Dissecting the antibacterial activity of oxadiazolone-core derivatives against *Mycobacterium abscessus*

Abdeldjalil Madani, Ivy Mallick, Alexandre Guy, Céline Crauste, Thierry Durand, Patrick Fourquet, Stéphane Audebert, Luc Camoin, Stéphane Canaan, Jean-François Cavalier

To cite this version:
Abdeldjalil Madani, Ivy Mallick, Alexandre Guy, Céline Crauste, Thierry Durand, et al.. Dissecting the antibacterial activity of oxadiazolone-core derivatives against *Mycobacterium abscessus*. PLoS ONE, Public Library of Science, 2020, 15 (9), pp.e0238178. 10.1371/journal.pone.0238178. hal-02950695

HAL Id: hal-02950695
https://hal-amanu.archives-ouvertes.fr/hal-02950695
Submitted on 28 Sep 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution 4.0 International License
Dissecting the antibacterial activity of oxadiazolone-core derivatives against *Mycobacterium abscessus*

Abdeldjalil Madani1*, Ivy Mallick1,2, Alexandre Guy3, Céline Crauste3, Thierry Durand3, Patrick Fourquet4, Stéphane Audebert4, Luc Camoin4, Stéphane Canaan1, JeanFrançois Cavalier1*

1 Aix-Marseille Univ., CNRS, LISM, Institut de Microbiologie de la Méditerranée FR3479, Marseille, France, 2 IHU Méditerranée Infection, Aix-Marseille Univ., Marseille, France, 3 IBMM, Univ Montpellier, CNRS, ENSCM, Montpellier, France, 4 Aix-Marseille Univ, INSERM, CNRS, Institut Paoli-Calmettes, CRCM, Marseille Proteomique, Marseille, France

☯ These authors contributed equally to this work.

* jfcavalier@imm.cnrs.fr

Abstract

*Mycobacterium abscessus* (*M. abscessus*), a rapidly growing mycobacterium, is an emergent opportunistic pathogen responsible for chronic bronchopulmonary infections in individuals with respiratory diseases such as cystic fibrosis. Most treatments of *M. abscessus* pulmonary infections are poorly effective due to the intrinsic resistance of this bacteria against a broad range of antibiotics including anti-tuberculosis agents. Consequently, the number of drugs that are efficient against *M. abscessus* remains limited. In this context, 19 oxadiazolone (*OX*) derivatives have been investigated for their antibacterial activity against both the rough (R) and smooth (S) variants of *M. abscessus*. Several *OXs* impair extracellular *M. abscessus* growth with moderated minimal inhibitory concentrations (MIC), or act intracellularly by inhibiting *M. abscessus* growth inside infected macrophages with MIC values similar to those of imipenem. Such promising results prompted us to identify the potential target enzymes of the sole extra and intracellular inhibitor of *M. abscessus* growth, i.e., compound *iBpPPOX*, via activity-based protein profiling combined with mass spectrometry. This approach led to the identification of 21 potential protein candidates being mostly involved in *M. abscessus* lipid metabolism and/or in cell wall biosynthesis. Among them, the Ag85C protein has been confirmed as a vulnerable target of *iBpPPOX*. This study clearly emphasizes the potential of the *OX* derivatives to inhibit the extracellular and/or intracellular growth of *M. abscessus* by targeting various enzymes potentially involved in many physiological processes of this most drug-resistant mycobacterial species.

Introduction

Non-tuberculous mycobacteria (NTM) are naturally-occurring bacterial species mostly found in soil and water that do not cause tuberculosis or leprosy [1]. NTM are opportunistic
pathogens able to infect humans with predisposing conditions like cystic fibrosis (CF) or immunosuppression and responsible for wide range of infections like skin infections, pulmonary infections or disseminated diseases [2–4]. In the last decades, NTM infections are increasing worldwide, the most frequently reported species being *Mycobacterium avium* complex (MAC) and *M. abscessus* complex [3, 5].

*M. abscessus* can be isolated from solid medium with either a smooth (S) or a rough (R) colony morphotype [6]. The difference between both morphotypes is related to the presence of glycopeptidolipids (GPLs) in the cell wall of the S variant, while absent in the R one [7]. This latter R strain is also associated with severe and persistent infections [8]. In CF patients, treatment of *M. abscessus* complex infections requires a multidrug therapy including a daily oral macrolide (clarithromycin or azithromycin) in conjunction with intravenous amikacin and a β-lactam (imipenem or cefoxitin) [9]. However, almost 60% of *M. abscessus* strains could develop both intrinsic and acquired resistance to currently available antibiotics, including macrolides [4, 10]. As a direct consequence, treatment of such infections has become very complicated with very limited alternative options [5, 11].

Due to the worldwide increasing incidence and prevalence of *M. abscessus* and the inherent difficulties to manage such resistant pulmonary infections, new active molecules are urgently needed. In this context, we recently investigated the antibacterial activities of 19 oxadiazolone-core (OX) derivatives (Fig 1) against three pathogenic slow-growing mycobacteria: *M. marinum, M. bovis* BCG as well as *M. tuberculosis* H37Rv the etiologic agent of tuberculosis [12].

These OX compounds exhibited not only encouraging minimal inhibitory concentrations (MIC), but above all, they were also found to display a diversity of actions by acting either only on extracellular *M. tuberculosis* growth, or both intracellularly on infected macrophages as well as extracellularly on bacterial growth. Remarkably, all OX derivatives exhibited very low
toxicity towards host cell macrophages [12]. Of interest, only the iBpPPOX derivative exhibited moderate (MIC$_{50}$ = 32.0 μM) to quite good (MIC$_{50}$ = 8.5 μM) antibacterial activity against both extracellular and intramacrophagic *M. tuberculosis* H37Rv, respectively [12]. Following an activity-based protein profiling (ABPP) approach combined with mass spectrometry, 18 putative target(s) of HPOX, a selective inhibitor of *M. tuberculosis* extracellular growth, were identified. All these proteins were (Ser/Cys)-enzymes possessing a catalytic serine or cysteine residue, and involved in *M. tuberculosis* lipid metabolism and/or in cell wall biosynthesis. Above all, the results of this study imply that such OX derivatives represent a novel class of multi-target mycobacterial inhibitors via the formation of a covalent bond with the catalytic residue of various mycobacterial (Ser/Cys)-containing enzymes involved in various physiological processes.

Given all these previous findings, in the present study we have further assessed the antibacterial activity of these 19 OXs against *M. abscessus* growth. The determined MIC revealed that some OXs were able to inhibit *M. abscessus* growth in vitro in culture broth medium and/or intracellularly inside macrophages. In addition, using a similar ABPP assay as previously reported for *M. tuberculosis* [12], the potential target enzymes of iBpPPOX, the most active inhibitor of extra- and intracellular bacterial growth, were further identified.

### Materials and methods

#### Bacterial strains and growth conditions

*M. abscessus* CIP104536$^T$ with either a smooth (S) or rough (R) morphotype was grown in Middlebrook 7H9 broth (BD Difco, Le Pont de Claix, France) supplemented with 0.2% glycerol, 0.05% Tween 80 and 0.2% glucose (Sigma-Aldrich, St. Quentin Fallavier, France) (7H9-S).

#### Chemicals

Clarithromycine and Imipenem mixture w/Cilastatin were purchased from Euromedex (Soffelwiesheim, France). The Oxadiazolone derivatives were synthesized as previously reported and were at least 98% pure as determined by HPLC analysis [12]. Stock solutions of each inhibitor (4 mg/mL) were prepared in DMSO and stored at -20 °C before use.

#### Resazurin microtiter assay (REMA) for MIC determination—Extracellular assay

Susceptibility testing was performed using the Middlebrook 7H9 broth microdilution method. MICs of the OXs were determined in 96-well flat-bottom Nunclon Delta Surface microplates with lid (Thermo-Fisher Scientific, ref. 167008) using the resazurin microtiter assay (REMA) [12–15]. Briefly, log-phase bacteria were diluted to a cell density of $5 \times 10^6$ cells/mL and 100 μL of this inoculum was grown in a 96-well plate in the presence of serial dilutions of each OX compound. After 3–5 days incubation at 37 °C, 20 μL of a 0.025% (w/v) resazurin solution was added to each well (200 μL) and incubation was continued until the appearance of a color change (from blue to pink) in the control well (i.e., bacteria without antibiotics). Fluorescence of the resazurin metabolite resorufin ($\lambda_{\text{excitation}}$, 530 nm; $\lambda_{\text{emission}}$, 590 nm) was then measured [13, 16] and the concentration leading to 50% and 90% growth inhibition was defined as the MIC$_{50}$ and MIC$_{90}$, respectively. See S1 Appendix for detailed protocol.
Intramacrophage killing assay—Intracellular assay

The intracellular growth of *M. abscessus* S was assessed following a 24 h exposure of infected Raw264.7 murine macrophages cell line (American Type Culture Collection TIB-71) to each of the 19 OX compounds at a final concentration of 30 μM [17]. To avoid growth of extracellular mycobacteria, cells were extensively washed and treated with amikacin (200 μg/mL = 340 μM; 87 × MIC<sub>50</sub>) prior to treatment with the OX analogs. Imipenem (IMP; 80 μg/mL = 267 μM; 64 × MIC<sub>50</sub>) was used as positive control for this intracellular killing assay. In each case, the viability of infected macrophages was checked by addition of trypan blue [18] before cell lysis and plating for CFU count. See S1 Appendix for detailed protocol.

iBpPPOX target enzymes identification

Activity-Based Protein Profiling (ABPP) for the identification of iBpPPOX target enzymes. Bacterial suspension of *M. abscessus* R in 7H9-S was adjusted at an OD<sub>600</sub> corresponding to 6 × 10<sup>9</sup> cells/mL and then incubated with iBpPPOX 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 iBpPPOX-treated *M. abscessus* 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 0.8 μm Nanolink streptavidin magnetic beads (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, *M. abscessus* R total lysates (500 μL – 1 mg total proteins) were further pre-incubated with iBpPPOX (400 μM final concentration) or DMSO as control for 60 min at 37°C, and then treated with 2 μM ActivX Desthiobiotin-FP probe (ThermoFisher Scientific) and processed as described above for *M. abscessus* R living cells. Detailed protocol regarding ABPP experiments is given in S1 Appendix.

