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Oxadiazolone derivatives, new promising multi-target inhibitors against *M. tuberculosis*

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ABSTRACT

A set of 19 oxadiazolone (OX) derivatives have been investigated for their antimycobacterial activity against two pathogenic slow-growing mycobacteria, *Mycobacterium marinum* and *Mycobacterium bovis* BCG, and the avirulent *Mycobacterium tuberculosis* (*M. tb*) mc²6230. The encouraging minimal inhibitory concentrations (MIC) values obtained prompted us to test them against virulent *M. tb* H37Rv growth either in broth medium or inside macrophages. The OX compounds displayed a diversity of action and were found to act either on extracellular *M. tb* growth only with moderated MIC₅₀, or both intracellularly on infected macrophages as well as extracellularly on bacterial growth. Of interest, all OX derivatives exhibited very low toxicity towards host macrophages. Among the six potential OXs identified, HPOX, a selective inhibitor of extracellular *M. tb* growth, was selected and further used in a competitive labelling/enrichment assay against the activity-based probe Desthiobiotin-FP, in order to identify its putative target(s). This approach, combined with mass spectrometry, identified 18 potential candidates, all being serine or cysteine enzymes involved in *M. tb* lipid metabolism and/or in cell wall biosynthesis. Among them, Ag85A, CaeA, TesA, KasA and MetA have been reported as essential for *in vitro* growth of *M. tb* and/or its survival and persistence inside macrophages. Overall, our findings support the assumption that OX derivatives may represent a novel class of multi-target inhibitors leading to the arrest of *M. tb* growth through a cumulative inhibition of a large number of Ser- and Cys-containing enzymes involved in various important physiological processes.

1. Introduction

With 10.4 million new cases and 1.7 million deaths in 2016, tuberculosis (TB) caused by the pathogenic species *Mycobacterium tuberculosis* (*M. tb*) remains the leading cause of death worldwide from a single infectious agent [1]. Despite the quadritherapy treatment

involving isoniazid (INH), pyrazinamide, rifampicin (RIF) and ethambutol, the introduction of new molecules on the market to strengthen or replace this first-line antibiotics regimen is a slow and tedious process [2,3]. Only a few drugs were able to pass the selection stages (e.g., bedaquiline [4], delamanid [5] and PA-824 [6]). However, the appearance and spread of multidrug-resistant (MDR), extensively drug-

Abbreviations: ABPP, activity-based protein profiling; CC₅₀, compound concentration leading to 50% of cell cytotoxicity; CyC, Cyclopostins & Cyclophostin analogs; ETO, ethionamide; FM, foamy macrophages; HSL, hormone-sensitive lipase; ILI, intracytoplasmic lipid inclusions; INH, isoniazid; MDR, multidrug-resistant strains; MIC₅₀, minimal inhibitory concentration leading to 50% of growth inhibition; *M. tb*, *Mycobacterium tuberculosis*; pNP, para-nitrophenyl; REMA, resazurin microtiter assay; RIF, rifampicin; TB, tuberculosis; TAG, triacylglycerols; TDR, totally drug-resistant strains; XDR, extensively drug-resistant strains; x_i, inhibitor molar excess related to 1 mol of enzyme; x_{i50}, inhibitor molar excess leading to 50% enzyme inhibition

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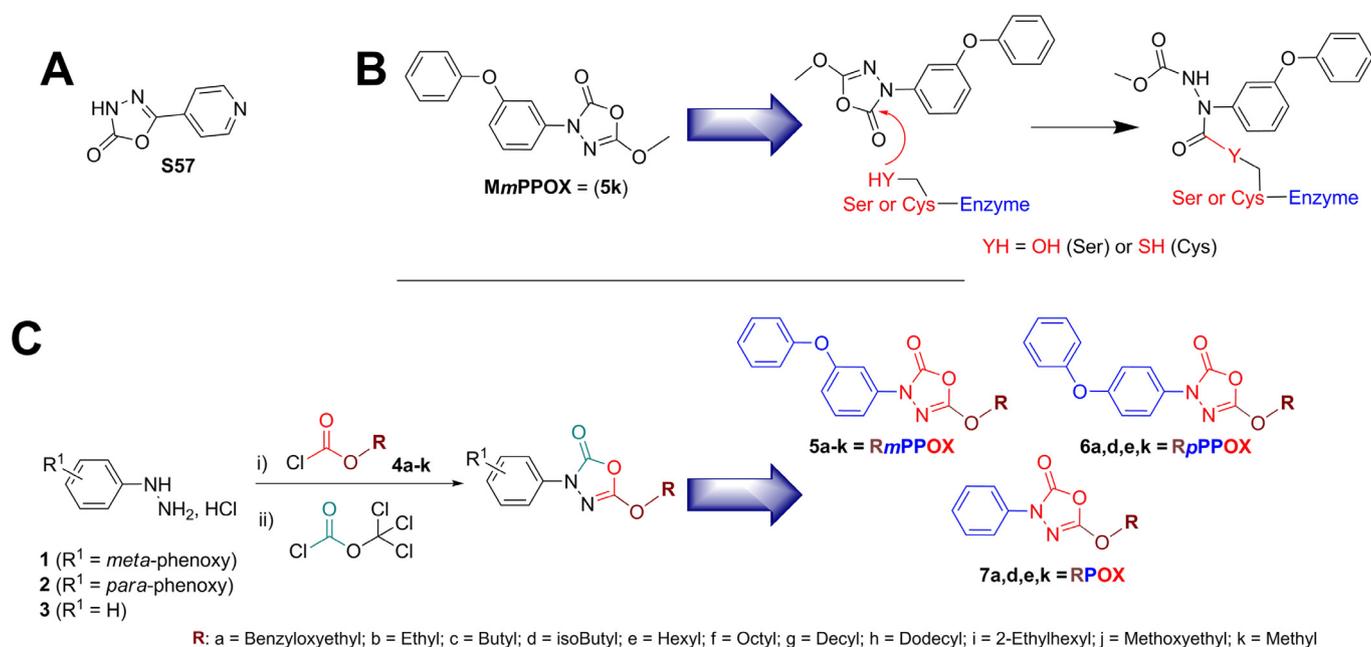


Fig. 1. Chemical structure of (A) 5-(pyridin-4-yl)-1,3,4-oxadiazol-2(3H)-one **S57**, and (B) 5-methoxy-3-(3-phenoxyphenyl)-1,3,4-oxadiazol-2(3H)-one **MmPPOX** and its mode of action. (C) General procedure for the one step preparation of 5-alkoxy-3-phenyl substituted-1,3,4-oxadiazol-2(3H)-one compounds from either (3-phenoxyphenyl)hydrazine hydrochloride (1), (4-phenoxyphenyl)hydrazine hydrochloride (2) or phenylhydrazine hydrochloride (3), giving **OX** derivatives **5a-k** (i.e., **RmPPOX**), **6a,d,e,k** (i.e., **RpPPOX**) or **7a,d,e,k** (i.e., **RPOX**), respectively. Reagents and conditions: (i) Alkyl chloroformate **4a-k**, Pyridine, 0 °C to RT; (ii) $ClCO_2CCl_3$, $CHCl_2$, Pyridine, 0 °C to RT, 40–85%. Adapted from [27].

resistant (XDR) and totally drug-resistant (TDR) strains [7–10] highlights the urgent need for finding new therapeutic options to fight against *M. tb*.

In this context, oxadiazolone-core (**OX**) compounds represent attractive tools. Compound **S57** (Fig. 1A), initially described in 1954 [11,12] as being active against TB [13–15], was used as template for the synthesis of 3,5-substituted 1,3,4-oxadiazole-2-one derivatives [16,17]. These molecules were found to exhibit interesting anti-mycobacterial activity against *M. tb* H37Rv, with minimal inhibitory concentrations (MIC) of 1.25–8 $\mu\text{g/mL}$, comparable to those of INH (0.5 $\mu\text{g/mL}$) and RIF (1.0 $\mu\text{g/mL}$) [16,17]. Molecular modeling indicated that these compounds possessed all necessary features to block the enzymatic activity of the mycobacterial cytochrome P450-dependent 14 α -sterol demethylase (P450_{14DM α}) [18], also a target for antifungal drug design [19]. These findings thus suggest the potential use of such **OX** derivatives as alternative therapeutic agents for TB [20].

