REVIEW

Revolutionizing tuberculosis treatment: Breakthroughs, challenges, and hope on the horizon

Martin Kufa[a,b], Vladimir Finger[a,b], Ondrej Kovar[a,b],
Ondrej Soukup[b], Carilyn Torruellas[c], Jaroslav Roh[a],
Jan Korabecny[b,*]

[a]Faculty of Pharmacy in Hradec Kralové, Charles University, Hradec Kralove 50003, Czech Republic
[b]Biomedical Research Center, University Hospital Hradec Kralove, Hradec Kralove 50003, Czech Republic
[c]U.S. Army CCDC Chemical Biological Center, MD 21010-5424, USA

Abstract   Tuberculosis (TB), an infectious disease caused by the bacterium *Mycobacterium tuberculosis* (*Mtb*), was responsible for the deaths of approximately 1.3 million people in 2022. In addition, 7.5 million new cases of TB have been reported. Present-day treatments require a daily dosing of a multiple-drug regimen for a minimum of six-month, but poor adherence and other factors often lead to treatment failure. Consequently, drug-resistant TB strains have become a growing concern, leading to more complex and expensive treatments. Promising drugs such as bedaquiline, delamanid, and pretomanid have been recently released, and 19 drug candidates are currently at different phases of clinical trials, addressing the problem of drug-resistant TB. Notwithstanding recent advances, the development of effective and safe drugs with novel mechanisms of action remains a challenge due to the unique nature of *Mtb*. Despite the persistent need for new treatments, TB research remains underfunded, highlighting the importance of collaborations between academia and the private sector in the advancement of anti-TB drug development. This review provides a perspective on the dynamic landscape of anti-TB drug discovery in recent years, offering hope for a more effective approach to combat this persistent global health threat.

*Corresponding author.
    E-mail address: jan.korabecny@fnhk.cz (Jan Korabecny).

1. Introduction

Tuberculosis (TB) is a transmissible infectious disease caused by the intracellular bacteria *Mycobacterium tuberculosis* (*Mtb*)[1]. TB stands as one of the principal causes of mortality in low and middle-income countries[2]. TB is primarily a pulmonary infection that is able to disseminate to other parts of the body. Although it is transmitted *via* airborne particles released by active TB patients, *Mtb* can also survive in the host for a long time in an asymptomatic form known as latent TB infection (LTBI). Those with LTBI are not infectious, but the LTBI can transform into active TB when the immunity system is compromised by other diseases such as human immunodeficiency virus (HIV)[3]. In 2022, 7.5 million newly diagnosed TB infection and 1.3 million deaths were recorded. Remarkably, 410,000 patients developed drug-resistant TB (DR-TB)[1], while LTBI prevailed in 25% of the World's population[3].

If inadequately treated, the active form of TB is often fatal, reaching a mortality rate up to 50%[4]. The standard treatment regimens for drug-susceptible TB (DS-TB) is driven by module 4 of the World's Health Organization (WHO) guidelines released in 2022, recommending daily dosing of the first-line drug for six months. During the first two months, isoniazid (INH), rifampicin (RIF), ethambutol (EMB) and pyrazinamide (PZA) are administered, followed by four months of INH and RIF therapy. This drug combination is successful in 85% of cases[5]. The failure of DS-TB treatment is caused by many factors: poor patient adherence, alcohol consumption, smoking, and co-infections. On the other hand, patients under 65 years of age, and females favor the success of TB treatment[6]. *Mtb* can quickly develop resistance against anti-TB drugs. If not cured adequately, DS-TB strains can convert into DR-TB. WHO categorizes these strains into five groups based on their resistance patterns: INH resistant TB (IR-TB); RIF resistant TB (RR-TB); strains resistant to both INH and RIF are referred to as multidrug-resistant (MDR-TB); strains resistant to RIF and any fluoroquinolone (FQ), a broad-spectrum bactericidal antibiotics, are referred to as pre-extensively drug-resistant (pre-XDR-TB). The last category is extensively drug-resistant strains (XDR-TB) showing resistance to RIF, any FQ, plus at least one of the following drugs: bedaquiline (BDQ) or linezolid (LNZ)[7,8]. These strains pose significant problem as they necessitate treatment with second-line drugs, which are associated with frequent and severe side effects, and higher costs[9].

In 2016, WHO recommended two regimens for the treatment of DR-TB infections: a standardized 9 to 12-month regimen and an individualized regimen lasting ≥20 months. The standardized regimen (Table 1) is used for patients who have not been treated with any second-line drug previously but are anticipated to be infected with strains sensitive to FQ and second-line injectable agents. In cases where the drugs in the standardized regimen cannot be administered, WHO recommends an individualized regimen (Table 2, revised in 2019)[10,11]. The most recent addition to the arsenal of anti-TB drugs is pretomanid, introduced to the WHO guidelines in 2020. In 2022, pretomanid became part of the newly recommended 6-month regimen BPaLM (BDQ, pretomanid, LNZ, and moxifloxacin) for the treatment of MDR/RR-TB and pre-XDR-TB[5].

Even in the case of DS-TB, the treatment for TB is a lengthy process, contributing to the emergence of drug-resistant strains. TB drug-resistance poses an imminent threat to developing countries, particularly in the context of globalization. For these reasons, the search for more effective drugs and shorter treatments become a critical task, yet TB research remains underfunded. In 2022, approximately $1 billion was allocated to TB research, half the annual target set by the member states of the United Nations during the 2018 high-level meeting on the Fight to End TB[12].

Despite the financial challenge, three new anti-TB agents: BDQ[13], delamanid[14] and pretomanid[15] have been approved. Moreover, 19 small molecule drugs are currently under investigation in clinical trials, with another four candidates in preclinical testing with prospects to enter clinical trials (Table 3). These advancements hold great promise, although resistance to some of these drugs has emerged shortly after their introduction into clinical practice[16]. The continuous search for safe anti-TB molecules is crucial to curb the spread of DR-TB.

Anti-TB agents research is a highly active field, encompassing numerous classes of compounds with diverse mechanisms of action. The elucidation of structural and biochemical differences between the bacterial and human species is key for the rational design of new antibacterial compounds that can selectively target mycobacteria[17]. A main feature responsible for mycobacteria's unique properties is their cell wall, which is significantly different from cells in other organisms[18], becoming the primary target for current drugs and drug candidates. Other targets stem from the differences in proteosynthesis, energy metabolism, and synthesis and repair of nucleic acids[19]. Despite the large number of research papers published each year on the design and synthesis of new anti-TB agents, only a small number of these molecules have the necessary drug-like properties and meet sufficient *in vivo* activity. Furthermore, only a fraction of qualifying candidates progress to clinical studies.

Current studies devoted to TB treatment from the perspective of developing new drugs are mainly concentrated on new drug regimen proposals and treatment strategies[20–22], or overviews current and potential drugs[23,24]. This review examines compounds that are currently being investigated in clinical trials or in advanced preclinical development. Individual agents are clustered based on their mechanisms of action on specific cellular structures

Table 1 Anti-TB drugs used in standardized MDR-TB treatment regimens and their mechanisms of action (MOA). The MOA for each drug is shown once only.

Phase	Drug	MOA (in *Mtb*)
Intensive (4–6 months)	Gatifloxacin or moxifloxacin	DNA gyrase inhibition
	Kanamycin	Proteosynthesis inhibition
	Prothionamide (PTH)	Mycolic acid biosynthesis inhibition
	Clofazimine	Binding to DNA, inhibition of bacterial proliferation
	High-dose isoniazid	Mycolic acid biosynthesis inhibition
	Pyrazinamide	The MOA is unknown. A potential mechanism may involve the inhibition of CoA biosynthesis.
	Ethambutol	Arabinogalactan biosynthesis inhibition
Continuation for additional 5 months	Gatifloxacin or moxifloxacin	
	Clofazimine	
	Pyrazinamide	
	Ethambutol	

Table 2 Anti-TB drugs recommended by WHO for individualized or long-term MDR-TB therapy with known or anticipated MOA. The MOA for each drug is shown once only.

Group (recommendation)	Drug	MOA (in *Mtb*)
Group A (all three agents are used in combination)	Levofloxacin or moxifloxacin	DNA gyrase inhibition
	Bedaquiline	Inhibition of ATP synthase
	Linezolid	Proteosynthesis inhibition
Group B (one or both agents are applied)	Clofazimine	
	Cycloserine or terizidone	Peptidoglycan biosynthesis inhibition
Group C (applied to complete the regimen and when drugs from Group A and B cannot be used)	Ethambutol	
	Delamanid	Mycolic acid biosynthesis inhibition
	Pyrazinamide	
	Imipenem-cilastatin or meropenem	Peptidoglycan biosynthesis inhibition
	Amikacin or streptomycin	Proteosynthesis inhibition
	Ethionamide (ETH) or PTH	Mycolic acid biosynthesis inhibition
	Para-aminosalicylic acid	Inhibition of folate metabolism

or enzyme pathways of *Mtb*. All minimum inhibitory concentrations (MIC) and half-maximal inhibitory concentration (IC_{50}) values are reported in micromolar (μmol/L) or nanomolar (nmol/L) values, to facilitate comparison. For MIC values, the percentage of inhibition is indicated by a subscript, and the incubation time and the strain evaluated are reported as recorded in the original publication.

2. Inhibitors of cell wall component synthesis

Targeting the mycobacterial cell wall (Fig. 1) biosynthesis has proven to be a highly effective strategy, as exemplified by first-line drugs such as INH[25] and EMB[26], as well as several second-line anti-TB agents, including the recently approved delamanid[14] and pretomanid[15]. The cell wall is an attractive target in *Mtb* as it possesses unique enzymes and transporters involved in cell wall biosynthesis, rendering highly selective antimycobacterial drugs with minimal inter-species toxicity. Another significant advantage lies in the specific localization of the targeted enzymes and transporters within the mycobacterial cell wall, specifically in the periplasm and cytoplasmic membrane. This strategic positioning enhances their accessibility as therapeutic targets compared to those located within the cytoplasm[27]. From this perspective, compounds that interfere with mycobacterial cell wall biosynthesis hold immense promise for developing highly selective anti-TB drugs.

Historically, the first known antibiotics targeting cell wall biosynthesis were the β-lactams. However, their effectiveness against *Mtb* was limited due to several factors: the presence of highly potent mycobacterial β-lactamases (BlaC, EC: 3.5.2.6)[30],

high expression of efflux pumps[31], low permeability through mycomembrane of the cell wall[18,32,33], and a slow cell cycle of *Mtb*[34]. Despite these drawbacks, β-lactams continue to be used in clinical practice. Carbapenems, a subgroup of β-lactam antibiotics, are widely employed for TB treatment in combination with other anti-TB drugs[35]. Their mode of action involves the inhibition of peptidoglycan synthesis. Peptidoglycan, the main component of the periplasm, maintains cell shape. Carbapenems act as inhibitors of L,D-transpeptidases (EC: 2.3.2.-) during cell division. The L,D-transpeptidase is essential for peptidoglycan synthesis by forming a crosslink between peptides and glycan chains formed from *N*-acetylglucosamines and *N*-acetylmuramic acids[36−38]. β-Lactam antibiotics are listed in the group C according to the WHO classification of anti-TB drugs for the treatment of MDR-TB in prolonged regimens (Table 2). Examples include imipenem (carbapenem) combined with the human dehydropeptidase inhibitor cilastatin, meropenem (carbapenem), and amoxicillin (aminopenicillin) combined with the β-lactamase inhibitor clavulanate[39]. Sanfetrinem cilexetil, a tricyclic carbapenem currently undergoing phase 2 clinical trials (Table 3), demonstrated promising intracellular activity with a MIC_{50} of 0.85 μmol/L against *Mtb* H37Rv in monocytes isolated from the blood of an acute monocytic leukemia patient (THP-1 cell line) after five days[40]. Its oral administration potential provides it with an advantage over meropenem[41].

Enoyl-[acyl-carrier-protein] reductase (InhA, EC: 1.3.1.9) serves as a target for the activated forms of INH, ethionamide (ETH), and prothionamide (PTH). InhA plays a pivotal role in the mycobacterial type II fatty acid synthase (FA*S* II) system, which is essential for the biosynthesis of mycolic acids[42,43]. These agents function as prodrugs: INH is activated by the catalase-peroxidase enzyme (KatG, EC: 1.11.1.21)[44], while ETH and PTH are activated by FAD-containing monooxygenases EthA (EC: 1.14.13.-), MymA (EC: 1.14.13.-), and Rv0565c (EC: 1.14.-.-)[45]. The active forms of these drugs share a common MOA; they form covalent adducts with the NAD cofactor, acting as tight-binding competitive inhibitors of InhA and thereby blocking mycolic acid biosynthesis[42,43]. The most prevalent cause of resistance to INH is the mutation of the KatG enzyme, preventing the activation of the prodrug and compromising its efficacy. The S315T variant can be found in 94% of IR-TB clinical isolates[46]. Conversely, resistance to ETH or PTH commonly arises from mutations in the promoter region of InhA, leading to its overexpression[47]. BVL-GSK098, currently in phase 2 clinical trials, is endowed with a unique MOA compared to other anti-TB drugs. BVL-GSK098 acts as a transcriptional regulator, stimulating the expression of MymA, a key enzyme activator for ETH and PTH. This stimulation enhances the activity of ETH and PTH, presenting a promising avenue for TB treatment[40,48,49]. From the perspective of structure−activity relationships, BVL-GSK098 allows several modifications that maintain high activity. The structure of BVL-GSK098 can be divided into three regions of potential medicinal-chemistry interest: the amidic, central spirocycle, and substituent in the 3-position of the spirocycle (Fig. 2). Molecule tolerates unbranched or branched aliphatic chains with fluorine being most advantageous. Specifically, 4,4,4-trifluorobutanoyl has shown to be the most active. Introducing an aromatic or saturated cycle into the side chain led to a decrease in activity. Replacing the piperidine ring of the central 1-oxa-2,8-diazaspiro[4.5]dec-2-ene moiety with pyrrolidine or azetidine reduced the activity. Various substituents were also tolerated in the 3-position, highlighting ethoxy, methoxy, and trifluoromethyl substituents.

Table 3   Anti-TB agents in clinical trials. Chemical structures, their target and the National Clinical Trial (NCT) identifier numbers are provided. Trial status is disclosed directly to NCT number.
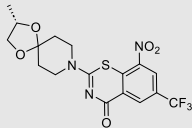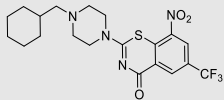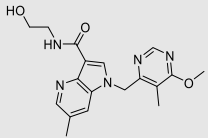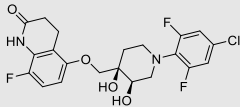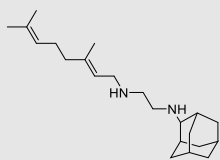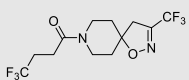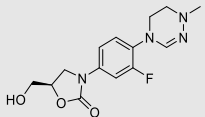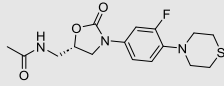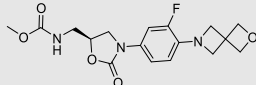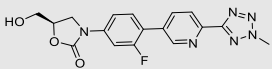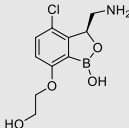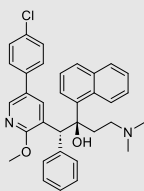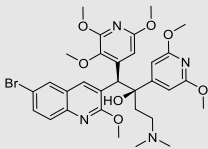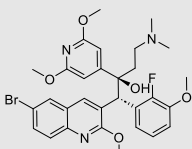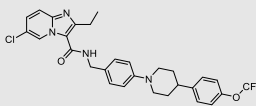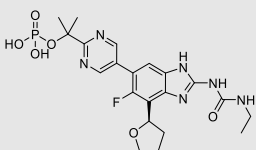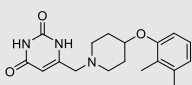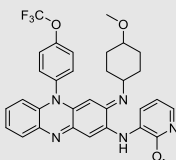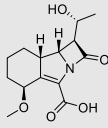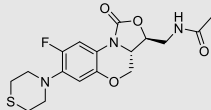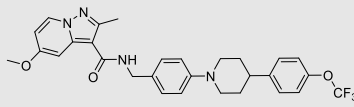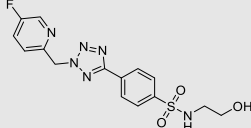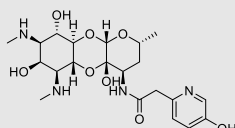
Name	Structure	Target	Phase in clinical trial[a]
BTZ-043		DprE1 (cell wall biosynthesis)	IIb/IIc NCT04044001 completed NCT03590600 completed NCT04874948 completed NCT05926466 recruiting NCT06114628 recruiting NCT05382312 recruiting NCT05807399 recruiting
Macozinone (PBTZ-169)		DprE1	Ib/IIa NCT04150224 completed with results NCT03423030 completed NCT03036163 completed with results NCT03776500 completed NCT03334734 terminated
TBA-7371		DprE1	IIa NCT03199339 completed NCT04176250 completed
OPC-167832		DprE1	IIb/IIc NCT03678688 completed with results NCT05221502 active, not recruiting NCT05971602 recruiting
SQ-109		MmpL3 (cell wall biosynthesis) MenA, MenG (energy metabolism)	IIb NCT01218217 completed NCT00866190 completed NCT01585636 completed NCT01358162 completed NCT01785186 completed with results NCT01874314 withdrawn
BVL-GSK098		Transcriptional regulator (activity boosting of ETH and PTH)	IIa NCT04654143 completed NCT05473195 recruiting
Delpazolid		50S ribosomal subunit (interfering with proteosynthesis)	IIb NCT04550832 completed NCT02836483 completed NCT01554995 completed NCT02538003 completed NCT02529241 terminated NCT04939779 completed NCT01842516 completed NCT02540460 completed NCT02882789 completed NCT03492996 completed
Sutezolid		50S ribosomal subunit	IIb/c NCT03199313 completed NCT03959566 completed NCT00990990 completed NCT01225640 completed NCT00871949 completed NCT05686356 recruiting NCT03237182 terminated NCT06192160 not yet recruiting NCT05971602 recruiting
TBI-223		50S ribosomal subunit	Ib NCT03758612 completed NCT04865536 completed NCT06192160 not yet recruiting

