# WORLDWIDE wwPDB PROTEIN DATA BANK

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

Jun 8, 2023 – 10:13 AM JST

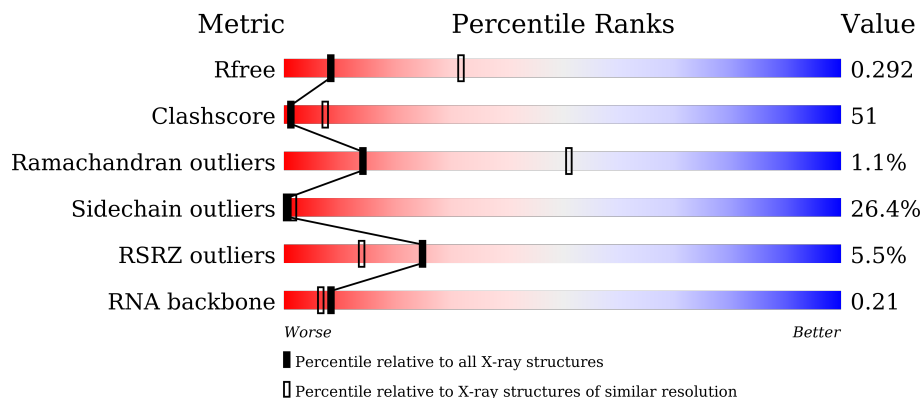|  |  |  |
|---|---|---|
| PDB ID | : | 7VYX |
| Title | : | Crystal structure of the selenomethionine(SeMet)-derived Cas12c1 (D969A) ternary complex |
| Authors | : | Zhang, B.; Lin, J.Y.; Perculija, V.; OuYang, S.Y. |
| Deposited on | : | 2021-11-15 |
| Resolution | : | 3.20 Å(reported) |

# 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 3.20 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.
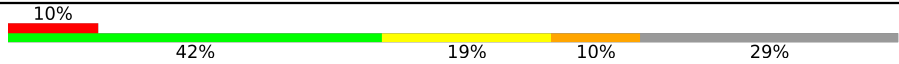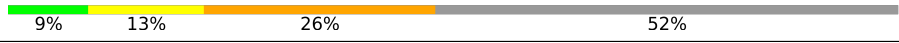
| Metric | Percentile Ranks | Value |
|--------|------------------|-------|
| Rfree | | 0.292 |
| Clashscore | | 51 |
| Ramachandran outliers | | 1.1% |
| Sidechain outliers | | 26.4% |
| RSRZ outliers | | 5.5% |
| RNA backbone | | 0.21 |

*Worse*        *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

| 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) |
| RNA backbone | 3102 | 1010 (3.50-2.90) |

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 | 1310 | 5%<br>36% · 41% · 15% · 8% |
| 1 | B | 1310 | 5%<br>33% · 42% · 15% · 9% |
| 2 | C | 136 | 7%<br>18% · 30% · 23% · 5% · 24% |
| 2 | D | 136 | 5%<br>16% · 21% · 25% · 5% · 33% |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 3 | E | 31 | 10% 42% 19% 10% 29% |
| 3 | F | 31 | 48% 26% 10% 16% |
| 4 | G | 23 | 9% 13% 26% 52% |
| 4 | H | 23 | 13% 35% 52% |

## 2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 24465 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 Selenomethionine (SeMet)-labeled Cas12c1 D969A mutant.

| Mol | Chain | Residues | Atoms | | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|---|---|---|---|---|---------|---------|-------|
| 1 | A | 1211 | Total | C | N | O | S | Se | 0 | 0 | 0 |
| | | | 9533 | 6075 | 1639 | 1788 | 20 | 11 | | | |
| 1 | B | 1193 | Total | C | N | O | S | Se | 0 | 0 | 0 |
| | | | 9369 | 5977 | 1607 | 1754 | 20 | 11 | | | |

- Molecule 2 is a RNA chain called sgRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|---|---|---|---|---------|---------|-------|
| 2 | C | 103 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 2188 | 978 | 387 | 720 | 103 | | | |
| 2 | D | 91 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 1934 | 865 | 344 | 634 | 91 | | | |

- Molecule 3 is a DNA chain called Target DNA strand.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|---|---|---|---|---------|---------|-------|
| 3 | E | 22 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 451 | 216 | 78 | 135 | 22 | | | |
| 3 | F | 26 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 534 | 256 | 92 | 160 | 26 | | | |

- Molecule 4 is a DNA chain called Non-target DNA strand.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|---|---|---|---|---------|---------|-------|
| 4 | G | 11 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 227 | 108 | 42 | 66 | 11 | | | |
| 4 | H | 11 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 227 | 108 | 42 | 66 | 11 | | | |

