Feb 13, 2017 – 08:56 pm GMT

PDB ID : 1PMD
Title : PENICILLIN-BINDING PROTEIN 2X (PBP-2X)
Authors : Pares, S.; Mouz, N.; Dideberg, O.
Deposited on : 1996-02-05
Resolution : 3.50 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the symbol.

The following versions of software and data (see references) were used in the production of this report:

- MolProbity : 4.02b-467
- Xtriage (Phenix) : NOT EXECUTED
- EDS : NOT EXECUTED
- Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
- Ideal geometry (proteins) : Engh & Huber (2001)
- Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
- Validation Pipeline (wwPDB-VP) : recalc28949
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
\textit{X-RAY DIFFRACTION}

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in
the following graphic. The table shows the number of entries on which the scores are based.

<table>
<thead>
<tr>
<th>Metric</th>
<th>Percentile Ranks</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clashscore</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

![Percentile graphic]

Note EDS was not executed.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Length</th>
<th>Quality of chain</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>675</td>
<td>100%</td>
</tr>
</tbody>
</table>
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 675 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PEPTIDOGLYCAN SYNTHESIS MULTIFUNCTIONAL ENZYME.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>ZeroOcc</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>675</td>
<td>Total C</td>
<td>675</td>
<td>0</td>
<td>675</td>
</tr>
</tbody>
</table>


3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: PEPTIDOGLYCAN SYNTHESIS MULTIFUNCTIONAL ENZYME

Chain A:

There are no outlier residues recorded for this chain.
4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Space group</td>
<td>P 6 1 2 2</td>
<td>Depositor</td>
</tr>
<tr>
<td>Cell constants</td>
<td>161.25Å 161.25Å 170.80Å</td>
<td>Depositor</td>
</tr>
<tr>
<td>a, b, c, α, β, γ</td>
<td>90.00° 90.00° 120.00°</td>
<td>Depositor</td>
</tr>
<tr>
<td>Resolution (Å)</td>
<td>6.00 – 3.50</td>
<td>Depositor</td>
</tr>
<tr>
<td>% Data completeness</td>
<td>78.3 (6.00-3.50)</td>
<td>Depositor</td>
</tr>
<tr>
<td>(in resolution range)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>R&lt;sub&gt;merge&lt;/sub&gt;</td>
<td>(Not available)</td>
<td>Depositor</td>
</tr>
<tr>
<td>R&lt;sub&gt;sym&lt;/sub&gt;</td>
<td>(Not available)</td>
<td>Depositor</td>
</tr>
<tr>
<td>Refinement program</td>
<td>X-PLOR</td>
<td>Depositor</td>
</tr>
<tr>
<td>R, R&lt;sub&gt;free&lt;/sub&gt;</td>
<td>0.225 , 0.211</td>
<td>Depositor</td>
</tr>
<tr>
<td>Estimated twinning fraction</td>
<td>No twinning to report.</td>
<td>Xtriage</td>
</tr>
<tr>
<td>Total number of atoms</td>
<td>675</td>
<td>wwPDB-VP</td>
</tr>
<tr>
<td>Average B, all atoms (Å²)</td>
<td>20.0</td>
<td>wwPDB-VP</td>
</tr>
</tbody>
</table>
5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Non-H</th>
<th>H(model)</th>
<th>H(added)</th>
<th>Clashes</th>
<th>Symm-Clashes</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>675</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>All</td>
<td>All</td>
<td>675</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.
5.3.2 Protein sidechains

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.
6  Fit of model and data

6.1  Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2  Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3  Carbohydrates

EDS was not executed - this section is therefore empty.

6.4  Ligands

EDS was not executed - this section is therefore empty.

6.5  Other polymers

EDS was not executed - this section is therefore empty.