



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:52 AM GMT

PDB ID : 2BYR  
Title : CRYSTAL STRUCTURE OF ACHBP FROM APLYSIA CALIFORNICA IN COMPLEX WITH METHYLLYCACONITINE  
Authors : Hansen, S.B.; Sulzenbacher, G.; Huxford, T.; Marchot, P.; Taylor, P.; Bourne, Y.  
Deposited on : 2005-08-03  
Resolution : 2.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

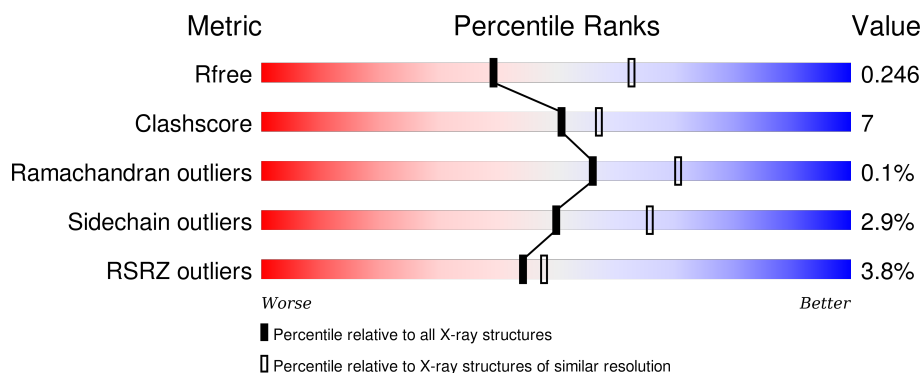
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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) | Similar resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|---|
| $R_{free}$            | 91344                       | 4776 (2.50-2.42)                                      |
| Clashscore            | 102246                      | 1030 (2.48-2.44)                                      |
| Ramachandran outliers | 100387                      | 1024 (2.48-2.44)                                      |
| Sidechain outliers    | 100360                      | 1024 (2.48-2.44)                                      |
| RSRZ outliers         | 91569                       | 4787 (2.50-2.42)                                      |

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ . 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     | 227    | <div> <div>80%</div> <div>11% • 6%</div> </div> |
| 1   | B     | 227    | <div> <div>81%</div> <div>11% • 7%</div> </div> |
| 1   | C     | 227    | <div> <div>81%</div> <div>11% • 7%</div> </div> |
| 1   | D     | 227    | <div> <div>82%</div> <div>11% 7%</div> </div>   |
| 1   | E     | 227    | <div> <div>82%</div> <div>12% 6%</div> </div>   |

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| Mol | Chain | Length | Quality of chain   |
|-----|-------|--------|--|
| 1   | F     | 227    | <div><div></div><div>3%</div><div>79%</div><div>12%</div><div>8%</div></div>   |
| 1   | G     | 227    | <div><div></div><div>3%</div><div>82%</div><div>7%</div><div>10%</div></div>   |
| 1   | H     | 227    | <div><div></div><div>14%</div><div>78%</div><div>10%</div><div>10%</div></div> |
| 1   | I     | 227    | <div><div></div><div>5%</div><div>83%</div><div>11%</div><div>6%</div></div>   |
| 1   | J     | 227    | <div><div></div><div>%</div><div>86%</div><div>7%</div><div>7%</div></div>     |

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18062 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 ACETYLCHOLINE-BINDING PROTEIN.