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 5 | A | 1 | Total 1 | Zn 1 | 0 | 0 |
| 5 | B | 1 | Total 1 | Zn 1 | 0 | 0 |

# 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.
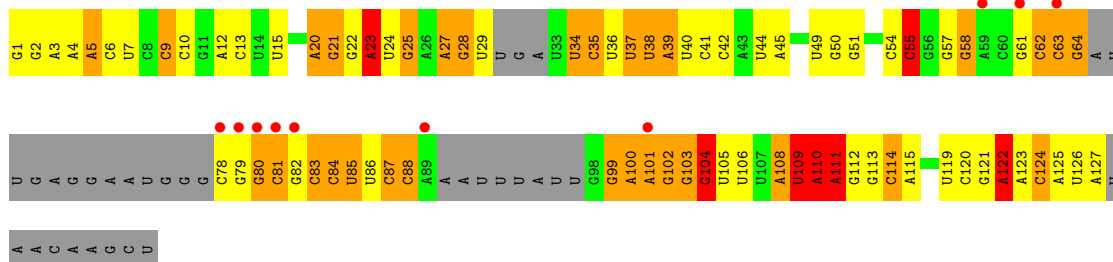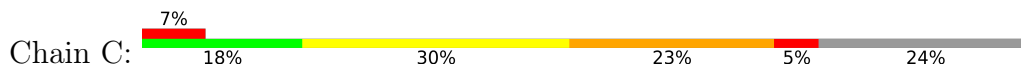
• Molecule 1: Selenomethionine (SeMet)-labeled Cas12c1 D969A mutant

• Molecule 1: Selenomethionine (SeMet)-labeled Cas12c1 D969A mutant



Chain B: 5%  33%  42%  15%  •  9%

V1252 Y1253 K1254 D1255 C1256 A1257 L1258 H1259 F1260 S1261 G1262 M1263 Q1264 A1265 D1266 E1267 N1268 A1269 A1270 I1271 N1272 I1273 G1274 R1275 R1276 F1277 L1278 T1279 A1280 L1281 R1282 K1283 N1284 ARG ARG SER ASP PHE PRO SER ASN VAL LYS ILE SER ASP ARG LEU LEU ASP ASN LEU GLU HIS HIS HIS HIS HIS HIS

• Molecule 2: sgRNA

Chain C:

G1 G2 A3 A4 A5 C6 U7 C8 C9 C10 G11 A12 C13 U14 U15 A20 G21 G22 A23 U24 A25 A26 A27 G28 U29 U G A U33 U34 G35 U36 U37 G38 A39 U40 C41 C42 A43 U44 A45 U49 G50 G51 C54 C55 G56 G57 G58 A59 C60 G61 C62 C63 G64 A U

U G A G G A U G G G G C78 G79 G80 C81 G82 C83 C84 U85 U86 C87 C88 A89 A A U U U A U U98 G99 A100 A101 G102 G103 G104 U105 U106 U107 A108 U109 A110 A111 G112 G113 C114 A115 U119 C120 G121 A122 A123 C124 A125 U126 A127 U
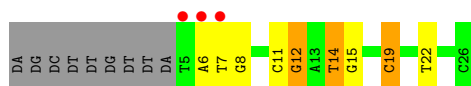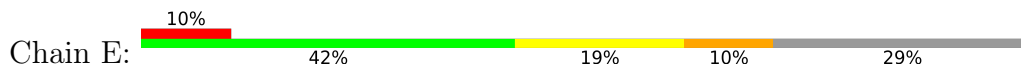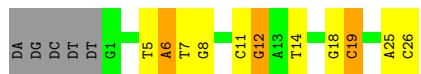
A A C A A G C U

• Molecule 2: sgRNA

Chain D:

G G2 A3 A4 A5 C6 U7 C8 C9 C10 G11 A12 C13 U14 U15 U18 C19 A20 G21 C22 A23 U24 G25 A26 A27 G28 U U G A U U C U36 U37 U38 A39 U40 C41 C42 A43 U44 A45 U52 G53 C54 C55 G56 G57 G58 A59 C60 G61 C62 C63 G64 A65 U

U G A G G A A U G G G C G G80 C81 G82 C83 C84 U85 U86 C C C A A A A U U U A U U G C G A100 A101 G102 G103 G104 U105 U106 U107 A108 U109 A110 A111 C114 A115 A116 U119 C120 G121 A122 A123 C124 A125 U126 A U

A A C A A G C U

• Molecule 3: Target DNA strand

Chain E:

DA DG DC DT DG DT DA T5 A6 T7 G8 C11 G12 A13 T14 G15 C19 T22 C26

• Molecule 3: Target DNA strand

Chain F:

