# wwPDB X-ray Structure Validation Summary Report  (i)

Sep 25, 2023 – 12:23 AM EDT

| | | |
|---|---|---|
| PDB ID | : | 5W94 |
| Title | : | Crystal structure of Scc4 in complex with Scc2n and Ctf19n |
| Authors | : | Hinshaw, S.M.; Harrison, S.C. |
| Deposited on | : | 2017-06-22 |
| Resolution | : | 3.19 Å(reported) |

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

| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.35.1 |
| 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) | : | 2.35.1 |

# 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 3.19 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.
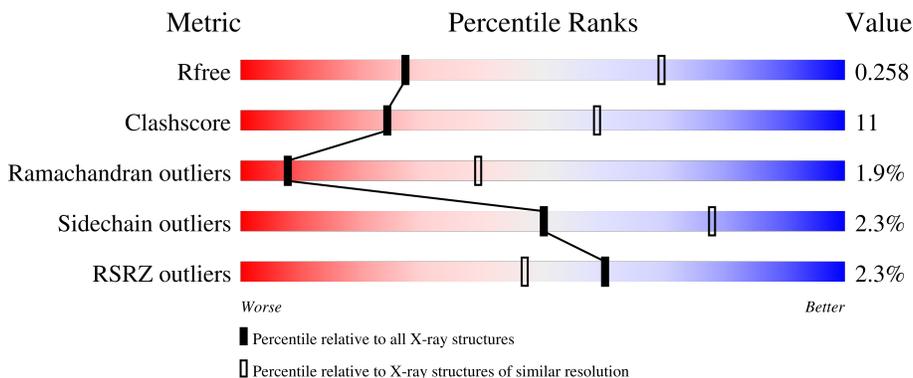


| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|---|---|---|
| $R_{free}$ | 130704 | 1133 (3.20-3.20) |
| Clashscore | 141614 | 1253 (3.20-3.20) |
| Ramachandran outliers | 138981 | 1234 (3.20-3.20) |
| Sidechain outliers | 138945 | 1233 (3.20-3.20) |
| RSRZ outliers | 127900 | 1095 (3.20-3.20) |

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 <=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.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 624 | %  72%  25%  ·· |
| 1 | C | 624 | %  76%  19%  ·· |
| 2 | B | 184 | 3%  36%  23%  ··  38% |
| 2 | D | 184 | 8%  44%  15%  ·  40% |
| 3 | E | 6 | 33%  17%  50%  33% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 3 | H | 6 | 17% 50% 33% |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|-----|-----------|----------|---------|------------------|
| 3 | TPO | E | 4 | - | - | - | X |
| 3 | SEP | E | 5 | - | - | - | X |

## 2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 11738 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 MAU2 chromatid cohesion factor homolog.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|---------|---------|-------|
| 1 | A | 617 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 5008 | 3216 | 840 | 915 | 37 | | | |
| 1 | C | 605 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 4928 | 3168 | 826 | 897 | 37 | | | |

- Molecule 2 is a protein called Sister chromatid cohesion protein 2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|---------|---------|-------|
| 2 | B | 114 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 874 | 553 | 150 | 170 | 1 | | | |
| 2 | D | 110 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 848 | 541 | 144 | 162 | 1 | | | |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|-------------|
| B | -2 | SER | - | expression tag | UNP Q04002 |
| B | -1 | ASN | - | expression tag | UNP Q04002 |
| B | 0 | ALA | - | expression tag | UNP Q04002 |
| D | -2 | SER | - | expression tag | UNP Q04002 |
| D | -1 | ASN | - | expression tag | UNP Q04002 |
| D | 0 | ALA | - | expression tag | UNP Q04002 |

- Molecule 3 is a protein called Ctf19n.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|---------|---------|-------|
| 3 | E | 4 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 40 | 20 | 4 | 14 | 2 | | | |
| 3 | H | 4 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 40 | 20 | 4 | 14 | 2 | | | |

# 3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

• Molecule 1: MAU2 chromatid cohesion factor homolog



• Molecule 1: MAU2 chromatid cohesion factor homolog

R601 V605 A614 L615 V616 K617 T620 S621 VAL LYS GLN

• Molecule 2: Sister chromatid cohesion protein 2

Chain B:

3%

36%          23%          ••          38%

SER ASN ALA MET S2 Y3 P4 D7 K8 E16 D20 L21 P22 L23 S24 V27 G31 L32 L35 V36 N37 A38 P39 K48 T49 I50 A54 D55 D56 D59 V60 N61 I62 N63 V64 L65 G66 T67 ALA ASN SER THR THR SER SER ILE LYS ASN GLU ALA E80

K81 E82 K87 R88 T93 S98 VAL ASP TYR VAL PRO THR N105 F106 L110 S111 P112 L113 A114 Q115 S116 V117 H121 L124 S127 I128 N129 I130 E131 K132 K133 SER GLU ILE VAL SER ARG PRO GLU ALA LYS HIS LYS LEU GLU SER VAL THR SER ASN ALA GLY ASN

LEU SER PHE ASN ASP ASN SER ASN SER ASN LYS LYS THR LYS THR SER THR GLY VAL THR MET THR GLN ALA ASN LEU ALA

• Molecule 2: Sister chromatid cohesion protein 2

Chain D:

8%

44%          15%          •          40%

SER ASN ALA MET SER Y3 P4 D7 K8 N9 I10 P11 G12 R13 E16 L21 P22 L23 S24 Y25 D30 G31 L35 V36 N37 L44 K48 D55 V60 N61 I62 N63 V64 LEU GLY THR ALA ASN SER THR THR SER SER ILE LYS ASN GLU ALA GLU LYS GLU

R83 R88 F92 A96 ASN SER VAL ASP Y101 T104 N105 F106 I110 L118 L124 N125 I128 N129 I130 E131 S134 GLU ILE VAL SER ARG PRO GLU ALA LYS HIS LYS LEU GLU SER VAL THR SER ASN ALA GLY ASN LEU SER PHE ASN ASP ASN SER SER ASN

LYS LYS THR LYS THR SER THR GLY VAL THR MET THR GLN ALA ASN LEU ALA

• Molecule 3: Ctf19n

Chain E:

33%

17%          50%          33%

MET ASP F3 T4 S5 D6

• Molecule 3: Ctf19n

Chain H:

17%          50%          33%

MET ASP F3 T4 S5 D6

# 4 Data and refinement statistics ⓘ

| Property | Value | Source |
|---|---|---|
| Space group | P 62 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 172.97Å    172.97Å    145.09Å<br>90.00°      90.00°      120.00° | Depositor |
| Resolution (Å) | 39.94   –   3.19<br>39.94   –   3.19 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 99.1 (39.94-3.19)<br>99.1 (39.94-3.19) | Depositor<br>EDS |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | 0.06 | Depositor |
| $< I/\sigma(I) >$ [1] | 1.36 (at 3.18Å) | Xtriage |
| Refinement program | PHENIX (1.11.1_2575: ???) | Depositor |
| R, $R_{free}$ | 0.209   ,   0.258<br>0.209   ,   0.258 | Depositor<br>DCC |
| $R_{free}$ test set | 1996 reflections (4.91%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 112.6 | Xtriage |
| Anisotropy | 0.384 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.30 , 66.6 | EDS |
| L-test for twinning[2] | $< |L| > = 0.48, < L^2 > = 0.31$ | Xtriage |
| Estimated twinning fraction | 0.037 for h,-h-k,-l | Xtriage |
| $F_o$,$F_c$ correlation | 0.95 | EDS |
| Total number of atoms | 11738 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 118.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.49% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

# 5 Model quality ⓘ

## 5.1 Standard geometry ⓘ

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

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 | 0.60 | 0/5107 | 0.79 | 4/6888 (0.1%) |
| 1 | C | 0.47 | 0/5025 | 0.70 | 2/6775 (0.0%) |
| 2 | B | 0.61 | 0/887 | 0.92 | 0/1198 |
| 2 | D | 0.46 | 0/863 | 0.71 | 0/1169 |
| 3 | E | 0.49 | 0/18 | 0.33 | 0/21 |
| 3 | H | 0.48 | 0/18 | 0.65 | 0/21 |
| All | All | 0.54 | 0/11918 | 0.76 | 6/16072 (0.0%) |

There are no bond length outliers.