Table 3 (*continued*)

Name	Structure	Target	Phase in clinical trial[a]
Tedizolid		50S ribosomal subunit	IIa NCT05534750 recruiting NCT01461460 completed NCT00876655 completed NCT01271998 completed NCT01623401 completed NCT00983255 completed NCT01496677 completed NCT01442831 completed NCT01156077 completed NCT00671814 completed NCT00671359 completed
GSK3036656		Leucyl-tRNA synthase (interfering with proteosynthesis)	IIa NCT03557281 completed with results NCT03075410 completed with results NCT05382312 recruiting NCT06114628 recruiting
Sudapyridine (WX-081)		ATP synthase (involved in energy metabolism)	IIa/IIb NCT06117514 completed NCT05824871 enrolling by invitation NCT04608955 completed
TBAJ-876		ATP synthase	Ib/IIa NCT05526911 completed NCT04493671 completed NCT06058299 recruiting
TBAJ-587		ATP synthase	Ia/Ib NCT04890535 completed
Telacebec (Q203)		QcrB subunit of cytochrome *bcc* complex (involved in energy metabolism)	IIa NCT02858973 completed NCT02530710 completed NCT03563599 completed
SPR720		DNA gyrase GyrB (DNA synthesis and reparation)	II NCT05955586 completed NCT03796910 completed NCT05966688 completed (clinical trials for the treatment of non-tuberculous mycobacterial infections) NCT05496374 recruiting NCT04553406 terminated with results
GSK2556286		cAMP-mediated inhibition of cholesterol catabolism	Ia/Ib NCT04472897 recruiting
Pyrifazimine (TBI-166)		Intracelullar redox cycling-release of oxygen species	IIa NCT04670120 unknown status

(continued on next page)

Table 3 (*continued*)

Name	Structure	Target	Phase in clinical trial[a]
Sanfetrinem		L,D-transpeptidases (cell wall biosynthesis)	II NCT05388448 recruiting
OTB-658		50S ribosomal subunit	Preclinical GLP toxicology studies
TB47		QcrB subunit of cytochrome *bcc* complex	Preclinical GLP toxicology studies
GSK839		Tryptophan synthase (essential enzyme for *Mtb* survival in macrophage)	Preclinical GLP toxicology studies
MBX-4888A		16S ribosomal RNA	Preclinical GLP toxicology studies

[a]Current status as of 5-2024; data gained from clinicaltrials.gov.
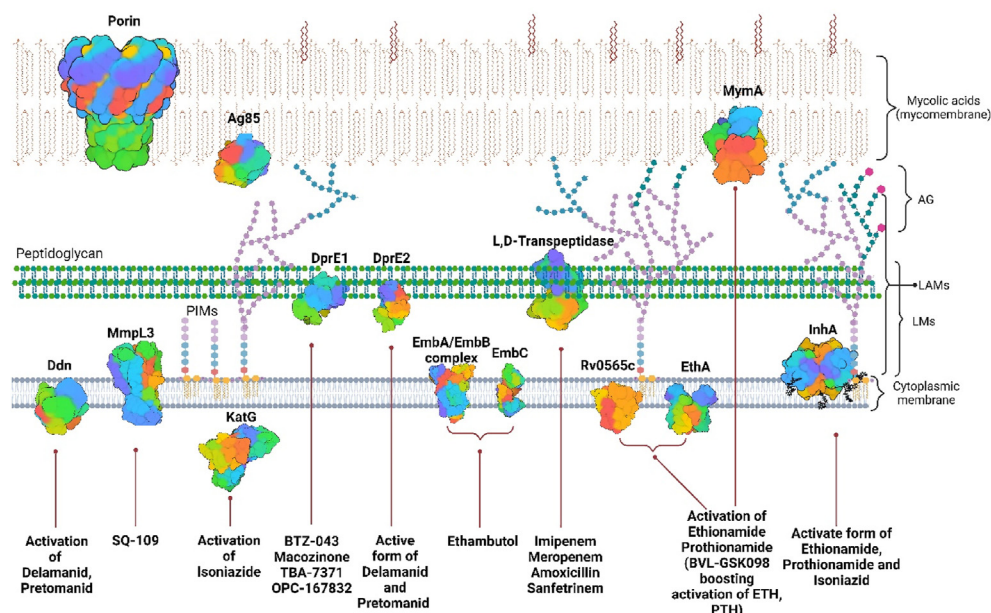
Figure 1 Composition of the mycobacterial envelope and drug targets of known anti-TB drugs. The mycobacterial cell envelope consists of four distinct units: the cytoplasmic membrane, the periplasm, the mycomembrane, and the capsule. Enzymes and transporters within this envelope intricately contribute to the synthesis of cell wall components and overall homeostasis. The cytoplasmic membrane is a glycerophospholipid bilayer incorporating essential molecules such as phosphatidylinositol mannosides (PIMs), lipomannans (LMs), and lipoarabinomannans (LAMs). Molecules derived from PIMs, are pivotal for maintaining cell wall integrity[28] and immune modulation[29].

However, derivatives with heteroaromatic or phenyl moieties in the 3-position also showed good activity[50,51].

Decaprenylphosphoryl-β-D-ribose oxidase (DprE1, EC: 1.1.98.3), a part of DprE1-DrpE2 complex, was first described in 2009[52]. DprE1 is a periplasmic flavoenzyme that catalyzes the first step of epimerization of decaprenylphosphoryl-D-ribose (DPR) into decaprenylphosphoryl-D-arabinose (DPA), providing the source of arabinose. Arabinose is an essential monosaccharide for
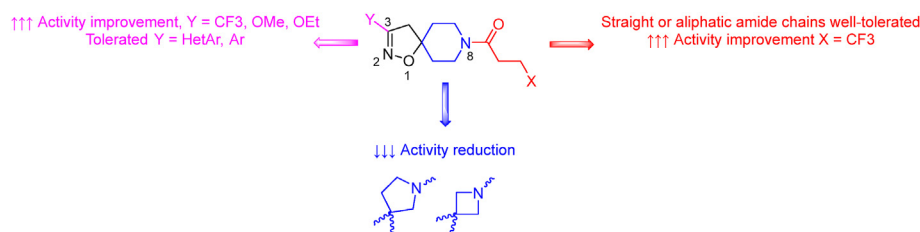
Figure 2 Structure and insight into structure−activity relationships of BVL-GSK098.

the synthesis of arabinans, lipoarabinomannans (LAMs) and arabinogalactans (AG). EMB targets this enzymatic pathway *via* arabinosyl transferases (EmbA-C, EC:2.4.2.-) inhibition[26]. DprE1 is located in the periplasm, allowing targeting by the xenobiotics[53]. Among them, benzothiazinones received particular attention, represented by macozinone[54] (*Mtb* $H_{37}R_v$ MIC_{99} = 0.65 nmol/L 7 days)[55] and BTZ-043[56] (*Mtb* $H_{37}R_v$ MIC_{99} = 2.3 nmol/L 7 days)[55] undergoing phase 1 and phase 2 clinical trials, respectively[40]. Benzothiazinones are prodrugs that act as suicide inhibitors of DprE1; they are activated *in situ* in the catalytic pocket of DprE1 by a reduced form of the cofactor dihydroflavine-adenine dinucleotide ($FADH_2$) *via* the reduction of the nitro group to its nitroso form, which subsequently forms a covalent bond with C387 of DprE1[57]. The MOA suggests that the nitro group in position 8 of the benzothiazinone scaffold is essential for the activity, implying limited possibilities for further structural modifications (Fig. 3). The strong electron acceptor substituents at position 6 and the unsubstituted positions 5 and 7 are pivotal for the activity. Position 2 of the core benzothiazinone moiety is the only allowing modifications. In this position, substituted saturated nitrogen heterocycles are preferred, providing the possibility of pharmacokinetic properties tunning[55,58,59].

3,4-Dihydrocarbostyril drug OPC-167832 (*Mtb* $H_{37}R_v$ MIC_{99} = 0.001 μmol/L) and 4-azaindole derivative TBA-7371 (*Mtb* $H_{37}R_v$ MIC_{80} = 1.56 μmol/L 5 days)[60] are other representatives from DprE1 inhibitors, currently undergoing phase 2 of clinical trials[40]. Notably, OPC-167832 is a non-covalent inhibitor, also acting in the catalytic pocket of DprE1, but unlike benzothiazinones, interaction with C387 is not crucial for its activity. Hence, the mutation in this position yields only moderate resistance. Highly OPC-167832 resistant strains rendered mutation at position Y314, being the cause of activity loss[61,62]. SAR study to OPC-167832 investigated three regions of the molecule, namely 2(1*H*)-quinolinone scaffold, the piperidine moiety attached to position 5 of the core *via* a methylenoxy linker, and an aromatic moiety attached to the piperidine (Fig. 4). Analogues of the 3,4-dihydrocarbostyril moiety displaying enhanced activity were those that were substituted within positions 7 or 8. The preferred substituents were mainly fluorine and chlorine. Regarding the linker, derivatives-bearing oxygen or sulfur atoms maintained notable activity. Nonetheless, for enhanced metabolic stability, oxygen was preferred, prompting the retention

of the methylenoxy linker in subsequent modifications. Piperidine ring modifications in positions 2′, 3′ and 4′ with substituents allowing the formation of hydrogen bonds, specifically amino, fluoro, and hydroxyl groups, all yielded activity improvement. Replacement of the piperidine ring with cyclohexane was tolerated in terms of activity, but the lipophilicity was also increased. The aromatic part attached to position 1′ of piperidine predominantly comprised a phenyl group; however, pyridine-2-yl and quinoline-2-yl were also tolerated. Introducing fluorine in positions 2″ and 6″ of the phenyl ring, or a proton-accepting functional group, conferred activity enhancement. Chloro or bromo substituents were the most potent for position 4″[61−63].

The TBA-7371 mode of action is deemed to be the same as for OPC-167832. The TBA-7371 resistant strain also revealed a mutation in DprE1-Y314 with no cross-resistance to benzothiazinones. Non-covalent interaction with DprE1 was confirmed by mass spectrometry analysis of DprE1 treated with TBA-7371. The pharmacological testing of TBA-7371 revealed inhibition of phosphodiesterase 6 (PDE6, EC: 3.1.4.34) IC_{50} = 4 μmol/L, which may lead to ocular side effects[60,64,65]. From a structure−activity relationship perspective, compound TBA-7371 was investigated in three regions; the amide part in position 3 of the 4-azaindole moiety, the heteroaromatic motif substitution attached to the 4-azaindole, and changes in positions 5, 6 and 7 of 4-azaindole (Fig. 5). The nature of the linker attached to *N*-amidic moiety was crucial for the solubility and microsomal stability of the compound. It also affected interaction with PDE6. For all these considerations, 2-hydroxyethyl substituent was the most advantageous. A bioisosteric pyrazole can also replace the amide bond while maintaining activity. Derivatives with nitrogen-containing heteroaromatics or phenyls were prepared to study position 1, revealing that the chosen aromatic moiety did not play a significant role in the activity. However, the substitution of the heteroaromatic moiety in this region significantly affects PDE6 inhibition and solubility. The most preferred heteroaromatic moieties reducing PDE6 inhibition were 6-methoxy-5-methylpyrimidine-4-yl, 6-(dimethylamino)-5-methylpyrimidine-4-yl and 6-(difluoromethoxy)-5-methylpyrimidine-4-yl. Substitutions in positions of 4-azaindole core pointed out to position 6, with a preference for methyl or methoxy substitutions, while a trifluoromethyl group, for instance, yielded in an inactive compound[66].

Figure 3 General structure of benzothiazinone and insight into their structure−activity relationships.
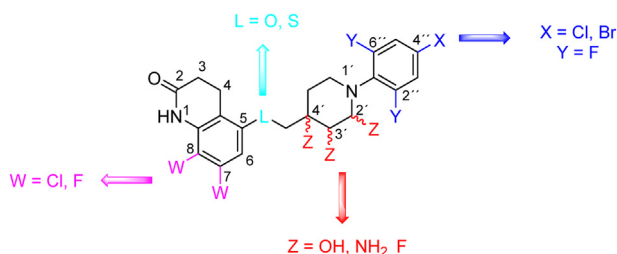
Figure 4 Tolerated structural modifications of OPC-167832.

Decaprenylphosphoryl-2-keto-β-D-erythropentose reductase (DprE2, EC: 1.1.1.333) the second enzyme of DprE1-DprE2 complex, is probably inhibited by active form of pretomanid and delamanid, the most recently approved anti-TB drug, which are prodrugs that are activated by the cytoplasmic enzyme deazaflavin-dependent nitroreductase (Ddn, EC: 1.1.98.-)[67].

Mycobacterial membrane protein large 3 (MmpL3) belongs to the resistance, nodulation and cell division (RND) superfamily of transporters and plays a vital role in many cellular processes such as cell wall biosynthesis, energy metabolism, and presumably iron uptake[68–70]. Depletion of MmpL3 is associated with the death of *Mtb*, thus representing a suitable target for potential anti-TB agents. MmpL3 is responsible for transporting trehalose monomycolates (TMM), which is crucial for cell wall synthesis. TMM is synthesized in the cytoplasm from trehalose and mycolic acids. TMM serves as a substrate for mycoloyltransferase AG85 in the biosynthesis of trehalose dimycolates (TDM), a mycomembrane component. TDM, located at the external cell wall layer, plays a key role in immunomodulation during TB pathogenesis[71]. The driving force for TMM transport is the proton cotransport. Inhibition of MmpL3 leads to the accumulation of TMM in the cytoplasm, impairing the cell wall stability, viability, and virulence of *Mtb*[72]. An ethylenediamine MmpL3 inhibitor SQ109 is currently in phase 2 clinical trials, reaching MIC$_{99}$ values of 1.59 µmol/L against *Mtb* H$_{37}$R$_v$ and 2.3–3.3 µmol/L against replicating and non-replicating *Mtb*, respectively[40,73,74]. SQ109, a transporter inhibitor, has been tested in combinations with standard drugs showing synergism with RIF, INH, and BDQ, increasing the accumulation of the drug in *Mtb*[75–77]. SQ109 was identified in a study of EMB analogues. However, a different MOA was subsequently determined, pointing out the inhibition of the MmpL3 transporter[78]. SQ109 acts as a multitarget ligand against MmpL3 and menaquinone (MK) biosynthesis-related enzymes, namely 1,4-dihydroxy-2-naphthoate octaprenyltransferase (MenA EC: 2.5.1.74) and demethylmenaquinone methyltransferase (MenG EC: 2.1.1.163). X-ray analysis of the SQ109 soaked in MmpL3 confirmed hydrophobic interactions between the geraniol appendage and the bulky adamantyl moiety and the hydrogen bonding between the two amino groups with D645. These

interactions block the proton channel, thus preventing its cotransport with TMM[79]. Several studies have focused on elucidating the structure−activity relationships of analogues of SQ109. Following structural modifications were considered, specifically the central ethylenediamine linker, and both sides of the molecule either containing geraniol or adamantyl moieties (Fig. 6). It has been confirmed that at least one nitrogen atom must be preserved to retain antimycobacterial activity. The second nitrogen atom can be replaced by oxygen to maintain the activity. The nitrogen attached to adamantyl moiety is vital to keep high *in vitro* activity. Bulky aliphatic substituents are preferred here, with adamant-2-yl moiety representing the drug lead candidate. The geraniol motif is more flexible for changes as saturated or partially unsaturated cycles are tolerated, as well as substituted aromatic rings linked *via* an ethylene linker, where the basic nitrogen is retained. Derivatives with geraniol proved to be the most potent ones[73,80].

