



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 06:39 AM EDT

PDB ID : 1KJX
Title : IMP Complex of E. Coli Adenylosuccinate Synthetase
Authors : Hou, Z.; Wang, W.; Fromm, H.J.; Honzatko, R.B.
Deposited on : 2001-12-05
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 1.20.1
EDS : 2.36.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

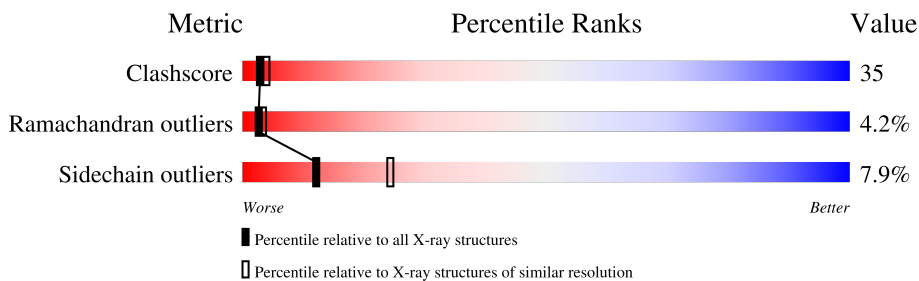
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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 | 141614 | 3518 (2.60-2.60) |
| Ramachandran outliers | 138981 | 3455 (2.60-2.60) |
| Sidechain outliers | 138945 | 3455 (2.60-2.60) |

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | A | 432 | |

2 Entry composition [i](#)

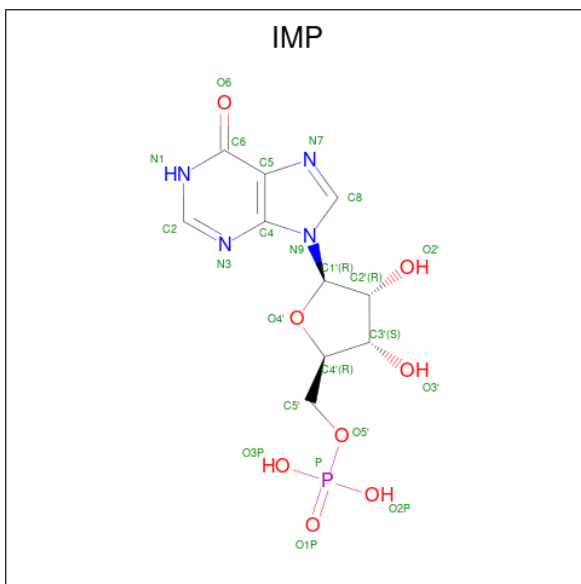
There are 3 unique types of molecules in this entry. The entry contains 3656 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Adenylosuccinate Synthetase.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 1 | A | 431 | 3321 | 2092 | 576 | 640 | 13 | 0 | 0 | 0 |

- Molecule 2 is INOSINIC ACID (three-letter code: IMP) (formula: C₁₀H₁₃N₄O₈P).



| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|---------|
| | | | Total | C | N | O | P | | |
| 2 | A | 1 | 23 | 10 | 4 | 8 | 1 | 0 | 0 |

- Molecule 3 is water.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------------|---------|---------|
| 3 | A | 312 | Total 312 O 312 | 0 | 0 |

4 Data and refinement statistics i

| Property | Value | Source |
|---|---|------------------|
| Space group | P 32 2 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 80.60Å 80.60Å 158.65Å 90.00° 90.00° 120.00° | Depositor |
| Resolution (Å) | 8.00 – 2.60 42.15 – 2.46 | Depositor EDS |
| % Data completeness (in resolution range) | (Not available) (8.00-2.60) 72.8 (42.15-2.46) | Depositor EDS |
| R_{merge} | (Not available) | Depositor |
| R_{sym} | 0.11 | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 0.71 (at 2.45Å) | Xtrriage |
| Refinement program | X-PLOR 3.1 | Depositor |
| R, R_{free} | 0.196 , 0.283 0.242 , (Not available) | Depositor DCC |
| R_{free} test set | No test flags present. | wwPDB-VP |
| Wilson B-factor (Å ²) | 24.8 | Xtrriage |
| Anisotropy | 0.866 | Xtrriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.38 , 88.3 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$ | Xtrriage |
| Estimated twinning fraction | 0.043 for -h,-k,l | Xtrriage |
| F_o, F_c correlation | 0.88 | EDS |
| Total number of atoms | 3656 | wwPDB-VP |
| Average B, all atoms (Å ²) | 28.0 | wwPDB-VP |

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.96% of the height of the origin peak. No significant pseudotranslation is detected.*

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: IMP

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 | 0.54 | 2/3379 (0.1%) | 0.79 | 0/4577 |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|--------|-------------|----------|
| 1 | A | 43 | LEU | C-N | -11.12 | 1.08 | 1.34 |
| 1 | A | 37 | HIS | C-N | 6.89 | 1.50 | 1.34 |

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 | 3321 | 0 | 3325 | 235 | 0 |
| 2 | A | 23 | 0 | 11 | 3 | 0 |
| 3 | A | 312 | 0 | 0 | 38 | 0 |
| All | All | 3656 | 0 | 3336 | 235 | 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 35.