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

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|-----|------|-------|---|----------|--------|
| 1 | A | 4 | LEU | CA-CB-CG | 5.54 | 128.05 | 115.30 |
| 1 | C | 390 | LEU | CA-CB-CG | 5.48 | 127.91 | 115.30 |
| 1 | A | 305 | LEU | CB-CG-CD1 | -5.38 | 101.85 | 111.00 |
| 1 | A | 123 | LEU | CA-CB-CG | 5.29 | 127.47 | 115.30 |
| 1 | C | 305 | LEU | CB-CG-CD1 | -5.18 | 102.19 | 111.00 |

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.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 5008 | 0 | 5059 | 138 | 1 |
| 1 | C | 4928 | 0 | 4986 | 89 | 0 |
| 2 | B | 874 | 0 | 885 | 52 | 1 |
| 2 | D | 848 | 0 | 864 | 22 | 1 |
| 3 | E | 40 | 0 | 21 | 2 | 0 |
| 3 | H | 40 | 0 | 22 | 0 | 0 |
| All | All | 11738 | 0 | 11837 | 259 | 2 |

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 11.

The worst 5 of 259 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:65:LEU:HD11 | 2:B:121:HIS:CD2 | 1.49 | 1.45 |
| 2:B:65:LEU:CD1 | 2:B:121:HIS:HD2 | 1.42 | 1.30 |
| 2:B:65:LEU:CD1 | 2:B:121:HIS:CD2 | 2.22 | 1.18 |
| 1:A:6:ASP:O | 1:A:7:LYS:HG3 | 1.53 | 1.08 |
| 2:B:61:ASN:ND2 | 2:B:63:ASN:OD1 | 1.99 | 0.93 |

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|--------|--------|--------------------------|-------------------|
| 2:B:2:SER:OG | 2:D:3:TYR:N[4_445] | 1.31 | 0.89 |
| 1:A:101:GLN:OE1 | 1:A:603:LYS:NZ[3_545] | 2.06 | 0.14 |

## 5.3   Torsion angles   ⓘ

### 5.3.1   Protein backbone   ⓘ

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 | 613/624 (98%) | 566 (92%) | 36 (6%) | 11 (2%) | 8 | 41 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------|----------|---------|----------|------|----|
| 1 | C | 599/624 (96%) | 561 (94%) | 33 (6%) | 5 (1%) | 19 | 58 |
| 2 | B | 108/184 (59%) | 89 (82%) | 13 (12%) | 6 (6%) | 2 | 14 |
| 2 | D | 104/184 (56%) | 90 (86%) | 9 (9%) | 5 (5%) | 2 | 17 |
| All | All | 1424/1616 (88%) | 1306 (92%) | 91 (6%) | 27 (2%) | 8 | 39 |

5 of 27 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 6 | ASP |
| 1 | A | 7 | LYS |
| 1 | A | 317 | CYS |
| 1 | A | 384 | THR |
| 1 | A | 386 | GLU |

### 5.3.2 Protein sidechains ⓘ

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 | 558/564 (99%) | 549 (98%) | 9 (2%) | 62 | 84 |
| 1 | C | 550/564 (98%) | 540 (98%) | 10 (2%) | 59 | 82 |
| 2 | B | 99/161 (62%) | 93 (94%) | 6 (6%) | 18 | 54 |
| 2 | D | 97/161 (60%) | 94 (97%) | 3 (3%) | 40 | 72 |
| 3 | E | 2/4 (50%) | 1 (50%) | 1 (50%) | 0 | 0 |
| 3 | H | 2/4 (50%) | 1 (50%) | 1 (50%) | 0 | 0 |
| All | All | 1308/1458 (90%) | 1278 (98%) | 30 (2%) | 50 | 78 |

5 of 30 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | B | 82 | GLU |
| 2 | D | 105 | ASN |
| 1 | C | 176 | ARG |
| 3 | H | 6 | ASP |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | C | 536 | ARG |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | B | 121 | HIS |
| 2 | B | 125 | ASN |
| 1 | C | 208 | ASN |
| 2 | D | 37 | ASN |

### 5.3.3   RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are 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 | $\#|Z| > 2$ |
| 3 | SEP | H | 5 | 3 | 8,9,10 | 1.70 | 1 (12%) | 8,12,14 | 1.82 | 2 (25%) |
| 3 | TPO | E | 4 | 3 | 8,10,11 | 2.08 | 2 (25%) | 10,14,16 | 1.79 | 1 (10%) |
| 3 | TPO | H | 4 | 3 | 8,10,11 | 1.91 | 3 (37%) | 10,14,16 | 1.58 | 1 (10%) |
| 3 | SEP | E | 5 | 3 | 8,9,10 | 1.76 | 2 (25%) | 8,12,14 | 1.80 | 1 (12%) |

