



## wwPDB EM Validation Summary Report ⓘ

May 18, 2026 – 08:08 PM JST

PDB ID : 9KDO / pdb\_00009kdo  
EMDB ID : EMD-62283  
Title : The structure of 2 ACTD bound to RNA polymerase II elongation complex with 3 CTG repeats  
Authors : Xu, J.; Zhao, W.; Zhu, L.  
Deposited on : 2024-11-03  
Resolution : 2.92 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at  
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
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>.

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

EMDB validation analysis : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : **NOT EXECUTED**  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

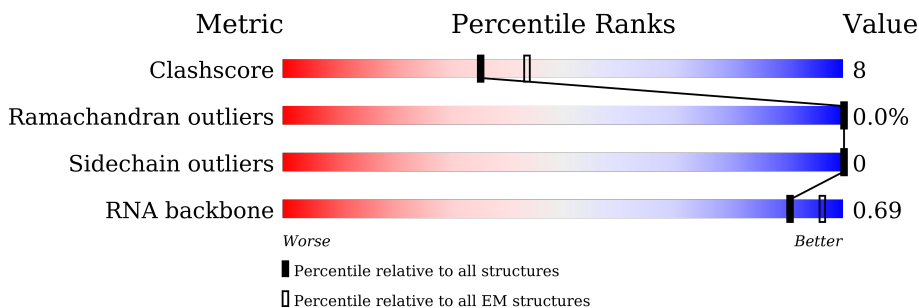
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.92 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.



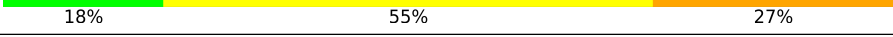
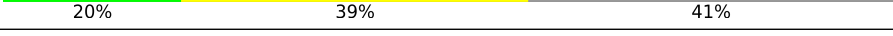
| Metric                | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|--------------------------|--------------------------|
| Clashscore            | 229148                   | 23984                    |
| Ramachandran outliers | 224038                   | 23583                    |
| Sidechain outliers    | 223484                   | 23102                    |
| RNA backbone          | 8273                     | 3508                     |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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     | 1733   | 66% 15% 18%      |
| 2   | B     | 1224   | 79% 17% .        |
| 3   | C     | 318    | 65% 18% 17%      |
| 4   | D     | 221    | 56% 19% 25%      |
| 5   | E     | 215    | 84% 15%          |
| 6   | F     | 155    | 46% 10% 44%      |
| 7   | G     | 171    | 70% 30%          |
| 8   | H     | 146    | 78% 18% .        |

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| Mol | Chain | Length | Quality of chain                                                                              |
|-----|-------|--------|-----------------------------------------------------------------------------------------------|
| 9   | I     | 122    |  74%21%5%   |
| 10  | J     | 70     |  81%17%.    |
| 11  | K     | 120    |  79%17%.    |
| 12  | L     | 70     |  54%10%36%  |
| 13  | M     | 11     |  18%55%27%  |
| 13  | O     | 11     |  18%55%27%  |
| 14  | N     | 49     |  10%24%65%  |
| 15  | P     | 12     |  33%50%8%8% |
| 16  | T     | 49     |  20%39%41%  |

## 2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 33071 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 DNA-directed RNA polymerase II subunit RPB1.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 1   | A     | 1418     | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 11153 | 7029 | 1947 | 2115 | 62 |         |       |

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 2   | B     | 1183     | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 9427  | 5958 | 1649 | 1765 | 55 |         |       |

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3   | C     | 265      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2086  | 1312 | 347 | 414 | 13 |         |       |

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | D     | 166      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1332  | 823 | 238 | 269 | 2 |         |       |

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5   | E     | 214      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1752  | 1111 | 309 | 321 | 11 |         |       |

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 6   | F     | 87       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 705   | 451 | 119 | 132 | 3 |         |       |

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 7   | G     | 171      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1339  | 861 | 222 | 248 | 8 |         |       |

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8   | H     | 140      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1120  | 704 | 188 | 224 | 4 |         |       |