Few years ago, we reported that the **OX** compound **MmPPOX** (Fig. 1B), a reversible inhibitor of the hormone-sensitive lipase (HSL) family of proteins [21,22], was able to inhibit the growth of *M. tb* with MIC values of around 15–25 $\mu\text{g/mL}$ as determined on solid medium [23]. Keeping in mind its strong affinity towards the HSL family member proteins (Lip-HSL), we further investigated the *in vitro* inhibition of recombinant *M. tb* Lip-HSL. As expected, the nine purified Lip-HSL enzymes tested were all strongly inhibited by **MmPPOX**, which reacted with the catalytic serine residue by forming a covalent but (slowly) reversible bond (i.e., carbamate or thiocarbamate bond, Fig. 1B). Such an inhibitor could then be considered as a long-life substrate rather than a true inhibitor as already observed with Orlistat (also named Tetrahydrolipstatine or THL), a representative member of reversible serine hydrolase inhibitors [24–26].

From these first results, a new series of 18 lipophilic **OX** derivatives based on **MmPPOX** core-structure have been synthesized (Fig. 1C) and tested for their anti-mycobacterial activities. More precisely, each oxadiazolone molecule has been tested against *M. tb* H37Rv for (i) its capacity to inhibit *in vitro* growth; (ii) its antitubercular activity on *M. tb*-infected macrophages, and (iii) its cytotoxicity towards

macrophages. Interestingly, some analogs were found to inhibit *M. tb* growth *in vitro* and/or inside macrophages without any significant toxicity to host cells. In addition, using an activity-based protein profiling (ABPP) assay, the potential target enzymes of **HPOX**, acting only on *M. tb* extracellular growth, were further identified.

2. Results and discussion

2.1. Synthesis of oxadiazolone-core (OX) derivatives

The set of new 18 lipophilic **OX** derivatives based on **MmPPOX** core-structure was designed by varying the nature of the R chain and/or the positioning of the phenoxy group (in *meta* or *para* position) when present (Fig. 1C), and synthesized as previously reported [27]. The (phenoxy)phenyl group, proposed to be responsible for strong hydrophobic interactions and structural stiffening [27], was conserved in most of the new candidate inhibitors. In addition, modifying the R chain born by the oxadiazolone ring allow an investigation of the influence of the lipophilicity on the antibacterial activity exerted by these molecules. To remain consistent with previous studies involving such compounds [23,27], we have decided to use the specific nomenclature already developed for these derivatives noted **Rm**(or **p**)**PPOX**; where **m** (or **p**)**P** represents the *meta* (or *para*)-Phenoxy group when present; **P** the phenyl group; **OX** the Oxadiazolone core; and **R** the alkyl chain (i.e., Be, benzyloxyethyl; M; methyl, E, ethyl; B, butyl; iB, isobutyl; H, hexyl; O, octyl; Eh, 2-ethylhexyl; D, decyl; Do, dodecyl; Me, methoxyethyl).

2.2. Susceptibility testing on selected mycobacteria

The antibacterial properties of the **OX** compounds were first evaluated towards three slow-growing mycobacteria: *M. marinum*, *M. bovis* BCG and *M. tb* mc²6230, a H37Rv strain with its RD1 region and *panCD* genes deleted, resulting in an avirulent pan(–) phenotype [28]. The corresponding MIC₅₀ values, as determined by the REMA assay [29–32], are reported in Table 1. First, it is noteworthy that the concentrations needed to inhibit 50% of the bacterial growth (MIC₅₀)

Table 1Antibacterial activities of the oxadiazolone derivatives against *M. marinum*, *M. Bovis* BCG and *M. tb* mc²6230 using the REMA method.^a

Compounds	MIC ₅₀ (μM)		
	<i>M. marinum</i>	<i>M. bovis</i> BCG	<i>M. tb</i> mc ² 6230
INH	20.5	0.71	1.5
RIF	1.4	0.027	0.015
MmPPOX	7.0	15.0	71.3
MpPPOX	11.5	39.9	> 120
MPOX	52.9	> 120	89.8
EmPPOX	3.4	7.1	> 120
MemPPOX	2.7	9.4	91.2
BmPPOX	4.1	6.6	52.2
iBmPPOX	13.6	4.4	57.2
iBpPPOX	6.9	8.5	31.1
iBPOX	2.5	5.7	> 120
HmPPOX	11.1	5.8	48.8
HpPPOX	3.4	14.0	41.3
HPOX	2.6	3.5	40.5
BemPPOX	5.6	10.5	49.5
BepPPOX	10.1	18.5	44.5
BePOX	1.9	6.6	33.2
OmPPOX	8.0	11.0	44.7
EhmPPOX	8.3	8.1	43.3
DmPPOX	10.5	80.8	> 120
DomPPOX	19.5	22.6	> 120

^a Experiments were performed as described in Section 4. MIC₅₀: compound minimal concentration leading to 50% of growth inhibition, as determined by the REMA assay. The best MIC₅₀ obtained for each strain are highlighted in bold. Values are mean of at least two independent assays performed in triplicate. INH, isoniazid; RIF, rifampicin.

obtained for rifampicin (RIF) and isoniazid (INH), used here as reference antibiotics, were in agreement with literature data [33–35].

Nearly all 19 OXs were active against *M. bovis* BCG and *M. marinum* growth (Table 1). However, with MIC₅₀ values in the range 1.9–53 μM, *M. marinum* was nearly 2-times more sensitive to OX compounds than *M. bovis* BCG (MIC₅₀ from 3.5 to > 120 μM). **BePOX**, **HPOX** and **iBPOX**, for which the phenoxy substituent is absent, exhibited the most potent antibacterial activity towards *M. marinum*, with mean MIC₅₀ of 2.3 ± 0.33 μM, comparable to that of RIF (1.4 μM). Interestingly, these three OX compounds were also among the best inhibitors of *M. bovis* BCG growth; **HPOX** being the best one (MIC₅₀ = 3.5 μM).

From these encouraging data obtained using two slow-growing mycobacteria, it was tempting to extrapolate that these OXs would behave in a similar way against *M. tb* growth and conclude that the same three compounds, i.e. **BePOX**, **HPOX** and **iBPOX**, would then be promising anti-TB molecules.

Drug susceptibility testing of the 19 OXs was thus further assessed using the non-virulent *M. tb* mc²6230 strain. Among all tested compounds, 14 OXs were active against *M. tb* mc²6230. The two best growth inhibitors obtained were **iBpPPOX** and **BePOX**, which displayed similar MIC₅₀ value (mean 32.1 ± 1.0 μM). In all other cases, MIC₅₀ values were indicative either of a weak (mean MIC₅₀ = 84.1 ± 9.1 μM for **MmPPOX**, **MPOX** and **MemPPOX**), or a moderate (mean MIC₅₀ = 46.9 ± 5.1 μM for **BmPPOX**, **iBmPPOX**, **HmPPOX**, **HpPPOX**, **HPOX**, **OmPPOX**, **EhmPPOX**, **BemPPOX** and **BepPPOX**) antibacterial activity (Table 1). From these data, *M. tb* mc²6230 was found nearly 13- and 5-times less sensitive to the OX compounds than *M. marinum* and *M. bovis* BCG, respectively.

Surprisingly, **iBPOX**, which differs from **BePOX** and **HPOX** by the length of its R substituent, was not active against this mycobacteria. Moreover, no clear trends or rules in terms of structure-activity relationships (SAR) have emerged regarding the potency of these oxadiazolone-core compounds against *M. marinum* and *M. bovis* BCG. Indeed, increasing the lipophilicity by varying the nature of the R chain

on the oxadiazolone ring and/or the positioning of the phenoxy group when present had no real impact on the anti-mycobacterial activity.

