepatic tuberculosis induced by rituximab treatment for C1q nephropathy with

minimal change disease: a case report.

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**BACKGROUND:** Rituximab is widely used for autoimmune nephropathy. It depletes B

cells, potentially increasing infection risk. Tuberculosis is a rare but severe

complication of rituximab treatment. We report a case of liver tuberculosis in a

patient with C1q nephropathy with Minimal Change Disease (MCD) treated with

rituximab.

**CASE PRESENTATION:** In March 2023, an 81-year-old male patient was admitted to

Shaoxing Second Hospital with a 2-month history of bilateral lower extremity

edema. He was diagnosed with C1q nephropathy with MCD through renal biopsy.

After treatment with 2 g rituximab, his proteinuria was relieved. In October

2024, due to B-cell rebound, 0.5 g of rituximab was added. In December 2023, the

patient visited our hospital due to a 7-day fever. Abdominal ultrasound revealed

a non-uniform hypoechoic liver mass suspected to be an abscess. Empirical

antibiotic treatment was ineffective and the condition worsened. A liver biopsy

was immediately performed, and the pathology showed characteristic granulomatous

inflammation and patchy coagulative necrosis. The patient was ultimately

diagnosed with hepatic tuberculosis and received a 1-year anti-tuberculosis

treatment, including rifampicin 450 mg qd, isoniazid 300 mg qd, pyrazinamide

1,500 mg qd, and ethambutol 1,000 mg qd. The patient's temperature returned to

normal and abdominal pain was relieved on the third day of treatment. Two months

later, a follow-up ultrasound showed a reduction in the left lobe liver mass,

and an 8-month CT scan showed complete disappearance of the mass. The patient is

currently under follow-up.

**CONCLUSION:** Rituximab may be an effective treatment option for C1q nephropathy

with MCD. Although the risk of infection with rituximab is relatively low, rare

infections such as tuberculosis still need to be vigilant, especially in elderly

or immunocompromised patients. Additionally, we recommend routine screening for

latent tuberculosis in elderly patients with nephropathy and

hypogammaglobulinemia before rituximab treatment.

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**2025 Aug 28.**

Development and validation of a diagnostic radiomics model for the differential

diagnosis of coexistent tuberculosis and lung cancer versus isolated lung

cancer.

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**BACKGROUND:** The coexistence of pulmonary tuberculosis with lung cancer (CTBLC)

and isolated lung cancer (ILC) often show similar appearances on computed

tomography (CT) images, making accurate diagnosis difficult and increasing the

risk of misdiagnosis. Despite the need for different treatment strategies for

CTBLC and ILC, research on predicting CTBLC using machine learning remains

scarce. Radiomics-based machine learning algorithms have demonstrated the

potential to improve diagnostic accuracy by identifying complex imaging patterns

through high-dimensional features such as shape, size, intensity, and subtle

textures beyond human perception. This study aims to develop and validate a

non-invasive combined model, integrating radiomics signatures with

clinicoradiological features, to differentiate CTBLC from ILC using CT imaging.

**METHODS**: A retrospective study was conducted on 171 patients (71 with CTBLC and

100 with ILC). The diagnosis of ILC or CTBLC was confirmed using multiple

diagnostic techniques including CT imaging, sputum smear analysis, blood tests,

and pathological examination following biopsy or surgical procedures.

Adenocarcinoma, squamous cell carcinoma, and small cell lung cancer types were

included for ILC. CTBLC lesions were identified in the same lobe and segment as

cancer. Two experienced radiologists manually segmented the regions of interest

(ROI) on CT images. Three-dimensional (3D) radiomics features were extracted,

out of which six important features were selected for the radiomics model. We

evaluated the performance of combined model with six radiomics signatures and

seven clinicoradiological features using accuracy (ACC), area under the curve

(AUC), among others. We also compared its effectiveness to that of

clinicoradiological model as well as radiomics model.

**RESULTS:** The combined model showed better efficacy (AUC =0.901, ACC =0.865,

sensitivity =0.900, and specificity =0.844) than the radiomics model (AUC

=0.892, ACC =0.827) and significantly outperformed the clinicoradiological model

(AUC =0.710, ACC =0.596). Among the clinicoradiological features, pleural

thickening, lymph node enlargement, and bronchial stenosis showed significant

differences between CTBLC and ILC groups (P<0.05), which contributed to the

model's performance. A radiomics nomogram integrating the Rad-score with

clinicoradiological features was also developed, enhancing the radiomics model's

utility for the clinical prediction of CTBLC.