Mass spectrometry analysis for enzyme 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 [19]. Peptides extracts were reconstituted with 0.1% trifluoroacetic acid in 4% acetonitrile and analyzed by liquid chromatography (LC)-tandem mass spectrometry (MS/MS) using Orbitrap Mass Spectrometers (Thermo Electron, Bremen, Germany) online with a nanoLC Ultimate 3000 chromatography system (Dionex, Sunnyvale, CA). Protein identification and quantification were processed using the MaxQuant computational proteomics platform, version 1.5.3.8 [20] using a UniProt *M. abscessus* ATCC 19977 (Taxon 561007) database (date 2017.02; 4940 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. Detailed Materials and Methods are given in S1 Appendix.

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (www.proteomexchange.org) [21] via the PRIDE partner repository with the dataset identifier PXD015680.
Validation of Ag85C<sub>Mabs</sub> by iBpPPOX

**Plasms and DNA manipulations.** All specific oligonucleotides and plasmids used in this study are listed in S1 Appendix (see S3 and S4 Tables—page S8). All cloned fragments were amplified using purified <i>M. abscessus</i> genomic DNA. The <i>mab</i><sub>0175</sub> gene encoding Ag85C was amplified by PCR using the specific forward (<i>pMyc</i>::<i>ag85C</i>-<i>F</i>) and reverse (<i>pMyc</i>::<i>ag85C</i>-<i>R</i>) primers. For the inactivated Ser124Ala mutant <i>pMyc</i>::<i>ag85C</i>-<i>R</i> were used, the second fragment containing the mutation was generated using the primer sets <i>pMyc</i>::<i>ag85C</i>-<i>F</i> and <i>pMyc</i>::<i>ag85C</i><sub>S124A</sub>-<i>R</i>. The two fragments were further purified, mixed in 1:1 (v/v) ratio and used as template to amplify the complete insert containing the mutation, using the primer pairs <i>pMyc</i>::<i>ag85C</i>-<i>F</i> and <i>pMyc</i>::<i>ag85C</i>-<i>R</i>. The respective PCR products were cloned into pMyC vector, following digestion with NcoI and HindIII, enabling the incorporation of a 6-His-tag in the C-terminus of the Ag85C or Ag85C<sub>S124A</sub> protein. Deletion mutant Δ<i>mab</i><sub>0175</sub> (= Δag85C) was obtained by a simple and rapid gene disruption strategy in <i>M. abscessus</i> developed by Viljoen et al. [22]. Ag85C gene was amplified using primer pairs <i>pUX1</i>::<i>Δag85C</i>-<i>F</i> and <i>pUX1</i>::<i>Δag85C</i>-<i>R</i>, then cloned into pUX1 vector using NheI and BamHI restriction sites by classical cloning. Finally, for complementation strain, the <i>mab</i><sub>0175</sub> gene was amplified using the primer pairs <i>pVV16</i>::<i>ag85C</i>-<i>F</i> and <i>pVV16</i>::<i>ag85C</i>-<i>R</i>, and cloned into pVV16 plasmid in frame with a 6-His-tag located in C-terminal and downstream of the <i>hsp60</i> promoter also containing a kanamycin resistance cassette using restriction free cloning (SLIC) [23] to generate <i>pVV16</i>::<i>ag85C</i>. Sequence integrity of each construct was confirmed by DNA sequencing (Eurofins Genomics). All the constructs were further transformed in electrocompetent <i>M. abscessus</i> S and R types and selected on respective antibiotic agar plates as described previously [22]. Positive transformants were further grown in 7H<i><sub>OADC</sub></i> medium (i.e., 7H9 broth + 0.2% glycerol + 0.05% Tween 80 + 10% oleic acid, albumin, dextrose, catalase) supplemented with either hygromycin (1000 μg/mL; i.e., overexpression and inactivated strains), kanamycin (250 μg/mL; i.e., deletion strain) or both antibiotics (1000 μg/mL hygromycin + 250 μg/mL kanamycin; i.e., complementation strain), up to OD<sub>600</sub> of 1. The overproduction of the recombinant proteins in the overexpression and inactivated strains as well as in the complementation strain was checked by Western blot using the HisProbe™ HRP conjugate (ThermoFisher Scientific). Regarding the deletion strain, the selection was made based on red fluorescent colonies followed by PCR amplification and sequencing strategy as described in [22].

**Functional validation of Ag85C<sub>Mabs</sub> target enzyme**

The abovementioned transformed bacteria, i.e., the <i>M. abscessus</i>_<i>pMyc</i>::<i>ag85C</i> overexpressing strains, the inactivated <i>M. abscessus</i>_<i>pMyc</i>::<i>ag85C</i><sub>S124A</sub> overexpressing strains, the <i>M. abscessus</i>_<i>Δag85C</i> deletion strains and their complemented counterparts <i>M. abscessus</i>_<i>Δag85C</i>::<i>C</i> were grown in 7H<i><sub>OADC</sub></i> medium supplemented with either hygromycin (1000 μg/mL; i.e., overexpression and inactivated strains), kanamycin (250 μg/mL; i.e., deletion strain), or both antibiotics (1000 μg/mL hygromycin + 250 μg/mL kanamycin; i.e., complementation strain) until the OD<sub>600</sub> reached 2. In the case of the overexpression and inactivated strains, induction was further done with 0.2% acetamide and the culture was incubated at 37°C for additional 24 h. Susceptibility testing of each of the <i>M. abscessus</i> mutant strains against various concentrations of iBpPPOX was further performed as described above.
Expression and purification of *M. abscessus* antigen Ag85C

The plasmid harboring the *mab_0175* gene was used to transform the *M. smegmatis ΔgroEl* expression strain. Transformed bacteria were grown in 7H9 medium containing hygromycin (200 μg/mL) until the OD<sub>600</sub> reached 2.0. Induction was done with 0.2% acetamide and the culture was further incubated at 37 °C for 24 h. One L of bacterial pellets were collected by centrifugation (8,000 × g, 4 °C, 1 h), re-suspended in 30 mL ice-cold buffer (50 mM Tris pH 8.0 containing 200 mM NaCl), and were broken using a French Pressure cell at 1,100 psi. The lysate was clarified by centrifugation (12,000 × g, 4 °C, 30 min) prior to purification by nickel affinity chromatography with Ni-NTA sepharose beads and elution with the previous Tris (pH 8.0) buffer containing 500 mM imidazole. Purified protein was concentrated at 1 mg/mL and stored at –80 °C [24, 25].

**In vitro** inhibition of pure recombinant *M. abscessus* Ag85C by iBpPPOX

A 14 μM (i.e., 25 μg) concentration of Ag85C<sub>Mabs</sub> was incubated for 1 h in its native form with increasing molar excess of iBpPPOX (i.e. enzyme/inhibitor molar ratio, E/I = 1:1; 1:5, 1:10, 1:25, 1:50, and 1:75) in a reaction mixture containing 10 mM Tris buffer (pH 8), 150 mM NaCl and 0.1% (w/v) Triton X-100. Each sample was further treated with 10 μM ActiveX TAMRA-FP fluorescent probe (ThermoFisher Scientific) for 1 h at room temperature in the darkness. The reaction was stopped by adding 5X Laemmli reducing buffer followed by boiling, and equal amounts of proteins (12 μg) were separated by 12% SDS-PAGE. Subsequently, TAMRA FP-labeled proteins were detected by fluorescent gel scanning (TAMRA: λ<sub>ex</sub> 557 nm, λ<sub>em</sub> 583 nm) using the Cy<sup>3</sup> filter of a ChemiDoc MP Imager (Bio-Rad) before staining the gel with Coomassie Brilliant Blue dye. Finally, relative fluorescence quantification of each band was performed using the ImageLab™ software version 5.0 (Bio-Rad) by taking the labeled Ag85C<sub>Mabs</sub>-TAMRA adduct as 100% absolute fluorescence level.