3. Small molecules as disruptors of mycobacterial protein synthesis

Approximately 50% of the cellular energy is used for protein synthesis, an essential process for cellular metabolism and proliferation[81]. This intricate mechanism occurs within ribosomes, complex ribonucleoprotein entities composed of two subunits: a large subunit (LSU), critical for peptide bond formation, and a small subunit (SSU), where the genetic information, encoded in mRNA, is translated into an amino acid sequence. The structural integrity of prokaryotic ribosomes, observed in gram-negative, gram-positive bacteria, and mycobacteria, is largely conserved across species. Subtle interspecies distinctions can be detected by a closer insight into the architecture of individual ribosomal subunits. The small 30S subunit shows minor interspecies structural differences; it is composed of 21 ribosomal proteins and 16S rRNA. In contrast, the 50*S* LSU displays more significant variability, encompassing differences in the number of ribosomal proteins (34 in *Mtb*) and the structural configuration of 23S and 5*S* rRNAs. Notably, mycobacterial ribosomes exhibit prominent disparities in the structure of LSU's 23S rRNA, particularly in the helices of domains I and II, as well as a significantly elongated helix 54a in domain III[82–84].

Streptomycin emerged as the pioneering drug for TB treatment in 1947, but monotherapy led to swift resistance development. Currently, streptomycin remains within Group C to treat MDR-TB, alongside other aminoglycosides such as amikacin and kanamycin (Table 2). The MOA of these aminoglycosides involves binding to 16S rRNA helix 44[85,86]. Capreomycin is another anti-TB agent from the aminoglycoside class, but its MOA accounts interaction with both subunits of the 70S ribosome[87]. LNZ, a protein synthesis inhibitor, impedes the formation of the 70*S* initiation complex by binding to the 23S rRNA of LSU[88]. In
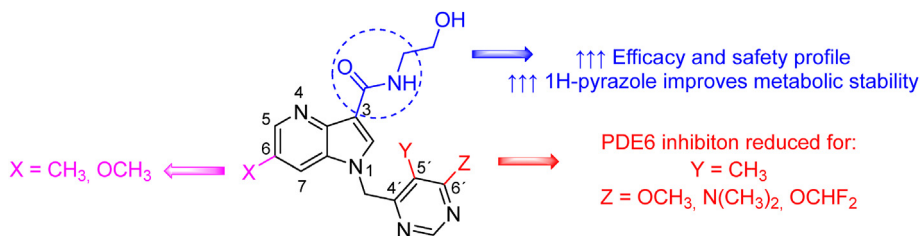

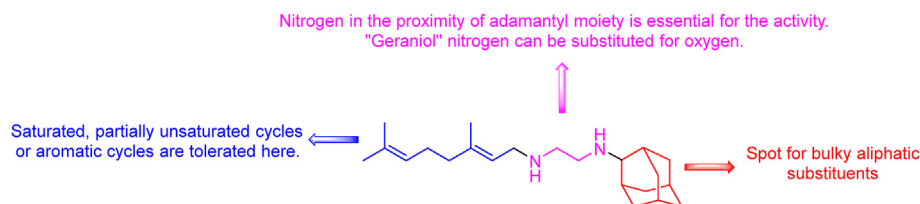**Figure 5** Modification for TBA-7371.

Figure 6 SQ109 and potential structural changes to retain high activity.

contrast, RIF acts as an inhibitor of DNA-dependent RNA polymerase (EC: 2.7.7.6), hindering RNA synthesis by blocking RNA elongation[89]. Remarkably, this group of protein synthesis inhibitors, excluding RIF, is associated with severe adverse effects including: nephrotoxicity, ototoxicity, and neurotoxicity for aminoglycosides, as well as thrombocytopenia, optic neuropathy, and peripheral neuropathy for LNZ[88,90].

Oxazolidinone compounds represent a prominent class of protein synthesis inhibitors, currently under investigation in clinical trials, inspired by the prototype drug LNZ (*Mtb* $H_{37}R_v$ $MIC_{90} = 0.981-1.245$ μmol/L 7 days, Fig. 7)[91]. LNZ inhibits cellular proliferation *via* disruption of protein synthesis by binding at the 23S rRNA, preventing the formation of a ribosome complex with *N*-formylmethionyl-tRNA. Clinically, LNZ was approved for the treatment of complicated skin infections and severe pneumonia caused by Gram-positive bacteria. LNZ shows antimycobacterial activity against the *Mtb in vitro,* including drug-resistant clinical isolates. LNZ is extensively used within the realm of MDR-TB therapy, as part of group A in prolonged regimen treatments. However, its usage is conveyed by deleterious side effects, including anemia, and peripheral neuropathy, often necessitating dose reduction or discontinuation[92,93]. Extensive efforts are under way in the oxazolidinone drug discovery field, to mitigate these adverse effects[94–97]. The mechanisms responsible for oxazolidinone's toxicity include the inhibition of monoamine

oxidases and mitochondrial protein synthesis (MPS), with LNZ MPS IC_{50} established at 6.40−7.98 μmol/L[98,99]. A side effects of long-term LNZ treatment caused by MPS inhibition is dose-dependent, reversible bone marrow suppression[100].

From the medicinal chemistry perspective, all oxazolidinones must preserve an aryl in position 3 and a polar substituent in position 5 attached *via* a methylene linker. The conservation of the spatial arrangement in position 5, which corresponds to the (*S*)-configuration in the LNZ, is crucial for their activity. Substitution of the aromatic moiety influences both activity and, notably, pharmacokinetic properties and solubility. The introduction of fluorine into the phenyl ring is beneficial for activity, while solubility and pharmackokinetics are modulated by the introduction of basic nitrogen in the form of morpholine or thiomorpholine, or the presence of acidic moiety like tetrazole (Fig. 7)[96,101,102].

A subtle modification in the structure, such as replacing morpholine with thiomorpholine in sutezolid (*Mtb* $H_{37}R_v$ $MIC_{90} = 0.34-0.58$ μmol/L 7 days, MPS $IC_{50} = 8.17$ μmol/L; Fig. 7), resulted in a slight improvement in the safety profile and a modest increase in antimycobacterial activity[91,103,104]. Delpazolid (*Mtb* $H_{37}R_v$ $MIC_{90} = 1.62$ μmol/L 7 days, MPS $IC_{50} = 3.2-11.0$ μmol/L; Fig. 7)[99,105] is another oxazolidinone currently investigated in phase 2 clinical trials. Replacement of morpholine in LNZ with a cyclic amidrazone, and the substitution of the amide moiety for alcohol enhanced the solubility in
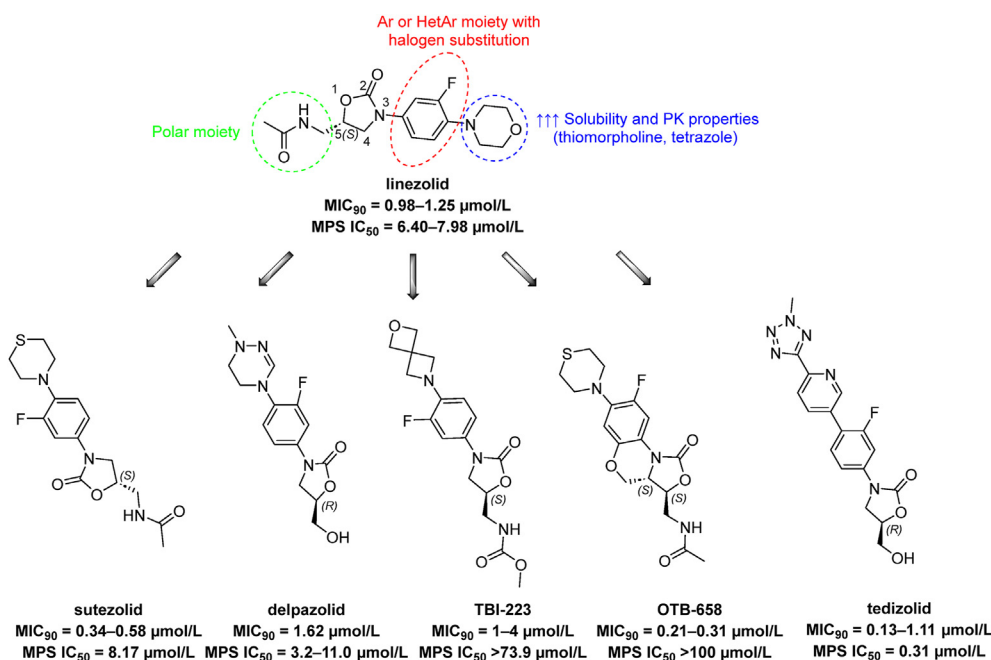

Figure 7 Anti-Tb agents from oxazolidinone family with highlighted regions of the molecule essential for the activity and ADME/PK properties. Examples of clinical candidates are displayed.

delpazolid while concomitantly boosting the safety profile and maintaining efficacy against *Mtb*[106]. The amide fragment in LNZ was replaced by methyl carbamate and the morpholine by spiromorpholine to propose TBI-223 (*Mtb* unspecified strain MIC = 1−4 μmol/L, MP*S* IC$_{50}$ > 73.9 μmol/L; Fig. 7)[23,99]. These structural changes substantially reduced mammalian MP*S* inhibition, thereby improving the safety profile[107]. OTB-658 (*Mtb* H$_{37}$R$_v$ MIC$_{90}$ = 0.21−0.30 μmol/L 7 days, MP*S* IC$_{50}$ > 100 μmol/L; Fig. 7) is an oxazolidinone derivative with *in vitro* potency superior to LNZ and sutezolid. Introducing an additional cycle in the structure led to a conformational constraint, enhancing activity and safety profiles[91,103]. The most recent oxazolidinone to enter phase 2 of the clinical trial as an anti-TB agent was tedizolid (Fig. 7). This drug, also known as Sivextro, was originally approved by the US Food and Drug Administration (FDA) in 2014 for the treatment of acute bacterial skin infections. The antimicrobial activity of tedizolid was evaluated across 120 DS-TB and DR-TB strains, exhibiting MIC$_{90}$ values in the range of 0.13−1.11 μmol/L. Unfortunately, tedizolid exhibited a higher inhibition of MP*S* with IC$_{50}$ = 0.31 μmol/L[98,108].

Spectinamides (Fig. 8) constitute a semisynthetic group of spectinomycin derivatives. In contrast to structurally analogous aminoglycosides, spectinomycins exhibit minimal adverse effects (ototoxicity and nephrotoxicity have not been observed in this class). Nonetheless, their efficacy against tubercular strains remains limited, primarily attributed to the mycobacterial efflux pump Rv1258c activity. This fact prompted an investigation into the potential structural modification of spectinomycin. Spectinomycin, a tricyclic aminoglycoside comprising actinamine (ring A) and actinospectose (ring C), connected *via* β-glycosidic and hemiketal linkages to form ring B, imposes a challenge for structural alteration due to structural complexity. Model predictions suggested that substituting the keto group in position 7 with an *R*-amine or amide moiety could provide a viable avenue for modification, offering opportunities for further derivatization to attenuate its affinity for the efflux pump. Modifying the amino group with acetamide alternatives emerged as a promising strategy. Among the derivatives synthesized, the (*tert*-butylamino) acetamide derivative displayed superior ribosomal efficacy, albeit with poor whole-cell activity. Subsequent modification with pyridine-2-yl or thiazol-4-yl acetamide groups demonstrated enhanced efficacy. Introduction of halogens in positions 4′ or 5′ of the pyridine moiety further augmented activity, yielding spectinamide-1599 (with a 5-chloropyridin-2-yl moiety, *Mtb* H$_{37}$R$_v$ MIC$_{90}$ = 1.64 μmol/L 7 days). Replacement of the chlorine in position 5′ with a hydroxyl group resulted in a remarkable increase in *in vivo* efficacy, as demonstrated in an infected mice model. Spectinamide-1810 (bearing 5-hydroxypyridin-2-yl moiety), known as MBX-4488A, also displayed intriguing activity

(*Mtb* H$_{37}$R$_v$ MIC$_{90}$ = 3.41 μmol/L 7 days, Table 3). These modifications have also augmented ribosome inhibition through hydrogen bonding within helix 34 of the 16S ribosomal RNA[109−113].

GSK3036656 (*Mtb* H$_{37}$R$_v$ MIC$_{95}$ = 0.08 μmol/L 14 days, Table 3) represents a groundbreaking advancement as the first boron-based anti-TB agent undergoing clinical trials. This compound belongs to a novel chemical class of 3-aminomethyl-4-halogen benzoxaboroles, exerting inhibitory effects on leucyl-tRNA synthetase (LeuRS, EC: 6.1.1.4). GSK3036656 exhibits remarkable selectivity for *Mtb*, displaying negligible activity against a spectrum of common bacteria and mammalian cell lines[114−116]. From a medicinal chemistry standpoint, three substitutions on the benzoxaborole scaffold at positions 3, 4, and 7 are pivotal (Fig. 9). Substitution in position 3 with an aminomethyl group has proven advantageous, with activity attributed to the (*S*)-enantiomer. Position 4 prefers halogen or methyl substitution, whereas longer alkyl chains or unoccupied position led to analogues with reduced activity. Introducing a methoxy or ethoxy group in position 7 has been beneficial; the most valuable turned out to be a 2-hydroxyethoxy appendage that improves ADME and PK properties. Substituent switch from position 7 to 6 significantly diminished the anti-TB activity[114−117].

4. Chemical drugs interfering with energy metabolism

Mtb is an obligate aerobic bacterium that relies on respiration and other alternative sources (such as fumarate and nitrate in low-oxygen environments) to generate the energy necessary for maintaining homeostasis. Under aerobic conditions, *Mtb* produces sufficient energy for growth through a series of enzymatic reactions, including the electron transport chain (ETC) and the oxidative phosphorylation system (Fig. 10). Mycobacteria respiration comprises the oxidation of electron donor molecules (*e.g.*,
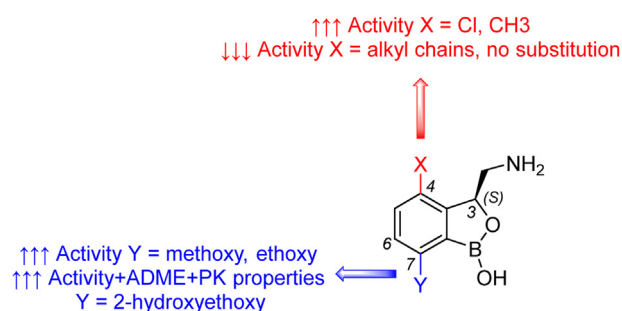
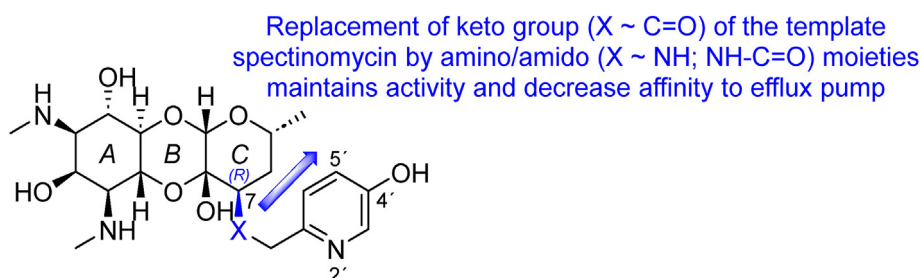**Figure 9** Insight into structure−activity relationships of benzoxaborole family.

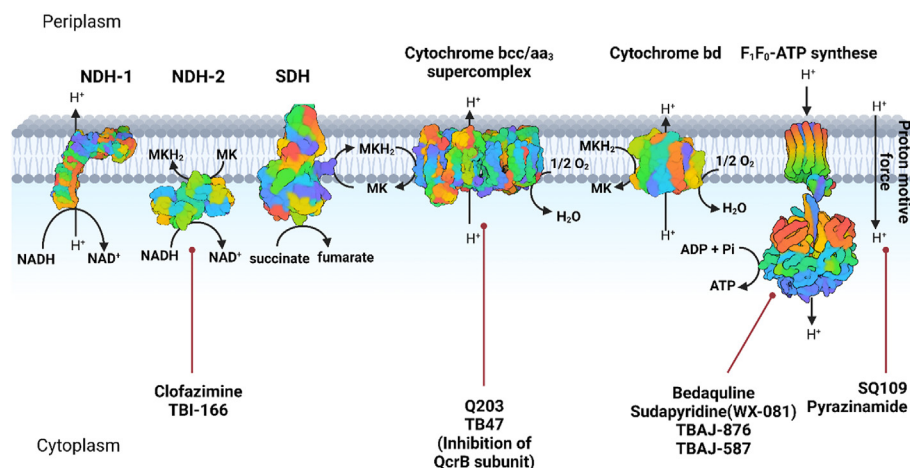**Figure 8** Structure−activity relationships of spectinamides.