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 9   | I     | 116      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 944   | 581 | 172 | 181 | 10 |         |       |

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10  | J     | 69       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 569   | 362 | 101 | 100 | 6 |         |       |

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11  | K     | 115      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 924   | 593 | 157 | 172 | 2 |         |       |

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 12  | L     | 45       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 359   | 221 | 71 | 63 | 4 |         |       |

- Molecule 13 is a protein called Actinomycin D.

| Mol | Chain | Residues | Atoms |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---------|-------|
| 13  | M     | 11       | Total | C  | N  | O  | 0       | 0     |
|     |       |          | 90    | 62 | 12 | 16 |         |       |
| 13  | O     | 11       | Total | C  | N  | O  | 0       | 0     |
|     |       |          | 90    | 62 | 12 | 16 |         |       |

- Molecule 14 is a DNA chain called NTS(non-template strand).

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 14  | N     | 17       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 346   | 166 | 59 | 104 | 17 |         |       |

- Molecule 15 is a RNA chain called RNA (5'-R(\*CP\*CP\*CP\*UP\*AP\*AP\*GP\*AP\*GP\*UP\*AP\*C)-3').

| Mol | Chain | Residues | Atoms |     |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 15  | P     | 11       | Total | C   | N  | O  | P  | 0       | 0     |
|     |       |          | 234   | 105 | 43 | 75 | 11 |         |       |

- Molecule 16 is a DNA chain called TS(template strand).

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 16  | T     | 29       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 592   | 284 | 103 | 176 | 29 |         |       |

- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 17  | A     | 2        | Total | Zn | 0       |
|     |       |          | 2     | 2  |         |
| 17  | B     | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |
| 17  | C     | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |
| 17  | I     | 2        | Total | Zn | 0       |
|     |       |          | 2     | 2  |         |
| 17  | J     | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |
| 17  | L     | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |

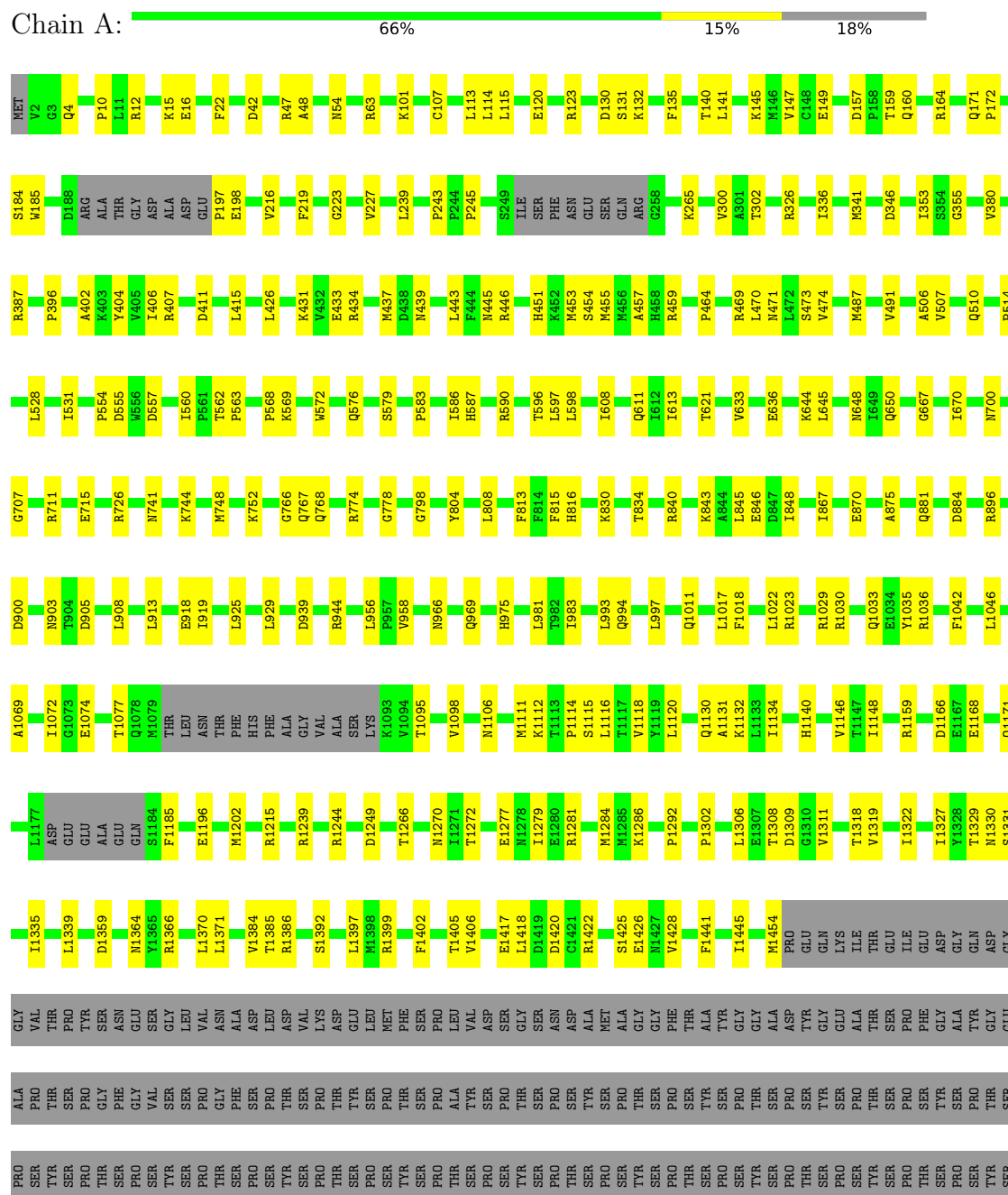
- Molecule 18 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 18  | A     | 1        | Total | Mg | 0       |
|     |       |          | 1     | 1  |         |