**Mass spectrometry analysis of Ag85C<sub>Mabs</sub>-iBpPPOX complex**

Purified Ag85C<sub>Mabs</sub> recombinant protein (14 μM– 100 μg) was further incubated for 1 h in its native form with iBpPPOX, using an enzyme/inhibitor molar ratio E/I = 1:100 to ensure total inhibition. Samples of the resulting Ag85C<sub>Mabs</sub>-iBpPPOX complex were analysed on a MALDI-TOF-TOF Bruker Ultraflex III spectrometer (Bruker Daltonics, Wissembourg, France) controlled by the Flexcontrol 3.0 package (Build 51), as described previously [24] (see S1 Appendix for full details). The total mass of the untreated protein (theoretical Mw = 32,057.83 Da; experimental Mw = 32,048.7 Da) is corresponding to the native enzyme lacking the 36 first N-terminal amino acids (i.e., M<sup>1</sup>SVRVKARRVLSALLAAFVMPVSM------TAH<sup>36</sup>) consisting of a Sec signal peptide cleaved at the Ala-X-Ala (i.e., A<sup>35</sup>-H<sup>36</sup>-A<sup>37</sup>) site, as confirmed by N-terminal Edman sequencing [26].

**Statistical analysis**

Graphpad Prism 5 was used to perform the statistical analyses of the intracellular activity of the OX compounds, and of all susceptibility testing on *M. abscessus* mutant strains. The statistical analysis related to MIC<sub>50Raw</sub> was completed using a Student’s t-test. The statistical significance of differences in the MIC<sub>50</sub> or MIC<sub>90</sub> values between each mutant strain was analyzed by one-way ANOVA followed by a post hoc Fisher’s test.
Results and discussion

*In vitro* activity of oxadiazolone derivatives against *M. abscessus*

Drug susceptibility testing of the OX derivatives was assessed against both S and R variants of *M. abscessus*, with amikacin (AMK) as standard drug. The corresponding MIC$_{50}$/MIC$_{90}$ values for each OX compound, as determined by the REMA assay [12–16], are reported in Table 1. Among all tested compounds, 14 OXs were able to block the growth of *M. abscessus* S variant. The best growth inhibitors were iBpPPOX (33.0 ± 2.0 μM), HpPPOX (32.5 ± 2.2 μM), MemPPOX (41.8 ± 1.6 μM) and BePOX (45.1 ± 3.4 μM) which displayed interesting MIC$_{50}$ values (Table 1). In all other cases, MIC$_{50}$ values were indicative either of a moderate (MIC$_{50}$ around

Table 1. Antibacterial activities of the oxadiazolone derivatives against *M. abscessus* growth in broth medium using the REMA method*.

| Compounds      | MIC$_{50}$/MIC$_{90}$ (μM) |
|----------------|----------------------------|
|                | *M. abscessus* CIP104536$^T$ |                          |
|                | S variant | R variant |
| AMK            | 3.9±0.19 / 5.8±0.20 | 7.4±0.26 / 10.1±0.45 |
| IMP            | 4.2±0.19 / 6.3±0.26 | 11.9±0.63 / 29.9±1.1 |
| MnPPPOX        | 60.7±5.0 / 119.3±4.2 | 181±9.0 / >200 |
| MpPPPOX        | 88.2±7.3 / 157.5±6.2 | >200 / >200 |
| MPOX           | >200       | >200       |
| EmPPPOX        | 82.8±6.5 / 101.8±4.6 | 191.8±10.2 / >200 |
| MemPPPOX       | 41.8±1.6 / 44.4±2.0 | 95.1±5.1 / 113.9±4.7 |
| BnPPPOX        | 78.1±5.3 / >200 | 167.4±8.5 / 174.1±8.1 |
| iBnPPPOX       | 122.1±7.8 / >200 | 133.5±8.0 / >200 |
| iBpPPPOX       | 33.0±2.0 / 85.9±5.5 | 53.2±1.8 / 104.3±5.1 |
| iPPOX          | 61.3±5.1 / 68.8±2.4 | >200 / >200 |
| HmPPPOX        | >200       | 120.3±7.1 / >200 |
| HpPPOX         | 32.5±2.2 / 79.4±3.3 | 45.8±1.9 / 103.8±4.0 |
| HPOX           | 92.9±4.2 / 99.9±5.5 | >200 / >200 |
| BemPPPOX       | 126.7±7.3 / 145.7±6.9 | 153.0±7.8 / >200 |
| BePPOX         | 53.7±3.1 / 73.5±3.2 | 52.6±2.5 / 111.1±4.1 |
| BePOX          | 45.1±3.4 / 46.5±2.0 | 98.0±5.8 / 170.2±6.2 |
| OmpPPOX        | >200       | >200       |
| EhmPPPOX       | 145.1±7.7 / >200 | 142.7±7.0 / 150.3±5.0 |
| DmPPPOX        | >200       | 144.0±7.8 / 167.5±5.8 |
| DomPPPOX       | >200       | 104.6±5.2 / >200 |

* Experiments were performed as described in Materials and Methods. MIC$_{50}$/MIC$_{90}$: compound minimal concentration leading to 50% or 90% of growth inhibition, respectively, as determined by the REMA assay. Values are mean of at least two independent assays performed in triplicate. AMK, amikacin, IMP, imipenem.

https://doi.org/10.1371/journal.pone.0238178.t001
Intramacrophagic susceptibility of *Mycobacterium abscessus* to OX derivatives

Macrophages, as the primary target, represent the host’s first line of defense but also an important reservoir of mycobacteria in lungs. From our previous work, the OXs were able to inhibit the growth of *M. tuberculosis* inside infected macrophages, and found to be non-toxic for Raw264.7 murine macrophages cell line with a CC50 > 100 μM (i.e., compound concentration leading to 50% cell toxicity) [12]. Considering such properties, we further investigated the ability of OXs to inhibit the intra-macrophagic growth of *M. abscessus*. The intrinsic nature of the R variant is to form bacterial clumps and cords in culture medium with time. As reported by Bernut *et al.*, *M. abscessus* R cording prevents its phagocytosis by macrophages. Consequently, the strain continues to grow extracellularly, and rapidly induces cell toxicity leading to cell death [29, 30]. Such cording characteristic makes macrophage infection experiments using *M. abscessus* R very difficult to handle. Indeed, nearly all macrophages were lysed at 24 h post-infection with *M. abscessus* R variant, making it impossible to quantify the intracellular effect of the OXs. This is, however, not the case with *M. abscessus* S for which more homogenous bacterial suspensions can be obtained for macrophages infection studies [25, 31, 32].

Therefore, Raw264.7 cells were infected with *M. abscessus* S at a multiplicity of infection (MOI) of 10, and then incubated for 24 h with all the OX compounds at a final concentration of 90, 60 and 30 μM, or with imipenem (IMP) used as positive drug control. Among the 19 compounds tested, only 3 OXs (i.e., MPOX, MpPPOX, and iBpPPOX) exhibited an antibacterial activity against intracellular *M. abscessus* growth. Interestingly, MpPPOX and MPOX, 53–61 μM for MmPPOX, iBPOX, and BepPPOX), a weak (MIC50 around 78–93 μM for MpPPOX, EmPPOX, BmPPOX, and HPOX), or a poor (MIC50 > 120 μM for iBmPPOX, EhmPPOX, and BemPPOX) antibacterial activity (Table 1). Considering the MIC50 values reached on *M. abscessus* S, they are up to 2.5-fold greater than the corresponding MIC50; except for HPOX (MIC50 = 92.9 ±4.2 μM / MIC90 = 99.9 ±5.5 μM), MemPPOX (MIC50 = 41.8 ±1.6 μM / MIC90 = 44.4 ±2.0 μM) and BiPPOX (MIC50 = 45.1 ±3.4 μM / MIC90 = 46.5 ±2.0 μM) for which both MICs are in the same order of magnitude (Table 1).

Compared to the S morphotype, *M. abscessus* R variant was nearly 1.3- to 3.6-times less sensitive to the OX compounds (Table 1); a property already observed for many drugs including AMK [27]. The best inhibitors of *M. abscessus* R growth were iBiPPOX (MIC50 = 53.2 ±1.8 μM / MIC90 = 104.3 ±5.1 μM), HpiPPOX (MIC50 = 45.8 ±1.9 μM / MIC90 = 103.8 ±4.0 μM), and BepPPOX (MIC50 = 52.6 ±2.5 μM / MIC90 = 111.1 ±4.1 μM) which exhibited similar MIC50 and MIC90 values, respectively (Table 1). Interestingly, MpPPOX bearing a short methyl chain has no antibacterial effect as compared to the three abovementioned para-phenoxyphenyl derivatives. In summary, iBiPPOX, HpiPPOX, and BepPPOX all possessing the phenoxy group in a para position as well as bulky ester chains, displayed the best antibacterial activity against *M. abscessus* R. No other clear trends or rules in terms of structure-activity relationships (SAR) have emerged regarding the potency of these oxadiazolone-core compounds against *M. abscessus*.

It is noteworthy that with MIC50 values ranging from 31 to >120 μM [12], *M. tuberculosis* susceptibility to the OX compounds is similar to that of the S variant of *M. abscessus*; iBiPPOX being the best growth inhibitor of both species. The increased tolerance of the most-virulent *M. abscessus* R variant towards the OX compounds is in line with its high resistance to classical antibiotics [4] compared to *M. tuberculosis*; a result that supports *M. abscessus* R’s nickname of “antibiotics nightmare” [28].
which are weakly and not active against extracellular bacilli, respectively, were however able to significantly decrease the intramacrophagic M. abscessus present 24 h after infection (Fig 2).