Interestingly, with *M. tb* mc²6230, some SAR tendencies can however be set up. First, and as mentioned above, the positioning of the phenoxy group in *meta* or *para* position has no real impact on the antibacterial activity of the corresponding compounds (i.e., **MmPPOX** vs. **MpPPOX**; **iBmPPOX** vs. **iBpPPOX**; **HmPPOX** vs. **HpPPOX**; **BemPPOX** vs. **BepPPOX**). Remarkably, **iBPOX** bearing the short chain isobutyl has no activity as compared to the phenoxyphenyl derivatives **iBpPPOX** and **iBmPPOX**. This is however not the case with the medium chains hexyl and benzyloxyethyl OXs, for which the respective activity of **HPOX** and **BePOX** is retained and even slightly better than **HmPPOX** & **HpPPOX** on the one hand, and **BemPPOX** & **BepPPOX** on the other hand. Finally, in absence of the bulky phenoxy group, the best MIC₅₀s against *M. tb* mc²6230 were also obtained with **HPOX** and **BePOX** vs. **MPOX** and **iBPOX**. In brief, the R chain length thus seems to affect the potency of the tested compounds. More globally, the best growth inhibitors were found to carry a middle chain length of around 6–9 carbon atoms (i.e., hexyl, 2-ethylhexyl, octyl or benzyloxyethyl chains). Longer or shorter chain's OXs (i.e., methyl, methoxyethyl, ethyl, decyl or dodecyl) exhibited no or only very poor activity.

In summary, **iBpPPOX** displayed the best, while still moderate, antibacterial activity against *M. tb* mc²6230. The reason why such differences exist between the activity of the OX compounds against *M. marinum* and *M. bovis* BCG, compared to *M. tb*, is not clear and will need further studies to be elucidated; but differences in membrane composition and permeability are likely playing a role in this phenotype.

2.3. High-content screening assay on virulent *M. tb* H37Rv

As recently observed for another class of potent *M. tb* growth inhibitors, the Cyclopiostins & Cyclophostin analogs (CyC) [31], MIC₅₀ values determined against *M. tb* mc²6230 do not necessarily correlate with the activity against *M. tb* H37Rv, particularly the activity against

Table 2
Antitubercular activities of the most active OX derivatives against *M. tb* H37Rv.^a

Compounds	Extracellular growth	Intracellular macrophage growth ^b	
	MIC ₅₀ (μM)	MIC ₅₀ (μM)	CC ₅₀ (μM)
INH ^c	1.2	1.2	> 150
RIF ^c	0.01	2.9	24
ETO ^c	6.0	6.0	120
iBpPPOX	32.0	8.5	> 100
iBPOX	> 50	17.1	> 100
HpPPOX	> 50	9.5	> 100
HPOX	44.6	No effect	> 100
BepPPOX	> 50	3.5	> 100
BePOX	30.8	No effect	> 100

^a Experiments were performed as described in Section 4. MIC₅₀: compound minimal concentration leading to 50% of growth inhibition. CC₅₀: compound concentration leading to 50% of cell cytotoxicity. Each value is the mean ± SD for a triplicated dose-response. Experiments were conducted at least twice with consistent results.

^b Raw264.7 macrophages were infected by *M. tb* H37Rv-GFP at a MOI of 2:1.

^c Data from [36]. INH, isoniazid; RIF, rifampicin; ETO, ethionamide.

intracellular bacteria.

Consequently, each of the 19 OX derivatives have been further evaluated for their specific antitubercular activity against extracellularly- and intracellularly-growing virulent *M. tb* H37Rv-GFP strain, using a high-content screening assay based on the fluorescence measurement of GFP-expressing bacteria. *In vitro* growth (i.e., extracellular assay) of *M. tb* H37Rv-GFP was first monitored after 5 days at 37 °C in presence of increasing concentrations of candidate inhibitors [31,36–38]. Intracellular growth of *M. tb* H37Rv-GFP was also assessed following a 5-day exposure of infected Raw264.7 murine macrophage cell line to the various OX compounds. In this case, the percentage of infected cells, the total number of bacteria, the number of bacteria per infected cells, as well as the number of living host cells allowed us to determine the MIC₅₀ of the compound [36,39,40]. In subsequent experiment, the concentration leading to 50% of host cell cytotoxicity, i.e. CC₅₀, were also determined in absence of infection.

Among all tested molecules, 6 potential OX candidates exhibited interesting antitubercular properties (Table 2 and Fig. 2). **BePOX** and **HPOX** impaired exclusively *M. tb* growth in culture broth medium with the same moderate MIC₅₀ (30.8 and 44.6 μM, respectively) than obtained previously on *M. tb* mc²6230. In contrast, **iBPOX**, **HpPPOX** and **BepPPOX** showed a clear preference against intracellularly-replicating mycobacteria with similar MIC₅₀ values (3.5–17.1 μM) than the first line antibiotics. Of interest, only **iBpPPOX** exhibited moderate (32.0 μM) to quite good (8.5 μM) activity against both extracellular and intramacrophagic *M. tb*, respectively (Fig. 2).

Beside antibacterial activity, significantly, all these 6 OX inhibitors exhibited very low toxicity towards host macrophages with

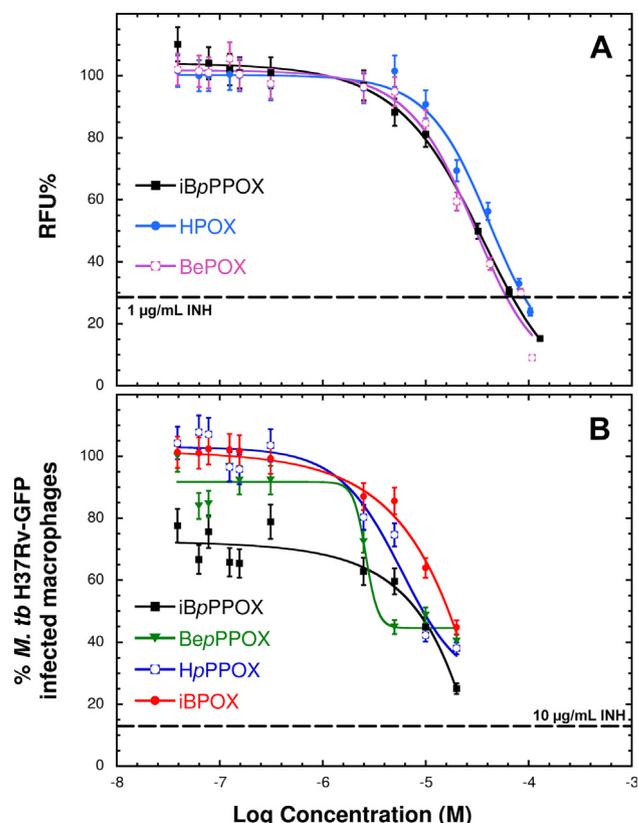


Fig. 2. *In vitro* and *ex vivo* dose-response activity of the OX derivatives against *M. tb* H37Rv. (A) Activity of **BePOX**, **iBpPPOX** and **HPOX** against GFP-expressing *M. tb* replicating in broth medium, expressed as normalized relative fluorescence units (RFU%). The dashed line represents the level of inhibition (~70%) reached with 1 μg/mL (=7.3 μM) INH as control. The MIC₅₀ of **BePOX**, **iBpPPOX** and **HPOX** replicating in culture broth medium were 30.8 μM, 32.0 μM and 44.6 μM, respectively. (B) Activity of **iBpPPOX**, **BepPPOX**, **HpPPOX** and **iBPOX** against *M. tb* replicating inside Raw264.7 macrophages. Results are expressed as the percentage of infected macrophages after 5 days post-infection. The dashed line represents the level of inhibition (~87%) reached with 10 μg/mL (=73 μM) INH as control. The MIC₅₀ of **BepPPOX**, **iBpPPOX**, **HpPPOX** and **iBPOX** replicating inside macrophages were 3.5 μM, 8.5 μM, 9.5 μM and 17.1 μM, respectively. Each value is the mean ± SD for a triplicated dose-response. Experiments were conducted at least twice with consistent results.