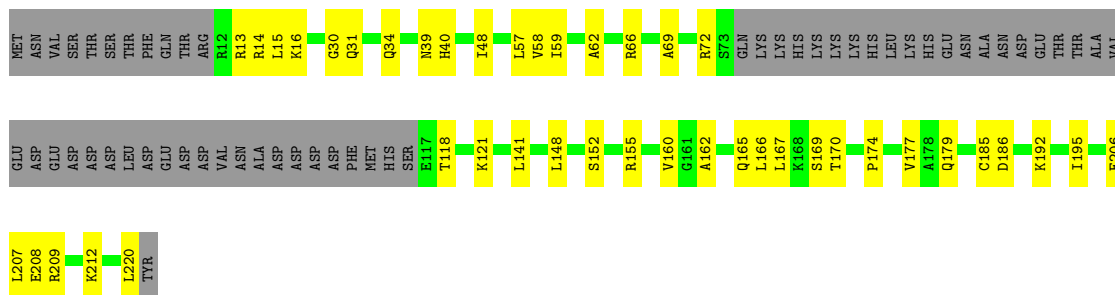
### 3 Residue-property plots [i](#)

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. 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. 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: DNA-directed RNA polymerase II subunit RPB1

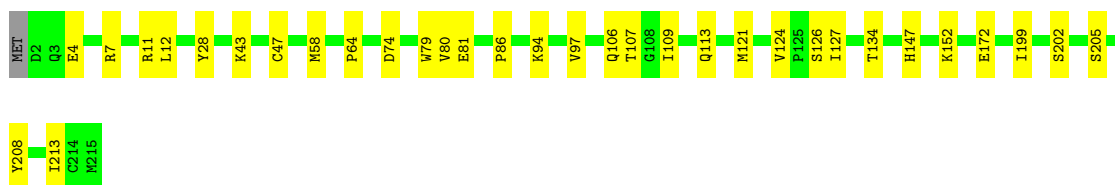






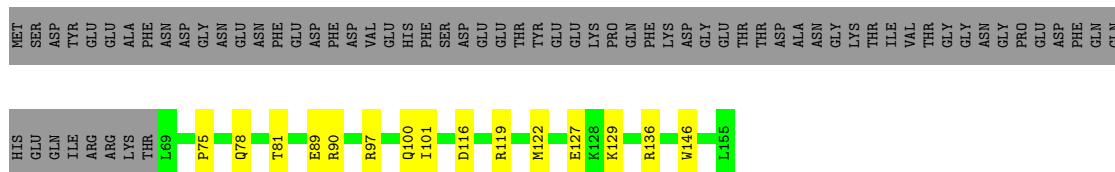
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 84% 15%



