Datasets, processing and refinement details for \textit{Mtb-}AnPRT: inhibitor structures with various space groups

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** Abstract

There are twenty-five published structures of \textit{Mycobacterium tuberculosis} anthranilate phosphoribosyltransferase (\textit{Mtb-}AnPRT) that use the same crystallization protocol. The structures include protein complexed with natural and alternative substrates, protein:inhibitor complexes, and variants with mutations of substrate-binding residues. Amongst these are varying space groups (\textit{i.e.} \textit{P2}_1, \textit{C2}, \textit{P2}_1\textit{2}_1\textit{2}_1, \textit{P2}_2\textit{1}_2\textit{2}_1). This article outlines experimental details for 3 additional \textit{Mtb-}AnPRT:inhibitor structures. For one protein:inhibitor complex, two datasets are presented – one generated by crystallization of protein in the presence of the inhibitor and another where a protein crystal was soaked with the inhibitor.
Automatic and manual processing of these datasets indicated the same space group for both datasets and thus indicate that the space group differences between structures of \textit{Mtb}-AnPRT:ligand complexes are not related to the method used to introduce the ligand.

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### Specifications Table

| Subject area          | Proteomics and Biochemistry |
|-----------------------|-----------------------------|
| More specific subject area | Structural biology |
| Type of data          | Tables, figures and X-ray diffraction images |
| How data was acquired | X-ray macromolecular crystallography; Australian Synchrotron MX1 and MX2 beamlines |
| Data format           | Unprocessed, processed, deposited with crystal packing analyzed. |
| Experimental factors  | Protein crystals soaked and co-crystallized with ligands |
| Experimental features | Contrast of the different protein crystal packing associated with different inhibitors and/or introduced by soaking or co-crystallization. |
|                       | X-ray diffraction datasets for co-crystallization and soaked-in experiments with the same inhibitor indicate space group changes are independent of method used to introduce the inhibitor. |
| Data source location  | Data collected in Melbourne, Australia. |
| Data accessibility    | The atomic coordinates and observed structure factors are available from Protein Data Bank with accession numbers: 5BO2, 5BO3 and 5BNE. The X-ray diffraction image files corresponding to datasets from two experiments are hosted by Mendeley: http://http://dx.doi.org/10.17632/2zrfgv34nb.1 http://http://dx.doi.org/10.17632/xgn5z8jn7r.1 |
| Related research article | Anthranilate phosphoribosyltransferase: Binding determinants for 5’-phospho-alpha-o-ribosyl-1’-pyrophosphate (PRPP) and the implications for inhibitor design “in press”. https://doi.org/10.1016/j.bbapap.2017.08.018 |

### Value of the data

- \textit{Mtb}-AnPRT is a target of interest in developing novel anti-tuberculosis agents. This protein’s capacity to crystallize thus yield new protein:ligand complexes makes it of interest for structure-based inhibitor design.
- Previously \textit{Mtb}-AnPRT:ligand complexes have been found with different space groups (e.g. \textit{P2}_1, \textit{C}2, \textit{P}2\textsubscript{1}2\textsubscript{1}2, and \textit{P}2\textsubscript{1}2\textsubscript{1}2\textsubscript{1}), generated by using the same crystallization protocol.
- \textit{Mtb}-AnPRT:inhibitor complex structures described herein have \textit{C}2 and \textit{P}2\textsubscript{1} space groups. These structures were solved using X-ray diffraction datasets from protein:ligand crystals generated by streak-seeded with wild-type \textit{P}2\textsubscript{1}2\textsubscript{1}2\textsubscript{1} crystal.
- For one inhibitor, X-ray diffraction datasets are presented for both co-crystallization and soaked crystal experiments. Space group \textit{C}2 occurred in both datasets and indicates the space group
change between ligand-free and inhibitor-bound structures are independent of method used to introduce the inhibitor.

