



## wwPDB EM Validation Summary Report ⓘ

May 10, 2026 – 12:14 AM JST

PDB ID : 9K16 / pdb\_00009k16  
EMDB ID : EMD-61966  
Title : A cryo-EM structure of *B. oleracea* RNA polymerase V in complex with 5U scaffold at 3.19 Angstrom  
Authors : Xie, G.; Du, X.; Du, J.  
Deposited on : 2024-10-16  
Resolution : 3.19 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>.

---

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

EMDB validation analysis : **FAILED**  
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

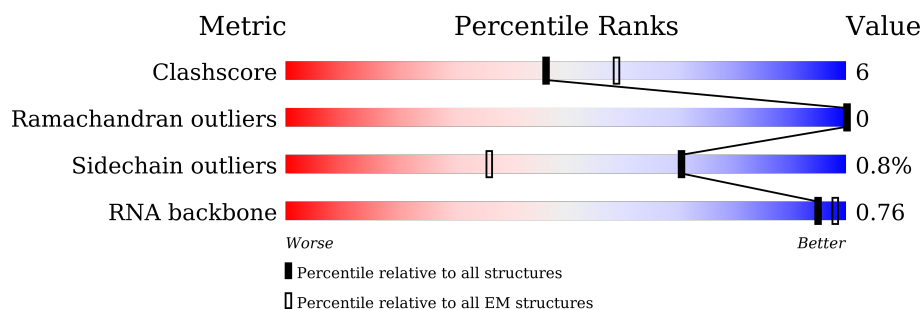
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 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<br>(#Entries) | EM structures<br>(#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   | T     | 34     | 9% 21% 71%       |
| 2   | N     | 34     | 32% 18% 50%      |
| 3   | P     | 20     | 15% 85%          |
| 4   | A     | 2032   | 34% 7% 59%       |
| 5   | C     | 319    | 80% 10% 10%      |
| 6   | F     | 144    | 42% 12% 44%      |
| 7   | J     | 71     | 85% 11%          |
| 8   | K     | 116    | 85% 8% 7%        |

Continued on next page...

*Continued from previous page...*

| Mol | Chain | Length | Quality of chain                                                                                  |
|-----|-------|--------|---------------------------------------------------------------------------------------------------|
| 9   | L     | 51     | <br>71% 18% 12% |
| 10  | H     | 146    | <br>73% 23% . . |
| 11  | I     | 114    | <br>68% 18% 15% |
| 12  | E     | 230    | <br>66% 25% 9%  |
| 13  | B     | 1169   | <br>76% 7% 17%  |

## 2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 23179 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 DNA chain called DNA (34-MER).

| Mol | Chain | Residues | Atoms |    |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|----|---------|-------|
| 1   | T     | 10       | Total | C  | N  | O  | P  | 0       | 0     |
|     |       |          | 205   | 98 | 40 | 57 | 10 |         |       |

- Molecule 2 is a DNA chain called DNA (34-MER).

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 2   | N     | 17       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 350   | 166 | 65 | 102 | 17 |         |       |

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

| Mol | Chain | Residues | Atoms |    |   |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---|---------|-------|
| 3   | P     | 3        | Total | C  | N | O  | P | 0       | 0     |
|     |       |          | 60    | 27 | 6 | 24 | 3 |         |       |

- Molecule 4 is a protein called DNA-directed RNA polymerase V largest subunit.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 4   | A     | 843      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 6597  | 4170 | 1132 | 1251 | 44 |         |       |

- Molecule 5 is a protein called DNA-directed RNA polymerase RpoA/D/Rpb3-type domain-containing protein.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5   | C     | 287      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2256  | 1418 | 380 | 445 | 13 |         |       |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference      |
|-------|---------|----------|--------|----------|----------------|
| C     | 2       | THR      | SER    | conflict | UNP A0A0D3D418 |

- Molecule 6 is a protein called DNA-directed RNA polymerase RpoA/D/Rpb3-type domain-containing protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 6   | F     | 80       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 660   | 420 | 114 | 122 | 4 |         |       |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference      |
|-------|---------|----------|--------|----------|----------------|
| F     | 51      | GLU      | ASP    | conflict | UNP A0A0D3BZZ8 |