Figure 10 The mycobacterial electron transport chain, and synthesis of ATP are outlined above. Each drug is paired with its target by red line. NADH:quinone oxidoreductases (NDH-1, NDH-2) and succinate dehydrogenase (SDH) function as electron transporters, facilitating the transfer of electrons from NADH and succinate to menaquinone (MK). In its reduced form, menaquinol (MKH2) serves as an electron carrier within the electron transport chain. MKH2 oxidizes back to MK through two pathways: the cytochrome *bcc/aa3* supercomplex and cytochrome bd. This oxidation process is coupled with the transfer of electrons to the terminal electron acceptor, oxygen. During the electron transport chain, protons are translocated across the membrane, forming a proton motive force (PMF).

NADH) derived from the catabolism of organic substrates, where oxygen serves as the final electron acceptor[118]. The mycobacterial proteome contains numerous enzymes participants in the ETC, utilizing two alternative pathways for terminal oxidation and electron transfer to oxygen. One pathway involves a cytochrome *bcc* complex and an aa$_3$-type family of cytochrome *c* oxidase, while the second pathway includes a cytochrome *bd*-type quinol oxidase. *Mtb* accumulates energy in two forms: adenosine triphosphate (ATP), acting as an energy carrier and store, and the proton motive force (PMF), which serves as the driving force for various metabolic and homeostatic processes, including ATP synthesis. PMF is predominantly harnessed by the membrane enzyme system F$_1$F$_0$-ATP synthase, and comprises the electric potential $\Delta\Psi$ (resulting from charge distribution across the membrane) and the chemical transmembrane proton gradient ΔpH[118−120].

Recently, the inhibition of energy metabolism emerged as a promising therapeutic target when BDQ has been marketed (*Mtb* H$_{37}$R$_v$ MIC$_{99}$ = 0.054−0.216 μmol/L 21 days)[121] in 2012[122]. However, its use is accompanied by severe adverse effects, specifically QT interval prolongation due to hERG inhibition, encoding the alpha subunit of the ether-à-go-go-related gene. hERG IC$_{50}$ value of BDQ is 1.6 μmol/L[123]. Shortly after BDQ was introduced into clinical practice, the first cases of resistance emerged, caused by a mutation in the MarR-like transcriptional regulator Rv0678 controlling the expression of the gene encoding mycobacterial membrane protein-small 5- mycobacterial membrane protein large 5 (MmpS5-MmpL5) transporter[124,125]. Several BDQ analogues have been developed to mitigate side effects and resistance of the parent drug, three of which (TBAJ-587, TBAJ-876, and sudapyridine) are currently in clinical trials (Table 3).

Diarylquinolines, including BDQ (Fig. 11), are currently the largest group of mycobacterial energy metabolism disruptors, acting as selective inhibitors of mycobacterial F$_1$F$_0$-ATP synthase. BDQ, despite its efficacy, is challenged by its exceptionally high lipophilicity (*c*log*P* = 7.25), leading to a protracted terminal elimination half-life of 5.5 months and significant tissue accumulation. Another critical task in BDQ drug development involves minimizing its affinity for hERG channel, a primary consideration

for cardiac safety[126,127]. The possibilities of structural optimization of BDQ have been the subject of numerous studies, primarily aiming to reduce lipophilicity, which was assumed to be directly linked with cardiotoxicity (Fig. 11). Based on insights into the activity dependence on structural modifications of BDQ, fundamental structural features were retained, namely the methoxy group in the 2-position and the bromine at the 6-position of the quinoline, although further modification also highlighted bromine replacement with a nitrile group[128,129]. The length of the liker chain between the quinoline moiety and the tertiary amine had to be fixed to preserve high anti-TB efficacy, promoting two potential sites for potential modification, a phenyl and a naphthalen-1-yl moiety. Analogues with a modified phenyl moiety included a variety of heterocyclic substitutions, maintaining activity at a low micromolar to nanomolar range, with 2,3-dimethoxypyridine-4-yl emerging as the most promising[130]. Replacing the naphthalen-1-yl moiety with 2,6-dimethoxypyridine-4-yl was the most effective one[123,131]. Two compounds codenamed TBAJ-587 and TBAJ-876 (Table 3) are currently under clinical trial evaluation[123]. In the case of TBAJ-587, the strategic modifications implemented the introduction of fluorine at the 2-position and methoxy at 3- position on the phenyl ring, along with the replacement of the naphthalen-1-yl moiety by a 2,6-dimethoxypyridin-4-yl group. These alterations led to a reduction in lipophilicity (*c*log*P* = 5.80) and mitigated cardiotoxicity (hERG IC$_{50}$ = 13 μmol/L) while maintaining potent antimycobacterial activity (*Mtb* H$_{37}$R$_v$ MIC$_{90}$ = 9.8 nmol/L). Concerning TBAJ-876, a substitution of the phenyl ring with the more hydrophilic 2,3,6-trimethoxypyridin-4-yl moiety lowered lipophilicity (*c*log*P* = 5.15) and remarkably improved safety (hERG IC$_{50}$ > 30 μmol/L) while retaining robust antimycobacterial activity (*Mtb* H$_{37}$R$_v$ MIC$_{90}$ = 9.1 nmol/L). Notably, the impact of the Rv0678 mutation on antimycobacterial activity in TBAJ-876 and TBAJ-587 was lower than BDQ, rendering them potential substitutes for BDQ in TB therapy[123,132,133].

Pyridine-based BDQ derivatives (Fig. 11) emerged as a new class of anti-TB agents acting as ATP synthase inhibitors. Sudapyridine (WX-081) is a clinical candidate that was discovered
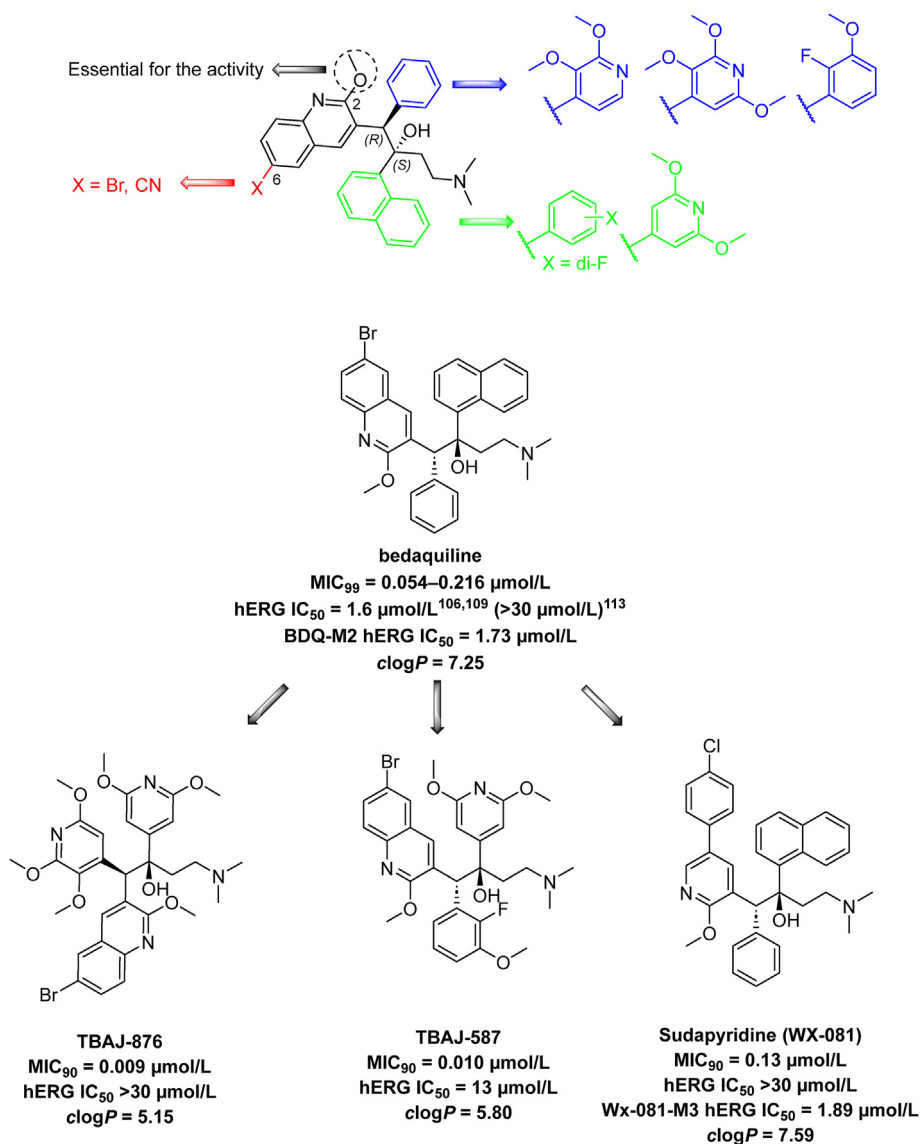
Figure 11 General structural aspects for bedaquiline and other diarylquinolines and biphenyl sudapyridine.

from an extensive structure–activity relationships campaign, replacing quinoline with phenylpyridine (Fig. 11). For the phenylpyridine moiety, attachment of phenyl to position 5 of the pyridine proved the most effective. Additionally, the substitution in this position with bulky substituents was tolerated but did not offer significant improvement. Further changes in the *para* position of the phenyl ring led to the identification of the two most effective derivatives bearing trifluoromethoxy group or chlorine. Replacement of naphthalene-1-yl moiety by phenyl aggravated toxicity and diminished the activity. Difluorophenyl derivatives were slightly more active and comparably toxic to naphthalene-1-yl-containing BDQ derivatives; however, their chemical synthesis required hardly available intermediates[134]. Consequently, sudapyridine (WX-081) was identified, bearing 5-(4-chlorophenyl)-2-methoxypyridin-3-yl moiety as a surrogate for BDQ quinoline moiety. Sudapyridine retained a potency comparable to BDQ (*Mtb* $H_{37}R_v$ MIC_{90} = 0.13 μmol/L 7 days); however, lipophilicity increased $clogP$ = 7.59, yielding high plasma protein binding. hERG inhibition assays revealed similar values for sudapyridine

and BDQ (both reaching hERG IC_{50} > 30 μmol/L). While the authors of this study suggest that sudapyridine exhibits a safer profile than BDQ, the evidence provided is inconclusive. This study identified metabolites that may be potentially responsible for cardiotoxicity, where WX-081-M3 and BDQ-M2 (metabolites of sudapyridine and BDQ, respectively) displayed comparable IC_{50} values (WX-081-M3 hERG IC_{50} = 1.89 μmol/L; BDQ-M2 hERG IC_{50} = 1.73 μmol/L)[134–136]. The results of the effect of BDQ on hERG reported in the study by Yao et al.[135] are inconsistent with other studies[123,128].

Imidazopyridine amides are novel anti-TB agents that function as inhibitors of the cytochrome *bcc* complex cytochrome *b* subunit (QcrB EC: 7.1.1.8). The cytochrome *bcc* complex is a crucial component of various enzyme complexes involved in electron transport and the formation of the respiratory ETC. Telacebec (Q203; Fig. 12) is currently in phase 2 clinical trials, exhibiting excellent antimycobacterial activity (*Mtb* $H_{37}R_v$ MIC_{50} = 2.7 nmol/L 21 days) with minimal hERG affinity (hERG IC_{50} > 30 μmol/L). Despite its high lipophilicity

Figure 12 The general structure of imidazopyridine amides and pyrazolopyridine carboxamides as QcrB inhibitors with highlighted key structural fragments and clinical candidate representatives telacebec and TB47.

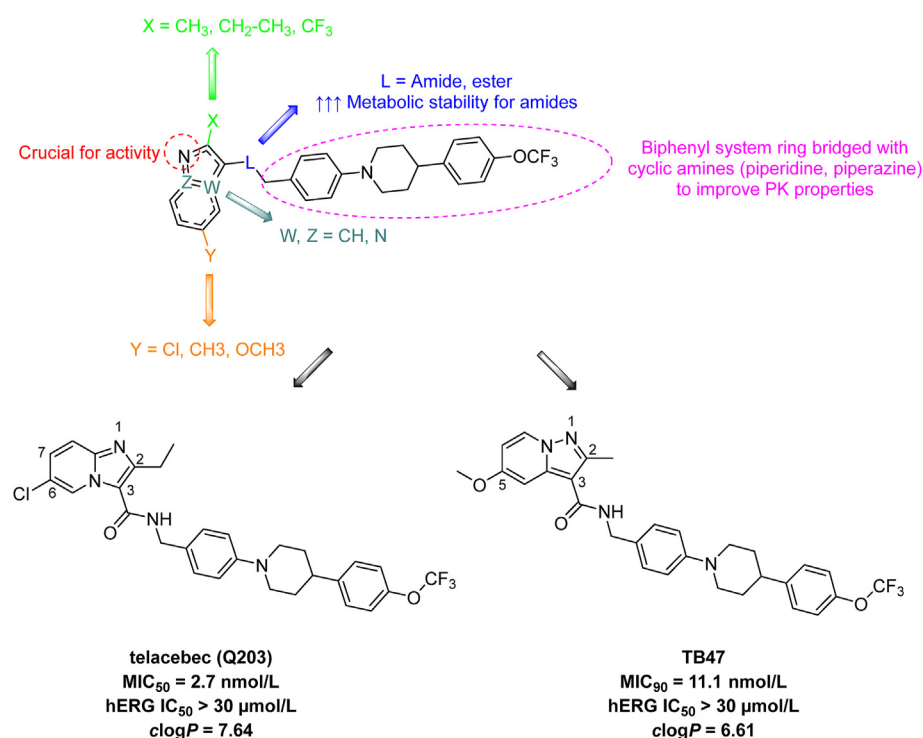($clogP$ = 7.64), telacebec has favorable pharmacokinetic properties (orally available, maximal plasma concentration after oral administration of 2 h and elimination half-life of 23.4 h)[137,138]. Telacebec was recognized as a part of the optimization study on imidazo[1,2-a]pyridine-3-carboxamides, identified through high-throughput screening of compounds against intracellular Mtb[138,139]. Several structural features necessary for activity were pinpointed during the drug modification (Fig. 12). A short alkyl chain or trifluoromethyl group in the 2-position were preferred. Position 3 tolerated carboxamide or ester groups as crucial for the activity, but amidic analogues were favored for higher metabolic stability. Core substitution of imidazo[1,2-a]pyridine highlighted positions 6 or 7, with chlorine or methyl being the top-ranked. The amidic side chain had a significant impact on activity and pharmacokinetic properties. Notably, the secondary amidic group had to be preserved to maintain high activity. The biphenyl system ring demonstrated high activity on the one hand, but sub-optimal pharmacokinetic properties on the other hand. Accordingly, the insertion of a cyclic amine (piperazine or piperidine) between two phenyl rings yielded excellent potency[137,140,141]. Subsequent studies highlighted the importance of spatial arrangement and electron distribution, particularly discussing the distance between the nitrogen in position 1 of the core moiety and the carboxamide in position 3. Thus, scaffold hopping approach enabled discovery of TB47 built on pyrazolo[2,1-a]pyridine-3-carboxamides, with nanomolar activity against Mtb[142−144].

Pyrazolopyridine carboxamides are structurally related to imidazopyridine amides, sharing a common target, namely QcrB. Derivatives structurally similar to telecabec emerged as the most potent members of the pyrazolopyridine carboxamide family (Fig. 12). Several pyrazolopyridines have been developed, displaying high activity against Mtb H$_{37}$R strains, but only TB47 (Fig. 12) exhibited sustained efficacy against DR-TB strains.

TB47 ($clogP$ = 6.61) demonstrated 10-fold lower lipophilicity compared to telacebec, while maintaining equivalent efficacy (Mtb H$_{37}$R$_v$ MIC$_{90}$ = 11.1 nmol/L 7 days) and low cardiotoxicity (hERG IC$_{50}$ > 30 μmol/L)[142,145,146].