The worst 5 of 235 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) |
|------------------|-----------------|--------------------------|-------------------|
| 1:A:20:VAL:HG21 | 1:A:221:GLU:HG3 | 1.48 | 0.96 |
| 1:A:104:PRO:HA | 1:A:147:ARG:HG2 | 1.56 | 0.86 |
| 1:A:100:SER:HB3 | 1:A:103:CYS:SG | 2.19 | 0.83 |
| 1:A:128:THR:HG22 | 1:A:130:GLY:H | 1.44 | 0.82 |
| 1:A:142:ALA:HB1 | 1:A:144:ARG:NH1 | 1.95 | 0.81 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|-----|-------|---------------|-----------|----------|----------|-------------------|
| 1 | A | 429/432 (99%) | 345 (80%) | 66 (15%) | 18 (4%) | 3 3 |

5 of 18 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 10 | GLN |
| 1 | A | 46 | ASN |
| 1 | A | 153 | ASP |
| 1 | A | 361 | ALA |
| 1 | A | 242 | ASN |

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|-----|-------|----------------|-----------|----------|-------------|
| 1 | A | 353/354 (100%) | 325 (92%) | 28 (8%) | 12 24 |

5 of 28 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 204 | VAL |
| 1 | A | 382 | THR |
| 1 | A | 239 | THR |
| 1 | A | 342 | LYS |
| 1 | A | 226 | THR |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 34 | GLN |
| 1 | A | 53 | HIS |
| 1 | A | 171 | GLN |
| 1 | A | 184 | GLN |
| 1 | A | 232 | HIS |

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 2 | IMP | A | 440 | - | 21,25,25 | 2.02 | 6 (28%) | 22,38,38 | 1.56 | 6 (27%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|-----------|---------|
| 2 | IMP | A | 440 | - | - | 0/6/26/26 | 0/3/3/3 |

The worst 5 of 6 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 2 | A | 440 | IMP | P-O3P | 4.27 | 1.70 | 1.54 |
| 2 | A | 440 | IMP | C1'-N9 | -3.90 | 1.39 | 1.50 |
| 2 | A | 440 | IMP | C8-N7 | -3.68 | 1.29 | 1.34 |
| 2 | A | 440 | IMP | C2-N3 | 3.18 | 1.35 | 1.29 |
| 2 | A | 440 | IMP | C5-C6 | -2.70 | 1.42 | 1.47 |

The worst 5 of 6 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|-------|-------------|----------|
| 2 | A | 440 | IMP | O2P-P-O5' | 2.84 | 114.07 | 106.67 |
| 2 | A | 440 | IMP | O3'-C3'-C2' | -2.63 | 103.40 | 111.82 |
| 2 | A | 440 | IMP | O5'-P-O1P | 2.59 | 113.44 | 106.44 |
| 2 | A | 440 | IMP | O4'-C4'-C5' | 2.33 | 116.81 | 109.33 |
| 2 | A | 440 | IMP | C4'-O4'-C1' | -2.25 | 107.86 | 109.92 |

There are no chirality outliers.

There are no torsion outliers.

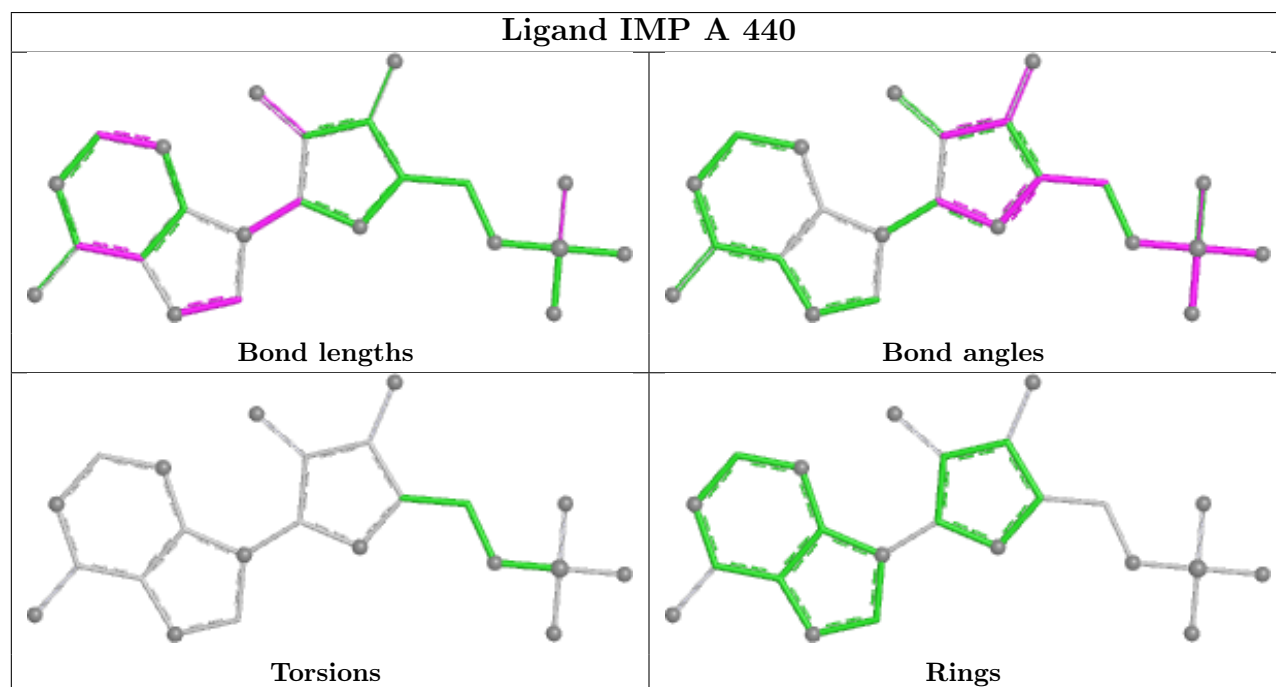
There are no ring outliers.