**CONCLUSIONS:** The proposed CT-based combined model effectively predicts CTBLC and

distinguishes it from ILC, proving a non-invasive, efficient auxiliary tool for

clinical diagnosis of CTBLC.

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**2025 Aug 26.**

The diagnostic value of CD101 in smear-negative pulmonary tuberculosis.

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**BACKGROUND:** Unlike smear-positive tuberculosis (TB) which is more easily

diagnosed due to the presence of Mycobacterium tuberculosis (MTB) in sputum,

smear-negative pulmonary tuberculosis (SN-TB) poses a diagnostic challenge that

can lead to delayed treatment hence new molecular diagnostic markers are

urgently needed. The aim of this study was to analyze the expression of CD101 in

peripheral blood mononuclear cells (PBMCs), T cells and natural killer (NK)

cells of patients with SN-TB through a case-control study and to assess the

value of CD101 alone or combined with other cytokines in the auxiliary diagnosis

of SN-TB.

**METHODS:** Sixty-three newly treated patients with TB and negative smear results

diagnosis by clinicians were included as the SN-TB group, while 59 healthy

individuals [healthy control (HC)] were included as the control group. The

expression of CD101 in PBMCs of the two groups was detected via real-time

quantitative polymerase chain reaction (RT-qPCR). The expression of CD101 on T

cells and NK cells, as well as the expression of T helper (Th) 1/2/17-related

cytokines was detected by flow cytometry. Spearman analysis was used to analyze

the correlation between CD101 expression, cytokines and clinical indicators in

patients with SN-TB. Receiver operating characteristic (ROC) curve analysis was

used to analyze the sensitivity and specificity of CD101 alone or in combination

with other cytokines in diagnosing SN-TB.

**RESULTS:** Compared with the control group, the experimental group showed high

CD101 expression in PBMCs and CD4+ T cells but not in CD8+ T cells or NK cells.

Th1/Th2-related cytokines interleukin-2 (IL-2), IL-4, IL-6, IL-10, tumor

necrosis factor-α (TNF-α) and interferon-γ (IFN-γ) were highly expressed in

patients with SN-TB, but there was no significant difference in the expression

of the Th17-related cytokine (IL-17A). The expression of CD101 on CD4+ T cells

in patients with SN-TB was positively correlated with cytokines IL-2 and IFN-γ

and the clinical indicators of ESR and CRP. CD101 on CD4+ T cells could well

distinguish patients with SN-TB from HC, with a sensitivity of 71.43%, a

specificity of 71.19% and an area under the curve (AUC) of 0.7604. The

sensitivity of CD101+CD4+ (%) combined with IL-2 was 73.25%, the specificity was

68.25% and the AUC was 0.7893. The sensitivity of CD101+CD4+ (%) combined with

IFN-γ was 72.88%, the specificity was 66.67% and the AUC was 0.7678. The

sensitivity of CD101+CD4+ (%) combined with IFN-γ and IL-2 was 74.58%, the

specificity was 74.60% and the AUC was 0.7899.

**CONCLUSIONS:** The expression of CD101 on CD4+ T cells could distinguish patients

with SN-TB from healthy individuals and was correlated with key TB infection

cytokines, including IL-2 and IFN-γ, as well as with ESR and CRP. CD101

demonstrated good diagnostic efficacy in combination with cytokines. It might

thus be an indicator for laboratory-assisted diagnosis of SN-TB.

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**2025 Aug 28.**

The role of the pleural fluid lactate dehydrogenase/adenosine deaminase ratio in

differentiating between tuberculosis pleural effusion and parapneumonic

effusion: a retrospective cohort study and meta-analysis.

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**BACKGROUND:** In regions with a high prevalence of tuberculosis, it is crucial to

accurately differentiate between tuberculosis pleural effusion (TPE) and

parapneumonic effusion (PPE). The current study aimed to evaluate the potential

role of the pleural fluid lactate dehydrogenase (LDH)/adenosine deaminase (ADA)

ratio in differentiating between TPE and PPE.

**METHODS:** In the first section, the pleural fluid LDH/ADA ratio was compared

between 45 patients with TPE and 81 patients with PPE within our study

population, and its diagnostic efficacy was assessed. In the second section, we

conducted a meta-analysis incorporating six previous publications and the

current study.

