Inhibiting *Mycobacterium tuberculosis* CoaBC by targeting a new allosteric site.

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Abstract

Coenzyme A (CoA) is a fundamental co-factor for all life, involved in numerous metabolic pathways and cellular processes and its biosynthetic pathway has raised substantial interest as a drug target against multiple pathogens including *Mycobacterium tuberculosis*. The biosynthesis of CoA is performed in five steps. However, in the vast majority of prokaryotes including *M. tuberculosis*, a single bifunctional protein, CoaBC, catalyses the second and third steps. Depletion of CoaBC was found to be bactericidal in *M. tuberculosis*. Here we report the first structure of a full length CoaBC, from the model organism *Mycobacterium smegmatis*, describe how it is organised as a dodecamer and regulated by CoA thioesters. A high-throughput biochemical screen focusing on CoaB identified two inhibitors with different chemical scaffolds. Hit expansion led to the discovery of potent inhibitors of *M. tuberculosis* CoaB. Crucially we further show that these compounds bind to a novel cryptic allosteric site within CoaB.

Introduction

Tuberculosis (TB) is the most prevalent and deadly infectious disease worldwide and remains a global epidemic. Despite the availability of treatment, this disease caused, by *Mycobacterium tuberculosis*, still claims 1.5 million lives each year [1]. Current treatment regimens are long which presents an obstacle for patient adherence and imposes a heavy social and economic burden on countries with a high incidence of TB. It is therefore critical to explore novel targets and find new and more effective drugs to combat this disease.

Coenzyme A (CoA) is an essential and ubiquitous cofactor, involved in numerous metabolic pathways with a large number of different enzymes requiring it for activity[2]. CoA is essential for the synthesis of phospholipids, fatty acids, polyketides, and non-ribosomal peptides, for the operation of the tricarboxylic acid cycle and in the degradation of lipids [3]. The importance of CoA for essential post-translational modifications of proteins is also well established in both eukaryotes and prokaryotes with various proteins post-translationally modified by thioester derivatives of CoA (acylation) or CoA itself (phosphopantetheinylation and CoAlation), while several other post-translational modifications depend indirectly on CoA through the mevalonate pathway [4-7]. Furthermore, dephospho-CoA, an intermediate of the CoA pathway, is incorporated into some RNA transcripts during transcription initiation thereby serving as a non-canonical transcription initiating nucleotide [8]. These RNA modifications have functional consequences and occur in both eukaryotes and bacteria [8]. In *M. tuberculosis*, CoA plays a pivotal role in the biosynthesis of complex lipids that are crucial components of the cell wall and required for pathogenicity [9]. It is also needed for the degradation of lipids, including cholesterol, which are the primary source of energy for this organism during infection [10,11]. The CoA pathway is therefore an attractive pathway for drug discovery for

many different infectious diseases, including TB, given its ubiquitous nature, wide metabolic and functional impact of its inhibition and lack of sequence conservation between prokaryotes and humans.

The biosynthesis of CoA from pantothenic acid (vitamin B_5) is performed in five steps, sequentially catalysed by the enzymes pantothenate kinase (CoaA, also known as PanK), phosphopantothenoylcysteine synthetase (CoaB), phosphopantothenoylcysteine decarboxylase (CoaC), phosphopantetheine adenylyltransferase (CoaD) and dephospho-CoA kinase (CoaE). However, in the vast majority of prokaryotes, including *M. tuberculosis*, CoaB and CoaC are encoded by a single gene to produce a fused bifunctional enzyme (CoaBC). Transcriptional silencing of individual genes of the CoA biosynthesis pathway of this pathogen identified CoaBC as uniquely bactericidal within the CoA pathway, highlighting it as a good candidate for drug discovery [12].

CoaBC comprises two enzymes in a single polypeptide chain and converts 4'-phosphopantothenate to 4'-phosphopantetheine in three steps. First, 4'-phosphopantothenate (*P*PA) reacts with CTP to form 4'-phosphopantothenoyl-CMP with the release of pyrophosphate. This intermediate subsequently reacts with cysteine to form 4'-phosphopantothenoylcysteine (*P*PC) with the release of CMP with these two steps being catalysed by CoaB. The product of CoaB is then decarboxylated by CoaC to 4'-phosphopantetheine an enzyme of the homo-oligomeric flavin-containing decarboxylase (HFCD) protein family. X-ray crystal structures have been reported for the individual CoaB and CoaC enzymes in several organisms, including a structure of CoaB from *Mycobacterium smegmatis*, a close relative of *M .tuberculosis* However, a structure of the full-length bifunctional CoaBC was missing.

Here we report the structure of the bifunctional CoaBC of *M. smegmatis* at 2.5 Å. We identify a previously unknown allosteric site in CoaB and crucially, we report the

identification of the first *M. tuberculosis* CoaBC allosteric inhibitors. Using X-ray crystallography and enzyme kinetic experiments, we define the mode of binding of one of the inhibitors and show its impact on the protein structure and function. These results further illustrate the potential of CoaBC as a novel drug target in *M. tuberculosis*.

Results

Overall structure of CoaBC

Because the HFCD protein family of flavin-binding proteins are known to form homo-oligomers [13], we performed native electrospray-ionization mass spectrometry (ESI-MS) to investigate the stoichiometry of CoaBC, previously proposed to form a dodecamer [13]. Both *M. tuberculosis* CoaBC (MtbCoaBC) (Figure S1A) and *M. smegmatis* CoaBC (MsmCoaBC) (Figure S1B) exclusively exhibited a dodecameric assembly, with no other oligomeric species observed in the spectra, consistent with a strong interaction between the subunits of the complex. The dodecamer of MtbCoaBC was centred around the 56+ charge state, with an observed mass of 537 kDa, while the dodecamer of MsmCoaBC was centred around the 52+ charge state, with an observed mass of 523 kDa. These masses are 1-2% higher than the expected masses of 525 and 518 kDa for MtbCoaBC and MsmCoaBC respectively, which can be attributed to the non-specific binding of solvent molecules or ions to the protein complexes under the soft ionization conditions employed. Structures of a few proteins of the HFCD family have been determined [14-18]. All of these structures show either a homo-trimeric or homo-dodecameric arrangement of the flavin-containing Rossmann-fold with trimers forming at each of the vertices of the tetrahedron in the case of a dodecameric arrangement [15]. However, all of these proteins, unlike CoaBC, contain only a single functional domain. We solved the structure of MsmCoaBC at 2.5 Å resolution (Figure 1A), in the presence of CTP and FMN (Figure 1B, S2A and

S2B), using crystals belonging to the $H3_2$ space group with an asymmetric unit containing four protomers forming two CoaBC dimers. Data collection and refinement statistics are summarized in (Table S1). The final model (residues 2-412) covers both CoaC and CoaB, but densities for several residues in three loop regions in CoaB are not observed (residues 290-298, 336-342, 363-376). However, all these residues except for 375 and 376 can be seen the MsmCoaB X-ray crystal structure (PDB: 6TH2) that we also solved in this work at 1.8 Å. The N-terminal CoaC of MsmCoaBC (residues 1-179) forms the same type of dodecameric arrangement seen in other HFCD family proteins such as the peptidyl-cysteine decarboxylase EpiD [15] and sits at the core of the dodecamer (Figure 1A and 1C). The active site of CoaC sits at the interface between two protomers of the CoaC trimer and a protomer of an adjacent CoaC trimer with the FMN site facing inwards towards the hollow centre of the dodecamer (Figure 2A). A flexible flap that was observed before covering a reaction intermediate bound to *Arabidopsis thaliana* CoaC [19] is also observed in some of the protomers, but in an open conformation (Figure 1B).