- Molecule 7 is a protein called DNA-directed RNA polymerase II, IV and V subunit 10.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 7   | J     | 63       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 507   | 324 | 85 | 91 | 7 |         |       |

- Molecule 8 is a protein called DNA-directed RNA polymerase RBP11-like dimerisation domain-containing protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8   | K     | 108      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 890   | 565 | 156 | 167 | 2 |         |       |

- Molecule 9 is a protein called DNA-directed RNA polymerase II, IV and V subunit 12.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 9   | L     | 45       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 365   | 224 | 70 | 67 | 4 |         |       |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference      |
|-------|---------|----------|--------|----------|----------------|
| L     | 18      | GLU      | LYS    | conflict | UNP A0A0D2ZPP3 |
| L     | 32      | CYS      | ARG    | conflict | UNP A0A0D2ZPP3 |

- Molecule 10 is a protein called DNA-directed RNA polymerase II, IV and V subunit 8.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10  | H     | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1129  | 729 | 183 | 208 | 9 |         |       |

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

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 11  | I     | 97       | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 787   | 482 | 150 | 143 | 12 |         |       |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference      |
|-------|---------|----------|--------|----------|----------------|
| I     | 20      | ARG      | LYS    | conflict | UNP A0A0D3A7P5 |
| I     | 40      | ASP      | ASN    | conflict | UNP A0A0D3A7P5 |

- Molecule 12 is a protein called RNA polymerase subunit H/Rpb5 C-terminal domain-containing protein.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 12  | E     | 209      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1706  | 1085 | 303 | 316 | 2 |         |       |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference      |
|-------|---------|----------|--------|----------|----------------|
| E     | 101     | GLY      | SER    | conflict | UNP A0A0D3DTU3 |
| E     | 182     | GLN      | HIS    | conflict | UNP A0A0D3DTU3 |
| E     | 210     | ILE      | VAL    | conflict | UNP A0A0D3DTU3 |

- Molecule 13 is a protein called DNA-directed RNA polymerase IV and V subunit 2.

| Mol | Chain | Residues | Atoms |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|----|---------|-------|
| 13  | B     | 967      | Total | C    | N    | O    | S  | 0       | 0     |
|     |       |          | 7660  | 4827 | 1357 | 1432 | 44 |         |       |

- Molecule 14 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 14  | A     | 1        | Total | Mg | 0       |
|     |       |          | 1     | 1  |         |

- Molecule 15 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms      |         | AltConf |
|-----|-------|----------|------------|---------|---------|
| 15  | A     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 15  | C     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 15  | J     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 15  | L     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 15  | I     | 2        | Total<br>2 | Zn<br>2 | 0       |





SER  
GLN  
ILE  
GLU  
ASP  
ILE  
GLN  
PRO  
ILE  
GLY  
ASN  
GLY  
GLU  
ASP  
SER  
GLN  
THR  
GLU  
PRO  
GLN  
ALA

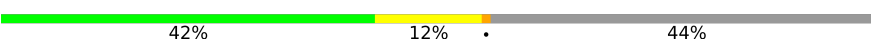
- Molecule 5: DNA-directed RNA polymerase RpoA/D/Rpb3-type domain-containing protein

Chain C: 

MET ASP THR G3 R8 T14 V40 M41 E56 S59 L62 R80 M84 E100 F101 V104 E105 F106 T114 D115 S127 V132 F137 GLY ASP SER SER GLY ALA ASP SER SER SER GLU Q148 V154 R157 E161 D175 T204 D205 D206

R227 Y237 E257 I258 K261 L280 L288 K291 D299 ASP THR VAL GLU ALA ASP ASP GLN PHE GLY GLU LEU GLY ALA HIS MET ARG GLY GLY

- Molecule 6: DNA-directed RNA polymerase RpoA/D/Rpb3-type domain-containing protein

Chain F: 

MET ALA GLU ASP TYR ASN GLU VAL ASP ASP LEU TYR GLU ASP GLU PRO ALA GLU PRO GLU ILE GLU GLY ILE GLU GLU ASP ASP MET LYS ASP ASN ASP ASP ILE ASN GLY GLY PRO LEU GLU THR GLU ASP LYS VAL THR GLU PRO VAL ARG P58 R70