| Mol | Chain | Residues | Atoms |      |     |     |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 1   | A     | 213      | Total | C    | N   | O   | S  | 0       | 7       | 0     |
|     |       |          | 1737  | 1096 | 289 | 342 | 10 |         |         |       |
| 1   | B     | 210      | Total | C    | N   | O   | S  | 0       | 8       | 0     |
|     |       |          | 1714  | 1082 | 288 | 334 | 10 |         |         |       |
| 1   | C     | 210      | Total | C    | N   | O   | S  | 0       | 5       | 0     |
|     |       |          | 1699  | 1073 | 284 | 333 | 9  |         |         |       |
| 1   | D     | 211      | Total | C    | N   | O   | S  | 0       | 6       | 0     |
|     |       |          | 1720  | 1084 | 290 | 337 | 9  |         |         |       |
| 1   | E     | 214      | Total | C    | N   | O   | S  | 0       | 4       | 0     |
|     |       |          | 1733  | 1090 | 290 | 343 | 10 |         |         |       |
| 1   | F     | 209      | Total | C    | N   | O   | S  | 0       | 6       | 0     |
|     |       |          | 1700  | 1074 | 284 | 333 | 9  |         |         |       |
| 1   | G     | 205      | Total | C    | N   | O   | S  | 0       | 1       | 0     |
|     |       |          | 1637  | 1035 | 267 | 326 | 9  |         |         |       |
| 1   | H     | 204      | Total | C    | N   | O   | S  | 0       | 1       | 0     |
|     |       |          | 1634  | 1032 | 270 | 324 | 8  |         |         |       |
| 1   | I     | 213      | Total | C    | N   | O   | S  | 0       | 4       | 0     |
|     |       |          | 1724  | 1085 | 287 | 343 | 9  |         |         |       |
| 1   | J     | 212      | Total | C    | N   | O   | S  | 0       | 5       | 0     |
|     |       |          | 1718  | 1084 | 285 | 339 | 10 |         |         |       |

There are 80 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| A     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| A     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| A     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| A     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| A     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| A     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| A     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| A     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| B     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |

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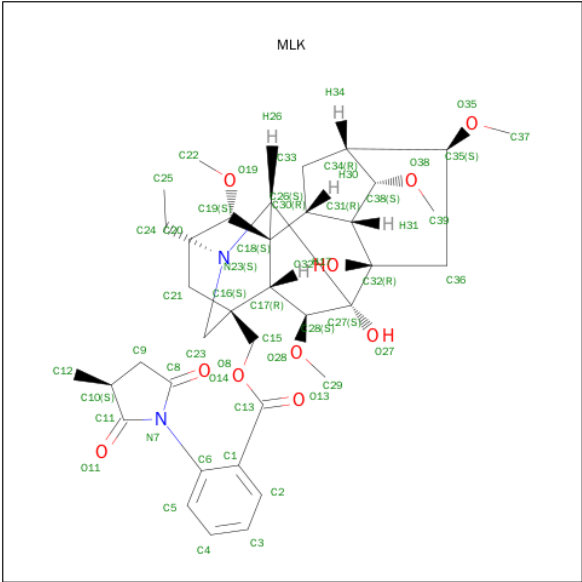
| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| B     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| B     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| B     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| B     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| B     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| B     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| B     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| C     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| D     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| E     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| F     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| G     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| G     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| G     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| G     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| G     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| G     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| G     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| G     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| H     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| I     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | -7      | TYR      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | -6      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | -5      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | -4      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | -3      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | -2      | ASP      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | -1      | LYS      | -      | EXPRESSION TAG | UNP Q8WSF8 |
| J     | 0       | LEU      | -      | EXPRESSION TAG | UNP Q8WSF8 |

- Molecule 2 is METHYLLYCACONITINE (three-letter code: MLK) (formula: C<sub>37</sub>H<sub>50</sub>N<sub>2</sub>O<sub>10</sub>).



| Mol | Chain | Residues | Atoms |    |   |    | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---|----|---------|---------|
| 2   | A     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | B     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | C     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | D     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | E     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | F     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | G     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | H     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | I     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |
| 2   | J     | 1        | Total | C  | N | O  | 0       | 0       |
|     |       |          | 49    | 37 | 2 | 10 |         |         |

- Molecule 3 is water.

| Mol | Chain | Residues | Atoms |     | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 3   | A     | 113      | Total | O   | 0       | 0       |
|     |       |          | 113   | 113 |         |         |
| 3   | B     | 91       | Total | O   | 0       | 0       |
|     |       |          | 91    | 91  |         |         |