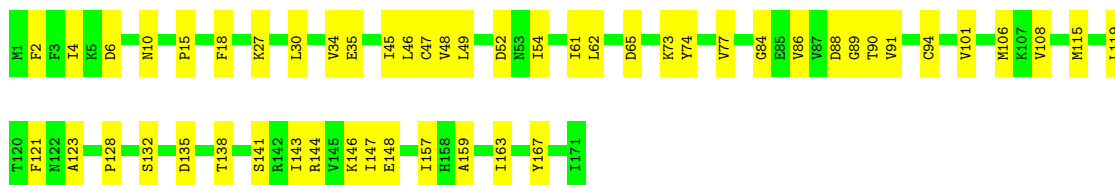
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F: 46% 10% 44%



- Molecule 7: DNA-directed RNA polymerase II subunit RPB7

Chain G: 70% 30%



- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 78% 18%



- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

Chain I: 74% 21% 5%



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J: 81% 17% .



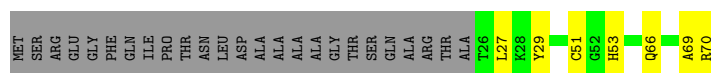
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11

Chain K: 79% 17% .



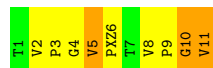
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain L: 54% 10% 36%



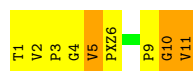
- Molecule 13: Actinomycin D

Chain M: 18% 55% 27%



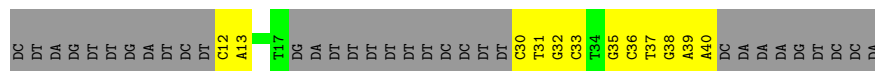
- Molecule 13: Actinomycin D

Chain O: 18% 55% 27%



- Molecule 14: NTS(non-template strand)

Chain N: 10% 24% 65%

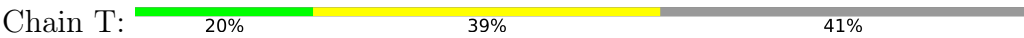


- Molecule 15: RNA (5'-R(\*CP\*CP\*CP\*UP\*AP\*AP\*GP\*AP\*GP\*UP\*AP\*C)-3')

Chain P: 33% 50% 8% 8%



● Molecule 16: TS(template strand)



## 4 Experimental information

| Property                             | Value                     | Source    |
|--------------------------------------|---------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE           | Depositor |
| Imposed symmetry                     | POINT, Not provided       |           |
| Number of particles used             | 77764                     | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF         | Depositor |
| CTF correction method                | NONE                      | Depositor |
| Microscope                           | TFS KRIOS                 | Depositor |
| Voltage (kV)                         | 300                       | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 49.4                      | Depositor |
| Minimum defocus (nm)                 | 1200                      | Depositor |
| Maximum defocus (nm)                 | 1800                      | Depositor |
| Magnification                        | Not provided              |           |
| Image detector                       | GATAN K2 SUMMIT (4k x 4k) | Depositor |