L74 R77 L91 E94 T95 D96 P97 L98 E99 I100 M102 L105 R106 Q107 R108 W126 G127 W137 LYS ARG GLN VAL GLY GLY ASP

- Molecule 7: DNA-directed RNA polymerase II, IV and V subunit 10

Chain J: 

V1 T2 C7 M48 R63 THR LEU GLU LYS SER ASP ALA ASN

- Molecule 8: DNA-directed RNA polymerase RBP11-like dimerisation domain-containing protein

Chain K: 

MET ASN ALA PRO ASP R6 F10 F11 V12 K26 I75 T78 S79 Q80 E97 E108 V109 S113 ASN PRO TYR

- Molecule 9: DNA-directed RNA polymerase II, IV and V subunit 12

Chain L: 

MET ASP GLN GLN SER GLU P7 V8 T9 Y10 V11 E18 R19 T20 T27 Q28 C29 C32 R35 R43 R51

- Molecule 10: DNA-directed RNA polymerase II, IV and V subunit 8

Chain H: 



- 



- 



- 



## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 59869                                   | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | FEI TALOS ARCTICA                       | Depositor |
| Voltage (kV)                         | 300                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 1.5625                                  | Depositor |
| Minimum defocus (nm)                 | 1000                                    | Depositor |
| Maximum defocus (nm)                 | 2500                                    | Depositor |
| Magnification                        | Not provided                            |           |
| Image detector                       | GATAN K3 (6k x 4k)                      | Depositor |

## 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: MG, 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   | T     | 0.19         | 0/229   | 0.36        | 0/348          |
| 2   | N     | 0.20         | 0/391   | 0.38        | 0/599          |
| 3   | P     | 0.07         | 0/65    | 0.19        | 0/98           |
| 4   | A     | 0.15         | 0/6710  | 0.41        | 1/9058 (0.0%)  |
| 5   | C     | 0.13         | 0/2286  | 0.37        | 0/3087         |
| 6   | F     | 0.15         | 0/673   | 0.43        | 0/905          |
| 7   | J     | 0.16         | 0/515   | 0.38        | 0/696          |
| 8   | K     | 0.15         | 0/908   | 0.33        | 0/1224         |
| 9   | L     | 0.15         | 0/369   | 0.40        | 0/493          |
| 10  | H     | 0.15         | 0/1155  | 0.44        | 0/1557         |
| 11  | I     | 0.15         | 0/804   | 0.41        | 0/1081         |
| 12  | E     | 0.16         | 0/1732  | 0.47        | 0/2332         |
| 13  | B     | 0.14         | 0/7809  | 0.35        | 0/10524        |
| All | All   | 0.15         | 0/23646 | 0.39        | 1/32002 (0.0%) |

There are no bond length outliers.

All (1) bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms   | Z    | Observed(°) | Ideal(°) |
|-----|-------|------|------|---------|------|-------------|----------|
| 4   | A     | 1002 | MET  | CB-CA-C | 5.17 | 117.79      | 109.51   |

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   | T     | 205   | 0        | 114      | 7       | 0            |
| 2   | N     | 350   | 0        | 193      | 6       | 0            |
| 3   | P     | 60    | 0        | 31       | 0       | 0            |
| 4   | A     | 6597  | 0        | 6648     | 101     | 0            |
| 5   | C     | 2256  | 0        | 2269     | 23      | 0            |
| 6   | F     | 660   | 0        | 669      | 16      | 0            |
| 7   | J     | 507   | 0        | 512      | 2       | 0            |
| 8   | K     | 890   | 0        | 883      | 5       | 0            |
| 9   | L     | 365   | 0        | 364      | 9       | 0            |
| 10  | H     | 1129  | 0        | 1128     | 29      | 0            |
| 11  | I     | 787   | 0        | 736      | 15      | 0            |
| 12  | E     | 1706  | 0        | 1759     | 41      | 0            |
| 13  | B     | 7660  | 0        | 7600     | 56      | 0            |
| 14  | A     | 1     | 0        | 0        | 0       | 0            |
| 15  | A     | 1     | 0        | 0        | 0       | 0            |
| 15  | C     | 1     | 0        | 0        | 0       | 0            |
| 15  | I     | 2     | 0        | 0        | 0       | 0            |
| 15  | J     | 1     | 0        | 0        | 0       | 0            |
| 15  | L     | 1     | 0        | 0        | 0       | 0            |
| All | All   | 23179 | 0        | 22906    | 281     | 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 6.