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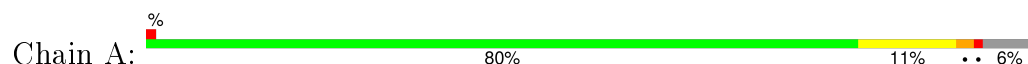
| Mol | Chain | Residues | Atoms       |         | ZeroOcc | AltConf |
|-----|-------|----------|-------------|---------|---------|---------|
| 3   | C     | 54       | Total<br>54 | O<br>54 | 0       | 0       |
| 3   | D     | 58       | Total<br>58 | O<br>58 | 0       | 0       |
| 3   | E     | 88       | Total<br>88 | O<br>88 | 0       | 0       |
| 3   | F     | 32       | Total<br>32 | O<br>32 | 0       | 0       |
| 3   | G     | 23       | Total<br>23 | O<br>23 | 0       | 0       |
| 3   | H     | 14       | Total<br>14 | O<br>14 | 0       | 0       |
| 3   | I     | 29       | Total<br>29 | O<br>29 | 0       | 0       |
| 3   | J     | 54       | Total<br>54 | O<br>54 | 0       | 0       |



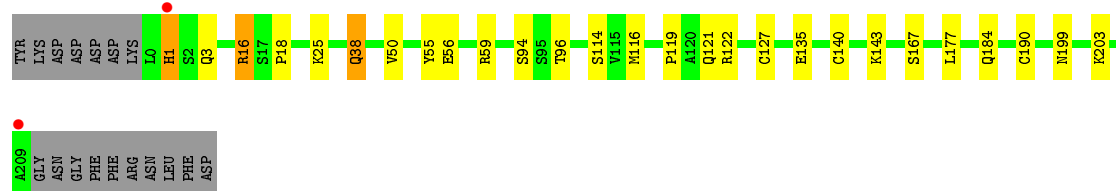
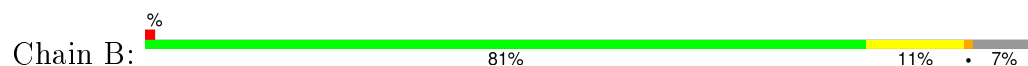
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

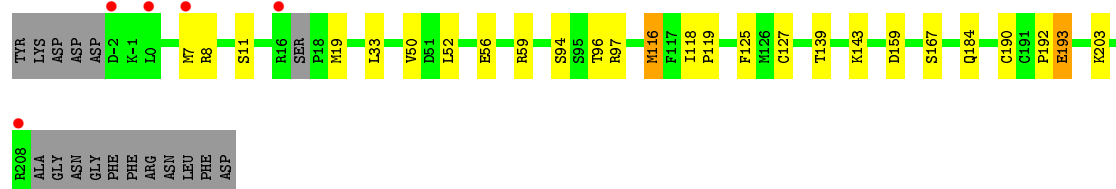
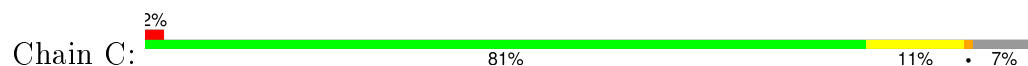
#### • Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



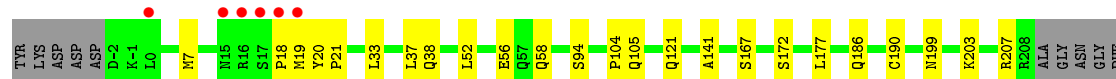
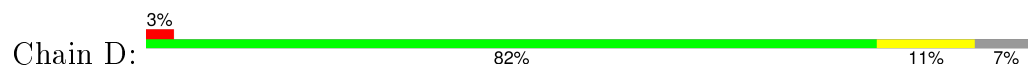
#### • Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



#### • Molecule 1: ACETYLCHOLINE-BINDING PROTEIN




#### • Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



PHE  
ARG  
ASN  
LEU  
PHE  
ASP


• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain E: 

