



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5ET9
Title : Racemic crystal structures of Pribnow box consensus promoter sequence (P21/n)
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Deposited on : 2015-11-17
Resolution : 1.83 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : **FAILED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027790

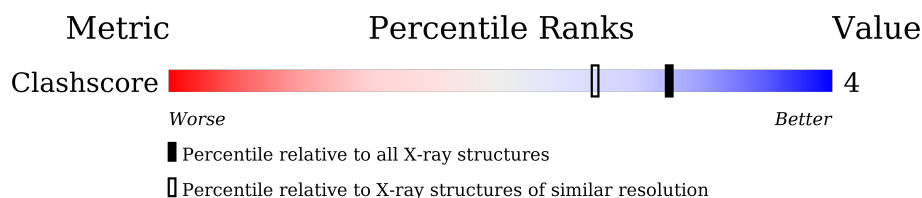
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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.



| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|------------|-----------------------------|---|
| Clashscore | 102246 | 2862 (1.86-1.82) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS failed to run properly.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | A | 12 | 83% 17% |
| 2 | B | 12 | 83% 17% |

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 501 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 DNA chain called Pribnow box consensus sequence- template strand.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|---------|-------|
| 1 | A | 12 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 243 | 117 | 45 | 70 | 11 | | | |

- Molecule 2 is a DNA chain called Pribnow box non-template strand.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|---------|-------|
| 2 | B | 12 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 243 | 117 | 45 | 70 | 11 | | | |

- Molecule 3 is BARIUM ION (three-letter code: BA) (formula: Ba).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 3 | B | 1 | Total | Ba | 0 | 0 |
| | | | 1 | 1 | | |
| 3 | A | 1 | Total | Ba | 0 | 0 |
| | | | 1 | 1 | | |

- Molecule 4 is water.


| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 4 | A | 7 | Total | O | 0 | 0 |
| | | | 7 | 7 | | |
| 4 | B | 6 | Total | O | 0 | 0 |
| | | | 6 | 6 | | |

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 errors 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 ($\text{RSRZ} > 2$). 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 failed to run properly.

- Molecule 1: Pribnow box consensus sequence- template strand

Chain A:  83% 17%



- Molecule 2: Pribnow box non-template strand

Chain B:  83% 17%



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

| Property | Value | Source |
|--|--|-----------|
| Space group | P 1 21/n 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 28.79Å 68.29Å 34.21Å 90.00° 90.05° 90.00° | Depositor |
| Resolution (Å) | 34.14 – 1.83 | Depositor |
| % Data completeness (in resolution range) | 92.1 (34.14-1.83) | Depositor |
| R_{merge} | 0.02 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 1.91 (at 1.83Å) | Xtriage |
| Refinement program | PHENIX (phenix.refine: 1.9_1692) | Depositor |
| R, R_{free} | 0.298 , 0.329 | Depositor |
| Wilson B-factor (Å ²) | 49.7 | Xtriage |
| Anisotropy | -2.419 | Xtriage |
| L-test for twinning ² | $\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available) | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| Total number of atoms | 501 | wwPDB-VP |
| Average B, all atoms (Å ²) | 61.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *None*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BA

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).

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------|-------------|-------------|
| | | RMSZ | $\# Z > 5$ | RMSZ | $\# Z > 5$ |
| 1 | A | 1.01 | 0/272 | 1.06 | 0/418 |
| 2 | B | 0.96 | 0/272 | 1.08 | 0/418 |
| All | All | 0.99 | 0/544 | 1.07 | 0/836 |

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 [i](#)

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.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 243 | 0 | 137 | 1 | 0 |
| 2 | B | 243 | 0 | 137 | 2 | 0 |
| 3 | A | 1 | 0 | 0 | 0 | 0 |
| 3 | B | 1 | 0 | 0 | 0 | 0 |
| 4 | A | 7 | 0 | 0 | 0 | 0 |
| 4 | B | 6 | 0 | 0 | 0 | 0 |
| All | All | 501 | 0 | 274 | 3 | 0 |

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 4.

All (3) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|-------------|--------------------------|-------------------|
| 2:B:8:DT:H2'' | 2:B:9:DA:C8 | 2.44 | 0.52 |
| 2:B:8:DT:H2'' | 2:B:9:DA:H8 | 1.80 | 0.46 |
| 1:A:4:DT:H2'' | 1:A:5:DA:C8 | 2.51 | 0.44 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.