DA DG DC DT DT G1 T5 A6 T7 G8 C11 G12 A13 T14 G18 C19 A25 C26

• Molecule 4: Non-target DNA strand

Chain G:

G1 T2 C3 T4 A5 G6 T7 G8 C9 A10 A11 DC DA DA DA DA DA DA DA DA DA DA DA DA

• Molecule 4: Non-target DNA strand

Chain H:

13%  35%  52%

G1 T2 C3 T4 A5 G6 T7 G8 C9 A10 A11 DC DA DA DA DA DA DA DA DA

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 1 21 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 93.13Å    149.85Å    173.25Å<br>90.00°    91.59°     90.00° | Depositor |
| Resolution (Å) | 49.73  &ndash;  3.20<br>49.68  &ndash;  3.20 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 79.4 (49.73-3.20)<br>79.4 (49.68-3.20) | Depositor<br>EDS |
| $R_{merge}$ | 0.13 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 3.96 (at 3.19Å) | Xtriage |
| Refinement program | REFMAC 5.8.0267 | Depositor |
| R, $R_{free}$ | 0.256  ,   0.292<br>0.256  ,   0.292 | Depositor<br>DCC |
| $R_{free}$ test set | 2973 reflections (4.78%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 53.0 | Xtriage |
| Anisotropy | 0.063 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.27 , 54.1 | EDS |
| L-test for twinning[2] | $< \lvert L \rvert > = 0.45, < L^2 > = 0.27$ | Xtriage |
| Estimated twinning fraction | 0.045 for h,-k,-l | Xtriage |
| $F_o$,$F_c$ correlation | 0.82 | EDS |
| Total number of atoms | 24465 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 73.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ 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: ZN

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 | 1.20 | 8/9713 (0.1%) | 0.96 | 31/13105 (0.2%) |
| 1 | B | 1.09 | 4/9549 (0.0%) | 0.95 | 34/12891 (0.3%) |
| 2 | C | 0.81 | 11/2441 (0.5%) | 0.89 | 6/3793 (0.2%) |
| 2 | D | 0.70 | 6/2158 (0.3%) | 0.96 | 9/3352 (0.3%) |
| 3 | E | 0.68 | 0/504 | 1.63 | 9/776 (1.2%) |
| 3 | F | 0.67 | 0/597 | 1.53 | 10/920 (1.1%) |
| 4 | G | 1.25 | 4/254 (1.6%) | 1.03 | 2/390 (0.5%) |
| 4 | H | 0.59 | 0/254 | 0.91 | 0/390 |
| All | All | 1.06 | 33/25470 (0.1%) | 0.99 | 101/35617 (0.3%) |

The worst 5 of 33 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|---|-------------|----------|
| 1 | A | 337 | PRO | N-CD | 13.97 | 1.67 | 1.47 |
| 1 | B | 956 | PRO | N-CD | 10.04 | 1.61 | 1.47 |
| 1 | A | 515 | PRO | N-CD | 9.92 | 1.61 | 1.47 |
| 1 | A | 460 | PRO | N-CD | -9.83 | 1.34 | 1.47 |
| 1 | A | 1190 | PHE | C-N | 9.49 | 1.55 | 1.34 |

The worst 5 of 101 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|-----|-------|-----|------|-------|---|----------------|-------------|
| 3 | E | 19 | DC | O5'-P-OP2 | -20.37 | 86.26 | 110.70 |
| 3 | F | 14 | DT | O5'-P-OP1 | -18.06 | 89.03 | 110.70 |
| 3 | F | 19 | DC | O5'-P-OP1 | -17.79 | 89.36 | 110.70 |
| 3 | E | 14 | DT | O5'-P-OP2 | -16.98 | 90.33 | 110.70 |
| 3 | E | 12 | DG | O5'-P-OP1 | -16.18 | 91.14 | 105.70 |

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 | 9533 | 0 | 9379 | 994 | 0 |
| 1 | B | 9369 | 0 | 9165 | 1088 | 0 |
| 2 | C | 2188 | 0 | 1113 | 138 | 0 |
| 2 | D | 1934 | 0 | 984 | 123 | 0 |
| 3 | E | 451 | 0 | 251 | 10 | 0 |
| 3 | F | 534 | 0 | 297 | 7 | 0 |
| 4 | G | 227 | 0 | 125 | 15 | 0 |
| 4 | H | 227 | 0 | 125 | 6 | 0 |
| 5 | A | 1 | 0 | 0 | 0 | 0 |
| 5 | B | 1 | 0 | 0 | 0 | 0 |
| All | All | 24465 | 0 | 21439 | 2321 | 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 51.