1 monomer is involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 2 | A | 440 | IMP | 3 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 1 | A | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | A | 43:LEU | C | 44:VAL | N | 1.08 |

6 Fit of model and data

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

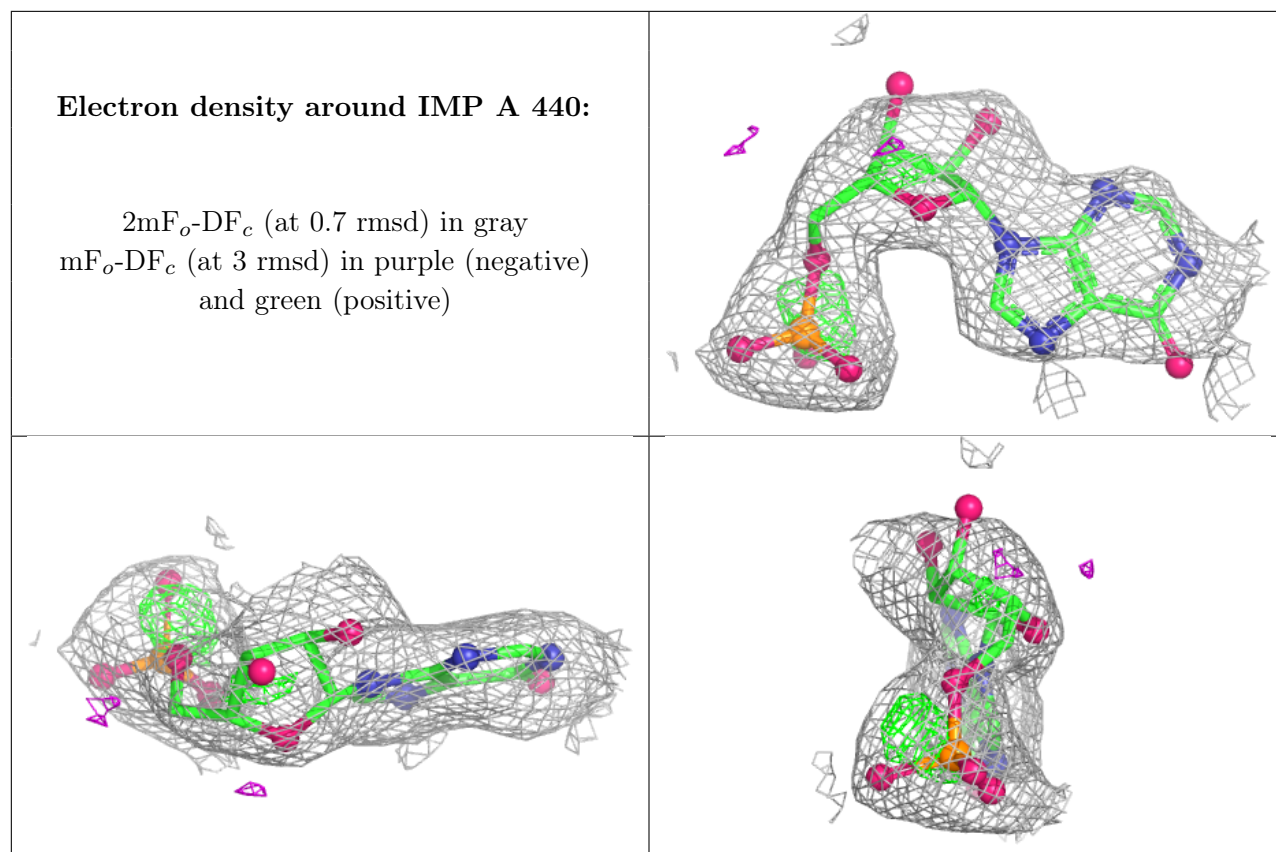
6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.