CC₅₀ > 100 μM, similarly to INH (CC₅₀ > 150 μM) and ethionamide (CC₅₀ ≥ 120 μM), two potent anti-TB drugs (Table 2). Their respective selectivity index (SI = CC₅₀/MIC₅₀) on intramacrophagic *M. tb* vs. Raw264.7 cells was thus found to be in a range from 5.8 and up to 28. While these are preliminary results that would need to be confirmed in other cell types including hepatocytes, they are encouraging for further improvement of the OX compounds. This absence of cytotoxicity was actually not obvious, given the number of (Ser/Cys)-enzymes present in host cells and the predicted potency of the OX compounds to target these classes of enzymes.

Interestingly, the observed differences in the behavior of OX compounds; in particular the higher activity against intracellular bacteria than against extracellular ones, have also been reported in the case of the CyC compounds family [31]. As previously discussed above, inhibition of *M. tb* H37Rv may result from several (and probably different) mechanisms of action or penetration of the OX derivatives. With the hexyl and benzyloxyethyl chain, the absence/presence of the phenoxy group in *para* position clearly shifted the activity of the corresponding OX from extracellular- (i.e., **HPOX** & **BePOX**) to intracellular-replicating bacilli (i.e., **HpPPOX** & **BepPPOX**). On the other hand, with the short isobutyl chain, both **iBpPPOX** and **iBPOX** are found most

active against intramacrophagic-replicating *M. tb*.

From these findings, it is tempting to assume that these OX compounds thus lead to the inhibition of specific but most likely distinct mycobacterial target enzymes between intramacrophagic- vs. extracellularly-replicating bacilli.

2.4. Targets identification by Activity-based protein profiling

Based on the aforementioned results, and taking into account their strong affinity for Serine and/or Cysteine (Ser/Cys)-based enzymes (Fig. 1B), one can hypothesize that OX inhibitors might target and impair the activity of various enzymes involved in several processes of *M. tb* pathogenic life cycle, thus resulting in bacterial death without any cytotoxicity towards host cells. Accordingly, target(s) identification experiments were conducted by applying an activity-based protein profiling (ABPP) approach [41–44]. In order to take into account the penetration/diffusion of the inhibitor through the mycobacterial cell wall, all experiments have been performed on living bacterial cells and not with a lysate, as previously described [31].

Here, HPOX, that selectively inhibits *M. tb* growth only in culture broth medium, was selected for such experiments. *M. tb* mc²6230 cells were grown to log phase and then incubated with HPOX compound or DMSO as a control. After cell lysis, part of the lysate was used for competitive probe labelling/enrichment assay using the Desthiobiotin-FP probe, targeting (Ser/Cys)-based enzymes [43] (Fig. 3). In parallel, the remaining lysate was incubated with TAMRA-FP, also targeting (Ser/Cys)-based enzymes [43], to reveal the candidates presumably reacting with HPOX on SDS-PAGE gel, using fluorescence scanning [31]. Around 9 distinct bands labelled by TAMRA-FP were visible in the fluorescence readout (Fig. 3B –lane E) and could also be detected by silver staining after release of the enzymes captured by Desthiobiotin-FP (Fig. 3B – lane B). In contrast, pre-treatment with HPOX (Fig. 3A) resulted in a decrease in fluorescence intensity of all visible bands, as exemplified by the black arrows in Fig. 3B – lane D. Indeed, the enzymes previously inactivated by HPOX inhibitor will thus be unable to further react with the probes. The respective enriched mixtures (Fig. 3B – lanes A-B) were digested with trypsin and the resulting peptides were analyzed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) followed by subsequent label free quantification analysis. The proteins that were also found in the control experiment (i.e., Fig. 3B – lane A: DMSO alone for unspecific binding to streptavidin-magnetic beads) were not taken into account.

The resulting mycobacterial targets of HPOX were displayed as volcano plot (Fig. 4). Only proteins identified with a permutation false discovery rate (pFDR) of 5% and a score threshold value ≥ 60 were selected, therefore leading to a panel of 18 distinct proteins (Table 3). These identified enzyme candidates ranged in their functional category from intermediary metabolism/respiration (6 proteins), lipid metabolism (5 proteins), cell wall/cell processes (6 proteins), and virulence/detoxification/adaptation (1 protein) (Table 3).

As expected, the identified proteins targeted by HPOX were all (Ser/Cys)-based enzymes. Among them, a variety of Ser/Cys hydrolases were detected. These included the putative β -lactamase Rv1367c possibly involved in cell wall biosynthesis; two amidases AmiC (Rv2888c) and AmiD (Rv3375); BpoC (Rv0554) a putative serine hydrolase [43]; two members of the lipase family Lip (LipH [45] and LipV [46]); three Cutinase-like proteins (Cfp21, Cut2 and Cut3) [47]; and the monoacylglycerol lipase Rv0183 [48].

More interestingly, 5 out of 18 identified proteins have been annotated as essential enzymes [49] (Table 3). These include the antigen 85 complex, Ag85A (Rv3804c), Ag85B (Rv1886c) and Ag85C (Rv0129c) [50]; the thioesterase TesA (Rv2928) [51]; the carboxylesterase CaeA (Rv2224c) [52]; the beta-ketoacyl synthase KasA (Rv2245) [53]; and the sole putative α/β -hydrolase MetA (Rv3341) belonging to the homoserine O-acetyltransferase family proteins in *M. tb* [54].

2.5. TesA, Rv0183 and Cfp21 are inhibited by HPOX

In order to validate some targets of HPOX inhibitor, we further investigated its ability to efficiently inhibit the activity of three identified proteins; i.e., TesA, Cfp21 and Rv0183. Coding sequences were amplified from *M. tb* genome, cloned in *E. coli* and the enzymes produced in recombinant form and purified as previously reported [48,55]. Purified proteins were then individually incubated for 30 min at room temperature with HPOX at various inhibitor molar excess (x_1). The residual enzyme activity was then measured using *para*-nitrophenyl caprylate (pNPC-8) as substrate for TesA and Cfp21 [55], and monoolein as substrate in the case of Rv0183 [48]. The variation in the residual enzyme activity allowed determination of the inhibitor molar excess leading to 50% enzyme inhibition, i.e., x_{150} value [27,56]. Thereby, a x_{150} value of 0.5 is synonymous with a 1:1 stoichiometric ratio between the inhibitor and the lipolytic enzyme, and is therefore the highest level of inhibitory activity that can be achieved.

As depicted in Fig. 5, a clear dose-dependent inhibition was observed with the three enzymes. TesA, Rv0183 and Cfp21 were indeed strongly inactivated, with 97.6% and 88.5% inhibition at $x_1 = 20$, respectively (Fig. 5, inset). Interestingly, HPOX was found to react almost stoichiometrically with pure TesA and Rv0183 as confirmed by their respective x_{150} values of around 0.60. These results clearly demonstrate that these three lipolytic enzymes are effective targets of HPOX.

The fact that these OXs derivatives behave against *M. tb* extracellular growth similarly to two other well-known non-specific (Ser/Cys)-enzyme inhibitors, namely Orlistat (MIC $\sim 25 \mu\text{M}$) [41,57] and the human lysosomal acid lipase inhibitor lalistat (MIC $\sim 25\text{--}50 \mu\text{M}$) [42], support the assumption that HPOX, and certainly all the other active OX compounds, may act as multi-target inhibitors by impairing the activities of multiple non-essential lipolytic enzymes as well as essential proteins involved in various important physiological pathways of *M. tb* life cycle.