MpPPOX displayed a moderate activity against intracellular M. abscessus S (Fig 2) with an approximated MIC$_{50_{Raw}}$ of around 75 μM which is 2.6 times higher that of IMP (MIC$_{50_{Raw}}$ = 28.3 μM). In contrast, 24 h-treatment with 30–60 μM MPOX led to a 53% reduction in mycobacteria which increased up to 73.5% at 90 μM, a percentage value comparable to the one elicited by IMP, i.e., 74.0% reduction following treatment with 60 μM (Fig 2). Remarkably, and as observed previously for M. tuberculosis [12], iBpPPOX was the sole identified inhibitor able to impair extracellular as well as intracellular growth of M. abscessus. A plateau value corresponding to 58.5 ±0.8% bacterial killing was indeed reached, whatever the iBpPPOX concentration used (30–90 μM) to treat the infected cells.

Such a difference between the intra and extracellular activities has already been reported in our previous works with the OX derivatives [12], as well as with another family of growth inhibitors, the Cyclipostins & Cyclophostin analogs [13, 14] acting against M. tuberculosis and M. abscessus [25]. Similar to M. tuberculosis [12], the intracellular and extracellular inhibition of M. abscessus growth may probably result from several different mechanisms of action or penetration of the OX derivatives. The short methyl chain MpPPOX and MPOX display a better antimycobacterial activity against intramacrophagic M. abscessus than in broth medium. This clear preference against intracellularly-replicating mycobacteria may imply that the intracellular activity and/or the targets of these two compounds might differ from that of OXs acting on extracellularly-replicating bacilli. Several factors may indeed account for these discrepancies, such as the metabolic status/fitness which varies between extra- and intracellular replicating bacteria. Another hypothesis could be that their corresponding target(s) would be more accessible and/or vulnerable during the intracellular lifestyle of M. abscessus. A specific response of the macrophage stimulated by the action of these compounds and leading to bacterial clearance cannot, however, be excluded. On the other hand, the iBpPPOX retains a similar
activity against \textit{M. abscessus} both extracellularly (MIC$_{50}$ = 33.0 μM) and inside macrophages (~59% bacterial clearance at 30 μM). Regarding its intracellular antibacterial activity, the presence of a plateau value, whatever the concentration used, might underline a different effect of \textit{iBpPPOX} towards infected macrophages compared to \textit{MmPPOX} and \textit{MPOX} for which a more classical dose-response has been reached. As mentioned above, one can speculate that the cellular stress caused by the action of \textit{iBpPPOX} on the infected macrophages might induce a specific stringent response of these host cells, such as possible cell metabolism, therefore leading to bacterial death.

Given the previously determined very low toxicity of the three selected compounds toward Raw264.7 cells with CC$_{50}$ > 100 μM [12] similar to AMK (CC$_{50}$ ≥ 150 μM) [33], the selectivity index (SI = CC$_{50}$/MIC$_{50}$Raw) of these best intracellular inhibitors on \textit{M. abscessus} vs. Raw264.7 cells was thus valued to be in a range from around 1.3 for \textit{MmPPOX} and up to >3 for \textit{iBpPPOX}.

From these findings, it can be assumed that the observed inhibitory potency of the OX compounds i) might result from the inhibition of specific but most likely distinct mycobacterial target enzymes between intramacrophagical vs. extracellularly-replicating bacilli; or ii) may reflect differences in the uptake and accumulation of the different compound inside the macrophage. Overall, these results suggest that both \textit{MmPPOX}, \textit{MPOX} and \textit{iBpPPOX} would be able to enter the macrophages and arrest bacterial replication without exhibiting significant toxicity for the host cell.

\textbf{iBpPPOX inhibit \textit{M. abscessus} by targeting various serine/cysteine enzymes}

Given the previous results obtained with the \textit{HPOX} on target enzymes identification during \textit{M. tuberculosis} \textit{in vitro} growth in broth medium [12], we thus performed a similar ABPP approach [12, 13, 34–37] to identify the potential target enzymes impacted by \textit{iBpPPOX}, the sole extra and intracellular inhibitor of \textit{M. abscessus} growth.

The R variant being associated to the most virulent form of \textit{M. abscessus} and thus to severe pulmonary infections [6, 28, 38]; a crude lysate of \textit{M. abscessus} R was, in the first approach, incubated with the \textit{iBpPPOX} inhibitor (or DMSO as a control) and then subjected to competitive probe labelling/enrichment assay with the ActivX™ Desthiobiotin-FP probe (Thermo-Fisher Scientific), as reported previously in the case of \textit{M. tuberculosis} [12, 13]. The obtained enriched mixtures were further 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 also found in the control experiment (\textit{i.e.}, DMSO alone for unspecific binding to streptavidin-magnetic beads) were not considered. A panel of 58 distinct protein candidates were then identified with a permutation false discovery rate (pFDR) of 10%, which was reduced to 21 and 11 when applying a pFDR of 5% and 1%, respectively (see S1 Table).

Since most of the identified proteins were putative in \textit{M. abscessus}, the corresponding orthologs in \textit{M. tuberculosis} H37Rv have been reported to bring more information about their essentiality, activity and predicted location [39]. Eleven out of 21 identified proteins (at a pFDR of 5%) were (Ser/Cys)-based enzymes, mainly involved in lipid metabolism and cell wall biosynthesis [40, 41]. These included the probable serine protease PepD (MAB_1078); the D-amino acid aminohydrolase MAB_2605c (\textit{i.e.}, Rv2913c); the probable carboxylesterase MAB_1919 (\textit{i.e.}, Rv2223c); and the putative β-lactamase MAB_2833 (\textit{i.e.}, Rv1367c) possibly involved in cell wall biosynthesis. Three members of the lipase family Lip [42], LipH (MAB_2039), LipN (MAB_3270c) and Lipl (MAB_2814); three Cutinase-like proteins [41], Cut2 (MAB_3263), Cut3 (MAB_3765) and Cut4 (MAB_3766); and MAB_175 (Ag85C), a
member of the antigen 85 (Ag85) complex [24, 43] which catalyzes the biosynthesis of trehalose dimycolate, triacylglycerol as well as the mycolylation of arabinogalactan, were also uncovered with iBpPPOX.

In a second approach, similar ABPP experiments were performed on living bacterial cells in order to take into account the ability of iBpPPOX to penetrate/diffuse through the mycobacterial cell wall. Accordingly, M. abscessus R cells were grown to log phase and incubated with iBpPPOX or DMSO as a control. After cell lysis, the obtained total lysate was processed as described above with ActivX™ Desthiobiotin-FP probe and streptavidin magnetic beads. Tryptic digestion followed by tandem mass spectrometry analysis led to the identification of 21 protein candidates at a pFDR of 5%, and only 5 at a pFDR of 1% (Table 2 and S2 Table).

Although 4 of the identified proteins are only conserved hypotheticals, the remaining 17 ranged in their functional category from intermediary metabolism/respiration (8 proteins), lipid metabolism (4 proteins), regulatory pathways (3 proteins), cell wall/cell processes (1 protein), and information pathways (1 protein). Among them, MAB_1675, the probable DNA repair protein RecO (i.e., Rv2362c), and MAB_1053c (i.e., Rv0948c) a putative chorismate mutase possibly involved in phenylalanine, tyrosine and tryptophan biosynthesis, are annotated as essential enzymes for the in vitro growth of M. tuberculosis [44, 45]. In good agreement with our previous work on M. tuberculosis target enzymes [12], several hydrolases were

Table 2. iBpPPOX target proteins identified at a pFDR of 1% and 5% in M. abscessus R culture by LC-ESI-MS/MS analysis.

| Protein Ids | Mol. Weight [kDa] | M. tuberculosis orthologs |
|-------------|-------------------|--------------------------|
| Rv number   | Essentiality a    | Location b               | Activity / Function | Functional category c |
| MAB_0176    | 35.825            | Rv3804c CF/M             | Secreted antigen 85-A FbpA (Ag85A) | LM |
| MAB_0177    | 34.909            | Rv3804c CF/M/WCL         | Antigen 85-A/B/C precursor | LM |
| MAB_0274c   | 20.371            |                          | uncharacterized protein | - |
| MAB_0401    | 46.209            | Rv6517                   | Possible acyltransferase | IM/R |
| MAB_0520    | 38.811            | Rv3626c                  | uncharacterized protein | - |
| MAB_0684c   | 26.813            | Rv0774c CF               | Hypothetical extracellular esterase | CW/CP |
| MAB_1053c   | 10.305            | Rv0948c In vitro growth  | WCL | Chorismate mutase | IM/R |
| MAB_1675    | 28.418            | Rv2362c In vitro growth  | CW | Possible DNA repair protein RecO | IP |
| MAB_2366    | 33.804            | Rv1701                   | - | Probable integrase | RP |
| MAB_2477c   | 55.217            | Rv1393c                  | - | Probable monooxygenase | IM/R |
| MAB_2478c   | 15.382            |                          | uncharacterized protein | - |
| MAB_2545c   | 35.436            | Rv0480c M/WCL            | Possible amidohydrolase | IM/R |
| MAB_2943c   | 31.546            | Rv1543 M/WCL             | Possible fatty acyl-CoA reductase | LM |
| MAB_3336c   | 54.339            | Rv2045c                  | - | Carboxylesterase LipT | IM/R |
| MAB_3398    | 17.635            | Rv3178                   | uncharacterized protein | - |
| MAB_3661    | 57.093            | Rv3508 M                 | Probable phosphomannomutase PmmB | IM/R |
| MAB_3689    | 26.374            | Rv3342 WCL               | Possible methyltransferase | IM/R |
| MAB_3705    | 19.995            | Rv3506 CF/M              | Putative TetR family regulatory protein | RP |
| MAB_4103c   | 30.192            | Rv1523                   | - | Probable methyltransferase | IM/R |
| MAB_4201c   | 22.905            | Rv3574 WCL               | Transcriptional regulatory protein KstR | RP |
| MAB_4750    | 27.932            | Rv1544 M/WCL             | Possible ketoacyl reductase | LM |

In bold, the 5 proteins identified at a pFDR of 1%.

a From [44, 45].