5. Disruptors of DNA replication and reparation

The survival and evolution of any living organism depend on its ability to reproduce. The Mtb life cycle is a unique process that allows it to survive in hostile environments. Mtb's *genome* spans approximately 4.4 million base pairs, constituting a circular chromosome. Replication initiates with a specific DNA segment known as the replicator, characterized by unique sequences that enable the binding of initiation proteins. This binding event triggers a cascade of processes culminating in the unwinding of the double helix into individual strands at the selected region (oriC sequence)[147,148]. DNA replication is orchestrated by an array of enzymes and proteins, among which gyrases play a key role by modifying the tertiary structure of DNA through negative super-coiling, thereby facilitating the functioning of helicase. Gyrases facilitate the functioning of the replisome, the molecular machinery upon which replication occurs. Various enzymes rigorously modulate the replisome activity to ensure the precision of DNA replication. This multienzyme complex comprises three catalytic compartments. The first compartment is the helicase−primase complex, responsible for unwinding the DNA strands into a replication fork and synthesizing RNA primers on the lagging strand. The second one is the core complex, harboring DNA polymerase III and facilitating the synthesis of complementary DNA strands, continuously in the case of the leading strand. However, the synthesis of the complementary strands on the lagging strand occurs discontinuously, involving the formation

of short DNA fragments known as Okazaki fragments. Primers are later replaced by DNA polymerase I, leading to the formation of a complete double strand. The final step in this complex process involves the sealing of the DNA fragments, a task accomplished by DNA ligase. The clamp loader complex forms the last compartment, which aids the core complex in its functions (Fig. 13). Many enzymes are responsible for DNA replication and are highly conserved across bacteria, including mycobacteria[148,149]. Within the portfolio of available anti-TB treatments, the FQ family stands as a unique group targeting DNA synthesis and repair through the inhibition of DNA gyrase (EC:5.6.2.2), undermining the DNA replication processes[150,151].

Benzimidazole urea derivatives are promising DNA gyrase inhibitors, with SPR720 (fobrepodacin) currently undergoing clinical trials. SPR720 (Table 3), a stable phosphate prodrug of SPR719, functions through a mechanism distinct to FQ, binding to the ATP subunit of DNA gyrase. In vitro activity of SPR719 (Mtb $H_{37}R_v$ MIC_{90} = 0.28−0.58 μmol/L) is approximately three times lower than moxifloxacin from the FQ family, but SPR720 prodrug and moxifloxacin showed similar efficacy in vivo[152,153]. Benzimidazole urea derivatives were first described as antimicrobial agents active against a broad spectrum of G+ and G-bacteria. Subsequent structural modifications focused on exploring the influence of substitution in positions 2, 5, 6 and 7 of the benzimidazole core in relationship to activity against S. aureus and other bacteria (Fig. 14). Ethyl urea in position 2 was found to be metabolically unstable, necessitating its replacement. However,

several urea mimics were inactive, except for the carbamoyl analogue which also revealed lower metabolic stability. For this reason, the ethylurea was preserved for sequential structural modifications. Nitrogen-containing heterocyclic compounds were favored in position 5, specifically pyridin-3-yl, pyrimidin-5-yl, and 2-(2-hydroxypropan-2-yl)pyrimidin-5-yl. The heterocyclic nitrogen played a pivotal role in the hydrogen bond formation with R136 of DNA gyrase subunit B (GyrB) from E. coli and R144 of GyrB from S. aureus. Position 6 tolerated a wide range of substituents; notably, fluorine derivatives exhibited slightly higher activity, suggesting enhanced permeability through the bacterial cell envelope. Position 7 accommodated preferably pyrazol-1-yl or tetrahydrofuran-2-yl [in (R)-configuration], allowing intramolecular hydrogen bonding with NH of benzimidazole moiety[154−156].

6. Anti-TB agents with miscellaneous mechanisms of action

Riminophenazines, a class of antibiotics represented by clofazimine (Mtb $H_{37}R_v$ MIC_{90} = 0.255 μmol/L 7 days (Table 2)[157], have been investigated for the treatment of infections caused by Mycobacterium leprae. Clofazimine was originally developed as a drug against Mtb, but it was discontinued due to low in vivo activity[158,159]. The drug was off-labeled as part of a combination regimen to treat DR-TB in Bangladesh[160], demonstrating good efficacy and reducing the treatment duration. Clofazimine is currently listed in the standardized regimen for DR-TB according
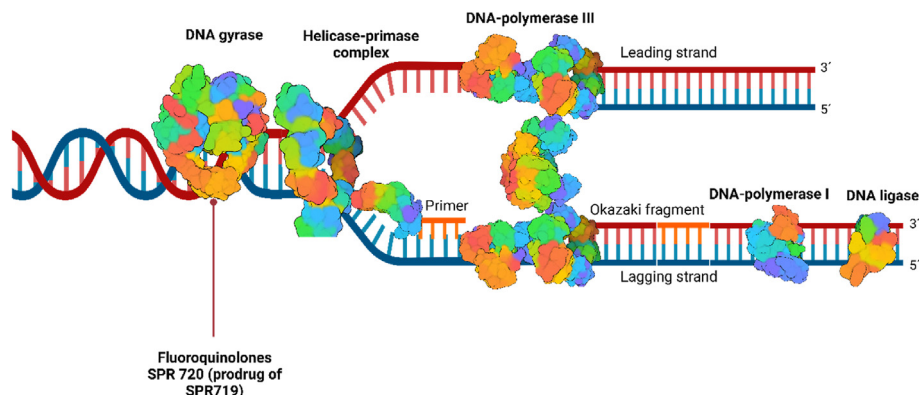

Figure 13 Mycobacterial replication fork as a drug target is a semi-conservative process in which two double strands of new DNA are formed, each carrying one original and one new strand. SPR720 and FQ are paired with its target enzyme by the red line.
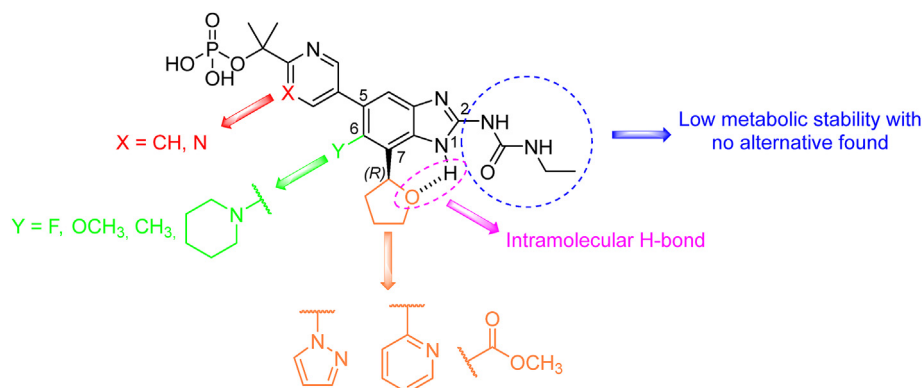

Figure 14 Insight into benzimidazole-urea derivatives structurally related to SPR720.

to WHO (Table 1) and Group B of the individualized regimen (Table 2). The MOA of riminophenazines is not fully understood; one hypothesis suggests the involvement of the drug in the intracellular redox cycle and the subsequent formation of reactive oxygen species that induce oxidative stress. The second hypothesis assumes the competition of clofazimine with MK for the enzyme type II NADH oxidoreductase (EC: 1.6.5.9), which functions early in the mycobacterial respiratory chain[159]. A major issue of clofazimine administration is associated with adverse side effects, mainly the discoloration of skin tissues caused by the deposition of this highly lipophilic drug ($clogP = 7.7$)[157−162]. The main goal of current drug development efforts has been to mitigate such undesirable effects, and this was successfully met in TBI-166 (Table 3). p-Chlorophenyl in clofazimine was replaced with a 2-methoxypyridin-3-yl moiety linked to the 2-amino group of the riminophenazine scaffold. This modification resulted in a reduction of lipophilicity ($clogP = 6.85$) and diminishing skin discoloration while at the same time slightly improving the activity (Mtb H$_{37}$R$_v$ MIC$_{90}$ = 0.027 μmol/L 7 days)[157,162]. Possible structural modifications of clofazimine have been studied since its discovery in the 1950's (Fig. 15). Simplification of the tricyclic arrangement by the omission of one benzene ring reduced the efficacy[163]. Aromatic amines were preferred in position 2, with pyridyl derivatives showing more activity than phenyl congeners[157,162,164]. Substitution of the imine nitrogen in position 3 with saturate cycles or branched alkyls improved the activity and physicochemical properties compared to aromatic counterparts[157,162,164−169]. Cyclopropyl or aromatic rings (like in TBI-166) were tolerated in position 5[169].

GSK2556286 (GSK286, Table 3) is a pyrimidine-2,4-dione derivative discovered *via* the high-throughput screening of compounds, with unknown MOA, against Mtb-infected macrophages. Based on the generated drug-resistant mutants, the putative MOA

lies in the alteration of cholesterol catabolism. A total 29 spontaneous GSK-286 resistant mutants were generated, out of which 14 possess a mutation in the *Rv1625c* gene, encoding class IIIa membrane-anchored adenylyl cyclase (cya, EC: 4.6.1.1), an important enzyme in the synthesis cyclic adenosine monophosphate (cAMP). cAMP serves as a second messenger, negatively regulating cholesterol utilization. The proposed MOA is consistent with experimental observations; the MIC values in cholesterol medium (with cholesterol being the sole carbon source) were significantly lowered (Mtb H$_{37}$R$_v$ MIC$_{90}$ = 2.12 μmol/L 7 days) compared to the glucose medium (Mtb H$_{37}$R$_v$ MIC$_{90}$ >125 μmol/L 7 days)[170−172].

Compound GSK839 (Table 3) was patented in 2017 as anti-TB agent inhibiting tryptophan synthase (EC: 4.2.1.20). This enzyme complex is responsible for the last two steps of L-tryptophan biosynthesis, allowing Mtb to supply L-tryptophan on its own and thus increasing its ability to survive in diverse environments. GSK839 exhibited an extracellular anti-TB activity value of Mtb H$_{37}$R$_v$ MIC = 0.07−0.16 μmol/L 7 days[173]. The compound represents four regions of interest that were inspected in detail by medicinal-chemistry principles, specifically the side chain of the amide, the benzenesulfonamide moiety, the 2H-tetrazole moiety, and the pyridine-2-yl moiety (Fig. 16). As for the side chain of the amide, the 2-hydroxyethyl chain proved to be the most potent, tolerating also nitrile or primary amide group. Shortening or elongation of the chain led to a decrease in efficacy. The benzenesulfonamide moiety was also examined, proving that the introduction of fluorine in position 3 or two fluorines in positions 2 and 6 of the phenyl ring is beneficial. Replacement of the 2H-tetrazole scaffold with 1H-1,2,3-triazole maintained the efficacy. Replacement of the pyridine-2-yl moiety with phenyl resulted in a slight increase in activity and lipophilicity. Additionally, the exchange for saturated cycles, specifically 4,4-difluorocyclohexyl and tetrahydropyran-2-yl, was tolerated[173].
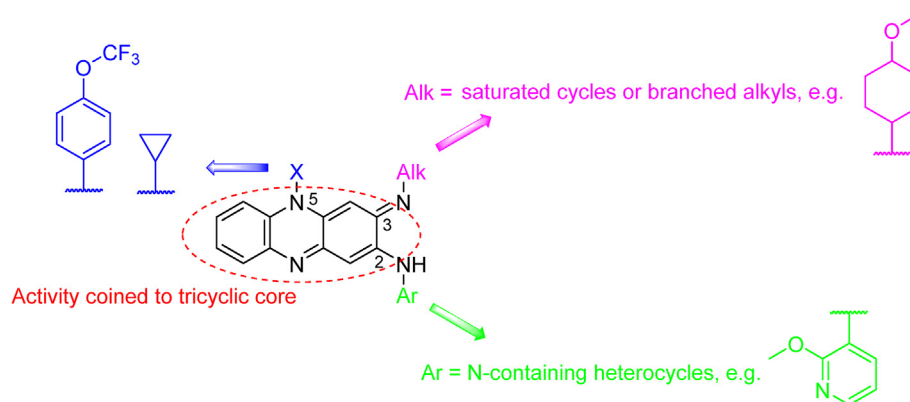

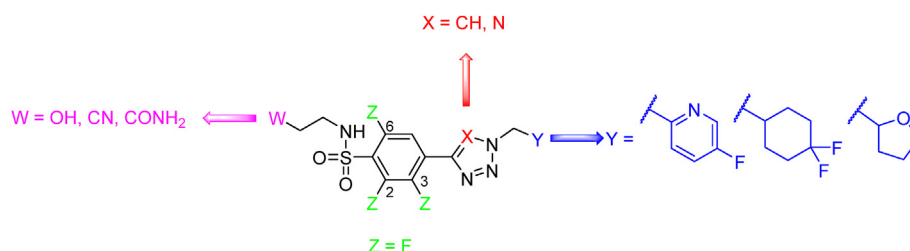**Figure 15** TBI-166 and structure−activity relationships of riminophenazines.

Figure 16 Tolerated changes to GSK839 preserving high anti-TB activity.

7.   Conclusions

TB remains a pervasive infectious disease with profound implications for public health and economies worldwide. The COVID-19 pandemic exacerbated the number of infected with TB, making both the diagnosis and treatment of TB less accessible in many countries, thereby increasing the risk of spreading DS-TB and MDR-TB cases[174−176]. The WHO emphasized the urgent need for intensified research to identify and develop new drugs and regimens that can lead to treatment shortening[175]. The increasing incidence of drug resistance in TB treatment is a critical indicator of the need for drugs with novel MOA. The important aspect to consider when developing new drugs is to shorten the treatment duration. A recent global surge in anti-TB research efforts led to the discovery of numerous potent molecules annually, yet only a fraction advance to late preclinical phases, and fewer will progress to clinical trials. Indeed, only three new drugs have been approved for the treatment of TB; namely BDQ, delamanid and, most recently, pretomanid, have been marketed. This challenge arises from the rigorous demands of creating compelling and safe drug candidates, with optimal pharmacokinetic and pharmacodynamic profiles, ideally endowed with novel MOA capable of treating DR-TB. The development hurdles are exacerbated by the unique lipophilic cell envelope of the *Mtb*. Besides, *Mtb* is an intracellular pathogen, requiring the drug to act inside the macrophage and being non-toxic to human cells at the same time[177]. The absence of reliable predictive models for mycobacterial cell wall permeation hampers successful biochemical screening. Therefore, whole-cell screening is an important component in developing potential new drugs, but the complexity of target identification and difficulty in hitting optimization are known limiting factors. This review highlighted the current state of anti-TB small molecules, focusing on those in late-stage preclinical development or clinical testing.

   Another factor that must be taken into account in the development of potential drugs is the requirement to act on slowly growing or nonreplicating bacteria. Most *in vivo* experiments performed in the development of anti-TB agents focus on determining efficacy in an acute infection model using BALB/c mice as model organisms, which is an excellent model for primary screening. However, it does not provide information on efficacy in the case of LTBI. Another issue with the use of BALB/c mice as a model organism is the different pathology of the disease compared to human, where the formation of granulomas (multicellular structures resulting from the immune response) is typical for the most common pulmonary form of TB. Pulmonary granulomas impose a significant barrier to drug permeation, with the diffused highly protein-rich lipophilic molecules. The use of C3HeB/FeJ mice, which develop granulomas during infection, appears to be a more advantageous model organism that provides more accurate information, yet most currently developed compounds continue to be tested using BALB/c mice model[178−182]. To promote the design of novel anti-TB agents, considering the complex environment in which the compounds must permeate before reaching the target cellular structure, a new metric has been proposed. This approach addresses the prediction of compound binding to caseum, which is pivotal for estimating permeation through the caseous environment of granulomas and necrotic lesions. The caseum binding is predicted based on c*log*P, the count of aromatic rings, and the count of sp^2 carbons in the molecule[181]. Despite this obstacle and slow progress, the pharmaceutical landscape has witnessed a surge in enthusiasm for the development of innovative

anti-TB agents. Currently, 19 promising drug candidates are undergoing clinical trials. Still, there is a scarcity of promising agents boasting novel MOA against MDR-TB infections.

   Phenotypic drug discovery is one of the main strategies used in the development of new anti-TB agents, yet it is hampered by difficulties in elucidating the specific MOA. A technique used to resolve this issue is the generation of spontaneous drug-resistant mutants and their subsequent genome sequencing using data analysis. This approach is not always successful; therefore, for some candidates, their MOA remains elusive[183]. Other compounds are difficult to categorize due to the complexity of their MOA, aiming at multiple targets simultaneously. Although nearly all small molecules undergoing concurrent clinical evaluation have been identified using this method, additional obstacles persist beyond the identification mentioned above. Firstly, a significant portion of these identified hits acts on known targets for which cases of resistant infections are documented, thereby posing a high risk of cross-resistance, minimizing the attractiveness of such hits[184]. Another challenge is the difficulty in translating *in vitro* activity into *in vivo*[185]; a large proportion of identified new anti-TB agents fail at this step, partly due to the routine applied for cultivation in a nutrient-rich broth, which does not mimic the real environment within a living organism[186]. Many scientists have long endeavored to address these challenges by developing novel screening methods. One promising approach involves assessing the efficacy in *Mtb*-infected macrophages. While considerably more costly and complex, the data obtained provide significantly better insights into potential *in vivo* efficacy, primarily due to assay conditions closely resembling real-life scenarios within a living organism. Additionally, this approach offers insight into the toxicity of tested compounds towards mammalian cells[187,188]. The discovery of telacebec is a successful example of *Mtb*-infected macrophage testing applied for this drug[137,138].