Overall, it is now acknowledged that the lipolytic enzymes containing a catalytic Ser or Cys residue in their active site are not only involved in the host-pathogen cross-talk [58], but also play several roles in the physiopathology of the disease, in particular by recycling fatty acids from host lipids, a key element favoring *M. tb* reactivation [48,59] and survival in dormancy [60]. *M. tb* indeed induces the formation of lipid bodies (LB) inside infected macrophages, giving the cells a foamy appearance. In foamy macrophages (FM), bacilli accumulate lipids within intracytoplasmic lipid inclusions (ILI) [61–64], which allow the bacteria to persist in a non-replicating state. In FM, several mycobacterial lipolytic enzymes of *M. tb* hydrolyze host triacylglycerols (TAG) from LB and the resulting fatty acids are stored within ILI as newly synthesized TAGs. Consequently, although they exhibited moderate MIC₅₀ values against *M. tb* H37Rv as compared to classical antibiotics or the more recent CyC analogs [31]; OX compounds may however represent attractive chemical tools for identifying such (Ser/Cys)-containing enzymes in living mycobacteria, studying the regulation of ILI formation in infected FM [65], and thus provide a better understanding of how bacilli can persist inside lipid-rich FM.

3. Conclusion

In conclusion, we have developed a new series of promising oxadiazolone-core compounds, active against three pathogenic mycobacteria. By blocking extracellular and/or intracellular *M. tb* growth, we anticipate that these OX probes could thus provide interesting insights in the mechanisms operating during mycobacterial replication, persistence and/or reactivation, which are major issues for deciphering the susceptibility and the general development of TB. Moreover, as these compounds target bacterial pathway yet unexploited by anti-TB compounds, the identification of the mycobacterial enzymes inhibited by these OX compounds *in vivo* may contribute to background information for the development of new therapeutic strategies for

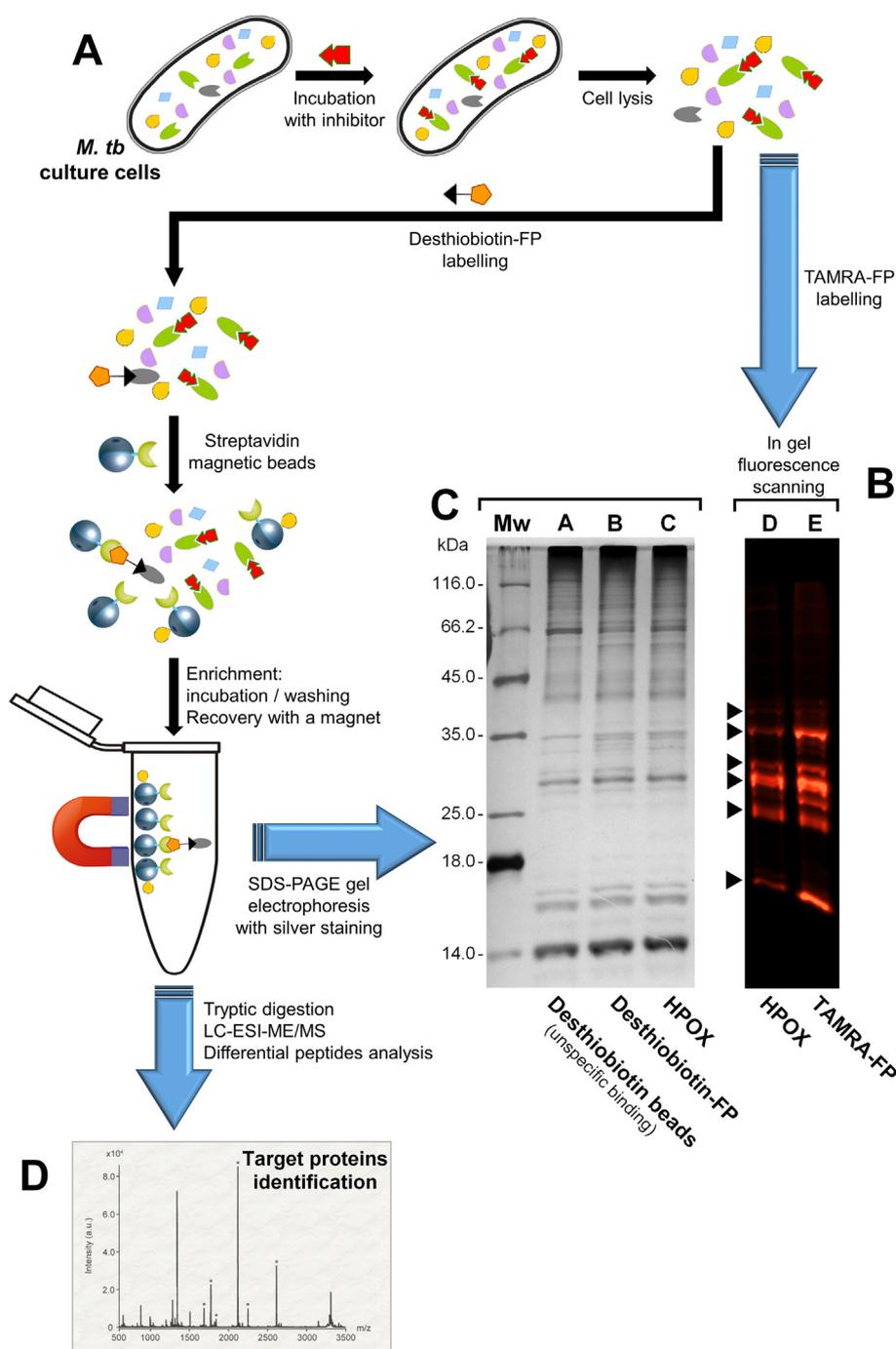


Fig. 3. Activity based protein profiling (ABPP) workflow for the identification of the proteins covalently bound to OX inhibitors. (A) Cell culture of *M. tb* mc²6230 was pre-treated with selected HPOX inhibitor prior to cell lysis and further incubation with TAMRA-FP or Desthiobiotin-FP probe. In this latter case, samples were then treated with streptavidin-magnetic beads for the capture and enrichment of labelled proteins. (B-C) Equal amounts of proteins obtained in A were separated by SDS-PAGE and visualized by in-gel fluorescence (right panel - lanes D-E: TAMRA detection) or silver staining (left panel - lanes A-C). Enzymes whose TAMRA-FP labelling is impeded because of the presence of HPOX in their active-site are shown by arrowheads. (D) Tryptic digestion followed by tandem mass spectrometry analyses and subsequent differential proteomics analysis allowed identifying the target proteins.

elimination of either actively replicating or latent bacilli from infected individuals. Accordingly, given the importance of such (Ser/Cys)-enzymes for *M. tb* viability during infection, they should represent new attractive drug targets. Such experiments are currently underway, and will be reported in due course.

4. Experimental Section

4.1. Chemistry

The first 13 oxadiazolone derivatives **5a-k**, **6k** and **7k** were synthesized as described previously [27,66]. The new six derivatives **6a,d,e** and **7a,d,e** were prepared from commercial (4-phenoxyphenyl) hydrazine hydrochloride (**2**) and phenylhydrazine hydrochloride (**3**), respectively, by performing both the coupling reaction with alkyl

chloroformate **2a-k** (step i) and the cyclization reaction with di-phosgene (step ii) in a one-pot two-steps reaction [27]. All compound were at least 98% pure as determined by HPLC analysis [27]. Stock solutions (4 mg/mL) in which the oxadiazolone compounds were found to be completely soluble in dimethyl sulfoxide (DMSO), were prepared prior to drug susceptibility testing. See [Supplementary Material](#) for NMR, HPLC analysis and HRMS spectra of the new six OX derivatives.