**RESULTS:** In our study population, a cut-off value of 18.63 for the pleural fluid

LDH/ADA ratio was established for diagnostic performance analysis. The area

under the curve (AUC) to discriminate between TPE and PPE was 0.960 [95%

confidence interval (CI): 0.902 to 0.989]. As for sensitivity, specificity,

positive likelihood ratio (PLR), negative likelihood ratio (NLR), positive

predictive value and negative predictive value, they were 94.44% (95% CI: 81.3%

to 99.3%), 84.85% (95% CI: 73.9% to 92.5%), 6.23 (95% CI: 3.50 to 11.09), 0.065

(95% CI: 0.017 to 0.25), 77.3% (95% CI: 65.6% to 85.8%), and 96.6% (95% CI:

87.9% to 99.1%), respectively. The diagnostic accuracy of the pleural fluid

LDH/ADA ratio was further tested and confirmed in the subsequent meta-analysis.

The meta-analysis demonstrated that the pooled sensitivity and specificity were

90% (95% CI: 82% to 94%) and 91% (95% CI: 84% to 95%), respectively.

**CONCLUSIONS:** The current study suggests that the pleural fluid LDH/ADA ratio is

a useful marker for distinguishing TPE from PPE.

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Mycobacterium tuberculosis, Mycobacterium kansasii and Rhodococcus equi induce

macrophage necroptosis in the presence of a caspase inhibitor acting on a

non-canonical target(s).

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Macrophages are the predominant cell type infected by Mycobacterium tuberculosis

(Mtb) in tuberculosis (TB). Death of Mtb-infected macrophages promotes tissue

pathology and releases Mtb to infect other cells, suggesting that inhibiting the

death of Mtb-infected macrophages could be an adjunctive treatment of TB.

Prospects for such an intervention depend on identifying the molecular pathways

leading to cell death. We previously reported that the death of Mtb-infected

mouse macrophages in vitro depends on type I interferon (IFN) and that the

ensuing upregulation of cis -aconitate decarboxylase (ACOD1; IRG1) contributes

to cell death by exacerbating Mtb-induced lysosomal membrane permeabilization.

Here we report that death of Mtb-infected primary mouse macrophages in vitro

became necroptotic and die faster in the presence of

benzyloxycarbonyl-Val-Ala-Asp-fluoromethylketone (z-VAD) acting on a target

other than caspase-8. Macrophages infected with Mycobacterium kansasii and

Rhodococcus equi likewise underwent z-VAD-dependent necroptosis. In C57BL/6

mice, which are relatively TB-resistant, we saw no impact of MLKL deficiency on

bacterial burden or pulmonary pathology. In contrast, in Sp140 -/- mice on the

C57BL/6 background, which express high levels of type I IFN after Mtb infection

and develop necrotic pulmonary lesions, MLKL-deficiency reduced bacterial burden

and pathology after high-dose infection. This report illustrates that off-target

action(s) of a caspase-8 inhibitor can switch the cell death pathway to

necroptosis in macrophages infected with various Gram-positive pathogens. In

turn, this opens the possibility that pathophysiologic circumstances may lead to

inhibition of the same target(s) that z-VAD inhibited in our studies. That may

be what allows MLKL to exacerbate tuberculosis in mice that are prone to

formation of necrotic lesions.

**AUTHOR SUMMARY:** Tuberculosis (TB), caused by the bacillus Mycobacterium

tuberculosis (Mtb), led to about 1.3 million deaths in 2023. The rapid emergence

of drug resistance and slow pace of new drug development prompt attention to

adjunctive host-directed therapies, an approach that relies on a thorough and

detailed understanding of host-Mtb interactions. Mtb infection of macrophages

can kill them, promoting tissue pathology and releasing of Mtb to infect other

cells. Here we find that a pan-caspase inhibitor z-VAD hastened the death of

Mtb-infected macrophages and converted the mode of cell death to

RIPK1-RIPK3-MLKL-dependent necroptosis. However, the functional target(s) of

z-VAD-FMK and the activation mechanism of RIPK3 differ from the canonical

pathways. The pan-caspase inhibitor also promoted rapid, necroptotic death of

macrophages infected with Mycobacterium kansasii and Rhodococcus equi . We

further found that MLKL-deficiency in Sp140 -/- mice on the C57BL/6 background

resulted in less weight loss, lower Mtb burdens and mitigation of lung pathology

after high-dose Mtb infection. Our findings suggest that necroptosis can

contribute to TB pathogenesis in some circumstances. Further identification of

the death pathway-switching mechanism could deepen our understanding of host-Mtb

interactions and aid in the design of adjunctive host-directed therapies.

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