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

c IM/R: intermediary metabolism/respiration; IP: information pathways; CW/CP: cell wall/cell processes; LM: lipid metabolism; RP: regulatory protein.

https://doi.org/10.1371/journal.pone.0238178.t002

In a second approach, similar ABPP experiments were performed on living bacterial cells in order to take into account the ability of iBpPPOX to penetrate/diffuse through the mycobacterial cell wall. Accordingly, M. abscessus R cells were grown to log phase and incubated with iBpPPOX or DMSO as a control. After cell lysis, the obtained total lysate was processed as described above with ActivX™ Desthiobiotin-FP probe and streptavidin magnetic beads. Tryptic digestion followed by tandem mass spectrometry analysis led to the identification of 21 protein candidates at a pFDR of 5%, and only 5 at a pFDR of 1% (Table 2 and S2 Table).

Although 4 of the identified proteins are only conserved hypotheticals, the remaining 17 ranged in their functional category from intermediary metabolism/respiration (8 proteins), lipid metabolism (4 proteins), regulatory pathways (3 proteins), cell wall/cell processes (1 protein), and information pathways (1 protein). Among them, MAB_1675, the probable DNA repair protein RecO (i.e., Rv2362c), and MAB_1053c (i.e., Rv0948c) a putative chorismate mutase possibly involved in phenylalanine, tyrosine and tryptophan biosynthesis, are annotated as essential enzymes for the in vitro growth of M. tuberculosis [44, 45]. In good agreement with our previous work on M. tuberculosis target enzymes [12], several hydrolases were
detected, including one hypothetical extracellular esterase (MAB_2181c), three putative methyltransferases (MAB_3689, MAB_4103c, MAB_0401); the carboxylesterase LipT (MAB_3336c) belonging to the Lip-family members, and the mycolyltransferases MAB_176 (Ag85A) and MAB_177 (Ag85-A/B/C precursor) two members of the Ag85 complex (Table 2 and S2 Table).

It is noteworthy that among these 21 potential hits, only Ag85 proteins were previously detected in the iBpPPOX-treated total lysate (see S1 and S2 Tables); thus, implying that nearly 19 proteins had not been detected in the previous treated M. abscessus total lysate, or at least at a pFDR ≤ 10%. On the other hand, such result suggests that Antigen 85 proteins may be the first target enzymes encountered and thus inhibited by the OX compounds.

**Validation of M. abscessus Ag85C as vulnerable target of iBpPPOX**

Knowing the importance of the Ag85 complex in mycobacterial membrane integrity due to its central role in cell envelope biogenesis, and given the fact that inhibiting the Ag85C was found to restrict *M. tuberculosis* growth [46], we decided to confirm the Ag85C<sub>Mabs</sub> which shares nearly 58% amino acid sequence identity with its *M. tuberculosis* ortholog and retains the same conserved catalytic triad (i.e., Ser<sup>124</sup>-Glu<sup>228</sup>-His<sup>260</sup>), as a potential target of the OX compounds.

We thus followed two different strategies: the first one was based on the susceptibility testing of various *M. abscessus* mutant strains to the iBpPPOX; and the second one relied on the molecular interaction between the iBpPPOX and the purified recombinant Ag85C<sub>Mabs</sub>.

In the first step, genes encoding either Ag85C<sub>Mabs</sub> or the inactivated Ag85C<sup>S124A</sup> protein were cloned and overexpressed in *M. abscessus* S and R variants using the pMyC::ag85C/ pMyC::ag85C<sup>S124A</sup> inducible plasmids, where genes were cloned under the control of an acetamide promoter (Fig 3A). Moreover, a deletion mutant of Ag85C<sub>Mabs</sub> named Δag85C was generated by using a recent one-step single cross-over system with the pUX1 vector [22]; and its complemented counterpart Δag85C::C (Fig 3B) was obtained using the pVV16::ag85C complementation plasmid which allows the constitutive production of recombinant Ag85C<sub>Mabs</sub> under the control of the hsp60 promoter (see S1 Appendix for cloning details). In each case, the overexpression/complementation of antigen 85C protein was confirmed by Western blotting as compared to the parental strain (WT) (Fig 3).

In order to examine whether the overexpression, inactivation or deletion/complementation of the Ag85C<sub>Mabs</sub> protein affect the strain susceptibility to the iBpPPOX compound, their respective MICs were further determined.

**p**-value: 0.05) and the **R** variant (148.2 ±2.1 μM; **p-value** <0.01), as well as in MIC<sub>90</sub> values (>200 μM), compared to the respective pMyc vector control and wild-type strains. These results clearly suggest that Ag85C<sub>Mabs</sub> is responsible for the decreased susceptibility to the iBpPPOX, thus confirming this protein as one of the targets of our compound.

Regarding the inactivated Ag85C<sup>S124A</sup> mutant *M. abscessus* S_pMyc::ag85C<sup>S124A</sup>, the gene deletion mutant *M. abscessus* S_Δag85C and its complemented counterpart *M. abscessus* S_Δag85C::C, as well as the wild-type *M. abscessus* S strain, they all responded similarly to iBpPPOX. In the case of *M. abscessus* R, although no significant variation was observed in MIC<sub>90</sub> values (mean MIC<sub>90</sub> = 111.1 ±8.4 μM), a slight decrease in MIC<sub>90</sub> of around 0.89- to 0.58-fold was reached for the inactivated Ag85C<sup>S124A</sup> (47.5 ±2.0 μM; **p-value** <0.05) and the Δag85C (30.9 ±2.1 μM; **p-value** <0.01) mutants, respectively, compared to the wild-type strain.
While complementation of Ag85C
Mabs
(i.e., Ag85C
Δag85C
::C) restored the wild-type R phenotype (51.8 ± 3.1 μM—Table 3).

Based on these results, purified Ag85C
Mabs recombinant protein [25] was further incubated with iBpPPOX, using increasing enzyme/inhibitor molar ratio (E/I) ranging from 1:1 to 1:75, and then treated with ActivX TAMRA-FP fluorescent probe, as reported previously [24, 25]. Equal amounts of proteins were separated on SDS-PAGE and visualized by Coomassie staining or in-gel fluorescence for TAMRA detection (Fig 4A). Relative fluorescence quantification of each band was done using the ImageLab™ software version 5.0 (Bio-Rad) by taking as 100% absolute fluorescence level, the labeled Ag85C
Mabs-TAMRA adduct (Fig 4A). As expected, pre-treating Ag85C
Mabs with iBpPPOX, resulted in a significant loss in fluorescence intensity by around 32.8 ± 1.8% (E/I = 1:1 to 1:10), 58.5 ± 0.70% (E/I = 1:25), 64.0 ± 1.8% (E/I = 1:50) and up
Fig 4. Inhibition of the Ag85C<sub>Mabs</sub> by iBpPPOX. (A) Ag85C<sub>Mabs</sub> was pre-treated with iBpPPOX (i.e. enzyme/inhibitor molar ratio of 1:1 to 1:75), incubated with ActiveX TAMRA-FP, separated by 12% SDS-PAGE, and visualized by Coomassie blue staining (upper panel) or in-gel fluorescence visualization (middle panel). The merged image is shown in the lower panel. Untreated protein (i.e., no TAMRA-FP and no iBpPPOX) was used as control. No TAMRA-FP labeling is detected in the presence of inactivated heat-treated Ag85C<sub>Mabs</sub>. TAMRA labeling of Ag85C<sub>Mabs</sub> is impaired when the Ag85C<sub>Mabs</sub>-iBpPPOX addsucts, as evidenced by the loss of fluorescence in the iBpPPOX lanes, presumably resulting from the covalent binding of iBpPPOX to the catalytic serine as previously observed [24, 25]. TAMRA-labeled Ag85C<sub>Mabs</sub> was detected by fluorescent gel scanning ($\lambda_{ex}$ 557 nm, $\lambda_{em}$ 583 nm) using the Cy5 filter of a ChemiDoc MP Imager (Bio-Rad) before staining of the gel with Coomassie Brilliant Blue dye. Relative fluorescence quantification of each band was performed using the ImageLab™ software version 5.0 (Bio-Rad) by taking as 100% absolute fluorescence level the TAMRA labeling of Ag85C<sub>Mabs</sub>, at an enzyme/inhibitor molar ratio of 1:1 to 1:75 (Fig 4A). This means that the TAMRA-FP probe cannot bind the catalytic serine when the Ag85C<sub>Mabs</sub>-iBpPPOX complex has been formed, as revealed by the significant loss in fluorescence emission (Fig 4A).