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PXZ, MVA, MG, ZN, SAR, DVA

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     | 0.13         | 0/11352 | 0.30        | 0/15350        |
| 2   | B     | 0.12         | 0/9613  | 0.31        | 2/12967 (0.0%) |
| 3   | C     | 0.12         | 0/2124  | 0.28        | 0/2879         |
| 4   | D     | 0.11         | 0/1340  | 0.30        | 0/1797         |
| 5   | E     | 0.12         | 0/1788  | 0.30        | 0/2406         |
| 6   | F     | 0.11         | 0/717   | 0.27        | 0/967          |
| 7   | G     | 0.11         | 0/1367  | 0.31        | 0/1844         |
| 8   | H     | 0.11         | 0/1139  | 0.28        | 0/1544         |
| 9   | I     | 0.11         | 0/962   | 0.32        | 0/1295         |
| 10  | J     | 0.12         | 0/578   | 0.26        | 0/775          |
| 11  | K     | 0.12         | 0/942   | 0.27        | 0/1272         |
| 12  | L     | 0.12         | 0/361   | 0.28        | 0/478          |
| 13  | M     | 0.28         | 0/26    | 0.40        | 0/30           |
| 13  | O     | 0.27         | 0/26    | 0.40        | 0/30           |
| 14  | N     | 0.49         | 0/385   | 0.85        | 0/589          |
| 15  | P     | 0.10         | 0/261   | 0.18        | 0/404          |
| 16  | T     | 0.50         | 0/662   | 0.80        | 0/1019         |
| All | All   | 0.15         | 0/33643 | 0.33        | 2/45646 (0.0%) |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|------|-------------|----------|
| 2   | B     | 503 | GLY  | CA-C-N | 5.58 | 132.20      | 121.54   |
| 2   | B     | 503 | GLY  | C-N-CA | 5.58 | 132.20      | 121.54   |

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     | 11153 | 0        | 11228    | 187     | 0            |
| 2   | B     | 9427  | 0        | 9419     | 149     | 0            |
| 3   | C     | 2086  | 0        | 2045     | 47      | 0            |
| 4   | D     | 1332  | 0        | 1353     | 36      | 0            |
| 5   | E     | 1752  | 0        | 1776     | 20      | 0            |
| 6   | F     | 705   | 0        | 731      | 9       | 0            |
| 7   | G     | 1339  | 0        | 1357     | 36      | 0            |
| 8   | H     | 1120  | 0        | 1086     | 18      | 0            |
| 9   | I     | 944   | 0        | 899      | 20      | 0            |
| 10  | J     | 569   | 0        | 585      | 10      | 0            |
| 11  | K     | 924   | 0        | 934      | 18      | 0            |
| 12  | L     | 359   | 0        | 381      | 7       | 0            |
| 13  | M     | 90    | 0        | 84       | 11      | 0            |
| 13  | O     | 90    | 0        | 84       | 11      | 0            |
| 14  | N     | 346   | 0        | 195      | 21      | 0            |
| 15  | P     | 234   | 0        | 120      | 7       | 0            |
| 16  | T     | 592   | 0        | 330      | 24      | 0            |
| 17  | A     | 2     | 0        | 0        | 0       | 0            |
| 17  | B     | 1     | 0        | 0        | 0       | 0            |
| 17  | C     | 1     | 0        | 0        | 0       | 0            |
| 17  | I     | 2     | 0        | 0        | 0       | 0            |
| 17  | J     | 1     | 0        | 0        | 0       | 0            |
| 17  | L     | 1     | 0        | 0        | 0       | 0            |
| 18  | A     | 1     | 0        | 0        | 0       | 0            |
| All | All   | 33071 | 0        | 32607    | 519     | 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 8.

The worst 5 of 519 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) |
|-----------------|-----------------|--------------------------|-------------------|
| 14:N:40:DA:H61  | 16:T:10:DT:H3   | 0.92                     | 0.92              |
| 2:B:763:GLN:HG2 | 2:B:765:PRO:HD2 | 1.56                     | 0.86              |
| 14:N:40:DA:N6   | 16:T:10:DT:H3   | 1.73                     | 0.86              |

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| Atom-1           | Atom-2          | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|-----------------|--------------------------|-------------------|
| 14:N:35:DG:H1'   | 13:O:1:THR:HG23 | 1.55                     | 0.86              |
| 2:B:1129:ARG:HG2 | 16:T:23:DA:H5'  | 1.57                     | 0.85              |

There are no symmetry-related clashes.