The worst 5 of 2321 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:B:1159:TRP:CH2 | 1:B:1183:ALA:HB2 | 1.29 | 1.67 |
| 1:B:565:VAL:HB | 1:B:708:ARG:CD | 1.31 | 1.60 |
| 1:B:565:VAL:CB | 1:B:708:ARG:HD3 | 1.34 | 1.52 |
| 1:A:444:VAL:HG21 | 1:A:471:PHE:CD2 | 1.43 | 1.49 |
| 1:A:1201:TYR:CE2 | 1:A:1209:PRO:HD2 | 1.48 | 1.47 |

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 | 1197/1310 (91%) | 1130 (94%) | 59 (5%) | 8 (1%) | 22 | 61 |
| 1 | B | 1177/1310 (90%) | 1092 (93%) | 68 (6%) | 17 (1%) | 11 | 46 |
| All | All | 2374/2620 (91%) | 2222 (94%) | 127 (5%) | 25 (1%) | 14 | 51 |

5 of 25 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 656 | ARG |
| 1 | B | 841 | ARG |
| 1 | A | 175 | ASN |
| 1 | A | 328 | LYS |
| 1 | A | 881 | VAL |

### 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 | 1018/1144 (89%) | 750 (74%) | 268 (26%) | 0 | 2 |
| 1 | B | 993/1144 (87%) | 730 (74%) | 263 (26%) | 0 | 2 |
| All | All | 2011/2288 (88%) | 1480 (74%) | 531 (26%) | 0 | 2 |

5 of 531 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 953 | LEU |
| 1 | B | 1018 | GLN |
| 1 | B | 944 | SER |
| 1 | B | 1244 | THR |
| 1 | A | 961 | GLN |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | B | 126 | GLN |
| 1 | B | 528 | GLN |
| 1 | B | 1284 | ASN |
| 1 | B | 1072 | GLN |
| 1 | B | 154 | ASN |

### 5.3.3   RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|----------|-------------------|-----------------|
| 2 | C | 99/136 (72%) | 51 (51%) | 9 (9%) |
| 2 | D | 87/136 (63%) | 49 (56%) | 5 (5%) |
| All | All | 186/272 (68%) | 100 (53%) | 14 (7%) |

5 of 100 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | C | 2 | G |
| 2 | C | 5 | A |
| 2 | C | 7 | U |
| 2 | C | 13 | C |
| 2 | C | 15 | U |

5 of 14 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | C | 110 | A |
| 2 | C | 114 | C |
| 2 | D | 114 | C |
| 2 | D | 82 | G |
| 2 | D | 110 | A |

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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 ⓘ

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 | 1200/1310 (91%) | 0.14 | 60 (5%) | 28 | 16 | 12, 61, 132, 179 | 0 |
| 1 | B | 1182/1310 (90%) | 0.23 | 66 (5%) | 24 | 13 | 16, 72, 129, 161 | 0 |
| 2 | C | 103/136 (75%) | 0.50 | 10 (9%) | 7 | 4 | 10, 81, 167, 198 | 0 |
| 2 | D | 91/136 (66%) | 0.66 | 7 (7%) | 13 | 7 | 13, 97, 168, 199 | 0 |
| 3 | E | 22/31 (70%) | 0.58 | 3 (13%) | 3 | 2 | 9, 44, 145, 166 | 0 |
| 3 | F | 26/31 (83%) | -0.07 | 0 | 100 | 100 | 14, 63, 139, 152 | 0 |
| 4 | G | 11/23 (47%) | 0.09 | 0 | 100 | 100 | 23, 41, 91, 122 | 0 |
| 4 | H | 11/23 (47%) | 0.02 | 0 | 100 | 100 | 26, 38, 78, 132 | 0 |
| All | All | 2646/3000 (88%) | 0.21 | 146 (5%) | 25 | 14 | 9, 67, 139, 199 | 0 |

The worst 5 of 146 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | A | 733 | ASN | 8.7 |
| 1 | A | 578 | ASN | 6.3 |
| 3 | E | 6 | DA | 5.8 |
| 1 | A | 1178 | GLY | 5.5 |
| 1 | B | 455 | ASP | 5.5 |

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

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

## 6.3   Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4   Ligands (i)

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($\text{Å}^2$) | Q<0.9 |
|-----|------|-------|------|-------|------|------|--------------------|-------|
| 5 | ZN | B | 1401 | 1/1 | 0.80 | 0.13 | 79,79,79,79 | 0 |
| 5 | ZN | A | 1401 | 1/1 | 0.96 | 0.10 | 61,61,61,61 | 0 |

## 6.5   Other polymers (i)

There are no such residues in this entry.