https://doi.org/10.1371/journal.pone.0238178.g004

**Table 3. Variation of MIC (μM) of iBpPPOX against *M. abscessus*-Ag85C-mutant strains*.**

| *M. abscessus* strains | MIC<sub>50</sub> / MIC<sub>90</sub> (μM) | MIC<sub>50</sub> / MIC<sub>90</sub> ratio mutant vs. WT |
|------------------------|-----------------------------------|-------------------------------------------------|
| *M. abscessus* S WT    | 33.0 ±2.0 / 85.9 ±5.5<sup>a</sup> | 1.0 / 1.0                                       |
| *M. abscessus* S_pMyc empty vector | 31.9 ±1.7 / 82.4 ±0.92<sup>a</sup> | 0.97 / 0.96                                     |
| *M. abscessus* S_pMyc::ag85C<sup>Δ124A</sup> | 34.4 ±3.0 / 83.1 ±6.8<sup>a</sup> | 1.04 / 0.97                                     |
| *M. abscessus* S_Aag85C | 33.7 ±1.9 / 81.5 ±7.4<sup>a</sup> | 1.02 / 0.95                                     |
| *M. abscessus* S_Aag85C::C | 32.6 ±1.3 / 87.4 ±1.5<sup>a</sup> | 0.99 / 1.02                                     |
| *M. abscessus* S_pMyc::ag85C<sup>Δ</sup> | 87.3 ±3.4<sup>a</sup> / >200<sup>a</sup> | 2.65 / >3.0                                     |
| *M. abscessus* R WT    | 53.2 ±1.8<sup>a</sup> / 104.3 ±5.1<sup>a</sup> | 1.0 / 1.0                                       |
| *M. abscessus* R_pMyc empty vector | 49.9 ±2.6 / 109.2 ±10.4<sup>a</sup> | 0.94 / 1.05                                     |
| *M. abscessus* R_pMyc::ag85C<sup>Δ124A</sup> | 47.5 ±2.0<sup>a</sup> / 119.0 ±9.6<sup>a</sup> | 0.89 / 1.14                                     |
| *M. abscessus* R_Aag85C | 30.9 ±2.1<sup>a</sup> / 114.9 ±8.2<sup>a</sup> | 0.58 / 1.10                                     |
| *M. abscessus* R_Aag85C::C | 51.8 ±3.1<sup>a</sup> / 108.2 ±4.6<sup>a</sup> | 0.97 / 1.04                                     |
| *M. abscessus* R_pMyc::ag85C<sup>Δ</sup> | 148.2 ±2.1<sup>a</sup> / >200<sup>a</sup> | 2.78 / >2                                       |

<sup>a</sup> Experiments were performed as described in Materials and Methods. MIC<sub>50</sub> / MIC<sub>90</sub> compound minimal concentration leading to 50% or 90% growth inhibition, respectively. Values are mean of two independent assays performed in triplicate. MIC values with a common symbol are significantly different ($^a$; p-value<0.05; $^b$, $^c$, $^d$, $^e$, $^f$, $^g$; p-value<0.01; ANOVA followed by Fisher’s test).

https://doi.org/10.1371/journal.pone.0238178.t003

$^*$ Experiments were performed as described in Materials and Methods. MIC<sub>50</sub> / MIC<sub>90</sub> compound minimal concentration leading to 50% or 90% growth inhibition, respectively. Values are mean of two independent assays performed in triplicate. MIC values with a common symbol are significantly different ($^a$; p-value<0.05; $^b$, $^c$, $^d$, $^e$, $^f$, $^g$; p-value<0.01; ANOVA followed by Fisher’s test).

https://doi.org/10.1371/journal.pone.0238178.t003

to >90% (E/I = 1:75) as compared to the non-treated protein labeled by the TAMRA-FP probe (Fig 4A). This means that the TAMRA-FP probe cannot bind the catalytic serine when the Ag85C<sub>Mabs</sub>-iBpPPOX complex has been formed, as revealed by the significant loss in fluorescence emission (Fig 4A).

https://doi.org/10.1371/journal.pone.0238178.g004
MALDI-TOF mass spectrometry was further used to confirm the (covalent) nature of the inhibition. Sample of the Ag85C<sub>Mabs</sub> iBpPPOX (E/I = 1:100) complex was subjected to MAL-DI-TOF mass spectrometry analyses. Mass increment of +305.3 Da was then observed within the global mass of the inhibited Ag85C<sub>Mabs</sub> as compared with the untreated protein (Fig 4B); whereas no changes in the global mass were observed with the inactivated heat-treated protein. Such result is thus consistent with the formation of a covalent enzyme-inhibitor adduct, as the reaction between the catalytic Ser124 and iBpPPOX is expected to yield a mass increase of +326 Da; and also, in agreement with the mechanism of action of such OX derivatives [42]. All these findings conclusively indicate that pure recombinant Ag85C<sub>Mabs</sub> protein is covalently modified by the iBpPPOX derivative (Fig 4C), in good agreement with the known classical mechanism of action of such OX compounds as previously demonstrated using pure lipolytic enzymes [12, 42].

Taken together, the in vitro inhibitory experiments conducted with iBpPPOX on pure recombinant Ag85C<sub>Mabs</sub> protein (Fig 4), as well as the statistically significant increased resistance levels when overexpressing the Ag85C<sub>Mabs</sub> protein in <i>M. abscessus</i> S and R variants (Table 3), thus confirm the assertion that this enzyme is an effective target of iBpPPOX.

Conclusion

As already highlighted in the case of <i>M. tuberculosis</i> [12], our series of oxadiazolone-core OX derivatives are able to impair different metabolic pathways during either extracellular and/or intracellular bacterial growth via the inhibition of various (Ser/Cys)-based enzymes, therefore resulting in <i>M. abscessus</i> death. Although the efficiency of these OX molecules could not be considered as sufficient enough to obtain powerful anti-mycobacterial agents, they may however represent attractive tools for deciphering the lipid metabolism in <i>M. abscessus</i> and/or in <i>M. tuberculosis</i>. We have indeed reported that the MmPPOX compound was able to prevent intracytoplasmic lipid inclusion (ILI) catabolism in vivo in <i>M. bovis</i> BCG infected murine bone-marrow-derived macrophages (mBMDM) [47–49]; as well as in vitro under carbon excess and nitrogen-deprived conditions allowing ILI biosynthesis and hydrolysis in <i>M. abscessus</i> [50]. Taken together, all these findings support that the OX derivatives are able to abolish the activity of several (Ser/Cys)-containing enzymes involved in mycobacterial lipid metabolism and/or in cell wall biosynthesis. This is the case of the Ag85 complex proteins which are essential players in the biosynthesis of lipids from mycobacterial membrane as well as in intracellular lipid metabolism, but also of proteins belonging to the hormone-sensitive lipase (HSL) family member proteins (i.e., Lip-HSL) [42], including LipY the major Lip-HSL lipase involved in mycobacterial lipid catabolism [49–52]. Therefore, the respective effects of these OX compounds against lipid-poor vs. lipid-rich bacteria deserve to be investigated in more details. More especially, deciphering how the presence of intracytoplasmic lipid inclusions (ILI) in lipid-rich bacteria can actively contribute to substantially enhanced mycobacterial virulence and pathogenesis as compared to lipid-poor strains, as reported recently [50], will provide major insights for understanding the general development of mycobacterial-related diseases. Such experiments are currently underway, and will be reported in due course.

Supporting information

S1 Appendix. Detailed protocols regarding the MIC determination, targets identification and mass spectrometry analysis of Ag85C<sub>Mabs</sub> as well as the list of plasmids and primers used in this study.

(PDF)
S1 Fig. Uncropped and unadjusted image for Western Blotting of Fig 3. Each overexpressed protein was revealed using the HisProbe™ HRP conjugate (ThermoFisher Scientific) and compared to the M. abscessus wild type strain as well as the pure recombinant Ag85C-Mabs protein. (TIF)

S2 Fig. Uncropped and unadjusted images for SDS-PAGE gel of Fig 4A. SDS-PAGE gel visualized by Coomassie blue staining (upper panel) or by in-gel fluorescence visualization (middle panel). Superimposition of both images is reported in the lower panel. Molecular weights were derived from the Unstained Protein Molecular Weight Marker (Euromedex). (TIF)

S1 Table. iBpPPOX target proteins identified in M. abscessus R total lysate by LC-ESI-MS/MS analysis. Only positive hits with a pFDR of 1%, 5% and 10% are reported. (XLSX)

S2 Table. iBpPPOX target proteins identified in M. abscessus R culture cell by LC-ESI-MS/MS analysis. Only positive hits with a pFDR of 1% and 5% are reported. (XLSX)

Acknowledgments
Authors would like to thank Dr. R. Lebrun and P. Mansuelle at the Proteomics platform of the Institut de Microbiologie de la Méditerranée FR3479 (Marseille, France) for N-Terminal Edman sequencing.

Author Contributions
Conceptualization: Stéphane Canaan, Jean François Cavalier.
Data curation: Abdeldjalil Madani, Ivy Mallick, Patrick Fourquet, Stéphane Audebert, Luc Camoin.
Formal analysis: Stéphane Audebert, Luc Camoin, Stéphane Canaan, Jean François Cavalier.
Funding acquisition: Jean François Cavalier.
Investigation: Abdeldjalil Madani, Ivy Mallick, Patrick Fourquet, Stéphane Audebert, Luc Camoin.
Project administration: Jean François Cavalier.
Resources: Alexandre Guy, Céline Crauste, Thierry Durand.
Supervision: Jean François Cavalier.
Validation: Stéphane Canaan, Jean François Cavalier.
Visualization: Jean François Cavalier.
Writing – original draft: Abdeldjalil Madani, Ivy Mallick.
Writing – review & editing: Céline Crauste, Thierry Durand, Stéphane Audebert, Luc Camoin, Stéphane Canaan, Jean François Cavalier.