- X-ray diffraction datasets utilizing different methods of ligand introduction and yielding equivalent protein:ligand structures are typically not made available. These publicly available datasets in the context of multiple space groups observed for Mtb-AnPRT:ligand structures, and the analysis presented herein, demonstrate that space group changes can be independent of co-crystallization and soaking methods of ligand introduction. This has relevance to academic and industrial researchers who are pursuing structure-based inhibitor design.

1. Data

1.1. Overview

The experimental and data processing details for 3 new protein:ligand structures of Mycobacterium tuberculosis anthranilate phosphoribosyl transferase (Mtb-AnPRT) are described herein (Table 1). The protein structures are complexed with Mtb-AnPRT inhibitors characterized in [1] and annotated as:

- 8k (2-(2-carboxyphenylamino)-5-(5-phosphonopentyloxy)benzoic acid)
- 8j (2-(2-carboxyphenylamino)-5-(4-phosphonobutoxy)benzoic acid)
- 8i (2-(2-carboxyphenylamino)-5-(3-phosphonopropoxy)benzoic acid)

These structures were determined with protein crystallized in presence of imidazole-malate and PEG4000. Crystallization drops seeded with crystal nuclei from a pre-existing Mtb-AnPRT crystal generate better crystal morphology for Mtb-AnPRT [2]. All new structures presented herein were generated by streak-seeding using wild-type P2_12_12 structures. Also presented are two X-ray diffraction datasets corresponding to protein crystals either soaked and co-crystallized with the same inhibitor (Table 2).

Of the previously published structures of Mtb-AnPRT, 25 were determined from protein crystallized using this protocol (Table 3). Most of these structures have a ligand bound (e.g. inhibitor or substrate) and/or are protein variants with mutations in substrate-binding residues (Table 3). Amongst both cohorts (Tables 1 and 3) several different space groups have been observed, including P2_1, C2, P2_12_12. Amongst the 28 structures referred to in this article (Tables 1 and 3), similar unit cells correspond to each space group.

P2_12_12 is the most common space group for macromolecular structures, and it has been proposed that this is due to its capacity to accommodate repositioning, i.e. rotations or translations, within the asymmetric unit, without loss of crystal contacts [3]. The structure of wild-type Mtb-AnPRT without ligands (PDB ID: 3QR9) has previously been solved from protein crystallized in imidazole-malate and PEG4000 in the space group P2_12_12, with two monomers (A, B) in the asymmetric unit, a unit cell of 79x92x120 Å, and 57% solvent content [2].

Mtb-AnPRT is a homodimeric protein with an extended “S”-shape, with each subunit containing two domains [4]. In the ligand-free structure, a single dimer (the biological assembly) is found in the Table 1

Summary of Mtb-AnPRT structures described herein.

| PDB ID | Ligand ID | Solvent content | Unit Cell | Space group | Resolution (Å) | Chains | PDB DOI |
|--------|-----------|-----------------|-----------|-------------|----------------|--------|---------|
| 5B02   | 8i        | 46%             | 91° 77 78 117 | P2_1        | 2.15           | A,B,C | 10.2210/pdb5bo2/pdb |
| 5B03   | 8j        | 46%             | 111° 95 78 103 | C2          | 2.00           | A,B   | 10.2210/pdb5bo3/pdb |
| 5BNE   | 8k        | 46%             | 111° 94 78 103 | C2          | 1.75           | A,B   | 10.2210/pdb5bne/pdb |
### Table 2
Crystallization of complexes, along with space group and unit cell from data processing.