   Another successful approach in the development of new anti-TB drugs is the repurposing of known therapeutics, wherein minor structural modification generates a new lead candidate capable of exhibiting efficacy against *Mtb* while maintaining the safety profile of the parent compound[189]. Sanfetrinem, an orally available tricyclic β-lactam antibiotic, is an example of the anti-TB clinical candidate discovered by this approach[190]. MBX-4888A was invented by delivering subtle structural modifications to spectinomycin. Indeed, MBX-4888A revealed decreased affinity to the mycobacterial efflux pump, which resulted in a higher intracellular concentration of the drug[109,112]. Another drug explored in the same way is lansoprazole, a proton pump inhibitor, which serves as a prodrug. Reduction of the sulfoxide moiety of lansoprazole to the sulphide forms an active agent[191].

   A critical aspect of TB drug discovery is evaluating the safety profile of the compounds, particularly related to potential drug−drug interactions. This concern is associated mainly with antiretrovirals, which are essential agents to treat HIV co-infection. Ensuring the safety and efficacy of new TB drugs, especially in combination with existing therapies, is indispensable for successful treatment outcomes and the prevention of further drug resistance.

   From a small molecule design perspective, 19 agents are currently undergoing clinical trials, with 8 introducing entirely new MOA. Notably, oxazolidinones dominate the clinical trials landscape, with delpazolid, sutezolid, and tedizolid in phase 2, TBI-223 in phase 1, and OTB-658 in preclinical studies. TBI-233 appears promising from a safety perspective, with a 10-fold decrease in inhibition of eukaryotic MP*S* while maintaining the same activity as LNZ. Another group of clinical candidates are

BDQ derivatives, whose development was aimed primarily at reducing the risk of QT interval prolongation, and this has been achieved by TBAJ-876. TBAJ-876, currently a phase 1 drug candidate, exhibits a superior safety profile and anti-TB activity comparable to BDQ. Among drug candidates with novel MOA, DprE1 inhibitors are prominent, represented by benzothiazinone derivatives like macozinone in phase 1 and BTZ-043 in phase 2 trials. While benzothiazinones act as covalent inhibitors of DprE1, two non-covalent inhibitors, namely OPC-167832 and TBA-7371, are currently ongoing phase 2 clinical trial testing. All DprE1 inhibitors except TBA-7371 show excellent *in vitro* activity in the low nanomolar range. Furthermore, QcrB subunit inhibitors of the cytochrome *bcc* complex, such as telacebec (phase 2), and TB47 (in preclinical studies), demonstrate efficacy comparable to DprE1 inhibitors.

The number of potential new drugs in preclinical studies continues to grow, increasing the odds of identifying more compounds that could advance to clinical trials. Finally, partnerships between academia and pharmaceutical companies are vital in the development of new anti-TB drug candidates. Organizations like TB-Alliance and initiatives like GSK's Tres Cantos Open Lab Foundation are crucial in advancing TB drug discovery. TB-Alliance is a non-profit organization established in 2000 that has made a significant contribution to bridging the private, academic, and philanthropic sectors. The GSK's project enables the use of private facilities, resources, and expertise to support independent research on infectious disease medicines. Despite considerable challenges, significant advances have been made in the development of new anti-TB candidates over the past decade, providing a positive outlook for the future of TB treatment.

Acknowledgments

Author contributions

Martin Kufa: Writing — review & editing, Writing — original draft, Visualization. Vladimir Finger: Writing — review & editing, Writing — original draft. Ondrej Kovar: Writing — review & editing, Writing — original draft. Ondrej Soukup: Writing — review & editing, Writing — original draft, Supervision, Funding acquisition. Carilyn Torruellas: Writing — review & editing, Writing — original draft. Jaroslav Roh: Writing — review & editing, Writing — original draft, Supervision, Funding acquisition. Jan Korabecny: Writing — review & editing, Writing — original draft, Visualization, Supervision, Funding acquisition.

Conflicts of interest

Authors declare no competing interest.

References

1. *Global tuberculosis report*. Available from: https://www.who.int/teams/global-tuberculosis-programme/tb-reports/global-tuberculosis-report-20232023. [Accessed 27 March 2024].

2. The top 10 causes of death. Available from: https://www.who.int/news-room/fact-sheets/detail/the-top-10-causes-of-death (accessed 2022-May-16).

3. Cohen A, Mathiasen VD, Schön T, Wejse C. The global prevalence of latent tuberculosis: a systematic review and meta-analysis. *Eur Respir J* 2019;**54**:1900655.

4. Tiemersma EW, van der Werf MJ, Borgdorff MW, Williams BG, Nagelkerke NJD. Natural history of tuberculosis: duration and fatality of untreated pulmonary tuberculosis in HIV negative patients: a systematic review. *PLoS One* 2011;**6**:e17601.

5. *WHO consolidated guidelines on tuberculosis. Module 4: treatment - drug-resistant tuberculosis treatment*. update. Available from: https://www.who.int/publications-detail-redirect/9789240063129, 2022. [Accessed 5 April 2023].

6. Torres NMC, Rodríguez JJQ, Andrade PSP, Arriaga MB, Netto EM. Factors predictive of the success of tuberculosis treatment: a systematic review with meta-analysis. *PLOS ONE* 2019;**14**:e0226507.

7. *Global tuberculosis report*. Available from: https://www.who.int/teams/global-tuberculosis-programme/tb-reports/global-tuberculosis-report-2022, 2022. [Accessed 4 April 2023].

8. Bea S, Lee H, Kim JH, Jang SH, Son H, Kwon JW, et al. Adherence and associated factors of treatment regimen in drug-susceptible tuberculosis patients. *Front Pharmacol* 2021;**12**:625078.

9. Nahid P, Mase SR, Migliori GB, Sotgiu G, Bothamley GH, Brozek JL, et al. Treatment of drug-resistant tuberculosis. An official ATS/CDC/ERS/IDSA clinical practice guideline. *Am J Respir Crit Care Med* 2019;**200**:e93−142.

10. *WHO treatment guidelines for drug-resistant tuberculosis*. update. Available from: https://www.who.int/publications-detail-redirect/9789241549639, 2016. [Accessed 5 April 2023].

11. WHO consolidated guidelines on drug-resistant tuberculosis treatment. Available from: https://www.who.int/publications-detail-redirect/9789241550529 (accessed 2023-April-5).

12. 2022 Report on TB Research Funding Trends. Treatment Action Group. Available from: https://www.treatmentactiongroup.org/resources/tbrd-report/tbrd-report-2022/(accessed 2023-April-6).

13. Diacon AH, Pym A, Grobusch MP, de los Rios JM, Gotuzzo E, Vasilyeva I, et al. Multidrug-resistant tuberculosis and culture conversion with bedaquiline. *N Engl J Med* 2014;**371**:723. 2.

14. Ryan NJ, Lo JH. Delamanid: first global approval. *Drugs* 2014;**74**:1041−5.

15. Keam SJ. Pretomanid: first approval. *Drugs* 2019;**79**:1797−803.

16. Kadura S, King N, Nakhoul M, Zhu H, Theron G, Köser CU, et al. Systematic review of mutations associated with resistance to the new and repurposed *Mycobacterium tuberculosis* drugs bedaquiline, clofazimine, linezolid, delamanid and pretomanid. *J Antimicrob Chemother* 2020;**75**:2031−43.

17. Harrison J, Cox JAG. Changing the rules of TB-drug discovery. *J Med Chem* 2019;**62**:10583−5.

18. Chiaradia L, Lefebvre C, Parra J, Marcoux J, Burlet-Schiltz O, Etienne G, et al. Dissecting the mycobacterial cell envelope and defining the composition of the native mycomembrane. *Sci Rep* 2017;**7**:12807.

19. Wellington S, Hung DT. The expanding diversity of *Mycobacterium tuberculosis* drug targets. *ACS Infect Dis* 2018;**4**:696−714.

20. Tiberi S, du Plessis N, Walzl G, Vjecha MJ, Rao M, Ntoumi F, et al. Tuberculosis: progress and advances in development of new drugs, treatment regimens, and host-directed therapies. *Lancet Infect Dis* 2018;**18**:e183−98.

21. Black TA, Buchwald UK. The pipeline of new molecules and regimens against drug-resistant tuberculosis. *J Clin Tuberc Other Mycobact Dis* 2021;**25**:100285.

22. Dartois VA, Rubin EJ. Anti-tuberculosis treatment strategies and drug development: challenges and priorities. *Nat Rev Microbiol* 2022;**20**:685−701.

23. Shetye GS, Franzblau SG, Cho S. New tuberculosis drug targets, their inhibitors, and potential therapeutic impact. *Transl Res* 2020;**220**:68−97.

24. Alsayed SSR, Gunosewoyo H. Tuberculosis: pathogenesis, current treatment regimens and new drug targets. *Int J Mol Sci* 2023;**24**:5202.

25. Timmins GS, Deretic V. Mechanisms of action of isoniazid. *Mol Microbiol* 2006;**62**:1220−7.

26. Zhang L, Zhao Y, Gao Y, Wu L, Gao R, Zhang Q, et al. Structures of cell wall arabinosyltransferases with the anti-tuberculosis drug ethambutol. *Science* 2020;**368**:1211−9.

27. Bhat ZS, Rather MA, Maqbool M, Lah HU, Yousuf SK, Ahmad Z. Cell wall: a versatile fountain of drug targets in *Mycobacterium tuberculosis*. *Biomed Pharmacother* 2017;**95**:1520−34.

28. Fukuda T, Matsumura T, Ato M, Hamasaki M, Nishiuchi Y, Murakami Y, et al. Critical roles for lipomannan and lipoarabinomannan in cell wall integrity of Mycobacteria and pathogenesis of tuberculosis. *mBio* 2013;**4**:e00472−12.

29. Koul A, Herget T, Klebl B, Ullrich A. Interplay between Mycobacteria and host signalling pathways. *Nat Rev Microbiol* 2004;**2**:189−202.

30. Hugonnet JE, Blanchard JS. Irreversible inhibition of the *Mycobacterium tuberculosis* β-lactamase by clavulanate. *Biochemistry* 2007;**46**:11998−2004.

31. Dinesh N, Sharma S, Balganesh M. Involvement of efflux pumps in the resistance to peptidoglycan synthesis inhibitors in *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2013;**57**:1941−3.

32. Brennan PJ, Nikaido H. The envelope of Mycobacteria. *Annu Rev Biochem* 1995;**64**:29−63.

33. Bansal-Mutalik R, Nikaido H. Mycobacterial outer membrane is a lipid bilayer and the inner membrane is unusually rich in diacyl phosphatidylinositol dimannosides. *Proc Natl Acad Sci U S A* 2014;**111**:4958−63.

34. Logsdon MM, Aldridge BB. Stable regulation of cell cycle events in Mycobacteria: insights from inherently heterogeneous bacterial populations. *Front Microbiol* 2018;**9**:514.

35. De Lorenzo S, Alffenaar JW, Sotgiu G, Centis R, D'Ambrosio L, Tiberi S, et al. Efficacy and safety of meropenem-clavulanate added to linezolid-containing regimens in the treatment of MDR-/XDR-TB. *Eur Respir J* 2013;**41**:1386−92.

36. Dubée V, Triboulet S, Mainardi JL, Ethève-Quelquejeu M, Gutmann L, Marie A, et al. Inactivation of *Mycobacterium tuberculosis* L,D-transpeptidase LdtMt1 by carbapenems and cephalosporins. *Antimicrob Agents Chemother* 2012;**56**:4189−95.

37. Martelli G, Pessatti TB, Steiner EM, Cirillo M, Caso C, Bisognin F, et al. *N*-Thio-β-lactams targeting L,D-transpeptidase-2, with activity against drug-resistant strains of *Mycobacterium tuberculosis*. *Cell Chem Biol* 2021;**28**:1321−32.

38. Cordillot M, Dubée V, Triboulet S, Dubost L, Marie A, Hugonnet JE, et al. *In vitro* cross-linking of *Mycobacterium tuberculosis* peptidoglycan by L,D-transpeptidases and inactivation of these enzymes by carbapenems. *Antimicrob Agents Chemother* 2013;**57**:5940−5.

39. WHO consolidated guidelines on tuberculosis, module 4: treatment - drug-resistant tuberculosis treatment. Available from: https://www.who.int/publications-detail-redirect/9789240007048 (accessed 2022-May-26).

40. Pipeline. Working group for new TB drugs. Available from: https://www.newtbdrugs.org/pipeline/clinical (accessed 2022-May-30).

41. Aguirre DB, Bates RH, Rio RGD, Losana AM, García SR. Sanfetrinem or a salt or ester thereof for use in treating mycobacterial infection. *WO2018206466A1* 2018. Available from: https://patents.google.com/patent/WO2018206466A1/en. [Accessed 28 June 2022].

42. Marrakchi H, Lanéelle G, Quémard AY. InhA, a target of the antituberculous drug isoniazid, is involved in a mycobacterial fatty acid elongation system, FAS-II. *Microbiology* 2000;**146**:289−96.

43. Wang F, Langley R, Gulten G, Dover LG, Besra GS, Jacobs WR, et al. Mechanism of thioamide drug action against tuberculosis and leprosy. *J Exp Med* 2007;**204**:73−8.

44. Quemard A, Dessen A, Sugantino M, Jacobs William R, Sacchettini JC, Blanchard JS. Binding of catalase-peroxidase-activated isoniazid to wild-type and mutant *Mycobacterium tuberculosis* enoyl-ACP reductases. *J Am Chem Soc* 1996;**118**:1561−2.

45. Hicks ND, Carey AF, Yang J, Zhao Y, Fortune SM. Bacterial genome-wide association identifies novel factors that contribute to ethionamide and prothionamide susceptibility in *Mycobacterium tuberculosis*. *mBio* 2019;**10**:e00616-19.

46. Vilchèze C, Jacobs WR. Resistance to isoniazid and ethionamide in *Mycobacterium tuberculosis*: genes, mutations, and causalities. *Microbiol Spectr* 2014;**2**:4.

47. Scardigli A, Caminero JA, Sotgiu G, Centis R, D'Ambrosio L, Migliori GB. Efficacy and tolerability of ethionamide versus prothionamide: a systematic review. *Eur Respir J* 2016;**48**:946−52.

48. Guieu B, Jourdan JP, Dreneau A, Willand N, Rochais C, Dallemagne P. Desirable drug−drug interactions or when a matter of concern becomes a renewed therapeutic strategy. *Drug Discov Today* 2021;**26**:315−28.

49. Blondiaux N, Moune M, Desroses M, Frita R, Flipo M, Mathys V, et al. Reversion of antibiotic resistance in *Mycobacterium tuberculosis* by spiroisoxazoline SMARt-420. *Science* 2017;**355**:1206−11.

50. Porras De Francisco E, Remuiñan-Blanco MJ, Bourotte M, Deprez B, Willand N. *WO2019034700 Novel compounds*. Available from: https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2019034700, 2019. [Accessed 16 April 2024].

51. Willand N, Deprez B, Baulard A, Brodin P, Desroses MF, Agouridas-Dutot L. *Spiroisoxazoline compounds having an activity potentiating the activity of an antibiotic*. Available from: https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2014096369, 2014. [Accessed 16 April 2024].

52. Gawad J, Bonde C. Decaprenyl-phosphoryl-ribose 2'-epimerase (DprE1): challenging target for antitubercular drug discovery. *Chem Cent J* 2018;**12**:72.

53. Piton J, Foo CSY, Cole ST. Structural studies of *Mycobacterium tuberculosis* DprE1 interacting with its inhibitors. *Drug Discov Today* 2017;**22**:526−33.

54. Makarov V, Mikušová K. Development of macozinone for TB treatment: an update. *Appl Sci* 2020;**10**:2269.

55. Makarov V, Lechartier B, Zhang M, Neres J, Sar AM, Raadsen SA, et al. Towards a new combination therapy for tuberculosis with next generation benzothiazinones. *EMBO Mol Med* 2014;**6**:372−3.

56. Makarov V, Manina G, Mikusova K, Möllmann U, Ryabova O, Saint-Joanis B, et al. Benzothiazinones kill *Mycobacterium tuberculosis* by blocking arabinan synthesis. *Science* 2009;**324**:801−4.

57. Richter A, Rudolph I, Möllmann U, Voigt K, Chung C, Singh OMP, et al. Novel insight into the reaction of nitro, nitroso and hydroxylamino benzothiazinones and of benzoxacinones with *Mycobacterium tuberculosis* DprE1. *Sci Rep* 2018;**8**:13473.

58. Wang A, Du N, Song H, Zhang Y, Zhong X, Wu J, et al. Design, synthesis and antitubercular activity of novel *N*-(amino)piperazinyl benzothiazinones with improved safety. *Eur J Med Chem* 2023;**258**:115545.