Tyr Lys D-5 D-4 D-3 H7 R16 S17 P18 K25 T30 Q38 V50 E51 L52 E56 D57 Q58 R59 N70 S94 V101 Q105 M116 P119 R122 F125 M126 C127 C140 K143 K157 S167 E175 Q184 R207 R208 ALA

GLY  
ASN  
GLY  
PHE  
PHE  
ARG  
ASN  
PHE  
ASP


• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain F: 

Tyr Lys Asp Asp Asp Lys L0 H1 N5 M15 R16 S17 P18 M19 Y20 L33 G34 F35 Q38 V50 D51 L52 E56 T75 V99 Q105 P119 A120 R122 C127 A141 V142 K143 V148 L156 S167 Y168 Y169 A170 S171 S172 E175

M199 R207 R208 ALA GLY ASN GLY PHE PHE ARG ASN LEU PHE ASP


• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain G: 

Tyr Lys Asp Asp Asp Lys Lys His His Ser Q3 A4 N5 L6 M7 L13 R16 S17 P18 M19 L33 T36 L37 Q38 E56 Q57 Q58 S94 S95 T96 P119 K157 L177 Q186 C190 C191 P192 L200 K203 R207 ARG ALA GLY ASN GLY PHE

PHE  
ARG  
ASN  
LEU  
PHE  
ASP


• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain H: 

Tyr Lys Asp Asp Asp Lys Lys His His Ser Pro Met Y20 L33 G34 F35 T36 Q38 D39 I40 L52 Y55 E56 Q57 Q58 L65 M70 E71 Y72 Q73 N74 R79 S94 Q105 V108 R122 F125 E135 A138

T139 C140 A141 V142 K143 Y149 F152 E153 I154 D155 L156 K157 T160 D161 S167 Y168 Y169 A170 S171 G172 K173 Y174 E175 V185 C190 E193 P194 S195 E196 R205 E206 R207 ARG ALA GLY ASN GLY PHE PHE ARG ASN PHE ASP

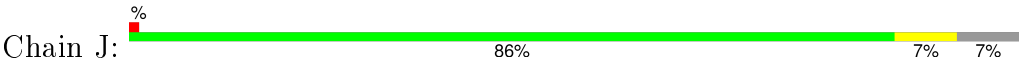
• Molecule 1: ACETYLCHOLINE-BINDING PROTEIN

Chain I: 

Tyr Lys D-5 L0 H1 H7 N15 R16 S17 P18 MET Y20 Y21 G22 K25 D26 D27 T36 L37 Q38 S45 V50 D51 L52 E56 Q57 Q58 R59 S94 S95 T96 M116 R122 C127 D128 P129 K157 K173 Q186 S189 C190 Y195



● Molecule 1: ACETYLCHOLINE-BINDING PROTEIN



## 4 Data and refinement statistics

| Property  | Value   | Source           |
|---|---|------------------|
| Space group   | P 1 21 1  | Depositor        |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$                | 67.27Å 135.78Å 147.29Å<br>90.00° 99.46° 90.00°              | Depositor        |
| Resolution (Å)  | 20.00 – 2.45<br>66.35 – 2.45                                | Depositor<br>EDS |
| % Data completeness<br>(in resolution range)                            | 100.0 (20.00-2.45)<br>98.5 (66.35-2.45)                     | Depositor<br>EDS |
| $R_{merge}$   | 0.08  | Depositor        |
| $R_{sym}$   | 0.08  | Depositor        |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>                              | 2.47 (at 2.45Å)   | Xtriage          |
| Refinement program  | REFMAC 5.2.0005   | Depositor        |
| R, $R_{free}$   | 0.193 , 0.232<br>0.213 , 0.246                              | Depositor<br>DCC |
| $R_{free}$ test set   | 1888 reflections (2.05%)                                    | DCC              |
| Wilson B-factor (Å <sup>2</sup> )                                       | 36.8  | Xtriage          |
| Anisotropy  | 0.237   | Xtriage          |
| Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> ) | 0.34 , 44.1   | EDS              |
| Estimated twinning fraction   | No twinning to report.                                      | Xtriage          |
| L-test for twinning <sup>2</sup>  | $\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$ | Xtriage          |
| Outliers  | 3 of 94321 reflections (0.003%)                             | Xtriage          |
| $F_o, F_c$ correlation  | 0.93  | EDS              |
| Total number of atoms   | 18062   | wwPDB-VP         |
| Average B, all atoms (Å <sup>2</sup> )                                  | 45.0  | wwPDB-VP         |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.38% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: MLK