| PDB ID | Ligand(s) bound | [Protein] mg mL$^{-1}$ | Reservoir condition | Cryoprotectant/Soak | Notes | Space group | Unit cell |
|--------|-----------------|------------------------|---------------------|--------------------|-------|-------------|-----------|
| 5BO2   | 8i :            | 3.0                    | 0.2 M imidazole.malate, pH 7.0, 9% PEG4000 | 0.2 M imidazole.malate, pH 7.0, 15% PEG4000, 1 mM 8i | Streak seeded; **soaked crystal** for 4 h; 2 day old crystal | C2 | 94×78×103 Å |
|        |                 |                        |                     |                    | X-ray images available at: [link](http://dx.doi.org/10.17632/xgn5z8jmr7.1) | | |
|        |                 |                        |                     |                    | β = 111° | | |
| Not applicable | 8i :         | 3.0                    | 0.2 M imidazole.malate, pH 7.0, 11% PEG4000, 1 mM 8i | 0.2 M imidazole.malate, pH 7.0, 15% PEG4000, 1 mM 8i | Streak seeded; **protein co-crystallized with ligand**; 2 day old crystal | C2 | 95×78×103 Å |
|        |                 |                        |                     |                    | X-ray images available at: [link](http://dx.doi.org/10.17632/2zrfgv34nb.1) | | |
|        |                 |                        |                     |                    | β = 111° | | |
| 5BO3   | 8j :            | 3.0                    | 0.2 M imidazole.malate, pH 7.0, 11% PEG4000, | 0.2 M imidazole.malate, pH 7.0, 15% PEG4000, 1 mM 8j | Streak seeded; **soaked crystal** for 10 min; 2 day old crystal | C2 | 95×78×103 Å |
|        |                 |                        |                     |                    | | | |
|        |                 |                        |                     |                    | β = 111° | | |
| 5BNE   | 8k :            | 3.1                    | 0.2 M imidazole.malate, pH 7.0, 15% PEG4000, 1 mM 8k | No cryo used, because crystallization condition contained 15% PEG4000 | Streak seeded; **protein co-crystallized with ligand**; 2 day old crystal | P2$_1$ | 77×78×117 Å |
|        |                 |                        |                     |                    | | | |
Table 3
Space groups, unit cells and other information for previously published Mtb-AnPRT structures crystallized in imidazole-malate and PEG4000.