CoaC and CoaB are connected through a small loop region (residues 180-189) that tightly interacts with both enzymes. CoaB also displays a Rossmann fold consistent with the several other CoaB structures solved previously, including both the eukaryotic form, in which CoaB exists as an individual polypeptide, and the bacterial form where CoaB is typically fused with CoaC [20-22]. Each CoaB of MsmCoaBC (residues 190-414) dimerises with a CoaB belonging to an adjacent trimer (Figure 1C). The full protein resembles a tetrahedron with CoaB dimers positioned at the six edges and CoaC trimers at the four vertices (Figure 1A).

The shortest distance between a pair of CoaB and CoaC active sites is ~30 Å (Figure 2B). Nevertheless, a flexible loop (residues 362-377) that covers the 4'-phosphopantothenate site when this substrate binds to the enzyme [20] can be seen in our MsmCoaB structure

away from the active site. A superposition of our MsmCoaB dimer structure with MsmCoaBC shows the loop extending towards the CoaC active site (Figure 2B). This long loop (15-16 amino acids) is present in all CoaBCs (Figure S3) and it is possible that it helps channel the substrate from the CoaB to the CoaC active site.

The small differences (RMSD = 1.147) in overall structure of CoaB dimers in the full length MsmCoaBC and the MsmCoaB crystal structure solved at 1.8 Å (PDB: 6TH2) can be attributed to artefacts of crystal packing (Figure S4). Similarly, the CoaC structure does not seem to differ between full length MsmCoaBC and the available individual CoaC structures. However, when MsmCoaB (residues 186-414) is expressed alone, the protein does not dimerise in solution and is inactive (not shown). This contrasts with *E. coli* CoaB, which still dimerises and is functional when expressed on its own without the N-terminal CoaC [23,24]. The CoaB dimer interface is mostly conserved, but there are clear differences in the dimerisation region between MsmCoaB and *E. coli* CoaB that could help to explain the different observed behaviours (Figure S3). The absence of dimerization for the MsmCoaB when expressed alone suggests that the interactions between CoaC and CoaB in *M. smegmatis,* and likely all other *Mycobacteriaceae*, are fundamental for CoaB dimerisation and activity. This idea is reinforced by the fact that the residues located at the interface of the two enzymes (CoaB and CoaC) are well conserved in all *Mycobacteriaceae* and somewhat conserved in the sub-order *Corynebacterineae* but not outside of this group (Figure S3).

The CoaB dimerisation region forms a β-sandwich composed of eight anti-parallel β-strands, related by 2-fold symmetry, that contacts with the active site (Figure 2C and 2D). Comparison of the MsmCoaB with human CoaB reveals that the human and many other eukaryotic CoaBs [21] possess two extra α-helices and β-strands involved in the dimerisation interface that help stabilise the dimer in the absence of CoaC (Figure S5).

The CoaB active site is enclosed by a loop that extends from the opposing protomer and is observed for the first time in this work. This loop contains a motif "K-X-K-K", which is widely conserved in bacteria (Figure S3), with few exceptions, and each lysine either interacts directly with the triphosphate group of CTP or through highly coordinated waters (Figure 2C). Also observed for the first time is the coordination of a cation by the triphosphate group and D281 (Figure 2C and S6). While magnesium or manganese are the favoured cations for CoaB activity [25], calcium is observed in our structures instead, due to the high concentration present in the crystallization condition.

CoaBC is regulated by CoA thioesters

It is known that CoA biosynthesis is regulated, in many organisms, at the first step of the pathway, catalysed by the enzyme CoaA [3]. *M. tuberculosis* and many other mycobacteria possess two isoforms of this enzyme (type I and III), however only the type I isoform seems to be active based on studies in *M. tuberculosis* [26]. CoA and its thioesters competitively inhibit this enzyme by binding to the ATP site with CoA being the strongest regulator [27,28]. Nevertheless, at physiologically relevant levels of CoA there is only a low level inhibition of CoaA [28]. It is also known that CoaD, the enzyme that catalyses the fourth step of the pathway, is competitively inhibited by CoA and its product dephospho-CoA [29,30]. However, nothing was known about the regulation of CoaBC. We therefore examined the effect of CoA and several of its thioesters (acetyl-CoA, malonyl-CoA and succinyl-CoA) on MtbCoaBC activity, using a coupled enzymatic assay that quantifies the release of pyrophosphate (EnzCheck pyrophosphate assay). Potent regulation of CoaB activity by CoA and acyl-CoAs was observed, with IC_{50} values ranging from 38 to 148 μM, far below the predicted intracellular concentrations of acyl-CoAs [31], with succinyl-CoA displaying the highest inhibition (Figure 3A and Table 1). Competition

assays with the three substrates and acetyl-CoA show a competitive mode of inhibition relative to CTP and *P*PA, and non-competitive inhibition for L-cysteine (Figure 3B). In the absence of a crystal structure to confirm the mode of binding, these results suggest that acyl-CoAs most likely bind to the active site itself, competing directly with CTP and *P*PA. Interestingly both acyl-CoAs, involved in fatty acid synthesis, as well as those, involved in the TCA cycle, show inhibition of CoaB with larger fatty acyl chains showing higher inhibition of CoaB.

Identification of CoaB inhibitors using high-throughput screening

Although the CoA biosynthetic pathway is considered an attractive target for drug discovery, CoA pathway inhibitors displaying potent whole cell activity are relatively rare. Few CoaBC inhibitors have been reported to date and these are in majority substrate mimicking [24,32].

In order to identify novel MtbCoaBC inhibitors, e conducted a high-throughput screen of 215,000 small molecules targeting CoaB activity. To do this an end-point pyrophosphate quantification assay was used (Biomol Green). The most potent hits identified were compounds **1a** and **2a** with IC_{50} values of 9 and 3.1 µM respectively (Table S2), originating from two different chemical series. A search was then performed for commercially available analogues. Testing of analogues of the initial hits resulted in the identification of more potent compounds with sub-micromolar IC_{50} values (Table 1, Figure 4A, Table S2 and Figure S7). Of these, compounds **1b** and **2b** (Figure 4A and Table 1) with IC_{50} values of 0.28 and 0.08 µM respectively were identified as the most potent of the two chemical series and therefore were selected for further work.

Elucidation of the mode of inhibition

Following the identification of potent MtbCoaB inhibitors we went on to determine their mode of inhibition using kinetic assays. For this, the EnzCheck coupled enzyme assay that measures the release of pyrophosphate was used. Control experiments were first performed to assess compound activity against the two coupling enzymes and the compounds were found to be inactive at 100 μM. The IC_{50} values for the compounds against CoaB were reassessed with this assay and the values obtained were in line with the primary screening assay (Table S2).

Competition experiments were then performed using the three CoaB substrates for the two most potent compounds of each chemical series (**1b** and **2b**). Compound **1b** was found to preferentially bind to the enzyme-substrate complex with uncompetitive inhibition observed for all substrates (Figure 4B), consistent with the compound binding preferentially when the three substrates are bound. Compound **2b** shows mixed inhibition relative to CTP and uncompetitive inhibition for L-cysteine and *P*PA (Figure 4C). It is known that CoaB forms the phosphopantothenoyl-CMP intermediate in the absence of L-cysteine [33] and it is likely, due to spatial constraints, that cysteine can only bind at the active site after the release of pyrophosphate. The data is therefore consistent with compound **1b** preferentially binding after L-cysteine enters the active site, for to the last step of catalysis and the formation of 4'-phosphopantothenoylcysteine and CMP. However, compound **2b** shows a mixed inhibition for CTP, reflecting a slightly different mechanism of action. These results obtained for both compounds suggest the existence of an allosteric site in the CoaB moiety of MtbCoaBC.