59. Gao C, Ye TH, Wang NY, Zeng XX, Zhang LD, Xiong Y, et al. Synthesis and structure−activity relationships evaluation of benzothiazinone derivatives as potential anti-tubercular agents. *Bioorg Med Chem Lett* 2013;**23**:4919−22.

60. Shirude PS, Shandil R, Sadler C, Naik M, Hosagrahara V, Hameed S, et al. Azaindoles: noncovalent DprE1 inhibitors from scaffold morphing efforts, kill *Mycobacterium tuberculosis* and are efficacious *in vivo*. *J Med Chem* 2013;**56**:9701−8.

61. Chikhale RV, Barmade MA, Murumkar PR, Yadav MR. Overview of the development of DprE1 inhibitors for combating the menace of tuberculosis. *J Med Chem* 2018;**61**:8563−93.

62. Hariguchi N, Chen X, Hayashi Y, Kawano Y, Fujiwara M, Matsuba M, et al. OPC-167832, a novel carbostyril derivative with

potent antituberculosis activity as a DprE1 inhibitor. *Antimicrob Agents Chemother* 2020;**64**:e02020-19.

63. Shimizu H, Kawano Y, Ishikawa S, Uematsu Y, Shinohara T, Itotani M, et al. *Heterobicyclic compounds and their use for the treatment of tuberculosis.* Available from: https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2016031255, 2016. [Accessed 7 May 2024].

64. Chatterji M, Shandil R, Manjunatha MR, Solapure S, Ramachandran V, Kumar N, et al. 1,4-Azaindole, a potential drug candidate for treatment of tuberculosis. *Antimicrob Agents Chemother* 2014;**58**:53251.

65. Shirude PS, Shandil RK, Manjunatha MR, Sadler C, Panda M, Panduga V, et al. Lead optimization of 1,4-azaindoles as antimycobacterial agents. *J Med Chem* 2014;**57**:5728−37.

66. Shirude PS, Shandil RK, Manjunatha MR, Sadler C, Panda M, Panduga V, et al. Lead optimization of 1,4-Azaindoles as antimycobacterial agents. *J Med Chem* 2014;**57**:5728−37.

67. Abrahams KA, Batt SM, Gurcha SS, Veerapen N, Bashiri G, Besra GS. DprE2 is a molecular target of the anti-tubercular nitroimidazole compounds pretomanid and delamanid. *Nat Commun* 2023;**14**:3828.

68. Su CC, Klenotic PA, Bolla JR, Purdy GE, Robinson CV, Yu EW. MmpL3 is a lipid transporter that binds trehalose monomycolate and phosphatidylethanolamine. *Proc Natl Acad Sci U S A* 2019;**116**:11241−6.

69. Degiacomi G, Benjak A, Madacki J, Boldrin F, Provvedi R, Palù G, et al. Essentiality of mmpL3 and impact of its silencing on *Mycobacterium tuberculosis* gene expression. *Sci Rep* 2017;**7**:43495.

70. Tullius MV, Harmston CA, Owens CP, Chim N, Morse RP, McMath LM, et al. Discovery and characterization of a unique mycobacterial heme acquisition system. *Proc Natl Acad Sci U S A* 2011;**108**:5051−6.

71. Lima VMF, Bonato VLD, Lima KM, Dos Santos SA, Dos Santos RR, Gonçalves EDC, et al. Role of trehalose dimycolate in recruitment of cells and modulation of production of cytokines and NO in tuberculosis. *Infect Immun* 2001;**69**:5305−12.

72. Li W, Obregón-Henao A, Wallach JB, North EJ, Lee RE, Gonzalez-Juarrero M, et al. Therapeutic potential of the *Mycobacterium tuberculosis* mycolic acid transporter, MmpL3. *Antimicrob Agents Chemother* 2016;**60**:5198−207.

73. Protopopova M, Hanrahan C, Nikonenko B, Samala R, Chen P, Gearhart J, et al. Identification of a new antitubercular drug candidate, SQ109, from a combinatorial library of 1,2-ethylenediamines. *J Antimicrob Chemother* 2005;**56**:968−74.

74. Li W, Upadhyay A, Fontes FL, North EJ, Wang Y, Crans DC, et al. Novel insights into the mechanism of inhibition of MmpL3, a target of multiple pharmacophores in *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2014;**58**:6413−23.

75. McNeil MB, Chettiar S, Awasthi D, Parish T. Cell wall inhibitors increase the accumulation of rifampicin in *Mycobacterium tuberculosis*. *Access Microbiol* 2019;**1**:e000006.

76. Chen P, Gearhart J, Protopopova M, Einck L, Nacy CA. Synergistic interactions of SQ109, a new ethylene diamine, with front-line antitubercular drugs *in vitro*. *J Antimicrob Chemother* 2006;**58**:332−7.

77. Reddy VM, Einck L, Andries K, Nacy CA. *In vitro* interactions between new antitubercular drug candidates SQ109 and TMC207. *Antimicrob Agents Chemother* 2010;**54**:2840−6.

78. Sacksteder KA, Protopopova M, Barry CE, Andries K, Nacy CA. Discovery and development of SQ109: a new antitubercular drug with a novel mechanism of action. *Future Microbiol* 2012;**7**:823−7.

79. Zhang B, Li J, Yang X, Wu L, Zhang J, Yang Y, et al. Crystal structures of membrane transporter MmpL3, an anti-TB drug target. *Cell* 2019;**176**:636−48.

80. Li K, Schurig-Briccio LA, Feng X, Upadhyay A, Pujari V, Lechartier B, et al. Multitarget drug discovery for tuberculosis and other infectious diseases. *J Med Chem* 2014;**57**:3126−39.

81. Russell JB, Cook GM. Energetics of bacterial growth: balance of anabolic and catabolic reactions. *Microbiol Rev* 1995;**59**:15.

82. Laughlin ZT, Nandi S, Dey D, Zelinskaya N, Witek MA, Srinivas P, et al. 50S S subunit recognition and modification by the *Mycobacterium tuberculosis* ribosomal RNA methyltransferase TlyA. *Proc Natl Acad Sci U S A* 2022;**119**:e2120352119.

83. Kushwaha AK, Bhushan S. Unique structural features of the Mycobacterium ribosome. *Prog Biophys Mol Biol* 2020;**152**:15−24.

84. Hentschel J, Burnside C, Mignot I, Leibundgut M, Boehringer D, Ban N. The complete structure of the Mycobacterium smegmatis 70S S ribosome. *Cell Rep* 2017;**20**:149−60.

85. Ruiz P, Rodríguez-Cano F, Zerolo FJ, Casal M. Investigation of the *in vitro* activity of streptomycin against *Mycobacterium tuberculosis*. *Microb Drug Resist* 2002;**8**:147−9.

86. Recht MI, Douthwaite S, Puglisi JD. Basis for prokaryotic specificity of action of aminoglycoside antibiotics. *EMBO J* 1999;**18**:3133−8.

87. Vianna JF, Bezerra KS, Oliveira JIN, Albuquerque EL, Fulco UL. Binding energies of the drugs capreomycin and streptomycin in complex with tuberculosis bacterial ribosome subunits. *Phys Chem Chem Phys* 2019;**21**:19192−200.

88. Zahedi Bialvaei A, Rahbar M, Yousefi M, Asgharzadeh M, Samadi Kafil H. Linezolid: a promising option in the treatment of Gram-positives. *J Antimicrob Chemother* 2017;**72**:354−64.

89. Wehrli W. Rifampin: mechanisms of action and resistance. *Rev Infect Dis* 1983;**5**:S407−11.

90. Arnold A, Cooke GS, Kon OM, Dedicoat M, Lipman M, Loyse A, et al. Adverse effects and choice between the injectable agents amikacin and capreomycin in multidrug-resistant tuberculosis. *Antimicrob Agents Chemother* 2017;**61**:e02586-16.

91. Guo S, Wang B, Fu L, Chen X, Zhang W, Huang H, et al. *In vitro* and *in vivo* activity of oxazolidinone candidate OTB-658 against *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2021;**65**:e0097421.

92. Zhang S, Chen J, Cui P, Shi W, Shi X, Niu H, et al. *Mycobacterium tuberculosis* mutations associated with reduced susceptibility to linezolid. *Antimicrob Agents Chemother* 2016;**60**:2542−4.

93. Eckmann C, Dryden M. Treatment of complicated skin and soft-tissue infections caused by resistant bacteria: value of linezolid, tigecycline, daptomycin and vancomycin. *Eur J Med Res* 2010;**15**:554.

94. Zhao Q, Xin L, Liu Y, Liang C, Li J, Jian Y, et al. Current landscape and future perspective of oxazolidinone scaffolds containing antibacterial drugs. *J Med Chem* 2021;**64**:10557−80.

95. Ndukwe ARN, Wiedbrauk S, Boase NRB, Fairfull-Smith KE. Strategies to improve the potency of oxazolidinones towards bacterial biofilms. *Chem Asian J* 2022;**17**:e202200201.

96. Fernandes GFS, Scarim CB, Kim SH, Wu J, Castagnolo D. Oxazolidinones as versatile scaffolds in medicinal chemistry. *RSC Med Chem* 2023;**14**:823−47.

97. Foti C, Piperno A, Scala A, Giuffrè O. Oxazolidinone antibiotics: chemical, biological and analytical aspects. *Molecules* 2021;**26**:4280.

98. Flanagan S, McKee EE, Das D, Tulkens PM, Hosako H, Fiedler-Kelly J, et al. Nonclinical and pharmacokinetic assessments to evaluate the potential of tedizolid and linezolid to affect mitochondrial function. *Antimicrob Agents Chemother* 2015;**59**:178−85.

99. Negatu DA, Aragaw WW, Cangialosi J, Dartois V, Dick T. Side-by-side profiling of oxazolidinones to estimate the therapeutic window against mycobacterial infections. *Antimicrob Agents Chemother* 2023;**67**:e0165522.

100. McKee EE, Ferguson M, Bentley AT, Marks TA. Inhibition of mammalian mitochondrial protein synthesis by oxazolidinones. *Antimicrob Agents Chemother* 2006;**50**:2042−9.

101. Poce G, Cocozza M, Consalvi S, Biava M. SAR analysis of new anti-TB drugs currently in pre-clinical and clinical development. *Eur J Med Chem* 2014;**86**:335−51.

102. Jadhavar PS, Vaja MD, Dhameliya TM, Chakraborti AK. Oxazolidinones as anti-tubercular agents: discovery, development and future perspectives. *Curr Med Chem* 2015;**22**:4379−97.

103. Zhao H, Wang B, Fu L, Li G, Lu H, Liu Y, et al. Discovery of a conformationally constrained oxazolidinone with improved safety and efficacy profiles for the treatment of multidrug-resistant tuberculosis. *J Med Chem* 2020;**63**:9316−39.

104. Wallis RS, Jakubiec W, Kumar V, Bedarida G, Silvia A, Paige D, et al. Biomarker-assisted dose selection for safety and efficacy in early development of PNU-100480 for tuberculosis. *Antimicrob Agents Chemother* 2011;**55**:567−74.

105. Zong Z, Jing W, Shi J, Wen S, Zhang T, Huo F, et al. Comparison of *In vitro* activity and MIC distributions between the novel oxazolidinone delpazolid and linezolid against multidrug-resistant and extensively drug-resistant *Mycobacterium tuberculosis* in China. *Antimicrob Agents Chemother* 2018;**62**:e00165-18.

106. Choi Y, Lee SW, Kim A, Jang K, Nam H, Cho YL, et al. Safety, tolerability and pharmacokinetics of 21 day multiple oral administration of a new oxazolidinone antibiotic, LCB01-0371, in healthy male subjects. *J Antimicrob Chemother* 2018;**73**:183−90.

107. TBI-223: a safer oxazolidinone in pre-clinical development for tuberculosis. Available from:: https://www.abstractsonline.com/pp8/#!/4358/presentation/6174 (accessed 2022-August-10).

108. Ruiz P, Causse M, Vaquero M, Casal M. *In vitro* activity of tedizolid against *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2019;**63**:e01939-18.

109. Lee RE, Hurdle JG, Liu J, Bruhn DF, Matt T, Scherman MS, et al. Spectinamides: a new class of semisynthetic antituberculosis agents that overcome native drug efflux. *Nat Med* 2014;**20**:152−8.

110. Liu J, Bruhn DF, Lee RB, Zheng Z, Janusic T, Scherbakov D, et al. Structure−activity relationships of spectinamide antituberculosis agents: a dissection of ribosomal inhibition and native efflux avoidance contributions. *ACS Infect Dis* 2017;**3**:72−88.

111. Scarff JM, Waidyarachchi SL, Meyer CJ, Lane DJ, Chai W, Lemmon MM, et al. Aminomethyl spectinomycins: a novel antibacterial chemotype for biothreat pathogens. *J Antibiot (Tokyo)* 2019;**72**:693−701.

112. Robertson GT, Scherman MS, Bruhn DF, Liu J, Hastings C, McNeil MR, et al. Spectinamides are effective partner agents for the treatment of tuberculosis in multiple mouse infection models. *J Antimicrob Chemother* 2017;**72**:770−7.

113. Wagh S, Rathi C, Lukka PB, Parmar K, Temrikar Z, Liu J, et al. Model-based exposure-response assessment for spectinamide 1810 in a mouse model of tuberculosis. *Antimicrob Agents Chemother* 2021;**65**:e01744-20.

114. Tenero D, Derimanov G, Carlton A, Tonkyn J, Davies M, Cozens S, et al. First-time-in-human study and prediction of early bactericidal activity for GSK3036656, a potent leucyl-tRNA synthetase inhibitor for tuberculosis treatment. *Antimicrob Agents Chemother* 2019;**63**:e00240−19.

115. Palencia A, Li X, Bu W, Choi W, Ding CZ, Easom EE, et al. Discovery of novel oral protein synthesis inhibitors of *Mycobacterium tuberculosis* that target leucyl-tRNA synthetase. *Antimicrob Agents Chemother* 2016;**60**:6271−80.

116. Li X, Hernandez V, Rock FL, Choi W, Mak YSL, Mohan M, et al. Discovery of a potent and specific M. tuberculosis leucyl-tRNA synthetase inhibitor: (*S*)-3-(aminomethyl)-4-chloro-7-(2-hydroxyethoxy)benzo[*c*][1,2]oxaborol-1(3H)-ol (GSK656). *J Med Chem* 2017;**60**:8011−26.

117. Alley MRK, Barros-Aguirre D, Giordano I, Hernandez V, Li X, Plattner JJ, et al. *Benzoxaborole compounds and uses thereof*. Available from: https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2016128949, 2016. [Accessed 16 April 2024].

118. Cook GM, Hards K, Dunn E, Heikal A, Nakatani Y, Greening C, et al. Oxidative phosphorylation as a target space for tuberculosis: success, caution, and future directions. *Microbiol Spectr* 2017;**5**. Available from: https://doi.org/10.1128/microbiolspec.tbtb2-0014-2016.

119. Cook GM, Hards K, Vilchèze C, Hartman T, Berney M. Energetics of respiration and oxidative phosphorylation in Mycobacteria. *Microbiol Spectr* 2014;**3**. Available from: https://doi.org/10.1128/microbiolspec.mgm2-0015-2013.

120. Bald D, Villellas C, Lu P, Koul A. Targeting energy metabolism in *Mycobacterium tuberculosis*, a new paradigm in antimycobacterial drug discovery. *mBio* 2017;**8**:e00272−17.

121. Lounis N, Vranckx L, Gevers T, Kaniga K, Andries K. *In vitro* culture conditions affecting minimal inhibitory concentration of bedaquiline against. *M Tuberculosis Med Mal Infect* 2016;**460**:220−5.

122. Mahajan R. Bedaquiline: first FDA-approved tuberculosis drug in 40 years. *Int J Appl Basic Med Res* 2013;**3**:1−2.

123. Sutherland HS, Tong AST, Choi PJ, Blaser A, Conole D, Franzblau SG, et al. 3,5-Dialkoxypyridine analogues of bedaquiline are potent antituberculosis agents with minimal inhibition of the hERG channel. *Bioorg Med Chem* 2019;**27**:1292−307.

124. Guo Q, Bi J, Lin Q, Ye T, Wang Z, Wang Z, et al. Whole genome sequencing identifies novel mutations associated with bedaquiline resistance in *Mycobacterium tuberculosis*. *Front Cel Infect Microbiol* 2022;**12**:807095.

125. Ismail N, Ismail NA, Omar SV, Peters RPH. *In vitro* study of stepwise acquisition of Rv0678 and atpE mutations conferring bedaquiline resistance. *Antimicrob Agents Chemother* 2019;**63**:e00292−19.

126. Sutherland HS, Tong AST, Choi PJ, Blaser A, Franzblau SG, Cooper CB, et al. Variations in the C-unit of bedaquiline provides analogues with improved biology and pharmacology. *Bioorg Med Chem* 2020;**28**:115213.