| PDB ID | Ref | Solvent content | Unit Cell | Space Group | Resolution (Å) | Chains | Notes | PDB DOI |
|--------|-----|-----------------|-----------|-------------|----------------|--------|-------|---------|
| 3QS8   | [2] | 46%             | 90°       | 78 81 111  | P2_1           | 2.00   | A,B,C,D Co-crystal | 10.2210/pdb3qs8/pdb |
| 3UU1   | [2] | 45%             | 90°       | 78 111 80  | P2_1           | 1.82   | A,B,C,D Co-crystal | 10.2210/pdb3uu1/pdb |
| 3R6C   | [2] | 44%             | 110°      | 94 78 100  | C2            | 1.83   | A,B   Co-crystal | 10.2210/pdb3r6c/pdb |
| 4ij1   | [5] | 45%             | 111 95    | 78 102    | C2            | 1.79   | A,B   Co-crystal | 10.2210/pdb4ij1/pdb |
| 4X58   | [6] | 50%             | 111 95    | 78 101    | C2            | 1.75   | A,B   Mutant   | 10.2210/pdb4x58/pdb |
| 4X59   | [6] | 50%             | 112 95    | 78 102    | C2            | 1.80   | A,B   Mutant   | 10.2210/pdb4x59/pdb |
| 4X5A   | [6] | 49%             | 112 94    | 78 102    | C2            | 1.93   | A,B   Mutant   | 10.2210/pdb4x5a/pdb |
| 4X5B   | [6] | 45%             | 111 94    | 78 100    | C2            | 2.47   | A,B   Mutant   | 10.2210/pdb4x5b/pdb |
| 4X5C   | [6] | 49%             | 111 94    | 78 101    | C2            | 2.33   | A,B   Mutant   | 10.2210/pdb4x5c/pdb |
| 4X5E   | [6] | 50%             | 110 95    | 79 101    | C2            | 1.77   | A,B   Mutant   | 10.2210/pdb4x5e/pdb |
| 4GIU   | [5] | 46%             | 90        | 111 81    | P2_2_2_2     | 1.67   | A,B   Co-crystal | 10.2210/pdb4giu/pdb |
| 4GKM   | [5] | 46%             | 90        | 111 81    | P2_2_2_2     | 1.67   | A,B   Co-crystal | 10.2210/pdb4gkm/pdb |
| 3QR9   | [2] | 57%             | 90        | 79 92     | P2_2_2_2_1   | 1.87   | A,B   Ligand-free | 10.2210/pdb3qr9/pdb |
| 4MOR   | [5] | 56%             | 90        | 79 92     | P2_2_2_2_1   | 1.96   | A,B   Co-crystal | 10.2210/pdb4mor/pdb |
| 4NSV   | [7] | 57%             | 90        | 80 93     | P2_2_2_2_1   | 1.90   | A,B   Soak     | 10.2210/pdb4nsv/pdb |
| 4N8Q   | [7] | 56%             | 90        | 80 91     | P2_2_2_2_1   | 2.08   | A,B   Soak     | 10.2210/pdb4n8q/pdb |
| 4N93   | [7] | 57%             | 90        | 80 92     | P2_2_2_2_1   | 2.03   | A,B   Soak     | 10.2210/pdb4n93/pdb |
| 4OWM   | [7] | 60%             | 90        | 79 92     | P2_2_2_2_1   | 1.99   | A,B   Soak     | 10.2210/pdb4owm/pdb |
| 4OWN   | [7] | 60%             | 90        | 80 92     | P2_2_2_2_1   | 2.11   | A,B   Soak     | 10.2210/pdb4own/pdb |
| 4OWO   | [7] | 60%             | 90        | 79 92     | P2_2_2_2_1   | 1.99   | A,B   Soak     | 10.2210/pdb4owo/pdb |
| 4OWQ   | [7] | 61%             | 90        | 79 92     | P2_2_2_2_1   | 1.89   | A,B   Soak     | 10.2210/pdb4owq/pdb |
| 4OWS   | [7] | 60%             | 90        | 80 92     | P2_2_2_2_1   | 2.43   | A,B   Soak     | 10.2210/pdb4ows/pdb |
| 4OWU   | [7] | 60%             | 90        | 79 92     | P2_2_2_2_1   | 1.89   | A,B   Soak     | 10.2210/pdb4owu/pdb |
| 4OWV   | [7] | 60%             | 90        | 80 92     | P2_2_2_2_1   | 1.90   | A,B   Soak     | 10.2210/pdb4owv/pdb |
| 4X5D   | [6] | 60%             | 90        | 80 92     | P2_2_2_2_1   | 2.30   | A,B   Mutant   | 10.2210/pdb4x5d/pdb |
asymmetric unit [2]. The two subunits of the dimer are related by a non-crystallographic two-fold symmetry axis (NCS).

1.2. Data for protein complexes with inhibitors

The three protein:inhibitor complexes (PDB IDs: 5BO2, 5BO3, 5BNE) were solved in the absence of metals and substrate. For these structures, the solvent content has decreased by ~ 10%, the unit cell has changed (i.e. dimension(s) decreased by 10–20 Å), and the space group has changed to P2₁ or C2, compared to the ligand-free wild-type structure.

In structures of AnPRT from other prokaryote species, domain movement is observed within subunits due to substrate binding and results in compression of the homodimer by 10 Å (e.g. Dmax (maximum distance) changes from 110 to 100 Å [8]). However, superposition of the subunits in the new Mtb-AnPRT structures onto the subunits of the ligand-free structure indicates there are no large changes (Table 4; [9]). Additionally, the longest dimension of the Mtb-AnPRT dimer is relatively unchanged between the ligand-free protein structure and the protein:ligand complex structures (Table 4; [10]). Thus, the changes in space group are not driven by domain movements within each subunit.

The P2₁ structure (PDB ID: 5BNE) contains an inhibitor annotated as 8k, and is the third structure of Mtb-AnPRT with this space group determined for protein crystallized in the imidazole-malate condition. The increased components in this structure’s asymmetric unit (chains A-D, vs. chains A and B; Fig. 1A) means that the lower symmetry described by P2₁ can generate equivalent protein content in a similarly-sized unit cell as is observed with structures defined by space groups P2₁2₁2₁ or P2₁2₁2. The β angle of 91° could be taken to suggest that the space group should be orthorhombic (e.g. P2₁2₁2₁ or P2₁2₁2₁). Both POINTLESS [11] and ZANUDA [12] indicated that P2₁ was the correct space group for this dataset, however.