Structural basis for inhibition of CoaB by allosteric inhibitors

In order to elucidate the binding mode of compound **1b** we used a truncation of the MsmCoaB (residues 187-414) that was previously crystallized before by others in the

presence of CTP (PDB code: 4QJI) at 2.65 Å resolution. The screening for new crystallization conditions allowed us to find a new CTP containing condition that gave excellent resolution (~1.8 Å). Comparison of this structure with the full length MsmCoaBC showed only minor differences that can be attributed to crystal packing (Figure S4). Hence this crystallization system could be used to validate CoaB inhibitors binding outside of the CTP site.

MsmCoaB was co-crystallized with CTP in the absence of compound **1b** and overnight soaking of the crystals with this compound was performed. A Co-crystal structure of MsmCoaB with compound **1b** was obtained and showed that the compound was bound to a site at the dimer interface of CoaB, in a deep cavity that is occluded when the compound is absent (Figure 5A-B and S8). Each CoaB dimer contains two of these sites, which are formed by a sandwich of eight β-strands and a long loop that contains the conserved "K-X-K-K" motif. This site opens to the active site and the inhibitor also contacts with D281 that is involved in the coordination of the cation (Figure 5C). The opening/closing of this cryptic allosteric site is mediated by the side chain of R207 of the opposing protomer (Figure 5D) that moves 5.5 Å at the furthest point and to a smaller extent by the side chain of F282 that moves 2 Å. R207 has previously been shown to be critical for the second half of the reaction catalysed by CoaB, the conversion of the 4'-phosphopantothenoyl-CMP intermediate to *P*PC, with almost no conversion of the intermediate to *P*PC detected when this arginine is mutated to glutamine [33]. Given the position of this arginine it is likely that it is involved in the binding of cysteine. Despite the absence of a crystal structure with cysteine, kinetic data showing uncompetitive inhibition with cysteine is consistent with this.

This allosteric site is comprised of a large group of hydrophobic residues (I209, F282 L304 of protomer A and L203, I292, P299 and I302 of protomer B) many of which form

hydrophobic interactions with compound **1b** (Figure 5C). Several π-interactions between the compound and the protein are also observed and involve D281 and F282 of protomer A and R207 of protomer B (Figure 5D). Hydrogen-bond interactions are formed with D281 and F282 of protomer A and R207 of protomer B. Water-mediated interactions are also observed for a group of residues that sit at the outer edge of the site (L203, H286 and D303) that is formed exclusively by protomer B (Figure 5C).

We propose that upon binding of L-cysteine, the R207 side chain moves towards the active site, and is likely involved in stabilizing/orienting L-cysteine to attack the phosphopantothenoyl-CMP intermediate. This movement opens the allosteric site, which allows binding of allosteric inhibitors to the newly created cavity. The allosteric inhibitors will then stabilize the enzyme in its substrate bound state with the position of R207 becoming locked by several hydrogen-bonds with the side chain of D281 of protomer A, the backbone carbonyl group of I292 and the side chain of D204 of protomer B but also by the π-interactions with the compound (Figure 5C). The residues around this site and crucially R207 are conserved across many microorganisms, suggesting that this allosteric site is present in most, if not all bacterial CoaBCs (Figure S3 and S9A). Interestingly, even though overall sequence identity is very low between the human CoaB and MsmCoaB (22%), the human enzyme also contains an arginine equivalent to R207 and a roughly similar interface with several conserved residues, but there are stark differences in the relative position of the residues at this site between the two enzymes (Figure S9B). While we were not able to obtain co-crystal structures with other inhibitors, *in silico* docking helped to provide a possible explanation for the structure-activity relationship observed for series one and two. The highest-scoring docking pose of compound **1b** the most potent inhibitor of series one, was almost identical to that observed in the co-crystal structure (Figure S10A), and the analogues for which docking was performed adopted a

similar binding pose. The lower activity of compound **1a** relative to compound **1b** could be explained by the loss of water-mediated hydrogen bonds (Figure 5C, S10B), while the lower activity of compound **1c** could be explained by the loss of the carbonyl group which faces a highly electropositive area of the protein (Figure S10C). Compound **2b** is predicted to form direct hydrogen bonds at the bottom of the allosteric site, similar to those formed by compound **1b** but also to interact directly with L203 and H286, forming extra hydrogen bonds at the top of the allosteric site (Figure 6). For compound **1b** the interactions at the top of the site are water mediated (Figure 5C). This could explain the higher potency of compound **2b**. Compounds **2c** and **2d** are also predicted to form direct hydrogen bond interactions at the top of the allosteric site, but the interactions at the bottom of the site are not as favourable due to the presence of extra hydroxyl groups (Figure S10D-F). The remaining compounds in series two, which have fewer hydroxyl groups and/or with hydroxyl groups in different positions, lose the ability to form hydrogen bonds, consistent with the weaker inhibitory effect observed (Table S2).

Screening of CoaBC inhibitors against *M. tuberculosis*

The in vitro whole cell activity of the compounds was further evaluated by their ability to inhibit *M. tuberculosis* growth on different carbon sources. None of the compounds exhibited activity in media containing glycerol or cholesterol as the main carbon source. We then tested whether the lack of inhibitory activity could be attributed to the presence of BSA by determining the whole cell activity of the three most potent inhibitors against *M. tuberculosis* in GAST/Fe minimal media. All the tested compounds exhibited moderate to low activity in this media with compound **2b** displaying the best activity of the three (Table 2). The observed differences in potency between the enzymatic assay and

whole cell activity are likely related to low compound permeation, high efflux or metabolisation.

Discussion

CoA is an essential co-factor ubiquitous in all domains of live. For many years, this pathway has been considered an attractive drug target to develop new antibiotics against a wide range of pathogens including *M. tuberculosis*. Furthermore, the recent identification of CoaBC as a key fragility point in the CoA pathway of this organism [12], combined with the extremely low sequence identity with the human CoaB (25%) makes this enzyme an highly attractive drug discovery target.

However, we were aware that the many questions remaining at the start of this work about the organization and regulation of this bi-functional enzyme could have significant implications for drug discovery. We therefore set out to obtain a full-length structure of a CoaBC from mycobacteria and we were successful in solving the full length MsmCoaBC but also MsmCoaB alone, which share very high sequence identity with the *M. tuberculosis* orthologue (86% full-length, 84% CoaB enzyme) and hence valuable tools for studying *M. tuberculosis* CoaBC. The CoaBC organization we revealed is similar to other HFCD family proteins [15] but unique in the sense that it contains more than one domain and highlights how the arrangement of the fused enzymes is essential for mycobacterial CoaB dimerisation and function.