127. Fox GJ, Menzies D. A review of the evidence for using bedaquiline (TMC207) to treat multi-drug resistant tuberculosis. *Infect Dis Ther* 2013;**2**:123−44.

128. Tong AST, Choi PJ, Blaser A, Sutherland HS, Tsang SKY, Guillemont J, et al. 6-Cyano analogues of bedaquiline as less lipophilic and potentially safer diarylquinolines for tuberculosis. *ACS Med Chem Lett* 2017;**8**:1019−24.

129. Guillemont J, Meyer C, Poncelet A, Bourdrez X, Andries K. Diarylquinolines, synthesis pathways and quantitative structure−activity relationship studies leading to the discovery of TMC207. *Future Med Chem* 2011;**3**:1345−60.

130. Choi PJ, Sutherland HS, Tong AST, Blaser A, Franzblau SG, Cooper CB, et al. Synthesis and evaluation of analogues of the tuberculosis drug bedaquiline containing heterocyclic B-ring units. *Bioorg Med Chem Lett* 2017;**27**:5190−6.

131. Sutherland HS, Tong AST, Choi PJ, Conole D, Blaser A, Franzblau SG, et al. Structure−activity relationships for analogs of the tuberculosis drug bedaquiline with the naphthalene unit replaced by bicyclic heterocycles. *Bioorg Med Chem* 2018;**26**:1797−806.

132. Xu J, Converse PJ, Upton AM, Mdluli K, Fotouhi N, Nuermberger EL. Comparative efficacy of the novel diarylquinoline TBAJ-587 and bedaquiline against a resistant Rv0678 mutant in a mouse model of tuberculosis. *Antimicrob Agents Chemother* 2021;**65**:e02418−20.

133. Almeida D, Converse PJ, Li SY, Upton AM, Fotouhi N, Nuermberger EL. Comparative efficacy of the novel diarylquinoline TBAJ-876 and bedaquiline against a resistant Rv0678 mutant in a mouse model of tuberculosis. *Antimicrob Agents Chemother* 2021;**65**:e01412-21.

134. Huang Z, Luo W, Xu D, Guo F, Yang M, Zhu Y, et al. Discovery and preclinical profile of sudapyridine (WX-081), a novel antituberculosis agent. *Bioorg Med Chem Lett* 2022;**71**:128824.

135. Yao R, Wang B, Fu L, Li L, You K, Li YG, et al. Sudapyridine (WX-081), a novel compound against *Mycobacterium tuberculosis*. *Microbiol Spectr* 2022;**10**:e0247721.

136. Barbaro L, Nagalingam G, Triccas JA, Tan L, West NP, Baell JB, et al. Synthesis and evaluation of pyridine-derived bedaquiline analogues containing modifications at the A-ring subunit. *RSC Med Chem* 2021;**12**:943−59.

137. Kang S, Kim RY, Seo MJ, Lee S, Kim YM, Seo M, et al. Lead optimization of a novel series of imidazo[1,2-a]pyridine amides leading to a clinical candidate (Q203) as a multi- and extensively-

drug-resistant anti-tuberculosis agent. *J Med Chem* 2014;**57**: 5293−305.

138. Pethe K, Bifani P, Jang J, Kang S, Park S, Ahn S, et al. Discovery of Q203, a potent clinical candidate for the treatment of tuberculosis. *Nat Med* 2013;**19**:1157−60.

139. Abrahams KA, Cox JAG, Spivey VL, Loman NJ, Pallen MJ, Constantinidou C, et al. Identification of novel imidazo[1,2-a]pyridine inhibitors targeting M. tuberculosis QcrB. *PLoS One* 2012;**7**:e52951.

140. Kang S, Kim YM, Kim RY, Seo MJ, No Z, Nam K, et al. Synthesis and structure−activity studies of side chain analogues of the anti-tubercular agent, Q203. *Eur J Med Chem* 2017;**125**:807−15.

141. No Z, Kim J, Brodin PB, Seo MJ, Kim YM, Cechetto J, et al, inventors. Anti-infective compounds. WO2011113606A1, September 22, 2011.

142. Tang J, Wang B, Wu T, Wan J, Tu Z, Njire M, et al. Design, synthesis, and biological evaluation of pyrazolo[1,5-a]pyridine-3-carboxamides as novel antitubercular agents. *ACS Med Chem Lett* 2015;**6**:814−8.

143. Moraski GC, Deboosère N, Marshall KL, Weaver HA, Vandeputte A, Hastings C, et al. Intracellular and *in vivo* evaluation of imidazo[2,1-b]thiazole-5-carboxamide anti-tuberculosis compounds. *PLoS One* 2020;**15**:e0227224.

144. Moraski GC, Seeger N, Miller PA, Oliver AG, Boshoff HI, Cho S, et al. Arrival of imidazo[2,1-*b*]thiazole-5-carboxamides: potent anti-tuberculosis agents that target QcrB. *ACS Infect Dis* 2016;**2**:393−8.

145. Lu X, Tang J, Cui S, Wan B, Franzblau SG, Zhang T, et al. Pyrazolo [1,5-a]pyridine-3-carboxamide hybrids: design, synthesis and evaluation of anti-tubercular activity. *Eur J Med Chem* 2017;**125**:41−8.

146. Lu X, Williams Z, Hards K, Tang J, Cheung CY, Aung HL, et al. Pyrazolo[1,5-a]pyridine inhibitor of the respiratory cytochrome *bcc* complex for the treatment of drug-resistant tuberculosis. *ACS Infect Dis* 2019;**5**:239−49.

147. Han SJ, Song T, Cho YJ, Kim JS, Choi SY, Bang HE, et al. Complete genome sequence of *Mycobacterium tuberculosis* K from a Korean high school outbreak, belonging to the Beijing family. *Stand Genom Sci* 2015;**10**:78.

148. Ditse Z, Lamers MH, Warner DF. DNA replication in *Mycobacterium tuberculosis*. Microbiol Spectr 2017;**5**. Available from: https://doi.org/10.1128/microbiolspec.tbtb2-0027-2016.

149. Baños-Mateos S, van Roon AMM, Lang UF, Maslen SL, Skehel JM, Lamers MH. High-fidelity DNA replication in *Mycobacterium tuberculosis* relies on a trinuclear zinc center. *Nat Commun* 2017;**8**: 855.

150. Moadebi S, Harder CK, Fitzgerald MJ, Elwood KR, Marra F. Fluoroquinolones for the treatment of pulmonary tuberculosis. *Drugs* 2007;**67**:2077−99.

151. Sarathy J, Blanc L, Alvarez-Cabrera N, O'Brien P, Dias-Freedman I, Mina M, et al. Fluoroquinolone efficacy against tuberculosis is driven by penetration into lesions and activity against resident bacterial populations. *Antimicrob Agents Chemother* 2019;**63**:e02516-18.

152. Locher CP, Jones SM, Hanzelka BL, Perola E, Shoen CM, Cynamon MH, et al. A novel inhibitor of gyrase B is a potent drug candidate for treatment of tuberculosis and nontuberculosis mycobacterial infections. *Antimicrob Agents Chemother* 2015;**59**: 1455−65.

153. Talley AK, Thurston A, Moore G, Gupta VK, Satterfield M, Manyak E, et al. First-in-human evaluation of the safety, tolerability, and pharmacokinetics of SPR720, a novel oral bacterial DNA gyrase (GyrB) inhibitor for mycobacterial infections. *Antimicrob Agents Chemother* 2021;**65**:e0120821.

154. Grillot AL, Le Tiran A, Shannon D, Krueger E, Liao Y, O'Dowd H, et al. Second-generation antibacterial benzimidazole ureas: discovery of a preclinical candidate with reduced metabolic liability. *J Med Chem* 2014;**57**:8792−816.

155. Charifson PS, Grillot AL, Grossman TH, Parsons JD, Badia M, Bellon S, et al. Novel dual-targeting benzimidazole urea inhibitors of DNA gyrase and topoisomerase IV possessing potent antibacterial activity: intelligent design and evolution through the judicious use of

structure-guided design and structure−activity relationships. *J Med Chem* 2008;**51**:5243−63.

156. Grossman TH, Bartels DJ, Mullin S, Gross CH, Parsons JD, Liao Y, et al. Dual targeting of GyrB and ParE by a novel amino-benzimidazole class of antibacterial compounds. *Antimicrob Agents Chemother* 2007;**51**:657−66.

157. Lu Y, Zheng M, Wang B, Fu L, Zhao W, Li P, et al. Clofazimine analogs with efficacy against experimental tuberculosis and reduced potential for accumulation. *Antimicrob Agents Chemother* 2011;**55**: 5185−93.

158. Barry VC, Belton JG, Conalty ML, Denneny JM, Edward DW, O'Sullivan JF, et al. A new series of phenazines (rimino-compounds) with high antituberculosis activity. *Nature* 1957;**179**:1013−5.

159. Cholo MC, Steel HC, Fourie PB, Germishuizen WA, Anderson R. Clofazimine: current status and future prospects. *J Antimicrob Chemother* 2012;**67**:290−8.

160. Van Deun A, Maug AKJ, Salim MAH, Das PK, Sarker MR, Daru P, et al. Short, highly effective, and inexpensive standardized treatment of multidrug-resistant tuberculosis. *Am J Respir Crit Care Med* 2010; **182**:684−92.

161. Murashov MD, LaLone V, Rzeczycki PM, Keswani RK, Yoon GS, Sud S, et al. The physicochemical basis of clofazimine-induced skin pigmentation. *J Invest Dermatol* 2018;**138**:697−703.

162. Zhang D, Lu Y, Liu K, Liu B, Wang J, Zhang G, et al. Identification of less lipophilic riminophenazine derivatives for the treatment of drug-resistant tuberculosis. *J Med Chem* 2012;**55**:8409−17.

163. Liu B, Liu K, Lu Y, Zhang D, Yang T, Li X, et al. Systematic evaluation of structure−activity relationships of the riminophenazine class and discovery of a C2 pyridylamino series for the treatment of multidrug-resistant tuberculosis. *Molecules* 2012;**17**:4545−59.

164. Zhang D, Liu Y, Zhang C, Zhang H, Wang B, Xu J, et al. Synthesis and biological evaluation of novel 2-methoxypyridylamino-substituted riminophenazine derivatives as antituberculosis agents. *Molecules* 2014;**19**:4380−94.

165. Jagannath C, Reddy MV, Kailasam S, O'Sullivan JF, Gangadharam PR. Chemotherapeutic activity of clofazimine and its analogues against *Mycobacterium tuberculosis*. *In vitro*, intracellular, and *in vivo* studies. *Am J Respir Crit Care Med* 1995;**151**:1083−6.

166. Reddy VM, Nadadhur G, Daneluzzi D, O'Sullivan JF, Gangadharam PR. Antituberculosis activities of clofazimine and its new analogs B4154 and B4157. *Antimicrob Agents Chemother* 1996; **40**:633−6.

167. van Rensburg CE, Jooné GK, Sirgel FA, Matlola NM, O'Sullivan JF. *In vitro* investigation of the antimicrobial activities of novel tetramethylpiperidine-substituted phenazines against *Mycobacterium tuberculosis*. *Chemotherapy* 2000;**46**:43−8.

168. Kamal A, Hari Babu A, Venkata Ramana A, Sinha R, Yadav JS, Arora SK. Antitubercular agents. part 1: synthesis of phthalimido- and naphthalimido-linked phenazines as new prototype antitubercular agents. *Bioorg Med Chem Lett* 2005;**15**:1923−6.

169. Li YL, Zhang CL, Zhang DF, Lu Y, Wang B, Zheng MQ, et al. Synthesis and anti-tubercular activity of novel alkyl substituted riminophenazine derivatives. *Yao Xue Xue Bao* 2012;**47**:745−54.

170. Nuermberger EL, Martínez-Martínez MS, Sanz O, Urones B, Esquivias J, Soni H, et al. GSK2556286 is a novel antitubercular drug candidate effective *in vivo* with the potential to shorten tuberculosis treatment. *Antimicrob Agents Chemother* 2022;**66**:e0013222.

171. Wilburn KM, Montague CR, Qin B, Woods AK, Love MS, McNamara CW, et al. Pharmacological and genetic activation of cAMP synthesis disrupts cholesterol utilization in *Mycobacterium tuberculosis*. *Plos Pathog* 2022;**18**:e1009862.

172. Brown KL, Wilburn KM, Montague CR, Grigg JC, Sanz O, Pérez-Herrán E, et al. Cyclic AMP-mediated inhibition of cholesterol catabolism in *Mycobacterium tuberculosis* by the novel drug candidate GSK2556286. *Antimicrob Agents Chemother* 2023;**67**: e0129422.

173. Alemparte-Gallardo C, Encinas L, Esquivias Provencio J. *Novel tetrazole compounds and their use in the treatment of tuberculosis.*

Available from: https://patentscope.wipo.int/search/en/detail.jsf?docId=WO2019034729, 2019. [Accessed 2 September 2022].

174. Tiberi S, Vjecha MJ, Zumla A, Galvin J, Migliori GB. Accelerating development of new shorter TB treatment regimens in anticipation of a resurgence of multi-drug resistant TB due to the COVID-19 pandemic. *Int J Infect Dis* 2021;**113**:S96−9.

175. WHO. *Glob tuberculosis Rep* 2021. Available from: https://www.who.int/publications-detail-redirect/9789240037021. [Accessed 16 May 2022].

176. Kyu HH, Ledesma JR. What is the impact of the COVID-19 pandemic on tuberculosis? *Lancet Glob Health* 2023;**11**:e1323−4.

177. Santucci P, Greenwood DJ, Fearns A, Chen K, Jiang H, Gutierrez MG. Intracellular localisation of *Mycobacterium tuberculosis* affects efficacy of the antibiotic pyrazinamide. *Nat Commun* 2021;**12**:3816.

178. Driver ER, Ryan GJ, Hoff DR, Irwin SM, Basaraba RJ, Kramnik I, et al. Evaluation of a mouse model of necrotic granuloma formation using C3HeB/FeJ mice for testing of drugs against *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2012;**56**:3181−95.

179. Rullas J, García JI, Beltrán M, Cardona PJ, Cáceres N, García-Bustos JF, et al. Fast standardized therapeutic-efficacy assay for drug discovery against tuberculosis. *Antimicrob Agents Chemother* 2010;**54**:2262−4.

180. Nuermberger EL. Preclinical efficacy testing of new drug candidates. *Microbiol Spectr* 2017;**5**. Available from: https://doi.org/10.1128/microbiolspec.tbtb2-0034-2017.

181. Sarathy JP, Zuccotto F, Hsinpin H, Sandberg L, Via LE, Marriner GA, et al. Prediction of drug penetration in tuberculosis lesions. *ACS Infect Dis* 2016;**2**:552−63.

182. Sarathy JP, Via LE, Weiner D, Blanc L, Boshoff H, Eugenin EA, et al. Extreme drug tolerance of *Mycobacterium tuberculosis* in caseum. *Antimicrob Agents Chemother* 2018;**62**:e02266-17.

183. Grzelak EM, Choules MP, Gao W, Cai G, Wan B, Wang Y, et al. Strategies in anti-*Mycobacterium tuberculosis* drug discovery based on phenotypic screening. *J Antibiot (Tokyo)* 2019;**72**:719−28.

184. Hoagland D, Liu J, Lee RB, Lee RE. New agents for the treatment of drug-resistant *Mycobacterium tuberculosis*. *Adv Drug Deliv Rev* 2016;**102**:55−72.

185. Pethe K, Sequeira PC, Agarwalla S, Rhee K, Kuhen K, Phong WY, et al. A chemical genetic screen in *Mycobacterium tuberculosis* identifies carbon-source-dependent growth inhibitors devoid of *in vivo* efficacy. *Nat Commun* 2010;**1**:57.

186. Herrmann J, Rybniker J, Müller R. Novel and revisited approaches in antituberculosis drug discovery. *Curr Opin Biotechnol* 2017;**48**:94−101.

187. Cole ST. Inhibiting *Mycobacterium tuberculosis* within and without. *Philos Trans R Soc Lond B Biol Sci* 2016;**371**:20150506.

188. Christophe T, Ewann F, Jeon HK, Cechetto J, Brodin P. High-content imaging of *Mycobacterium tuberculosis*-infected macrophages: an *in vitro* model for tuberculosis drug discovery. *Future Med Chem* 2010;**2**:1283−93.

189. An Q, Li C, Chen Y, Deng Y, Yang T, Luo Y. Repurposed drug candidates for antituberculosis therapy. *Eur J Med Chem* 2020;**192**:112175.

190. Roubert C, Fontaine E, Upton AM. "Upcycling" known molecules and targets for drug-resistant TB. *Front Cel Infect Microbiol* 2022;**12**:1029044.

191. Rybniker J, Vocat A, Sala C, Busso P, Pojer F, Benjak A, et al. Lansoprazole is an antituberculous prodrug targeting cytochrome Bc1. *Nat Commun* 2015;**6**:7659.