(A) Superposition of the dimer (cartoon) from a Mtb-AnPRT:inhibitor structure defined by space group P2₁, PDB ID: 5BNE (chain A, B, C and D in green, cyan, pink and yellow, respectively), onto that of the ligand-free Mtb-AnPRT structure (PDB ID: 3QR9 [2]; P2₁2₁2₁; chain A and B in dark and light grey, respectively). The figure includes adjacent dimers (ribbons) in equivalent crystal layers (c-b plane in 3QR9 [2] and c-a plane in 5BNE). In (B) the superposition is re-colored with the Mtb-AnPRT: inhibitor structure in yellow and the ligand-free Mtb-AnPRT structure in dark grey. Arrows highlight the reorientation of dimers relative to each other. (C) Superposition of the dimer (cartoon) from a Mtb-AnPRT:inhibitor structure defined by space group C2, PDB ID: 5BO2 (marine blue) onto that of the ligand-free Mtb-AnPRT structure (PDB ID: 3QR9 [2]; P2₁2₁2₁; dark grey). In (D) superpositions in panels B-C are combined.

Structural superposition of the dimers from Mtb-AnPRT:inhibitor structures (PDB ID: 5BNE and 5BO2) onto the dimer present in the P2₁2₁2₁ ligand-free Mtb-AnPRT structure (PDB ID: 3QR9 [2]) revealed a reorientation of the protein dimers relative to each other (Fig. 1B and C). The combination

| Table 4 |
| Comparison Mtb-AnPRT subunits found in the 3 new structures to ligand-free structure. |
|-------------------------|-------------------------|-------------------------|
|                        | RMSD⁺ to chain A-3QR9 (Å) | RMSD⁺ to chain B-3QR9 (Å) | Longest dimension of dimer (Å) |
| 3qr9.pdb;A             | –                       | 0.89                    | 109                       |
| 3qr9.pdb;B             | 0.89                    | –                       | 110                       |
| 5bo2.pdb;A             | 0.67                    | 0.68                    | 110                       |
| 5bo2.pdb;B             | 0.66                    | 0.73                    |                           |
| 5bo3.pdb;A             | 0.63                    | 0.53                    | 110                       |
| 5bo3.pdb;B             | 0.62                    | 0.73                    |                           |
| 5bne.pdb;A             | 0.57                    | 0.53                    | 109                       |
| 5bne.pdb;B             | 0.46                    | 0.74                    |                           |
| 5bne.pdb;C             | 0.46                    | 0.92                    | 109                       |
| 5bne.pdb;D             | 0.55                    | 0.60                    |                           |

⁺ Root mean standard difference (RMSD) between the Cα atoms
of these superpositions (Fig. 1D) indicates that the lattice in the $P2_1$ structure corresponds to an intermediate position between the lattice observed for $P2_1\overline{2}1_2$ and $C2$ structures. We propose the subunits that are related by crystallographic symmetry elements in the $P2_1\overline{2}1_2$ structures are related by pseudosymmetry elements in the $P2_1$ structure. Pseudosymmetry occurs where a non-crystallographic symmetry element within the asymmetric unit is close to a crystallographic symmetry operators [13]. Thus, the $P2_1$ space group has been correctly assigned, even though the unit cell has a $\beta$ of approximately 90°.