Regulation of the CoA biosynthesis pathway by its product (CoA) was known to occur for other enzymes of the pathway but no information was available for CoaBC. We demonstrate that both CoA as well as several CoA thioesters regulate CoaBC by inhibiting CoaB activity with succinyl-CoA showing the greatest inhibition of the tested acyl-CoAs, and that these molecules act in a competitive manner with CTP and PPA and

353 a non-competitive manner with L-cysteine. This is consistent with these molecules
354 binding to the CoaB active site but not to the L-cysteine sub-site.
355 CoA and acyl-CoAs inhibit both CoaA and CoaD enzymes to varying extents [28,30,34].
356 However, the inhibitory effect of CoA and its thioesters in their activity is low when
357 compared to what we observed in CoaBC and consequently the impact of the intracellular
358 level of these molecules will be higher in CoaBC . We therefore report a new and
359 important mechanism of regulation of de novo CoA biosynthesis, mediated by the action
360 of CoA thioesters on CoaBC. Since the reported intracellular levels of these molecules
361 are normally above the observed IC_{50} the activity of CoaBC is highly inhibited. This
362 correlates well with previous work showing that "de novo" CoA biosynthesis closely
363 matches dilution due to cell division [35].
364 Although the CoA pathway and CoaBC have been the subject of many drug discovery
365 efforts, few non-substrate-mimicking inhibitors of CoaBC have been reported [24]. Our
366 work identifies two related chemical scaffolds that potently inhibit the activity of the
367 CoaB moiety of MtbCoaBC through a new cryptic allosteric site that sits in the dimer
368 interface region of the CoaB enzyme. This site is closed in the CTP-bound structure, by
369 the side chain of R207 a residue known to be involved in the second and final step of the
370 reaction catalysed by CoaB – the conversion of the 4'-phosphopantothenoyl-CMP
371 intermediate to *P*PC [33]. Considering the role of this in the final step of product formation
372 and that compound **1b** shows uncompetitive inhibition relative to all CoaB substrates, we
373 propose that the opening of this site occurs upon binding of the final substrate L-cysteine.
374 Currently it is not clear whether this new allosteric site is exploited by a natural ligand,
375 as we were unable to identify such a biomolecule. Nevertheless, the conservation of
376 residues at this site, across a variety of bacteria, indicates that this feature might be
377 common to many, if not all, bacterial CoaBs.

Drug discovery against *M. tuberculosis* is rich in examples of compounds with potent activity against an essential enzyme but with a complete lack of whole cell activity due to the impermeable cell wall of this organism, efflux pumps, target modification enzymes and extensive capacity to metabolise compounds [36]. The lack of in vitro whole cell activity displayed by the CoaB inhibitors reported in this work, may relate to any of these issues. However, the activity observed in albumin free media (GAST media) also points to the possibility of compound binding to albumin interfering with the assay. Nevertheless, the promising biochemical and structural data described herein further validates CoaBC as a promising novel anti-tubercular drug target by showing a new allosteric site that can be targeted by potent inhibitors.

Materials and methods

Cloning and protein purification

Mycobacterium tuberculosis and *Mycobacterium smegmatis coaBC* genes were amplified from genomic DNA of *M. tuberculosis* H37Rv strain, obtained from ATCC (ATCC25618D-2) and genomic DNA of *M. smegmatis* mc^2 155 (graciously provided by Dr. Nuno Empadinhas), and cloned into a pET28a vector (Novagen), modified to include an N-terminal 6xHis-SUMO tag. *M. smegmatis coaB* construct was obtained from Seattle Structure Genomics Center for Infectious Disease. The same protein purification protocol was used for both *M. tuberculosis* and *M. smegmatis* CoaBC constructs.

E. coli BL21(DE3) containing pET28aSUMO-CoaBC was grown in 2XYT media at 37 ºC until an $O.D._{600}$ = 0.6. IPTG was then added to a final concentration of 0.5 mM at the temperature changed to 18 ºC for 18-20h. Cells were then harvested by centrifugation, re-suspended in 50 mM TRIS pH 8.0, 250 mM NaCl, 20% (w/v) glycerol, 20 mM imidazole, 5 mM $MgCl_2$ with protease inhibitors tablets (Roche) and DNAseI (Sigma). Cells were

lysed with an Emulsiflex (Avestin) and the resultant cell lysate was centrifuged at 27000 x *g* for 30 min to remove cell debris. Recombinant CoaBCs were purified with a HiTrap IMAC Sepharose FF column (GE-Healthcare), equilibrated with 50 mM TRIS pH 8.0, 250 mM NaCl, 20% glycerol (w/v) and 20mM Imidazole. Elution was performed in the same buffer with 500mM Imidazole. Protein was dialysed in 25 mM TRIS pH 8 and 150 mM and SUMO tag was cleaved overnight at 4 ºC by adding Ulp1 Protease at 1:100 ratio. CoaBC was concentrated and loaded in a Superdex 200 column equilibrated with 25mM TRIS pH 8.0, 150 mM NaCl. Fraction purity was determined by SDS-page and the purest fractions were pooled, concentrated to ~10 $mg.ml^{-1}$ for *M. tuberculosis* CoaBC and 30 $mg.ml^{-1}$ for *M. smegmatis* CoaBC, flash frozen in liquid nitrogen and stored at -80 ºC.

E. coli BL21(DE3) containing the *M. smegmatis* CoaB construct with a N-terminal non--cleavable 6xhis tag was grown and harvested as above and re-suspended in 20 mM HEPES pH 7.0, 500 mM NaCl, 20 mM imidazole, 5 mM $MgCl_2$ with protease inhibitors tablets (Roche) and DNAseI (Sigma). Cells were lysed with an Emulsiflex (Avestin) and cell lysate was centrifuged at 27000 g for 30 mins to remove cell debris. Recombinat *M. smegmatis* CoaB was purified with a HiTrap IMAC Sepharose FF column (GE-Healthcare), equilibrated with 20 mM HEPES pH 7.0, 500 mM NaCl and 20 mM imidazole. Elution was carried in the same buffer with 500 mM imidazole. Protein was concentrated and loaded on a Superdex 200 column equilibrated with 20mM HEPES pH 7.0 and 500 mM NaCl. Fraction purity was assessed by SDS-page and the purest fractions were pooled concentrated to 22 $mg.\ ml^{-1}$, flash frozen in liquid nitrogen and stored at -80 ºC.

Native mass spectrometry

Spectra were recorded on a Synapt HDMS mass spectrometer (Waters) modified for studying high masses. MtCoaBC and MsCoaBC were exchanged into NH_4OAc (500 mM, pH 7.0) solution using Micro Bio-Spin 6 chromatography columns (Bio-Rad). 2.5 µL of sample solution was injected into a borosilicate emitter (Thermo Scientific) for sampling. Instrument conditions were optimized to enhance ion desolvation while minimizing dissociation of macromolecular complexes. Typical conditions were capillary voltage 1.8–2.0 kV, sample cone voltage 100 V, extractor cone voltage 1 V, trap collision voltage 60 V, transfer collision voltage 60 V, source temperature 20 °C, backing pressure 5 mbar, trap pressure 3–4 × 10^{-2} mbar, IMS (N_2) pressure 5–6 × 10^{-1} mbar and TOF pressure 7–8 × 10^{-7} mbar. Spectra were calibrated externally using cesium iodide. Data acquisition and processing were performed using MassLynx 4.1 (Waters).

Crystallization

For both full length *M. smegmatis* CoaBC and CoaB alone, the crystallization screens and optimization were performed at 18 ºC using the sitting-drop vapour diffusion method. For CoaBC 300 nL of pure protein at 30 $mg.ml^{-1}$, pre-incubated with 3 mM CTP and 10 mM $MgCl_2$, was mixed in 1:1 and 1:2 (protein to reservoir) ratio with well solution using a mosquito robot (TTP labtech). Initial conditions were obtained in the Classics lite crystallization screen (Qiagen), solution 1. Crystals obtained in this condition diffracted poorly, therefore several rounds of optimization were performed. The final optimised condition consisted of 0.1 M BisTris pH 6.5, 10 mM $CoCl_2$ 0.8 M 1,6-hexanediol. Crystals appeared after three days in both conditions. A cryogenic solution was prepared by adding ethylene glycol up to 30% (v/v) to mother liquor. Crystals were briefly transferred to this solution, flash frozen in liquid nitrogen and stored for data collection.