References
1. Porvaznik I, Solovic I, Mokry J. Non-Tuberculous Mycobacteria: Classification, Diagnostics, and Therapy. Adv Exp Med Biol. 2017; 944:19–25. Epub 2016/11/09. https://doi.org/10.1007/5584_2016_45 PMID: 27826888.
2. Claeyts TA, Robinson RT. The many lives of nontuberculous mycobacteria. J Bacteriol. 2018. Epub 2018/02/28. https://doi.org/10.1128/JB.00739-17 PMID: 29483164.

3. Lee MR, Sheng WH, Hung CC, Yu CJ, Lee LN, Hsueh PR. Mycobacterium abscessus Complex Infections in Humans. Emerg Infect Dis. 2015; 21(9):1638–46. Epub 2015/08/22. https://doi.org/10.3201/2109.141634 PMID: 26295364.

4. Luthra S, Rominski A, Sander P. The Role of Antibiotic-Target-Modifying and Antibiotic-Modifying Enzymes in Mycobacterium abscessus Drug Resistance. Front Microbiol. 2018; 9:2179. Epub 2018/09/28. https://doi.org/10.3389/fmicb.2018.02179 PMID: 30258428.

5. Brown-Elliott BA, Nash KA, Wallace RJ Jr. Antimicrobial susceptibility testing, drug resistance mechanisms, and therapy of infections with nontuberculous mycobacteria. Clin Microbiol Rev. 2012; 25 (3):545–82. Epub 2012/07/06. https://doi.org/10.1128/CMR.05039-11 PMID: 22763637.

6. Catherino E, Clarissou J, Etienne G, Ripoll F, Emile JF, Daffe M, et al. Hypervirulence of a rough variant of the Mycobacterium abscessus type strain. Infect Immun. 2007; 75(2):1055–8. Epub 2006/12/06. https://doi.org/10.1128/IAI.00835-06 PMID: 17145951.

7. Howard ST, Rhoades E, Recht J, Pang X, Alsup A, Kolter R, et al. Spontaneous reversion of Mycobacterium abscessus from a smooth to a rough morphotype is associated with reduced expression of glycopeptidolipid and reacquisition of an invasive phenotype. Microbiology. 2006; 152(Pt 6):1581–90. Epub 2006/06/01. https://doi.org/10.1099/mic.0.28625-0 PMID: 16735722.

8. Pawlik A, Gamier G, Orgeur M, Tong P, Lohan A, Le Chevalier F, et al. Identification and characterization of the genetic changes responsible for the characteristic smooth-to-rough morphotype alterations of clinically persistent Mycobacterium abscessus. Mol Microbiol. 2013; 90(3):612–29. Epub 2013/09/04. https://doi.org/10.1111/mmi.12387 PMID: 23998761.

9. Floto RA, Olivier KN, Saiman L, Daley CL, Herrmann JL, Nick JA, et al. US Cystic Fibrosis Foundation and European Cystic Fibrosis Society consensus recommendations for the management of non-tuberculous mycobacteria in individuals with cystic fibrosis: executive summary. Thorax. 2016; 71(1):88–90. Epub 2015/12/19. https://doi.org/10.1136/thoraxjnl-2015-207983 PMID: 26678435.

10. Nash KA, Brown-Elliott BA, Wallace RJ Jr. A novel gene, erm(41), confers inducible macrolide resistance to clinical isolates of Mycobacterium abscessus but is absent from Mycobacterium chelonae. Antimicrob Agents Chemother. 2009; 53(4):1367–76. Epub 2009/01/28. https://doi.org/10.1128/AAC.01275-08 PMID: 19171799.

11. Bastian S, Veziris N, Roux AL, Brossier F, Gaillard JL, Jarlier V, et al. Assessment of clarithromycin susceptibility in strains belonging to the Mycobacterium abscessus group by erm(41) and rrl sequencing. Antimicrob Agents Chemother. 2011; 55(2):775–81. Epub 2010/12/08. https://doi.org/10.1128/AAC.00861-10 PMID: 21351815.

12. Nguyen PC, Delorme V, Bénarouche A, Guy A, Landry V, Audebert S, et al. Oxadiazolone derivatives, new promising multi-target inhibitors against M. tuberculosis. Bioorg Chem. 2018; 81:414–24. https://doi.org/10.1016/j.bioorg.2018.08.025 PMID: 30212765.

13. Nguyen PC, Delorme V, Bénarouche A, Martin BP, Paudel R, Gnawali GR, et al. Cyclopiostins and Cyclophostin analogs as promising compounds in the fight against tuberculosis. Scientific Reports. 2017; 7(1):11751. https://doi.org/10.1038/s41598-017-11843-4 PMID: 28924204.

14. Nguyen PC, Madani A, Santucci P, Martin BP, Paudel RR, Delattre S, et al. Cyclophostin and Cyclopiostin analogs, new promising molecules to treat mycobacterial-related diseases. Int J Antimicrob Agents. 2018; 51:651–4. https://doi.org/10.1016/j.ijantimicag.2017.12.001 PMID: 29241819.

15. Palomino JC, Martin A, Camacho M, Guerra H, Swings J, Portaels F. Resazurin microtiter assay plate: simple and inexpensive method for detection of drug resistance in Mycobacterium tuberculosis. Antimicrob Agents Chemother. 2002; 46(8):2720–2. Epub 2002/07/18. https://doi.org/10.1128/aac.46.8.2720-2722.2002 PMID: 12121966.

16. Rybniker J, Vocat A, Sala C, Busso P, Pojer F, Benjak A, et al. L Lansoprazole is an antituberculous drug-targeting cytochrome bcl. Nat Commun. 2015; 6:7659. Epub 2015/07/15. https://doi.org/10.1038/ncomms8659 PMID: 26158909.

17. Rodrigues Felix C, Gupta R, Geden S, Roberts J, Winder P, Pomponi SA, et al. Selective Killing of Dormant Mycobacterium tuberculosis by Marine Natural Products. Antimicrob Agents Chemother. 2017; 61 (8):e00743–17. https://doi.org/10.1128/aac.00743-17 PMID: 28607021.

18. Strober W. Trypan blue exclusion test of cell viability. Curr Protoc Immunol. 2001; Appendix 3(1):Appendix 3B. Epub 2008/04/25. https://doi.org/10.1002/0471142735.imato3bs21 PMID: 18432654.

19. Shevchenko A, Wilm M, Vorm O, Mann M. Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels. Anal Chem. 1996; 68(5):850–8. Epub 1996/03/01. https://doi.org/10.1021/ac950914h PMID: 8779443.
20. Cox J, Mann M. MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. Nat Biotechnol. 2008; 26(12):1367–72. Epub 2008/11/26. https://doi.org/10.1038/nbt.1511 PMID: 19029910.

21. Vizcaino JA, Deutsch EW, Wang R, Csordas A, Reisinger F, Rios D, et al. ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nat Biotechnol. 2014; 32(3):223–6. Epub 2014/04/15. https://doi.org/10.1038/nbt.2839 PMID: 24727771.

22. Viljoen A, Gutierrez AV, Dupont C, Ghigo E, Kremer L. A Simple and Rapid Gene Disruption Strategy in Mycobacterium abscessus: On the Design and Application of Glycopeptidolipid Mutants. Front Cell Infect Microbiol. 2018; 8:69. Epub 2018/03/30. https://doi.org/10.3389/fcimb.2018.00069 PMID: 29594066.

23. Jeong J-Y, Yim H-S, Ryu J-Y, Lee HS, Lee J-H, Seen D-S, et al. One-Step Sequence- and Ligation-Independent Cloning as a Rapid and Versatile Cloning Method for Functional Genomics Studies. Appl Environ Microbiol. 2012; 78(15):5440–3. https://doi.org/10.1128/AEM.00844-12 PMID: 22610439.

24. Hawke D, Yuan P. S-Pyridylethylation of cystine residues. Applied Biosystems Bulletin 28. 1987:

25. Madani A, Ridenour JN, Martin BP, Paudel RR, Abdul Basir A, Le Moigne V, et al. Cyclophostin Analogues as Multitarget Inhibitors That Impair Growth of Mycobacterium abscessus. ACS Infect Dis. 2019; 5(9):1597–608. Epub 2019/07/13. https://doi.org/10.1021/acsinfecdis.9b00172 PMID: 31299146.

26. Singh S, Bouzinbi N, Chaturvedi V, Godreuil S, Kremer L. In vitro evaluation of a new drug combination against clinical isolates belonging to the Mycobacterium abscessus complex. Clin Microbiol Infect. 2014; 20(12):O1124–O7. https://doi.org/10.1111/1469-0691.12780 PMID: 25301937.

27. Madani A, Ridenour JN, Martin BP, Paudel RR, Abdul Basir A, Le Moigne V, et al. Cyclophostins and Cyclophosphatin analogs inhibit the antigen 85C from Mycobacterium tuberculosis both in vitro and in vivo. J Biol Chem. 2018; 293(8):2755–69. https://doi.org/10.1074/jbc.RA117.007760 PMID: 29301937.