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     | 0.48         | 0/1806      | 0.71        | 3/2458 (0.1%)  |
| 1   | B     | 0.46         | 0/1787      | 0.64        | 2/2432 (0.1%)  |
| 1   | C     | 0.43         | 0/1761      | 0.63        | 0/2397         |
| 1   | D     | 0.40         | 0/1785      | 0.62        | 0/2430         |
| 1   | E     | 0.46         | 0/1790      | 0.63        | 1/2437 (0.0%)  |
| 1   | F     | 0.40         | 0/1765      | 0.65        | 2/2405 (0.1%)  |
| 1   | G     | 0.39         | 0/1681      | 0.57        | 0/2293         |
| 1   | H     | 0.38         | 0/1677      | 0.55        | 0/2286         |
| 1   | I     | 0.39         | 0/1779      | 0.57        | 0/2422         |
| 1   | J     | 0.41         | 0/1779      | 0.58        | 0/2422         |
| All | All   | 0.42         | 0/17610     | 0.62        | 8/23982 (0.0%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | B     | 0                   | 1                   |
| 1   | C     | 0                   | 1                   |
| 1   | D     | 0                   | 1                   |
| 1   | F     | 0                   | 1                   |
| 1   | G     | 0                   | 1                   |
| 1   | H     | 0                   | 1                   |
| All | All   | 0                   | 6                   |

There are no bond length outliers.

All (8) bond angle outliers are listed below:

| Mol | Chain | Res    | Type | Atoms     | Z     | Observed(°) | Ideal(°) |
|-----|-------|--------|------|-----------|-------|-------------|----------|
| 1   | A     | 208    | ARG  | NE-CZ-NH1 | 7.39  | 124.00      | 120.30   |
| 1   | F     | 207[A] | ARG  | NE-CZ-NH2 | 6.34  | 123.47      | 120.30   |
| 1   | F     | 207[B] | ARG  | NE-CZ-NH2 | 6.34  | 123.47      | 120.30   |
| 1   | A     | 16     | ARG  | NE-CZ-NH1 | 6.00  | 123.30      | 120.30   |
| 1   | B     | 140    | CYS  | CA-CB-SG  | -5.54 | 104.04      | 114.00   |
| 1   | B     | 16     | ARG  | NE-CZ-NH1 | 5.37  | 122.99      | 120.30   |
| 1   | A     | 207    | ARG  | NE-CZ-NH1 | 5.10  | 122.85      | 120.30   |
| 1   | E     | 140    | CYS  | CA-CB-SG  | -5.03 | 104.95      | 114.00   |

There are no chirality outliers.

All (6) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group   |
|-----|-------|-----|------|---------|
| 1   | B     | 1   | HIS  | Peptide |
| 1   | C     | 190 | CYS  | Peptide |
| 1   | D     | 190 | CYS  | Peptide |
| 1   | F     | 0   | LEU  | Peptide |
| 1   | G     | 190 | CYS  | Peptide |
| 1   | H     | 190 | CYS  | Peptide |