For MsmCoaB 200 nL of pure protein at 22-24 mg.mL^{-1} with 10 mM CTP was mixed in 1:1 ratio with well solution using a Phoenix robot (Art Robbins). Crystals were obtained in Wizards classics III&IV (Rigaku) solution G4 consisting of 20% (w/v) PEG 8000, 0.1M MES pH 6.0 and 0.2 M calcium acetate. Crystals appeared after 2 days.

To obtain ligand-bound structures, soaking was performed condition using the hanging-drop vapour-diffusion method as follows: 2 uL of a solution containing 20% (w/v) PEG 8000, 0.1M MES pH 6.0, 0.2 M calcium acetate, 0.25 M NaCl 10% (v/v) DMSO and 1-5 mM inhibitors was left to equilibrate against 500 µl of reservoir solution for 3 days. Crystals were then transferred to the pre-equilibrated drops and incubated for 24h. A cryogenic solution was prepared by adding 2-Methyl-2,4-pentanediol up to 25% (v/v) to mother liquor. Crystals were briefly transferred to this solution, flash frozen in liquid nitrogen and stored for data collection.

While we have also obtained *M. tuberculosis* CoaBC crystals they did not diffract and our optimization efforts failed to improve them.

Data collection and processing

The data sets were collected at stations I02 and I03 at Diamond Light Source (Oxford, UK). The diffraction images were processed with AutoPROC [37] using XDS [38] for indexing and integration with AIMLESS [39] and TRUNCATE [40] from CCP4 Suite [41] for data reduction, scaling and calculation of structure factor amplitudes and intensity statistics.

Structure solution and refinement

MsmCoaB and MsmCoaBC structures were solved by molecular replacement using PHASER [42] from the PHENIX software package [43]. For MsmCoaB the atomic

coordinates of MsmCoaB structure (PDB entry 4QJI) were used as a search model. Ligand bound structures were solved using our highest resolution MsmCoaB apo form structure (PDB entry 6TH2). For MsmCoaBC atomic coordinates of *Arabidopsis thaliana* CoaC (PDB entry 1MVL) [19] and our highest resolution CoaB structure (PDB entry 6TH2) were used as search models. Model building was done with Coot [44] and refinement was performed in PHENIX [43]. Structure validation was performed using Coot and PHENIX tools [43,44]. All figures were prepared using Pymol (The PyMOL Molecular Graphics System, Version 2.0 Schrödinger, LLC.) and ligand interactions calculated with Arpeggio [45].

High-throughput screening

Potential inhibitors of CoaBC were assessed at room temperature using a PHERAStar microplate reader (BMG Labtech). Pyrophosphate produced by CoaB was converted to two molecules of inorganic phosphate using a pyrophosphatase. Phosphate was then detected using the BIOMOL® Green reagent (Enzo Life Sciences), which when bound to phosphate absorbs light at 650 nm. An end-point assay was carried out in clear, flat-bottom, polystyrene, 384-well plates (Greiner) in an 50 µl reaction volume containing 100 mM TRIS, pH 7.6; 1 mM $MgCl_2$; 1 mM TCEP; 0.03 U/mL pyrophosphatase; 2 µM CTP; 40 µM L-cysteine; 30 µM *P*PA and 30 nM MtbCoaBC. Assays were performed by adding 25 µL of a 2-times concentrated reaction mixture containing all components with the exception of the enzymes to all wells, and the reactions started by adding 25 µL of a 2-times concentrated enzyme mixture. The reaction was carried out for 2 h at room temperature, before 50 µL of BIOMOL® Green reagent was added and incubated for a further 20 min prior to reading.

Inorganic pyrophosphatase-purine nucleoside phosphorylase PNP-PPIase assay. The commercially available EnzCheck pyrophosphate assay kit (E-6645) (Life Technologies) was used for this assay. The final reaction composition used was 0.03 U/mL inorganic pyrophosphatase, 1 U/mL purine nucleoside phosphorylase, 1 mM $MgCl_2$, 200 µM MESG, 100 mM TRIS pH 7.5, 1 mM TCEP, 32 nM MtbCoaBC, 125 µM CTP, 125 µM *P*PA, 500 µM L-cysteine, and various concentrations of compounds being tested for inhibition all prepared from DMSO stock solutions (compounds of series one and two) or water (CoA and CoA thioesters). Assays were performed on either a CLARIOStar or PHERAStar microplate reader (BMG Labtech) in 96-well plates (Greiner). A substrate mixture containing the substrates and the inhibitor was pre-incubated at 25 °C for 10 min. An enzyme solution was prepared and separately pre-incubated at 25 °C for 10 min. The reaction was initiated by the addition of the substrates to the solution containing the enzyme to a final volume of 75 µL. Enzymatic activity was monitored by following the absorbance at 360 nm for 30 min (100 cycles/20 s each cycle). Assays were performed in triplicates, including a negative control (lacking *P*PA) and a positive control (lacking inhibitor).

Competition assays were performed using the same conditions but with variable substrate concentrations (31.25 µM, 62.5 µM, 125 µM, 250 µM and 500 µM for CTP and *P*PA, 31.25 µM, 62.5 µM, 93.75 µM 125 µM and 250 µM for L-cysteine).

M. tuberculosis strains and growth conditions

MIC determination for *M. tuberculosis* H37RvMA was performed as previously described [46] in the following media: 7H9/ADC/glycerol (4.7 g/L Difco Middlebrook 7H9 base, 100mL/L Middlebrook albumin (BSA)-dextrose-catalase (ADC) Difco Middlebrook, 0.2% glycerol and 0.05% Tween-80) , 7H9/Cholesterol/Tyloxapol (4.7 g/L

527 7H9 base, 0.81 g/L NaCl, 24 mg/L cholesterol, 5 g/L BSA fraction V and 0.05%
528 Tyloxapol), GAST/Fe (0.3 g/L of Bacto Casitone (Difco), 4.0/L g of dibasic potassium
529 phosphate, 2.0 g/L of citric acid, 1.0 g/L of L-alanine, 1.2 g/L of magnesium chloride
530 hexahydrate, 0.6 g/L of potassium sulfate, 2.0 g/L of ammonium chloride, 1.80 ml/L of
531 10 N sodium hydroxide, 10.0 ml of glycerol 0.05% Tween 80 and 0.05 g of ferric
532 ammonium citrate adjusted to pH 6.6.
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554 **Figure Legends**

555 **Figure 1: X-ray crystal structure of FMN and CTP bound MsmCoaBC.**

556 (A) Full aspect of the dodecameric CoaBC with CoaC represented in teal and CoaB in
557 gold. (B) View of a CoaBC dimer with FMN and CTP shown. Each protomer is coloured
558 differently. The CoaC active site flexible flap is highlighted in blue. (C) In the left panel,
559 a CoaBC trimer is shown with the CoaC coloured in teal and CoaB in gold. On the right
560 panel dimerization of two CoaBC trimers is shown with CoaC coloured in teal or grey for
561 different trimers. Each CoaB forms a dimer with protomers from different trimers.