The generation of the protein: inhibitor structures, involved experiments, with all three inhibitors, using both co-crystallization and soaking-in methods. The structures deposited on the PDB correspond to those where the clearest density was observed for the inhibitor (i.e. modelled with full occupancy; Fig. 2). In Table 5 there are data statistics corresponding to Mtb-AnPRT co-crystallized with inhibitor 8i. In Table 6 are data statistics corresponding to inhibitor 8i soaked into a wild-type Mtb-APRT crystal. In both cases, with no manual intervention, the datasets processed in XDS [14] and AIMLESS [11] as space group C2. Thus, in this study, there no correlation was found between space group type and the method by which the ligand was introduced (i.e. soaking vs. co-crystallization).
2. Experimental design, materials and methods

2.1. Materials

Unless otherwise stated, all chemicals were obtained from Sigma-Aldrich, Scharlau, or Pure Science. The purification of \textit{Mtb}-AnPRT, as well as the synthesis and biochemical characterization of its inhibitors annotated as \textit{8i}, \textit{8j} and \textit{8k} (Table 2), are outlined in the article entitled “\textit{Anthranilate phosphoribosyltransferase: Binding determinants for 5’-phospho-alpha-D-ribose-1’-pyrophosphate (PRPP) and the implications for inhibitor design}” [1].

\textbf{Fig. 2.} Omit and fitted map for inhibitors bound in \textit{Mtb}-AnPRT structures. The $F_o$-$F_c$ map calculated (green, contoured at 3 $\sigma$) prior to the addition of ligands to the model for A) 8k, B) 8j and C) 8i (PDB entries 5BNE, 5BO3 and 5BO2, respectively). The 2$F_o$-$F_c$ map calculated (blue, contoured at 1 $\sigma$) after final refinement, with model including the ligands for D) 8k (black), E) 8j (green) and F) 8i (pink).
Table 6
Data and refinement statistics for AnPRT complexes with inhibitors.

| Data collection | AnPRT complexed with | 8i | 8j | 8k |
|-----------------|----------------------|----|----|----|
| **Space group** | C2                   | C2 | C2 | P2_1 |
| **Cell dimensions** |                         |    |    |     |
| a, b, c (Å) | 94.6, 78.1, 102.8 | 95.0, 78.1, 102.6 | 77.3, 78.4, 117.2 |
| β (deg) | 111.0 | 111.1 | 90.7 |
| **Unique reflections** |                         |    |    |     |
| 47170 (3415) | 68993 (3669) | 75079 (4387) |
| **Resolution range (Å)** | 47-2.00 (2.05-2.00) | 48-1.75 (1.78-1.75) | 47-2.15 (2.19-2.15) |
| Rmerge | 0.138 (1.237) | 0.121 (1.762) | 0.111 (0.711) |
| R_p.i.m. | 0.054 (0.488) | 0.046 (0.688) | 0.073 (0.477) |
| **CC1/2** | 8.5 (1.5) | 13.3 (1.2) | 6.9 (1.5) |
| Completeness (%) | 99.8 (97.7) | 97.8 (93.7) | 98.4 (77.3) |
| **Redundancy** | 3.4 (3.3) | 7.8 (7.4) | 3.0 (2.9) |
| **Wilson B factor** | 15.1 | 16.3 | 21.4 |

Refinement
Atoms, B factor (Å^2)

| Protein | Solvent | Ligands | R_work/R_free (%/%) | Ramachandran outliers (%) | R.m.s.d. of bond lengths (Å) | R.m.s.d. of bond angles (°) |
|---------|---------|---------|---------------------|---------------------------|----------------------------|----------------------------|
| 4788, 25.8 | 352, 29.7 | 79, 33.2 | 0.192/0.232 (0.276/0.324) | 0.31 (0.16) | 0.003 | 0.074 |

a Outer resolution shell is shown in parentheses.
b The average atomic temperature factor.
c R_work=(|F_{o}| - |F_{c}|)/|F_{o}| and R_free=Σ(T(|F_{o}| - |F_{c}|))/Σ|F_{o}|, where T is a test dataset of 5% of the total reflections randomly chosen and set aside before refinement.
d RMSD from ideal geometry values from Engh and Huber (1991) [15].