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 |
|-----|------|-------|-----|------|---------|----------|-------|
| 3 | SEP | H | 5 | 3 | - | 4/5/8/10 | - |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------|-------|
| 3 | TPO | E | 4 | 3 | - | 4/9/11/13 | - |
| 3 | TPO | H | 4 | 3 | - | 1/9/11/13 | - |
| 3 | SEP | E | 5 | 3 | - | 3/5/8/10 | - |

The worst 5 of 8 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|---|-------------|----------|
| 3 | E | 4 | TPO | P-O1P | 3.73 | 1.62 | 1.50 |
| 3 | E | 5 | SEP | P-O1P | 3.68 | 1.62 | 1.50 |
| 3 | H | 4 | TPO | P-O1P | 3.67 | 1.62 | 1.50 |
| 3 | H | 5 | SEP | P-O1P | 3.55 | 1.62 | 1.50 |
| 3 | E | 4 | TPO | CB-CA | 3.00 | 1.60 | 1.53 |

All (5) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|-----|------|-------|---|----------------|-------------|
| 3 | E | 4 | TPO | P-OG1-CB | -5.22 | 107.44 | 123.21 |
| 3 | E | 5 | SEP | OG-CB-CA | 4.41 | 112.43 | 108.14 |
| 3 | H | 4 | TPO | P-OG1-CB | -4.29 | 110.26 | 123.21 |
| 3 | H | 5 | SEP | OG-CB-CA | 4.03 | 112.07 | 108.14 |
| 3 | H | 5 | SEP | P-OG-CB | -2.25 | 112.11 | 118.30 |

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-------|
| 3 | E | 4 | TPO | N-CA-CB-CG2 |
| 3 | E | 4 | TPO | N-CA-CB-OG1 |
| 3 | E | 4 | TPO | C-CA-CB-CG2 |
| 3 | H | 4 | TPO | CB-OG1-P-O1P |
| 3 | H | 5 | SEP | CB-OG-P-O3P |

There are no ring outliers.

2 monomers are involved in 2 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 3 | E | 4 | TPO | 1 | 0 |
| 3 | E | 5 | SEP | 1 | 0 |

## 5.5 Carbohydrates ⓘ

There are no monosaccharides 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 ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95$^{th}$ percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | | | OWAB(Å$^2$) | Q<0.9 |
|-----|-------|----------|--------|---------|-----|-----|-------------|-------|
| 1 | A | 617/624 (98%) | -0.19 | 6 (0%) | 82 | 72 | 67, 101, 151, 191 | 0 |
| 1 | C | 605/624 (96%) | -0.04 | 6 (0%) | 82 | 72 | 90, 125, 161, 182 | 0 |
| 2 | B | 114/184 (61%) | 0.17 | 5 (4%) | 34 | 21 | 80, 107, 148, 165 | 0 |
| 2 | D | 110/184 (59%) | 0.69 | 14 (12%) | 3 | 2 | 95, 142, 171, 180 | 0 |
| 3 | E | 2/6 (33%) | 3.68 | 2 (100%) | 0 | 0 | 182, 182, 182, 183 | 0 |
| 3 | H | 2/6 (33%) | 0.24 | 0 | 100 | 100 | 170, 170, 170, 177 | 0 |
| All | All | 1450/1628 (89%) | -0.02 | 33 (2%) | 60 | 47 | 67, 116, 161, 191 | 0 |

The worst 5 of 33 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 3 | E | 6 | ASP | 4.5 |
| 1 | C | 231 | PRO | 3.9 |
| 1 | A | 449 | SER | 3.8 |
| 2 | D | 7 | ASP | 3.8 |
| 1 | A | 451 | ASP | 3.6 |

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95$^{th}$ percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|-----|------|-------|-----|-------|------|-----|------------------|-------|
| 3 | TPO | E | 4 | 11/12 | 0.65 | 0.58 | 194,208,242,254 | 0 |
| 3 | SEP | E | 5 | 10/11 | 0.73 | 0.44 | 189,200,212,225 | 0 |
| 3 | SEP | H | 5 | 10/11 | 0.77 | 0.26 | 176,197,209,213 | 0 |
| 3 | TPO | H | 4 | 11/12 | 0.85 | 0.41 | 183,196,215,229 | 0 |

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.