## 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     | 1737  | 0        | 1672     | 35      | 0            |
| 1   | B     | 1714  | 0        | 1655     | 27      | 0            |
| 1   | C     | 1699  | 0        | 1634     | 15      | 0            |
| 1   | D     | 1720  | 0        | 1656     | 23      | 0            |
| 1   | E     | 1733  | 0        | 1661     | 23      | 0            |
| 1   | F     | 1700  | 0        | 1637     | 31      | 0            |
| 1   | G     | 1637  | 0        | 1565     | 14      | 0            |
| 1   | H     | 1634  | 0        | 1563     | 16      | 0            |
| 1   | I     | 1724  | 0        | 1650     | 36      | 0            |
| 1   | J     | 1718  | 0        | 1652     | 17      | 0            |
| 2   | A     | 49    | 0        | 50       | 4       | 0            |
| 2   | B     | 49    | 0        | 50       | 3       | 0            |
| 2   | C     | 49    | 0        | 50       | 3       | 0            |
| 2   | D     | 49    | 0        | 50       | 3       | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 2   | E     | 49    | 0        | 50       | 7       | 0            |
| 2   | F     | 49    | 0        | 50       | 6       | 0            |
| 2   | G     | 49    | 0        | 50       | 4       | 0            |
| 2   | H     | 49    | 0        | 50       | 6       | 0            |
| 2   | I     | 49    | 0        | 50       | 6       | 0            |
| 2   | J     | 49    | 0        | 50       | 3       | 0            |
| 3   | A     | 113   | 0        | 0        | 1       | 0            |
| 3   | B     | 91    | 0        | 0        | 3       | 0            |
| 3   | C     | 54    | 0        | 0        | 0       | 0            |
| 3   | D     | 58    | 0        | 0        | 1       | 0            |
| 3   | E     | 88    | 0        | 0        | 3       | 0            |
| 3   | F     | 32    | 0        | 0        | 1       | 0            |
| 3   | G     | 23    | 0        | 0        | 0       | 0            |
| 3   | H     | 14    | 0        | 0        | 0       | 0            |
| 3   | I     | 29    | 0        | 0        | 1       | 0            |
| 3   | J     | 54    | 0        | 0        | 0       | 0            |
| All | All   | 18062 | 0        | 16845    | 237     | 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 7.

All (237) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1              | Atom-2              | Interatomic distance (Å) | Clash overlap (Å) |
|---------------------|---------------------|--------------------------|-------------------|
| 1:A:59[B]:ARG:HD3   | 1:A:116[B]:MET:CE   | 1.17                     | 1.60              |
| 1:I:59[B]:ARG:CG    | 1:I:116[B]:MET:HE3  | 1.31                     | 1.54              |
| 1:I:59[B]:ARG:CG    | 1:I:116[B]:MET:CE   | 1.94                     | 1.46              |
| 1:A:59[B]:ARG:CD    | 1:A:116[B]:MET:CE   | 2.09                     | 1.28              |
| 1:A:59[B]:ARG:CD    | 1:A:116[B]:MET:HE2  | 1.65                     | 1.19              |
| 1:I:59[B]:ARG:HG3   | 1:I:116[B]:MET:CE   | 1.60                     | 1.19              |
| 1:I:59[B]:ARG:CD    | 1:I:116[B]:MET:HE3  | 1.88                     | 1.03              |
| 1:A:59[B]:ARG:HD3   | 1:A:116[B]:MET:HE1  | 1.43                     | 1.01              |
| 1:I:59[B]:ARG:CD    | 1:I:116[B]:MET:CE   | 2.37                     | 1.00              |
| 1:I:59[B]:ARG:HG2   | 1:I:116[B]:MET:HE3  | 0.95                     | 0.94              |
| 1:G:186:GLN:HE22    | 2:G:301:MLK:H4      | 1.34                     | 0.91              |
| 1:I:59[B]:ARG:HG3   | 1:I:116[B]:MET:HE1  | 1.53                     | 0.91              |
| 1:A:59[B]:ARG:HD3   | 1:A:116[B]:MET:SD   | 2.14                     | 0.86              |
| 1:F:171:SER:HA      | 1:F:207[B]:ARG:HH12 | 1.40                     | 0.86              |
| 1:A:59[B]:ARG:CD    | 1:A:116[B]:MET:HE1  | 2.01                     | 0.86              |
| 1:F:207[A]:ARG:HH21 | 1:F:207[A]:ARG:HG2  | 1.39                     | 0.86              |
| 1:D:37:LEU:HD11     | 1:D:52:LEU:HD11     | 1.57                     | 0.85              |