## 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 PDB entries followed by that with respect to all EM entries.

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     | 1408/1733 (81%) | 1376 (98%) | 32 (2%)  | 0        | 100         | 100 |
| 2   | B     | 1173/1224 (96%) | 1136 (97%) | 36 (3%)  | 1 (0%)   | 48          | 76  |
| 3   | C     | 263/318 (83%)   | 255 (97%)  | 8 (3%)   | 0        | 100         | 100 |
| 4   | D     | 162/221 (73%)   | 156 (96%)  | 6 (4%)   | 0        | 100         | 100 |
| 5   | E     | 212/215 (99%)   | 206 (97%)  | 6 (3%)   | 0        | 100         | 100 |
| 6   | F     | 85/155 (55%)    | 82 (96%)   | 3 (4%)   | 0        | 100         | 100 |
| 7   | G     | 169/171 (99%)   | 163 (96%)  | 6 (4%)   | 0        | 100         | 100 |
| 8   | H     | 136/146 (93%)   | 133 (98%)  | 3 (2%)   | 0        | 100         | 100 |
| 9   | I     | 114/122 (93%)   | 109 (96%)  | 5 (4%)   | 0        | 100         | 100 |
| 10  | J     | 67/70 (96%)     | 67 (100%)  | 0        | 0        | 100         | 100 |
| 11  | K     | 113/120 (94%)   | 112 (99%)  | 1 (1%)   | 0        | 100         | 100 |
| 12  | L     | 43/70 (61%)     | 42 (98%)   | 1 (2%)   | 0        | 100         | 100 |
| 13  | M     | 2/11 (18%)      | 2 (100%)   | 0        | 0        | 100         | 100 |
| 13  | O     | 2/11 (18%)      | 2 (100%)   | 0        | 0        | 100         | 100 |
| All | All   | 3949/4587 (86%) | 3841 (97%) | 107 (3%) | 1 (0%)   | 100         | 100 |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | B     | 504 | ARG  |

### 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 PDB entries followed by that with respect to all EM entries.

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     | 1240/1520 (82%) | 1240 (100%) | 0        | 100         | 100 |
| 2   | B     | 1026/1061 (97%) | 1026 (100%) | 0        | 100         | 100 |
| 3   | C     | 233/274 (85%)   | 233 (100%)  | 0        | 100         | 100 |
| 4   | D     | 148/200 (74%)   | 148 (100%)  | 0        | 100         | 100 |
| 5   | E     | 196/197 (100%)  | 196 (100%)  | 0        | 100         | 100 |
| 6   | F     | 77/137 (56%)    | 77 (100%)   | 0        | 100         | 100 |
| 7   | G     | 152/152 (100%)  | 152 (100%)  | 0        | 100         | 100 |
| 8   | H     | 123/128 (96%)   | 123 (100%)  | 0        | 100         | 100 |
| 9   | I     | 110/116 (95%)   | 110 (100%)  | 0        | 100         | 100 |
| 10  | J     | 64/65 (98%)     | 64 (100%)   | 0        | 100         | 100 |
| 11  | K     | 99/102 (97%)    | 99 (100%)   | 0        | 100         | 100 |
| 12  | L     | 40/57 (70%)     | 40 (100%)   | 0        | 100         | 100 |
| 13  | M     | 4/4 (100%)      | 4 (100%)    | 0        | 100         | 100 |
| 13  | O     | 4/4 (100%)      | 4 (100%)    | 0        | 100         | 100 |
| All | All   | 3516/4017 (88%) | 3516 (100%) | 0        | 100         | 100 |

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 4   | D     | 28  | GLN  |
| 8   | H     | 139 | ASN  |
| 7   | G     | 24  | GLN  |
| 7   | G     | 122 | ASN  |
| 9   | I     | 116 | ASN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed    | Backbone Outliers | Pucker Outliers |
|-----|-------|-------------|-------------------|-----------------|
| 15  | P     | 10/12 (83%) | 1 (10%)           | 0               |

All (1) RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 15  | P     | 9   | G    |

There are no RNA pucker outliers to report.