4.1.1. General procedure for the one step preparation of 5-alkoxy-3-aryl-1,3,4-oxadiazol-2(3H)-one compounds

4.1.1.1. 5-(2-(benzyloxy)ethoxy)-3-(3-phenoxyphenyl)-1,3,4-oxadiazol-2(3H)-one (**6a** = **BepPPOX**). (4-phenoxyphenyl)hydrazine hydrochloride [66] **2** (8.2 g, 34.6 mmol, 1 equiv.) and 1-methyl pyrrolidone (2.41 mL, 31.1 mmol, 0.9 equiv.) were dissolved in dry pyridine (700 mL). The solution was cooled in an ice bath to 0 °C. Then, 2-benzyloxyethyl

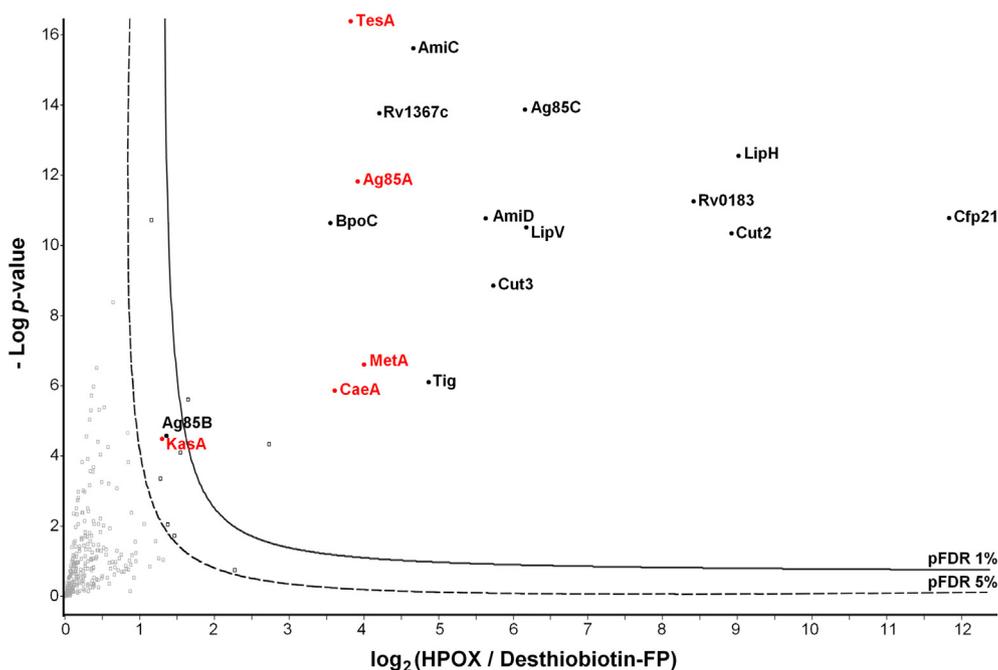


Fig. 4. Volcano plot of proteomic analysis of HPOX in *M. tb mc²6230* culture. Volcano plot showing the significance two-sample *t*-test ($-\log p$ -value) versus fold-change (\log_2 (LFQ normalized intensity in HPOX versus Desthiobiotin-FP condition) on the y and x axes, respectively. Here the plot is zoomed on the positive difference between the two conditions. The full line is indicative of protein hits obtained at a permutation false discovery rate of 1% (pFDR). Only protein hits obtained at a pFDR of 5% (dashed line) and with a score threshold value ≥ 60 were selected, and are highlighted in black (non-essential) or in red (essential). Data results from two different experiments processed three times. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

chloroformate **4a** (6.87 mL, 38.6 mmol, 1.1 equiv.) was added dropwise over a period of 30 min at 0–5 °C and allowed to stir for 1 h at 0 °C and 1 h at room temperature. The reaction mixture was diluted by addition of methylene chloride (300 mL) and dry pyridine (70 mL) and the mixture was cooled at -10 °C using an ice-salt bath. A solution of diposgene (6.26 mL, 51.8 mmol, 1.5 equiv.) in methylene chloride (30 mL) was added dropwise using a syringe pump over a period of 1 h while maintaining -10 °C with an ice-salt bath. After the addition is complete the reaction mixture stirred 1 h at -10 °C and 2 h at room temperature. The reaction mixture was diluted with water (1 L) and extracted with diethyl ether (3 × 250 mL). The combined organic layers were washed with water (2 × 250 mL) and brine (3 × 100 mL), dried over MgSO_4 , and filtered. Purification by column chromatography using cyclohexane/ethyl acetate (98/2 to 95/5, v/v) as eluent gave the title compound **6a** (**BepPPOX**) as a yellow oil (9.94 g, 71%). Analytical data for **BepPPOX**: R_f (AcOEt/Cyclohexane 1:3, v/v) 0.36. HRMS (ESI) m/z $[\text{M}+\text{H}]^+$ calcd. for $\text{C}_{23}\text{H}_{21}\text{N}_2\text{O}_5$: 405.1445 Da; found:

405.1446 Da. ^1H NMR δ 7.71 (dd, $J = 9.1$ Hz, $J = 2.2$ Hz, 2H), 7.31 (m, 7H), 6.98–7.13 (m, 5H), 4.60 (s, 2H), 4.54 (m, 2H), 3.83 (m, 2H). ^{13}C NMR δ 157.14 (s), 155.23 (s), 154.77 (s), 148.29 (s), 137.43 (s), 131.56 (s), 129.85 (2 × d), 128.55 (2 × d), 127.99 (d), 127.79 (2 × d), 123.47 (d), 119.83 (2 × d), 119.47 (2 × d), 118.74 (2 × d), 73.42 (t), 70.56 (t), 66.99 (t).

4.1.1.2. *5-isoButyloxy-3-(4-phenoxyphenyl)-1,3,4-oxadiazol-2(3H)-one* (**6d** = **iBpPPOX**). Prepared using Isobutyl chloroformate **4d** applying similar method as described above for **6a**. Analytical data for **iBpPPOX**: pale yellow oil (87%). R_f (AcOEt/Cyclohexane 1:3, v/v) 0.55. HRMS (ESI) m/z $[\text{M}+\text{H}]^+$ calcd. for $\text{C}_{18}\text{H}_{19}\text{N}_2\text{O}_4$: 327.1339 Da; found: 327.1342 Da. ^1H NMR δ 7.72 (dd, $J = 9.2$ Hz, $J = 2.3$ Hz, 2H), 7.30 (m, 2H), 6.97–7.12 (m, 5H), 4.14 (t, $J = 6.6$ Hz, 2H), 2.15 (m, 1H), 1.0 (d, 6H). ^{13}C NMR δ 157.17 (s), 155.42 (s), 154.67 (s), 148.36 (s), 131.66 (s), 129.83 (2 × d), 123.42 (d), 119.79 (2 × d), 119.49 (2 × d), 118.69 (2 × d), 71.39 (t), 22.75 (t), 18.70 (2 × q).

Table 3
HPOX target proteins identified in *M. tb mc²6230* culture by LC-ESI-MS/MS analysis.^a

Protein name	Rv number	Mol. weight [kDa]	Essentiality	Location ^b	Function	Functional category ^c
Cutinase Cfp21	Rv1984c	21.8		CF; CW; M	Lipase/esterase	CW/CP
Probable cutinase Cut2	Rv2301	23.9		M, WCL, CF	hydrolase	CW/CP
Probable cutinase Cut3	Rv3451	26.5		M, CF	hydrolase	CW/CP
Lipase LipV	Rv3203	27.9		WCL	Lipase/esterase	IM/R
Non-heme bromoperoxidase BpoC	Rv0554	28.4		M	hydrolase	V/D/A
Thioesterase TesA	Rv2928	29.2	<i>in vitro</i> growth	M	Lipase/esterase	LM
Monoglyceride lipase Rv0183	Rv0183	30.3		M	Lipase/esterase	IM/R
Lipase LipH	Rv1399c	33.9		M	Lipase/esterase	IM/R
Secreted antigen 85-B FbpB (Ag85B)	Rv1886c	34.6		CF; CW; M	Lipase/esterase	LM
Secreted antigen 85-A FbpA (Ag85A)	Rv3804c	35.7	<i>in vitro</i>	CF; CW; M	Lipase/esterase	LM
Secreted antigen 85-C FbpC (Ag85C)	Rv0129c	36.8		CF; CW	Lipase/esterase	LM
Probable homoserine O-acetyltransferase MetA	Rv3341	39.8	essential gene	M	Acytransferase	IM/R
β -ketoacyl-ACP synthase KasA	Rv2245	43.3	essential gene	CF; CW; M	Lipase/esterase	LM
Hypothetical protein LH57_07490	Rv1367c	43.7		M	β -lactamase	CW/CP
Trigger factor Tig	Rv2462c	50.6		M, WCL, CF	Protein export	CW/CP
Amidase AmiD	Rv3375	50.6		CW; M	Amidase	IM/R
Amidase AmiC	Rv2888c	50.9		CW; M	Amidase	IM/R
Putative Carboxylesterase A CaeA	Rv2224c	55.9	Macrophage and <i>in vitro</i>	M, WCL, CF	Lipase/esterase	CW/CP

^a Only positive hits with a pFDR of 5% and a score threshold value ≥ 60 were selected.