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| Atom-1              | Atom-2              | Interatomic distance (Å) | Clash overlap (Å) |
|---------------------|---------------------|--------------------------|-------------------|
| 1:C:139:THR:OG1     | 1:C:203:LYS:NZ      | 2.10                     | 0.84              |
| 1:I:59[A]:ARG:HH11  | 1:I:116[A]:MET:CE   | 1.90                     | 0.84              |
| 1:I:59[B]:ARG:CG    | 1:I:116[B]:MET:HE1  | 2.03                     | 0.82              |
| 1:H:38:GLN:HA       | 1:H:38:GLN:HE21     | 1.41                     | 0.82              |
| 1:I:59[B]:ARG:HD3   | 1:I:116[B]:MET:CE   | 2.12                     | 0.80              |
| 1:I:59[B]:ARG:CD    | 1:I:116[B]:MET:HE1  | 2.10                     | 0.79              |
| 1:A:59[B]:ARG:CG    | 1:A:116[B]:MET:SD   | 2.72                     | 0.78              |
| 1:A:59[B]:ARG:HD3   | 1:A:116[B]:MET:HE2  | 0.78                     | 0.77              |
| 1:I:59[B]:ARG:HG2   | 1:I:116[B]:MET:CE   | 1.82                     | 0.76              |
| 2:F:301:MLK:C12     | 1:J:38[B]:GLN:HE21  | 1.99                     | 0.76              |
| 1:B:143:LYS:HE3     | 1:B:184:GLN:HE22    | 1.51                     | 0.75              |
| 1:I:59[A]:ARG:HH11  | 1:I:116[A]:MET:HE1  | 1.51                     | 0.73              |
| 1:C:97[B]:ARG:HH11  | 1:C:97[B]:ARG:HG3   | 1.53                     | 0.73              |
| 2:F:301:MLK:H122    | 1:J:38[B]:GLN:HE21  | 1.53                     | 0.73              |
| 1:H:173:LYS:NZ      | 1:I:45:SER:O        | 2.22                     | 0.72              |
| 1:A:59[B]:ARG:NE    | 1:A:116[B]:MET:HE1  | 2.05                     | 0.71              |
| 1:D:207[B]:ARG:HG3  | 1:D:207[B]:ARG:HH21 | 1.55                     | 0.71              |
| 1:I:59[B]:ARG:HG3   | 1:I:116[B]:MET:HE2  | 1.68                     | 0.70              |
| 1:B:59[B]:ARG:HH21  | 1:B:59[B]:ARG:HG3   | 1.55                     | 0.70              |
| 1:G:38[B]:GLN:NE2   | 2:H:301:MLK:H122    | 2.06                     | 0.70              |
| 1:I:186:GLN:HE22    | 2:I:301:MLK:C4      | 2.05                     | 0.69              |
| 1:F:171:SER:CA      | 1:F:207[B]:ARG:HH12 | 2.06                     | 0.69              |
| 1:C:192:PRO:HD2     | 1:C:193:GLU:OE2     | 1.93                     | 0.68              |
| 1:C:50:VAL:HG21     | 1:C:127:CYS:SG      | 2.34                     | 0.68              |
| 1:C:52:LEU:HG       | 1:C:125:PHE:HE2     | 1.60                     | 0.67              |
| 1:J:177:LEU:HB2     | 1:J:203[A]:LYS:HG2  | 1.77                     | 0.66              |
| 1:B:50:VAL:HG21     | 1:B:127:CYS:SG      | 2.36                     | 0.66              |
| 1:J:143:LYS:NZ      | 1:J:184:GLN:HE22    | 1.94                     | 0.66              |
| 1:F:119:PRO:HB2     | 1:F:121[B]:GLN:HE21 | 1.62                     | 0.65              |
| 1:D:172:SER:O       | 1:D:207[A]:ARG:HD2  | 1.95                     | 0.65              |
| 1:H:38:GLN:HE22     | 1:H:167:SER:HB2     | 1.61                     | 0.65              |
| 1:F:1:HIS:CE1       | 1:F:5:ASN:HD21      | 2.14                     | 0.65              |
| 1:A:59[B]:ARG:CD    | 1:A:116[B]:MET:SD   | 2.79                     | 0.64              |
| 1:B:25:LYS:NZ       | 3:B:2004:HOH:O      | 2.31                     | 0.64              |
| 1:E:207[B]:ARG:HH11 | 1:E:207[B]:ARG:HG3  | 1.64                     | 0.63              |
| 1:F:38[A]:GLN:HE22  | 1:F:167:SER:HB3     | 1.64                     | 0.63              |
| 1:D:207[B]:ARG:HH21 | 1:D:207[B]:ARG:CG   | 2.12                     | 0.63              |
| 1:A:139:THR:HG23    | 1:A:203[A]:LYS:HD3  | 1.79                     | 0.63              |
| 1:A:-3:ASP:OD2      | 1:A:-3:ASP:C        | 2.38                     | 0.62              |
| 1:D:38[A]:GLN:HE21  | 2:E:301:MLK:H122    | 1.65                     | 0.62              |
| 1:B:143:LYS:NZ      | 3:B:2059:HOH:O      | 2.34                     | 0.61              |