562

563 **Figure 2: Detailed view of MsmCoaBC active sites and MsmCoaB dimerisation**
564 **interface.**

565 (A) View of CoaC active site with FMN bound. The active site sits between two
566 protomers of one trimer (gold and red) and a third protomer from an adjacent trimer
567 (green). Hydrogen bonds are depicted in yellow and π-interactions are in blue. (B)
568 Superposition of a CoaB crystal structure (PDB code: 6TH2) in green, with full length
569 CoaBC (teal) showing the active site flaps (brown) of the CoaB and CoaC enzymes. (C)
570 Detailed view of the CTP binding site. Cartoon and residues belonging to each protomer
571 are coloured differently. Hydrogen bonds and π-interactions are coloured as in B.
572 Important waters are represented as red spheres and calcium as a green sphere. Calcium
573 coordination is depicted in purple. (D) CoaB dimerization interface. Each protomer is
574 coloured as in C. (D)

575

576 **Figure 3: Regulation of MtbCoaBC by CoA and CoA thioesthers.**

(A) Inhibition of MtbCoaBC by CoA, acetyl-CoA, malonyl-CoA and succinyl-CoA. (B) Lineweaver-Burk plots showing the effect of varying the concentration of each substrate in the presence of different concentrations of acetyl-CoA.

Figure 4: Inhibition of MtbCoaBC by compounds 1b and 2b.

(A) Dose response profiles and chemical structure of compounds **1b** and **2b** is shown. (B) Lineweaver-burke plots showing the effect of varying concentrations of compound **1b** (left) and **2b** (right) in the presence of varying concentrations of CTP, *P*PA and L-cysteine.

Figure 5: MsmCoaB X-ray structure showing the cryptic allosteric site.

CoaB with the cryptic allosteric site closed (A) and opened conformation (B) with compound **1b** (pink) bound. (C) Detailed view of the allosteric site with compound **1b** (yellow) bound. The individual protomers of the CoaB dimer are coloured in green or pink.. Hydrogen bonds are depicted in red, π-interactions are in grey, and hydrophobic interaction in green. Important waters are represented as red spheres and calcium as a green sphere. Calcium coordination is depicted in purple. (D) Gating mechanism of the cryptic allosteric site showing the movement of R207 with the closed conformation in yellow and the open conformation in pink. An *E. coli* structure (PDB code: 1U7Z) with the 4'-phosphopantothenoyl-CMP (purple) intermediate bound is superimposed.

Figure 6: Docking of compound 2b into MsmCoaB showing the highest scoring pose.

Hydrogen bonds are shown in red. The individual protomers of the CoaB dimer are either coloured in green or pink.

Tables

Table 1: Inhibition of CoaB domain by CoA, CoA thioesters and the most potent inhibitors from of series one and two. IC_{50} values determined using the EnzChek pyrophosphate assay are shown.

Compound	IC_{50} EnzCheck (μM)
CoA	148 ± 11
AcCoA	121 ± 9
MlCoA	49 ± 3
SucCoA	38 ± 2
1b	0.28 ± 0.05
1c	4.6 ± 0.4
2b	0.08 ± 0.01
2c	0.41 ± 0.03
2d	0.54 ± 0.06
2e	3.0 ± 0.2

Table 2: Minimum inhibitory concentration (MIC) values of CoaB inhibitors against *M. tuberculosis* H37Rv cultured in different media (μM).

Compound	7H9/ADC/ Glycerol	7H9/ Cholesterol/ Tyloxapol	GAST/ Fe
1b	>250	>250	125
1c	>250	ND	ND
2b	>250	>250	50
2c	>250	>250	125
2d	>250	>250	ND
2e	>250	ND	ND

*ND – Not determined.

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Author contributions

VMendes wrote the manuscript. VM designed and performed all the crystallographic experiments with the help of MB, OB and JCW. VMendes and JH designed and performed the kinetic experiments. JH synthesised 4'-phosphopantothenate. PHMT

747 performed docking experiments. DSC performed the native mass spectrometry
748 experiments. SG, TB, SON, SD, JP and CS developed and performed the high-throughput
749 screening. JCE, SLL and HIMB performed the microbiology experiments on *M.*
750 *tuberculosis* H37Rv. VMendes, JCE, SG, AGC, PCR, KR, CA, HIMB, CEB, VMizrahi,
751 PGW and TLB managed the project. All authors approved the manuscript.
752
753 **Accession numbers**
754 Coordinates and structure factors related to this work have been deposited in the PDB
755 with accession numbers: **6TGV**, **6TH2** and **6THC**.