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

12 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 | $\# Z  > 2$ |
| 13  | SAR  | M     | 10  | 13   | 4,4,5        | 1.07 | 0           | 1,3,5       | 2.67 | 1 (100%)    |
| 13  | MVA  | M     | 11  | 13   | 6,7,8        | 1.09 | 1 (16%)     | 7,8,10      | 2.07 | 3 (42%)     |
| 13  | MVA  | M     | 5   | 13   | 6,7,8        | 0.79 | 0           | 7,8,10      | 1.29 | 2 (28%)     |
| 13  | SAR  | M     | 4   | 13   | 4,4,5        | 1.11 | 0           | 1,3,5       | 2.73 | 1 (100%)    |
| 13  | MVA  | O     | 5   | 13   | 6,7,8        | 0.80 | 0           | 7,8,10      | 1.29 | 2 (28%)     |
| 13  | MVA  | O     | 11  | 13   | 6,7,8        | 1.07 | 1 (16%)     | 7,8,10      | 2.07 | 3 (42%)     |
| 13  | SAR  | O     | 4   | 13   | 4,4,5        | 1.12 | 0           | 1,3,5       | 2.70 | 1 (100%)    |
| 13  | SAR  | O     | 10  | 13   | 4,4,5        | 1.06 | 0           | 1,3,5       | 2.69 | 1 (100%)    |

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 |
|-----|------|-------|-----|------|---------|----------|-------|
| 13  | SAR  | M     | 10  | 13   | -       | 1/1/2/3  | -     |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------|-------|
| 13  | MVA  | M     | 11  | 13   | -       | 5/6/8/10 | -     |
| 13  | MVA  | M     | 5   | 13   | -       | 6/6/8/10 | -     |
| 13  | SAR  | M     | 4   | 13   | -       | 1/1/2/3  | -     |
| 13  | MVA  | O     | 5   | 13   | -       | 6/6/8/10 | -     |
| 13  | MVA  | O     | 11  | 13   | -       | 5/6/8/10 | -     |
| 13  | SAR  | O     | 4   | 13   | -       | 1/1/2/3  | -     |
| 13  | SAR  | O     | 10  | 13   | -       | 1/1/2/3  | -     |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z    | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|------|-------------|----------|
| 13  | M     | 11  | MVA  | O-C   | 2.57 | 1.30        | 1.19     |
| 13  | O     | 11  | MVA  | O-C   | 2.53 | 1.30        | 1.19     |

The worst 5 of 14 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 13  | O     | 11  | MVA  | O-C-CA | -4.25 | 112.98      | 124.83   |
| 13  | M     | 11  | MVA  | O-C-CA | -4.24 | 113.01      | 124.83   |
| 13  | M     | 4   | SAR  | O-C-CA | -2.73 | 117.52      | 125.42   |
| 13  | O     | 4   | SAR  | O-C-CA | -2.70 | 117.61      | 125.42   |
| 13  | O     | 10  | SAR  | O-C-CA | -2.69 | 117.64      | 125.42   |

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms       |
|-----|-------|-----|------|-------------|
| 13  | M     | 4   | SAR  | C-CA-N-CN   |
| 13  | O     | 4   | SAR  | C-CA-N-CN   |
| 13  | M     | 5   | MVA  | N-CA-CB-CG1 |
| 13  | M     | 5   | MVA  | N-CA-CB-CG2 |
| 13  | M     | 5   | MVA  | C-CA-CB-CG1 |

There are no ring outliers.

6 monomers are involved in 7 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 13  | M     | 10  | SAR  | 1       | 0            |
| 13  | M     | 11  | MVA  | 1       | 0            |
| 13  | M     | 5   | MVA  | 2       | 0            |

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| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 13  | O     | 5   | MVA  | 1       | 0            |
| 13  | O     | 11  | MVA  | 1       | 0            |
| 13  | O     | 10  | SAR  | 1       | 0            |

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 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 [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.