^b CF: Culture filtrate; CW: Cell wall; M: Membrane fraction; WCL: Whole cell lysate.

^c IM/R: Intermediary metabolism/respiration; CW/CP: cell wall/cell processes; LM: Lipid metabolism; V/D/A: Virulence, detoxification, adaptation.

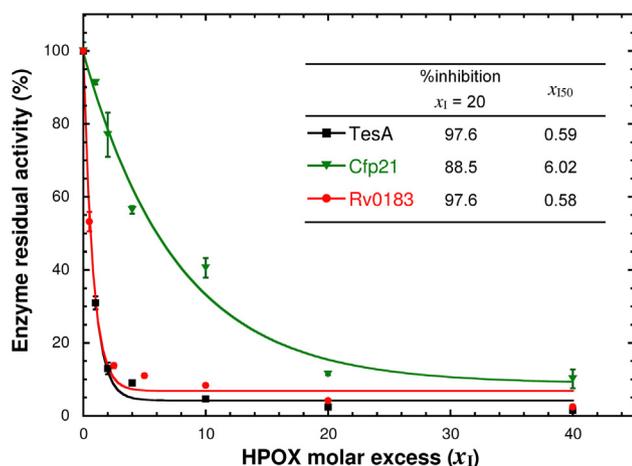


Fig. 5. HPOX efficiently impairs TesA, Cfp21 and Rv0183 activities *in vitro*. Variation of the residual activities of TesA, Cfp21 and Rv0183 as a function of increasing molar excess (x_1) of HPOX. Each enzyme was pre-incubated at various inhibitor molar excess (x_1) for 30 min at 25 °C. The inset displays the determined values of x_{150} and the level of inhibition at $x_1 = 20$. Kinetic assays were performed as described in Section 4. Results are expressed as mean values \pm SD of at least two independent assays.

4.1.1.3. 5-Hexyloxy-3-(4-phenoxyphenyl)-1,3,4-oxadiazol-2(3H)-one (6e = HpPPOX). Prepared using Hexyl chloroformate **4e** applying similar method as described above for **6a**. Analytical data for **HpPPOX**: yellow oil (85%). R_f (AcOEt/Cyclohexane 1:3, v/v) 0.95. HRMS (ESI) m/z $[M+H]^+$ calcd. for $C_{20}H_{23}N_2O_4$: 355.1652 Da; found: 355.1652 Da. 1H NMR δ 7.72 (dd, $J = 9.0$ Hz, $J = 2.0$ Hz, 2H), 7.30 (m, 2H), 6.97–7.12 (m, 5H), 4.37 (t, $J = 6.6$ Hz, 2H), 1.80 (m, 2H), 1.30–1.58 (m, 6H), 0.90 (t, $J = 6.8$ Hz, 3H). ^{13}C NMR δ 157.16 (s), 155.33 (s), 154.67 (s), 148.38 (s), 131.65 (s), 129.83 (2 \times d), 123.42 (d), 119.78 (2 \times d), 119.49 (2 \times d), 118.68 (2 \times d), 71.79 (t), 31.36 (t), 28.35 (t), 25.17 (t), 22.50 (t), 13.99 (q).

4.1.1.4. 5-Benzyloxyethoxy-3-phenyl-1,3,4-oxadiazol-2(3H)-one (7a = BePOX). Prepared using 2-benzyloxyethyl chloroformate **4a** and phenylhydrazine hydrochloride **3** applying similar method as described above for **6a**. Analytical data for **BePOX**: pale yellow oil (79%). R_f (AcOEt/Cyclohexane 1:3, v/v) 0.36. HRMS (ESI) m/z $[M+H]^+$ calcd. for $C_7H_{17}N_2O_4$: 313.1183 Da; found: 313.1183 Da. 1H NMR δ 7.75 (m, 2H), 7.18–7.73 (m, 8H), 4.60 (s, 2H), 4.54 (m, 2H), 3.83 (m, 2H). ^{13}C NMR δ 155.23 (s), 148.23 (s), 137.44 (s), 136.17 (s), 129.12 (2 \times d), 128.55 (2 \times d), 127.98 (d), 127.79 (2 \times d), 125.56 (d), 117.95 (2 \times d), 73.41 (t), 70.55 (t), 66.98 (t).

4.1.1.5. 5-isoButyloxy-3-phenyl-1,3,4-oxadiazol-2(3H)-one (7d = iBPOX). Prepared using Isobutyl chloroformate **4d** and phenylhydrazine hydrochloride **3** applying similar method as described above for **6a**. Analytical data for **iBPOX**: white crystals (77%). Mp: 76–77 °C. R_f (AcOEt/Cyclohexane 1:3, v/v) 0.55. HRMS (ESI) m/z $[M+Na]^+$ calcd. for $C_{12}H_{14}N_2O_3Na$: 257.0897 Da; found: 257.0895 Da. 1H NMR δ 7.80 (m, 2H), 7.42 (m, 2H), 7.25 (m, 1H), 4.18 (d, $J = 6.6$ Hz, 2H), 1.85 (m, 1H), 1.05 (d, 6H). ^{13}C NMR δ 155.63 (s), 148.51 (s), 136.44 (s), 129.29 (2 \times d), 125.67 (d), 118.14 (2 \times d), 77.57 (t), 27.94 (d), 18.89 (2 \times q).

4.1.1.6. 5-Hexyloxy-3-phenyl-1,3,4-oxadiazol-2(3H)-one (7e = HPOX). Prepared using Hexyl chloroformate **4e** and phenylhydrazine hydrochloride **3** applying similar method as described above for **6a**. Analytical data for **HPOX**: white crystals (71%). Mp: 34–35 °C. R_f (AcOEt/Cyclohexane 1:3, v/v) 0.59. HRMS (ESI) m/z $[M+H]^+$ calcd. for $C_{14}H_{19}N_2O_3$: 263.1390 Da; found: 263.1390 Da. 1H NMR δ 7.80 (ddd, $J = 8.4$ Hz, $J = 2.3$ Hz,

$J = 0.75$ Hz, 2H), 7.42 (dd, $J = 7.6$ Hz, $J = 1.7$ Hz, 2H), 7.22 (t, $J = 7.4$ Hz, 1H), 4.40 (t, $J = 6.6$ Hz, 2H), 1.85 (m, 2H), 1.33–1.49 (m, 6H), 0.93 (t, 3H). ^{13}C NMR δ 155.54 (s), 148.53 (s), 136.45 (s), 129.30 (2 \times d), 125.67 (d), 118.13 (2 \times d), 71.97 (t), 31.45 (t), 28.55 (t), 25.36 (t), 22.68 (t), 14.17 (q).

4.2. Biological evaluation

4.2.1. Bacterial strains and growth condition

M. marinum ATCC BAA-535/M, *M. bovis* BCG Pasteur 1173P2 and *M. tb* mc²6230 (H37Rv Δ RD1 Δ panCD [28]) strains were routinely grown in Middlebrook 7H9 broth (BD Difco) supplemented with 0.2% glycerol, 0.05% Tween 80 (Sigma-Aldrich), 10% oleic acid, albumin, dextrose, catalase (OADC enrichment; BD Difco) (7H9-S) and 24 μ g/mL D-pantothenate (*M. tb* mc²6230). For further intra and extracellular assays, *M. tb* H37Rv expressing GFP [36] was grown for 14 days in 7H9-S supplemented with 50 μ g/mL hygromycin B (Euromedex). All cultures were kept at 37 °C without shaking, except *M. marinum* which was grown at 32 °C.