Figure 1

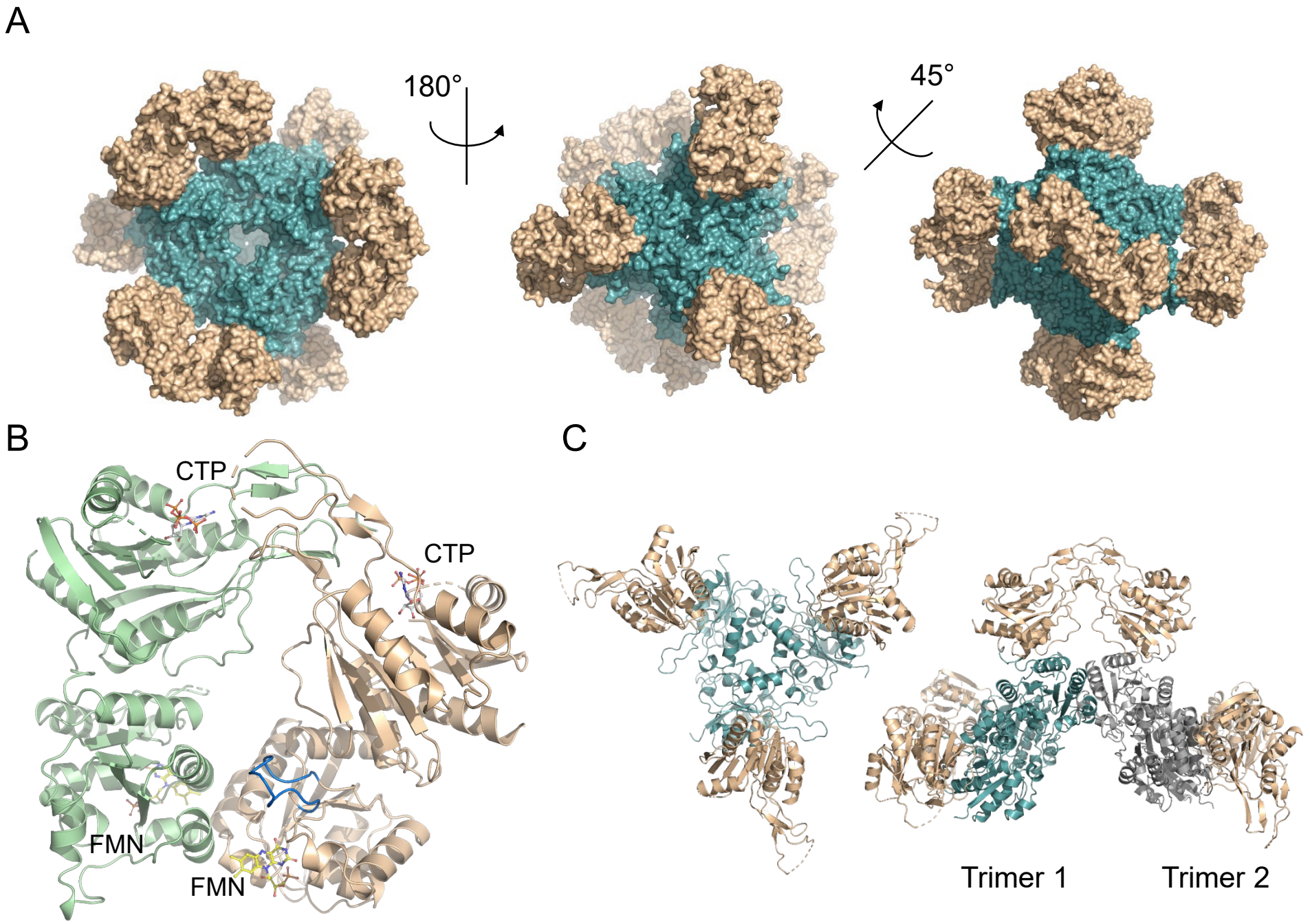
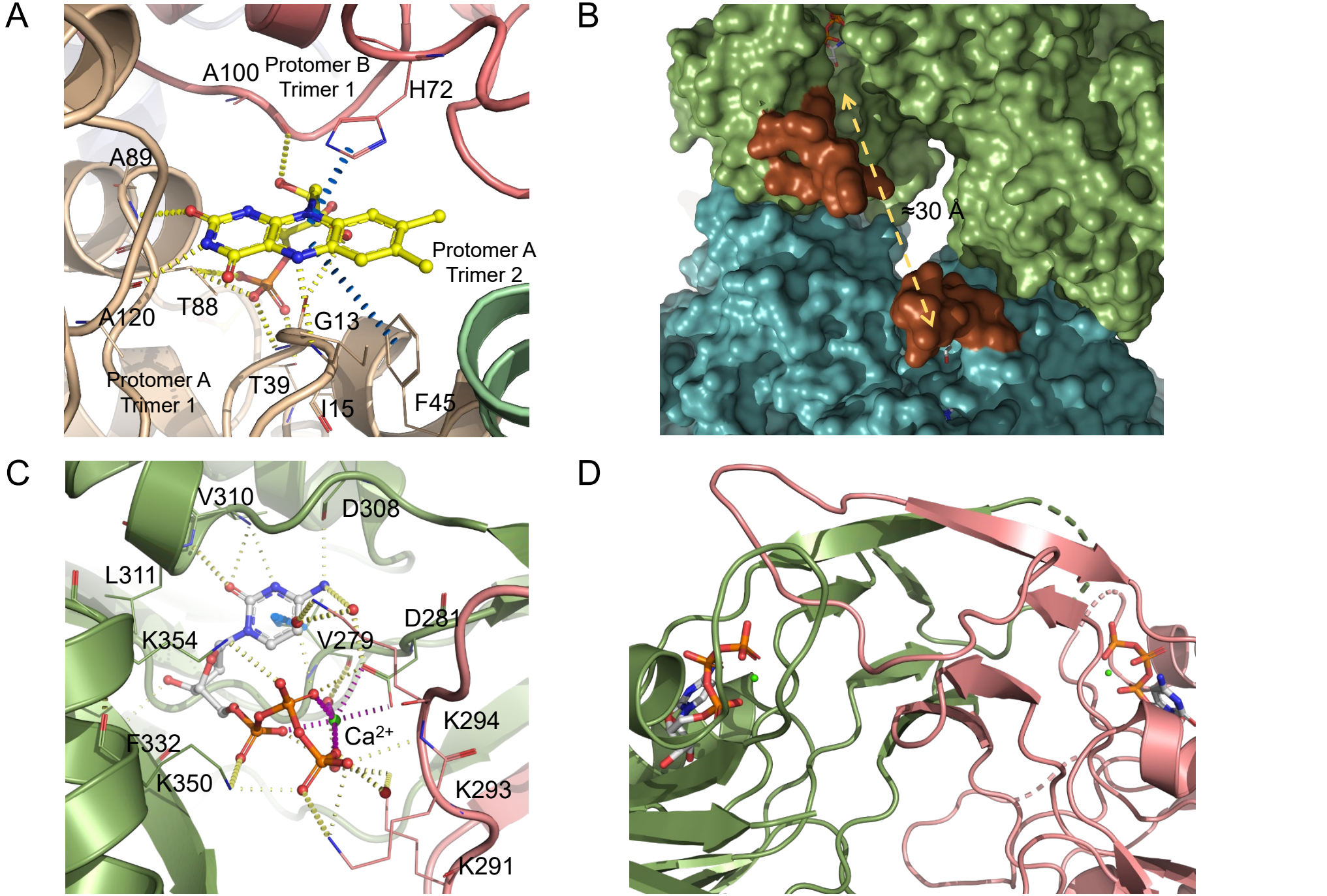


Figure 2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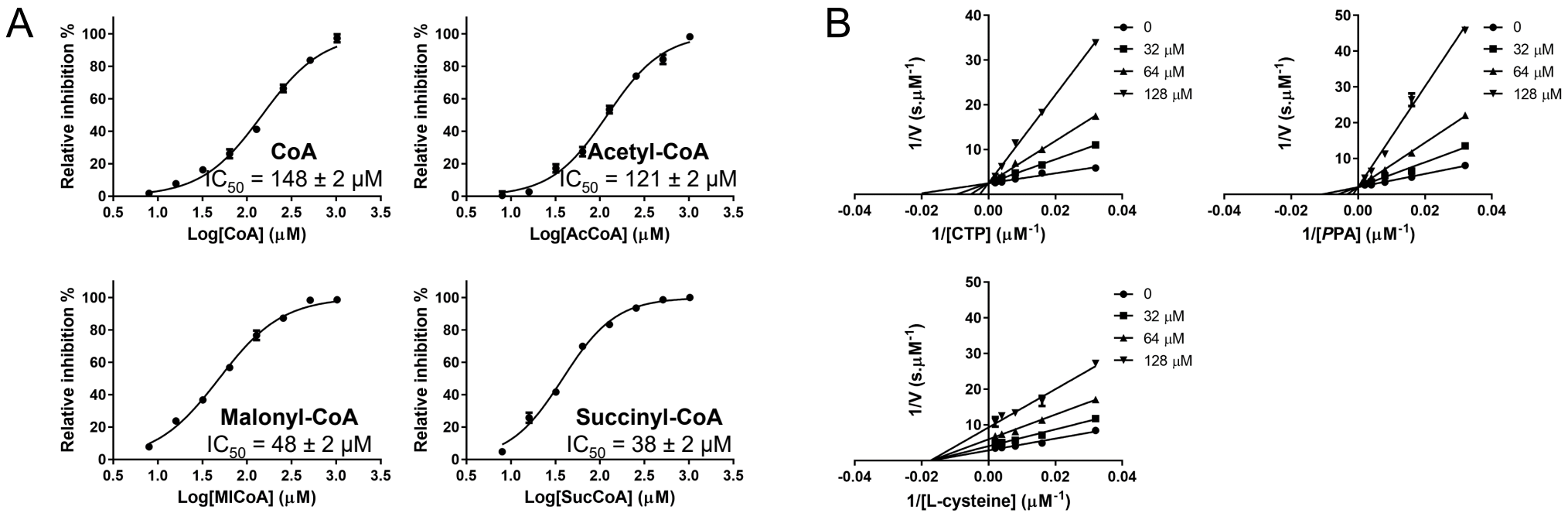
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Succinyl-CoA
IC50 = 38 ± 2 μM
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Figure 4