The worst 5 of 281 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:N:10:DG:H22    | 13:B:463:LYS:HD3 | 1.46                     | 0.81              |
| 12:E:100:THR:HA  | 12:E:129:GLN:HG2 | 1.70                     | 0.73              |
| 4:A:938:HIS:HE2  | 4:A:1006:MET:HE3 | 1.54                     | 0.72              |
| 11:I:68:LEU:HD11 | 11:I:87:PHE:HB2  | 1.73                     | 0.70              |
| 4:A:592:LYS:HG3  | 4:A:596:GLU:HG3  | 1.74                     | 0.70              |

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 |     |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 4   | A     | 833/2032 (41%)  | 805 (97%)  | 28 (3%)  | 0        | 100         | 100 |
| 5   | C     | 283/319 (89%)   | 271 (96%)  | 12 (4%)  | 0        | 100         | 100 |
| 6   | F     | 78/144 (54%)    | 73 (94%)   | 5 (6%)   | 0        | 100         | 100 |
| 7   | J     | 61/71 (86%)     | 58 (95%)   | 3 (5%)   | 0        | 100         | 100 |
| 8   | K     | 106/116 (91%)   | 103 (97%)  | 3 (3%)   | 0        | 100         | 100 |
| 9   | L     | 43/51 (84%)     | 39 (91%)   | 4 (9%)   | 0        | 100         | 100 |
| 10  | H     | 139/146 (95%)   | 126 (91%)  | 13 (9%)  | 0        | 100         | 100 |
| 11  | I     | 93/114 (82%)    | 89 (96%)   | 4 (4%)   | 0        | 100         | 100 |
| 12  | E     | 207/230 (90%)   | 198 (96%)  | 9 (4%)   | 0        | 100         | 100 |
| 13  | B     | 953/1169 (82%)  | 927 (97%)  | 26 (3%)  | 0        | 100         | 100 |
| All | All   | 2796/4392 (64%) | 2689 (96%) | 107 (4%) | 0        | 100         | 100 |

There are no Ramachandran outliers to report.

### 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 |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 4   | A     | 748/1709 (44%) | 741 (99%)  | 7 (1%)   | 70          | 81  |
| 5   | C     | 253/276 (92%)  | 253 (100%) | 0        | 100         | 100 |
| 6   | F     | 72/128 (56%)   | 71 (99%)   | 1 (1%)   | 59          | 77  |
| 7   | J     | 56/63 (89%)    | 55 (98%)   | 1 (2%)   | 51          | 74  |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Analysed        | Rotameric  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 8   | K     | 98/105 (93%)    | 95 (97%)   | 3 (3%)   | 35          | 66  |
| 9   | L     | 40/46 (87%)     | 40 (100%)  | 0        | 100         | 100 |
| 10  | H     | 123/127 (97%)   | 122 (99%)  | 1 (1%)   | 73          | 82  |
| 11  | I     | 85/101 (84%)    | 85 (100%)  | 0        | 100         | 100 |
| 12  | E     | 190/209 (91%)   | 187 (98%)  | 3 (2%)   | 55          | 75  |
| 13  | B     | 846/1026 (82%)  | 842 (100%) | 4 (0%)   | 81          | 85  |
| All | All   | 2511/3790 (66%) | 2491 (99%) | 20 (1%)  | 70          | 82  |

5 of 20 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 12  | E     | 203  | TYR  |
| 13  | B     | 279  | PHE  |
| 13  | B     | 670  | TRP  |
| 13  | B     | 291  | VAL  |
| 4   | A     | 1073 | ASP  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 13  | B     | 473 | ASN  |
| 13  | B     | 648 | HIS  |
| 13  | B     | 720 | GLN  |
| 13  | B     | 529 | ASN  |
| 10  | H     | 106 | GLN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed   | Backbone Outliers | Pucker Outliers |
|-----|-------|------------|-------------------|-----------------|
| 3   | P     | 2/20 (10%) | 0                 | 0               |

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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.