4.2.2. Susceptibility testing on *M. marinum*, *M. Bovis* BCG and *M. tb* mc²6230

The concentrations of compound leading to 50% of bacterial growth (MIC_{50}) were first determined using the resazurin microtiter assay (REMA) [29,30]. Briefly, log-phase bacteria were diluted to a cell density of 5×10^6 cells/mL and 100 μ L of this inoculum was grown in a 96-well plate in the presence of serial dilutions of compounds. After 7–14 days incubation, 20 μ L of a 0.025% (w/v) resazurin solution was added to each well (200 μ L) and incubation was continued until the appearance of a color change (from blue to pink) in the control well (bacteria without antibiotics). Fluorescence of the resazurin metabolite resorufin ($\lambda_{excitation}$, 530 nm; $\lambda_{emission}$, 590 nm) was then measured [30] and the concentration leading to 50% growth inhibition was defined as the MIC_{50} . See [Supplementary Material](#) for detailed protocol.

4.2.3. High-content screening assay – extracellular assay

A 14 days old culture of *M. tb* H37Rv-GFP was washed twice with PBS and resuspended in 7H9 medium containing 10% OADC, 0.5% glycerol, 0.05% Tween 80 and 50 μ g/mL hygromycin B. Bacteria were seeded in 384 well plates (7×10^5 bacteria/mL) containing 2-fold dilutions of the compounds in DMSO. The final volume of DMSO was kept under 0.3%. Plates were incubated at 37 °C, 5% CO₂ for 5 days. Bacterial fluorescence levels (RFU) were recorded using a fluorescent microplate reader (Victor X3, Perkin-Elmer). The MIC_{50} of all tested compounds were determined using ten-point dose-response curves. In each plate, negative control with 1% DMSO; and positive controls containing 1 μ g/mL INH and RIF were also included.

4.2.4. High-content screening assay in infected macrophages – intracellular assay

The growth of *M. tb* H37Rv-GFP strain in macrophages was monitored by automated fluorescence confocal microscope (Opera, Perkin-Elmer) as already described [36,67]. Briefly, bacteria were washed twice with PBS and resuspended in RPMI 1640 medium (Invitrogen) supplemented with 10% heat-inactivated fetal bovine serum (FBS, Invitrogen). Murine (Raw264.7) macrophages (American Type Culture Collection TIB-71) were infected at a multiplicity of infection (MOI) of 2:1 and incubated 2 h at 37 °C in RPMI 1640 medium containing 10% FBS. Cells were then washed, treated with 50 μ g/mL amikacin (Euromedex) for 1 h at 37 °C to kill all extra-cellular bacteria, washed again and finally seeded in 384-well plates (5×10^5 cells/mL), containing 2-fold dilutions of compounds in DMSO. The final volume of DMSO was kept under 0.3%. Plates were incubated for 5 days at 37 °C, 5% CO₂. Infected cells were stained for 30 min using Syto60 dye (Invitrogen) at a final concentration of 5 μ M before reading using fluorescence confocal microscope (20X water objective; GFP: λ_{ex} 488 nm, λ_{em} 520 nm;

Syto60: λ_{ex} 640 nm, λ_{em} 690 nm). Dose-responses were fitted using Prism software (sigmoidal dose-response, variable slope model). The MIC₅₀ was determined using ten-point dose-response curves as an average of the MIC₅₀ of 4 parameters, the ratio of infected cells, the total area of bacteria, the cells number and the bacterial area per infected cell. In each plate, negative control with 1% DMSO (*i.e.*, infected macrophages only); as well as positive controls containing 10 $\mu\text{g}/\text{mL}$ INH, ETO and RIF were also included.

4.3. HPOX target enzymes identification

4.3.1. Activity-based protein profiling (ABPP)

Homogeneous bacterial suspension of *M. tb* mc²6230 in 7H9-S was adjusted at an OD₆₀₀ of 60 and then incubated with the selected HPOX inhibitor (400 μM final concentration) or DMSO (control) at 37 °C for 2–3 h. under gentle shaking at 75 rpm. Bacteria were then washed 3 times with PBS containing 0.05% Tween 80, resuspended in PBS buffer at a 1:1 (*w/v*) ratio and then lysed by mechanical disruption on a BioSpec Beadbeater. Both HPOX-treated *M. tb* mc²6230 and DMSO-control lysate samples (750 μL –0.75 mg total proteins) were labeled with 2 μM Desthiobiotin-FP probe for 90 min at room temperature. Samples were enriched for biotinylated proteins using Nanolink streptavidin magnetic beads 0.8 μm (Solulink), according to the manufacturer's instructions. The resulting captured biotinylated proteins solution was mixed with 5X Laemmli reducing sample buffer, and heated at 95 °C for 5 min. The released denatured proteins were subjected to tryptic digestion, peptide extraction, and LC-MS/MS analysis as described below.

Alternatively, the HPOX-treated *M. tb* mc²6230 and DMSO-control lysate samples (100 μL –100 μg total proteins) were incubated with 2 μM ActivX TAMRA-FP probe (Thermo Fisher Scientific) for 90 min at room temperature and in absence of light. The reaction was stopped by adding 5 \times Laemmli reducing sample buffer and boiling at 95 °C for 5 min. The labeled proteins were further separated by SDS-PAGE electrophoresis. TAMRA fluorescence (TAMRA: λ_{ex} 557 nm, λ_{em} 583 nm) was detected using a ChemiDoc MP Imager (Bio-Rad). Detailed Materials and Methods is given in [Supplementary Material](#).

4.3.2. Protein identification and quantification

Protein extract were loaded and stacked on a NuPAGE gel (Life Technologies). Stained bands were submitted to an in-gel trypsin digestion [68]. Peptides extracts were reconstituted with 0.1% trifluoroacetic acid in 4% acetonitrile and analyzed by liquid chromatography (LC)-tandem mass spectrometry (MS/MS) using an Orbitrap Fusion Lumos Tribrid Mass Spectrometer (Thermo Electron, Bremen, Germany) online with a an Ultimate 3000RSLC nano chromatography system (Thermo Fisher Scientific, Sunnyvale, CA). Protein identification and quantification were processed using the MaxQuant computational proteomics platform, version 1.5.3.8 [69] using a UniProt *M. tuberculosis* ATCC 25,618 database (date 2018.01; 2164 entries). The statistical analysis was done with Perseus program (version 1.5.6.0). Differential proteins were detected using a two-sample *t*-test at 0.01 and 0.05 permutation based FDR. The mass spectrometry proteomics data, including search results, have been deposited to the ProteomeXchange Consortium (www.proteomexchange.org) [70] via the PRIDE partner repository with the dataset identifier PXD010255. Detailed Materials and Methods is given in [Supplementary Material](#).

4.4. Inhibition assays on pure recombinant proteins

The three lipolytic enzymes from *M. tb*, the thioesterase TesA, the monoacylglycerol lipase Rv0183, and the Cutinase-like protein Cfp21 were produced and purified as previously reported [48,55].

The lipase-inhibitor pre-incubation method was used to test, in aqueous medium and in the absence of substrate, the possible direct reactions between lipases and inhibitors as previously described

[27,56,71]. Briefly, an aliquot of each enzyme was pre-incubated at 25 °C with HPOX at various inhibitor molar excess (x_1) ranging from 1 to 40 related to 1 mol of enzyme. A sample of the incubation medium was collected after 30 min incubation period and the residual enzyme activity was measured. The variation in the residual lipase activity allowed determination of the inhibitor molar excess which reduced the enzyme activity to 50% of its initial value (x_{150}) [27,56,71]. In each case, control experiments were performed in the absence of inhibitor. The respective enzymatic activity of TesA and Cfp21 were assessed using *para*-nitrophenyl (pNP) ester assay with pNP caprylate (pNP-C8) as substrate, as described previously [23]. Rv0183 residual activity was determined using monoolein as substrate, as reported in [48,56]. Dose-response curves were fitted in Kaleidagraph 4.2 Software (Synergy Software). Results are expressed as mean values \pm SD of at least two independent assays.

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Appendix A. Supplementary material

Supplementary data associated with this article can be found, in the online version, at <https://doi.org/10.1016/j.bioorg.2018.08.025>.

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