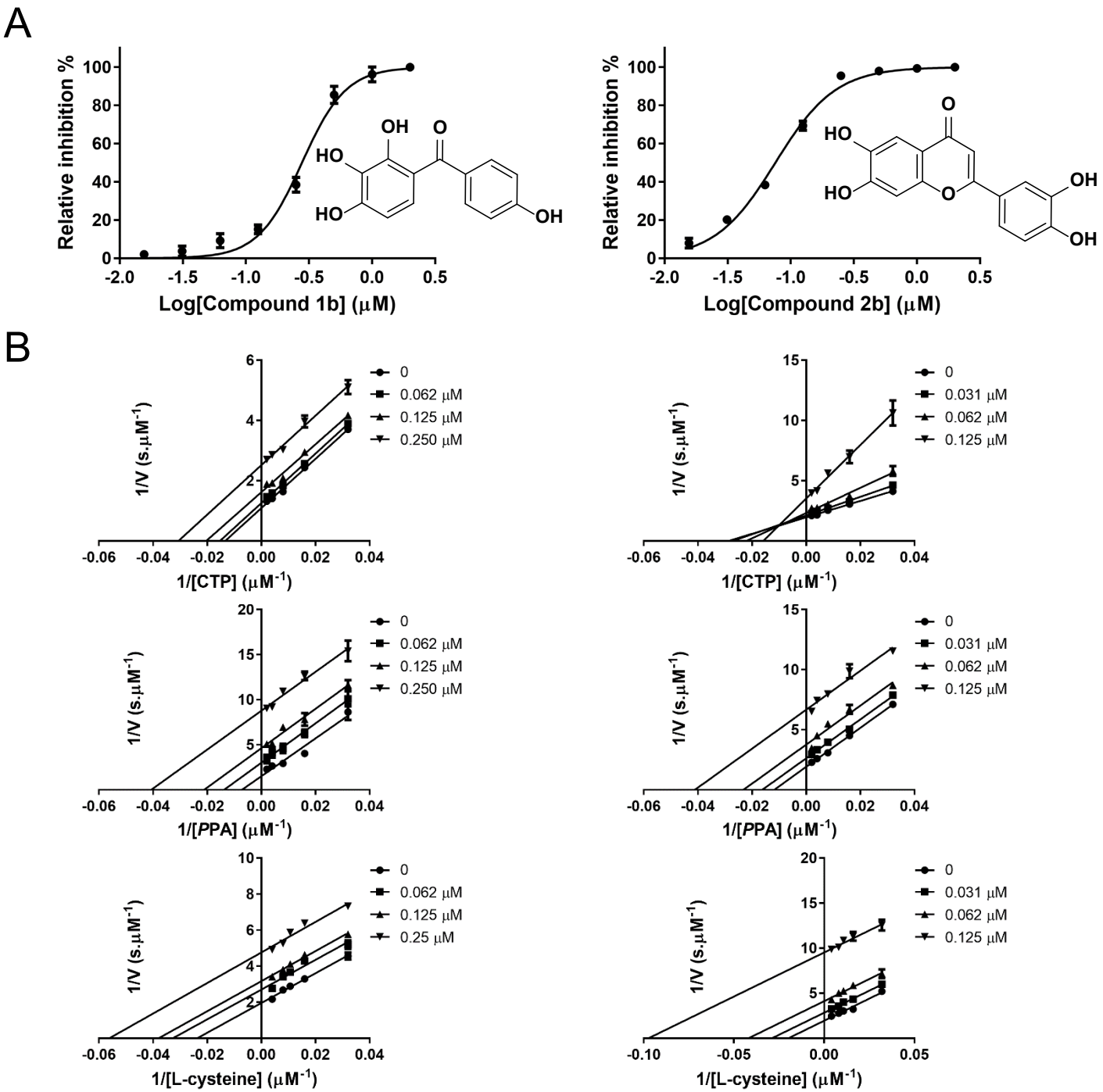
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Figure 5

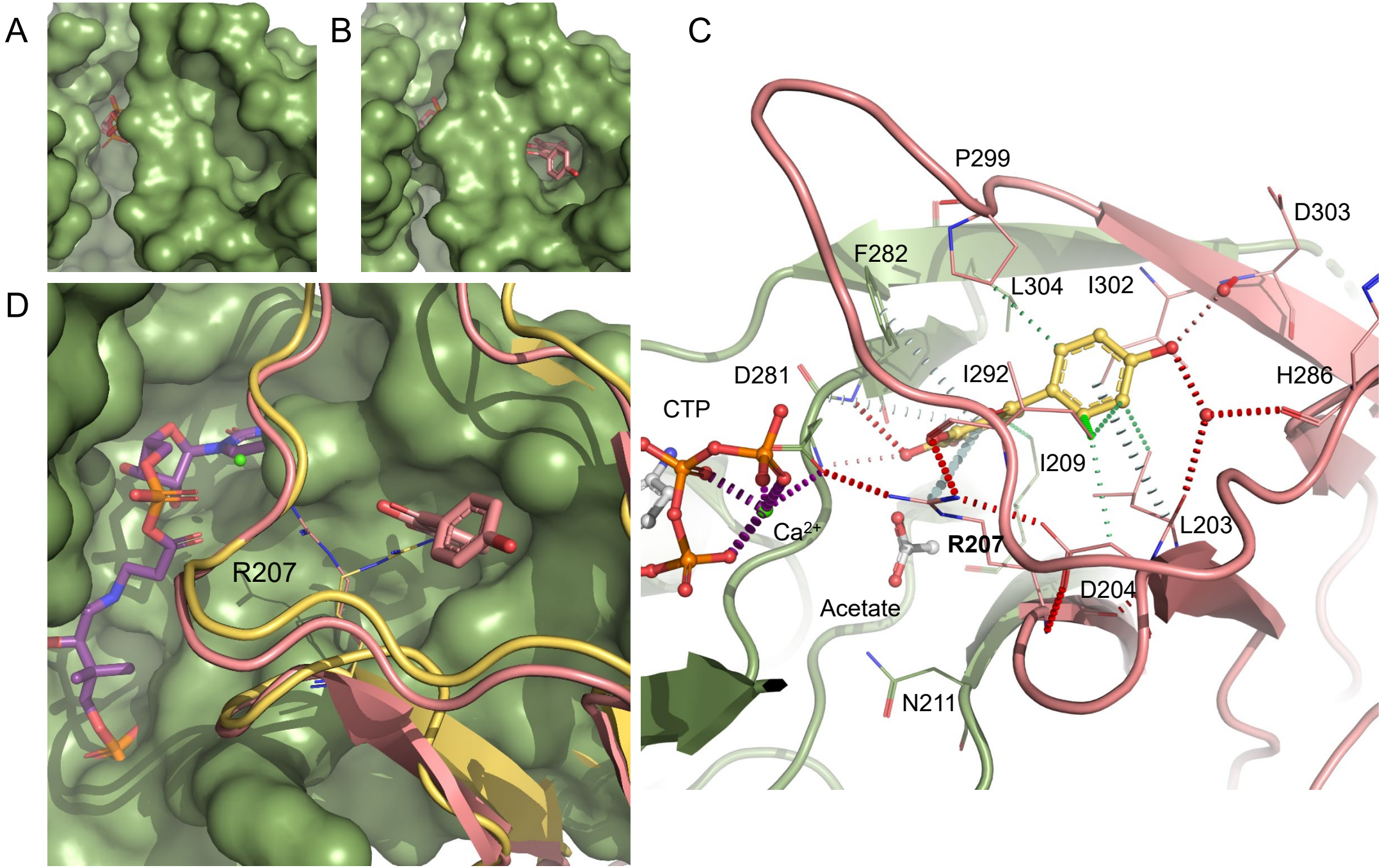
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Figure 6