28. Nesser R, Cambau E, Reyrat JM, Murray A, Gicquel B. Mycobacterium abscessus: a new antibiotic nightmare. J Antimicrob Chemother. 2012; 67(4):810–8. https://doi.org/10.1093/jac/dkr576 PMID: 22290346.

29. Bernut A, Hermann JL, Kiss a K, Dubremetz JF, Gaillard JL, Lutfalla G, et al. Mycobacterium abscessus cording prevents phagocytosis and promotes abscess formation. Proceedings of the National Academy of Sciences of the United States of America. 2014; 111(10):E943–52. Epub 2014/02/26. https://doi.org/10.1073/pnas.1321390111 PMID: 24567393.

30. Johansen MD, Hermann JL, Kremer L. Non-tuberculous mycobacteria and the rise of Mycobacterium abscessus. Nat Rev Microbiol. 2020. Epub 2020/02/26. https://doi.org/10.1038/s41579-020-0331-1 PMID: 32086501.

31. Le Run E, Arthur M, Mainardi JL. In Vitro and Intracellular Activity of Imipenem Combined with Tetrahydrolipstatin (THL). Mol Cell Proteomics. 2014; 13(2):435–48. https://doi.org/10.1074/mcp.M113.029942 PMID: 24345785.

32. Le Run E, Arthur M, Mainardi JL. In Vitro and Intracellular Activity of Imipenem Combined with Tetrazolid, Rifabutin, and Avibactam against Mycobacterium abscessus. Antimicrob Agents Chemother. 2017; 61(4):e02440–16. Epub 2017/01/18. https://doi.org/10.1128/AAC.02440-16 PMID: 28096155.

33. Ravn DR, Ravn DR, Ravn DR. In Vitro and Intracellular Activity of Imipenem Combined with Tetrazolid, Rifabutin, and Avibactam against Mycobacterium abscessus. Antimicrob Agents Chemother. 2017; 61(4):e02440–16. Epub 2017/01/18. https://doi.org/10.1128/AAC.02440-16 PMID: 28096155.

34. Christophe T, Jackson M, Jeon HK, Fenistein D, Contreras-Dominguez M, Kim J, et al. High content screening identifies decaprenyl-phosphoribose 2’ epimerase as a target for intracellular antimycobacterial inhibitors. PLoS Pathog. 2009; 5(10):e1000645. Epub 2009/10/31. https://doi.org/10.1371/journal.ppat.1000645 PMID: 19876393.

35. Ravindran MS, Rao SP, Cheng X, Shukla A, Cazenave-Gassiot A, Yao SQ, et al. Targeting Lipid Esterases in Mycobacteria Grown Under Different Physiological Conditions Using Activity-based Profiling with Tetrahydrolipstatin (THL). Mol Cell Proteomics. 2014; 13(2):435–48. https://doi.org/10.1074/mcp.M113.029942 PMID: 24345785.

36. Tallman KR, Levine SR, Beatty KE. Small Molecule Probes Reveal Esterases with Persistent Activity in Dormant and Reactivating Mycobacterium tuberculosis. ACS Infect Dis. 2016; 2(12):936–44. Epub 2016/10/04. https://doi.org/10.1021/acsiinfecdis.6b00135 PMID: 27690385.

37. Lehmann J, Cheng TY, Aggarwal A, Park AS, Zeiler E, Raju RM, et al. An Antibacterial beta-Lactone Kills Mycobacterium tuberculosis by Disrupting Mycolic Acid Biosynthesis. Angew Chem Int Ed Engl. 2018; 57(1):349–53. Epub 2017/10/27. https://doi.org/10.1002/anie.201709365 PMID: 29067779.

38. Lehmann J, Vomacka J, Esser K, Kodwell M, Kolbe K, Ramer P, et al. Human lysosomal acid lipase inhibitor listatid impairs Mycobacterium tuberculosis growth by targeting bacterial hydrolases. MedChemComm. 2016; 7:1797–801. https://doi.org/10.1039/c6md00231e.
38. Catherinot E, Roux AL, Macheras E, Hubert D, Matmar M, Dannhoffer L, et al. Acute respiratory failure involving an R variant of Mycobacterium abscessus. J Clin Microbiol. 2009; 47(1):271–4. Epub 2008/11/21. https://doi.org/10.1128/JCM.01478-08 PMID: 19020061.

39. Koonin EV. Orthologs, Paralogs, and Evolutionary Genomics. Annu Rev Genet. 2005; 39(1):309–38. https://doi.org/10.1146/annurev.genet.39.073003.114725 PMID: 16285863.

40. Dedieu L, Serveau-Avesque C, Kremer L, Canaan S. Mycobacterial lipolytic enzymes: a gold mine for tuberculosis research. Biochimie. 2013; 95(1):66–73. https://doi.org/10.1016/j.biochi.2012.07.008 PMID: 22819994.

41. Johnson G. The alpha/beta Hydrolase Fold Proteins of Mycobacterium tuberculosis, with Reference to their Contribution to Virulence. Curr Protein Pept Sci. 2017; 18(3):190–210. Epub 2016/08/03. https://doi.org/10.2174/1389203717666160729093515 PMID: 27480283.

42. Delorme V, Diomandé SV, Dedieu L, Carrière F, Kremer L, et al. MmpPox Inhibits Mycobacterium tuberculosis Lipolytic Enzymes Belonging to the Hormone-Sensitive Lipase Family and Alters Mycobacterial Growth. PLoS ONE. 2012; 7(9):e46493. https://doi.org/10.1371/journal.pone.0046493 PMID: 23029536.

43. Sacchettini JC, Ronning DR. The mycobacterial antigens 85 complex—from structure to function: response. Trends Microbiol. 2000; 8(10):441. Epub 2001/02/24. https://doi.org/10.1016/S0966-842X(00)01843-6 PMID: 11203233.

44. Griffin JE, Gawronski JD, Dejesus MA, Ieroerger TR, Akerley BJ, Sassetti CM. High-resolution phenotypic profiling defines genes essential for mycobacterial growth and cholesterol catabolism. PLoS Pathog. 2011; 7(9):e1002251. Epub 2011/10/08. https://doi.org/10.1371/journal.ppat.1002251 PMID: 21980284.

45. Sassetti CM, Boyd DH, Rubin EJ. Genes required for mycobacterial growth defined by high density mutagenesis. Mol Microbiol. 2003; 48(1):77–84. https://doi.org/10.1046/j.1365-2958.2003.03425.x PMID: 12657046.

46. Warrier T, Tropis M, Werngren J, Diehl A, Gengenbacher M, Schlüter B, et al. Antigen 85C inhibition restricts Mycobacterium tuberculosis growth through disruption of cord factor biosynthesis. Antimicrob Agents Chemother. 2012; 56(4):1735–43. Epub 2012/02/01. https://doi.org/10.1128/AAC.05742-11 PMID: 22290959.

47. Caire-Brandili I, Papadopoulos A, Maliga W, Marais D, Canaan S, Thilo L, et al. Reversible lipid accumulation and associated division arrest of Mycobacterium avium in lipoprotein-induced foamy macrophages may resemble key events during latency and reactivation of tuberculosis. Infect Immun. 2014; 82(2):476–80. https://doi.org/10.1128/IAI.01196-13 PMID: 24478064.

48. Santucci P, Bouzid F, Smichi N, Poncin I, Kremer L, De Chastellier C, et al. Experimental Models of Foamy Macrophages and Approaches for Dissecting the Mechanisms of Lipid Accumulation and Consumption during Dormancy and Reactivation of Tuberculosis. Front Cell Infect Microbiol. 2016; 6:122. Epub 2016/10/25. https://doi.org/10.3389/fcimb.2016.00122 PMID: 27774438.

49. Santucci P, Diomandé S, Poncin I, Ailbaud L, Viljoen A, Kremer L, et al. Delineating the physiological roles of the PE and catalytic domain of LipY in lipid consumption in mycobacteria-infected foamy macrophages. Infect Immun. 2018; 86(9):e00394–18. https://doi.org/10.1128/IAI.00394-18 PMID: 29986895.

50. Santucci P, Johansen MD, Point V, Poncin I, Viljoen A, Cavalier J-F, et al. Nitrogen deprivation induces triacylglycerol accumulation, drug tolerance and hypervirulence in mycobacteria. Scientific Reports. 2019; 9(1):8667. https://doi.org/10.1038/s41598-019-45164-5 PMID: 31209261.

51. Deb C, Daniel J, Sirakova TD, Abomoleak B, Dubey VS, Kolattukudy PE. A novel lipase belonging to the hormone-sensitive lipase family induced under starvation to utilize stored triacylglycerol in Mycobacterium tuberculosis. J Biol Chem. 2006; 281(7):3866–75. Epub 2005/12/16. https://doi.org/10.1074/jbc.M505556200 PMID: 16354661.

52. Mishra KC, de Chastellier C, Narayana Y, Bifani P, Brown AK, Besra GS, et al. Functional role of the PE domain and immunogenicity of the Mycobacterium tuberculosis triacylglycerol hydrolase LipY. Infect Immun. 2008; 76(1):127–40. Epub 2007/10/17. https://doi.org/10.1128/IAI.00410-07 PMID: 17938218.