Table 5
Statistics for dataset of Mtb-AnPRT co-crystallized with inhibitor 8i.

| Data collection | AnPRT complexed with | 8i |
|-----------------|----------------------|----|
| **Space group** | C2                   |    |
| **Cell dimensions** |                         |    |
| a, b, c (Å) | 94.6, 78.1, 102.8 |
| β (deg) | 111.0 |
| **Unique reflections** |                         |    |
| 47170 (3415) | 68993 (3669) |
| **Resolution range (Å)** | 47-2.00 (2.05-2.00) |
| Rmerge | 0.138 (1.237) |
| R_p.i.m. | 0.054 (0.488) |
| **CC1/2** | 8.5 (1.5) |
| Completeness (%) | 99.8 (97.7) |
| **Redundancy** | 3.4 (3.3) |
| **Wilson B factor** | 15.1 |

b The average atomic temperature factor.
c R_work=(|F_{o}| - |F_{c}|)/|F_{o}| and R_free=Σ(T(|F_{o}| - |F_{c}|))/Σ|F_{o}|, where T is a test dataset of 5% of the total reflections randomly chosen and set aside before refinement.
d RMSD from ideal geometry values from Engh and Huber [15].

a Outer resolution shell is shown in parentheses.
2.2. Crystallization

Crystals of Mtb-AnPRT were obtained in hanging drops of 1–2 μL protein solution (3.0–3.1 mg mL\(^{-1}\) in final storage buffer) with the equivalent amount of reservoir solution in a fine screen of 0.2 M imidazole-malate pH 7.0–8.5, 5–15% polyethylene glycol (PEG) 4000, as previously reported [2]. Complexes were prepared either by co-crystallization or by soaking with ligands (details in Table 2). The crystallization drops were seeded from previously formed crystals of Mtb-AnPRT, by streak seeding using a cat whisker. Data collection occurred within a few days after crystallization. In preparation for data collection, crystals were typically soaked in a reservoir solution containing cryoprotectant 15% PEG4000 and appropriate ligands (details in Table 2), before being flash-cooled in liquid nitrogen.

2.3. Data collection, structure solution and refinement

Data were collected at the Australian Synchrotron, Beamlines MX1 and MX2 at 110 K. The crystals of the Mtb-AnPRT complexes diffracted to a maximum resolution that varied between 1.75 and 2.15 Å. X-ray diffraction spots were indexed and integrated with XDS [14] and scaled with AIMLESS [11]. The high resolution cut-off was determined based on a correlation coefficient (CC\(_{1/2}\)) [16] exceeding 0.5, with mean I/σ between 1 and 1.5, and a R\(_{p.i.m.}\) of 0.7 or less, as calculated by AIMLESS [11]. R\(_{p.i.m.}\) is defined as \(\sum_{hkl} \frac{1}{(n-1)} \times R_{merge}\) with R\(_{merge}\) defined as \(\sum_{hkl} |I(hkl) - \langle I(hkl) \rangle| / \sum_{hkl} \langle I(hkl) \rangle\), where \(\langle I(hkl) \rangle\) is the mean of symmetry-equivalent reflections of I(hkl) [17]. Data and refinement statistics are given in Tables 5 and 6.

Mtb-AnPRT (chain A of 3QR9 [2]), without solvent or ligands, and with loops I and II removed, was used as the search model for structure determination by molecular replacement using Phaser [18]. Refinement and model building was performed with COOT [19], Refmac5 [20], and PHENIX [21]. After positioning waters, omit maps were examined (Fig. 2) and ligands placed, with subsequent refinement including restraints for the ligands generated by phenix.elbow [21]. Restraints on protein bond lengths and angles were based on the ideal values of Engh and Huber [15] and model quality was assessed using MolProbity [22]. Figures illustrating structural details were prepared using PyMOL.

The Fo-Fc map calculated (green, contoured at 3 σ) prior to the addition of ligands to the model for A) 8k, B) 8j and C) 8i (PDB entries 5BNE, 5BO3 and 5BO2, respectively). The 2Fo-Fc map calculated (blue, contoured at 1 σ) after final refinement, with model including the ligands for D) 8k (black), E) 8j (green) and F) 8i (pink).

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Transparency document. Supporting information

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2017.10.051.
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