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| Atom-1             | Atom-2              | Interatomic distance (Å) | Clash overlap (Å) |
|--------------------|---------------------|--------------------------|-------------------|
| 1:G:38[B]:GLN:HE22 | 2:H:301:MLK:H122    | 1.63                     | 0.61              |
| 2:A:301:MLK:H9C1   | 1:E:167:SER:HB2     | 1.82                     | 0.61              |
| 1:I:186:GLN:HE22   | 2:I:301:MLK:H4      | 1.66                     | 0.60              |
| 1:I:59[A]:ARG:HH11 | 1:I:116[A]:MET:HE2  | 1.65                     | 0.60              |
| 1:F:175:GLU:HB3    | 1:F:207[B]:ARG:CD   | 2.31                     | 0.60              |
| 1:B:38[A]:GLN:NE2  | 1:B:167:SER:O       | 2.35                     | 0.60              |
| 1:H:38:GLN:CA      | 1:H:38:GLN:HE21     | 2.13                     | 0.60              |
| 1:A:16:ARG:HH11    | 1:A:16:ARG:HG2      | 1.67                     | 0.59              |
| 1:A:16:ARG:HH11    | 1:A:16:ARG:CG       | 2.15                     | 0.59              |
| 1:G:36:THR:HG22    | 1:G:38[A]:GLN:HE22  | 1.67                     | 0.59              |
| 1:G:36:THR:HG22    | 1:G:38[A]:GLN:NE2   | 2.17                     | 0.59              |
| 1:I:59[B]:ARG:HD3  | 1:I:116[B]:MET:HE3  | 1.73                     | 0.59              |
| 1:I:36:THR:HG22    | 1:I:38[B]:GLN:HE22  | 1.66                     | 0.59              |
| 1:D:38[A]:GLN:HE21 | 2:E:301:MLK:C12     | 2.16                     | 0.58              |
| 1:G:186:GLN:HE22   | 2:G:301:MLK:C4      | 2.11                     | 0.58              |
| 1:E:207[B]:ARG:CG  | 1:E:207[B]:ARG:HH11 | 2.17                     | 0.58              |
| 1:D:172:SER:O      | 1:D:207[A]:ARG:CD   | 2.52                     | 0.58              |
| 1:A:104:PRO:C      | 1:A:105[B]:GLN:HE21 | 2.08                     | 0.58              |
| 1:I:207:ARG:HG3    | 1:I:207:ARG:HH21    | 1.69                     | 0.57              |
| 1:F:171:SER:HA     | 1:F:207[B]:ARG:NH1  | 2.15                     | 0.57              |
| 1:H:94:SER:HB3     | 2:H:301:MLK:H121    | 1.87                     | 0.56              |
| 1:F:119:PRO:HG2    | 1:F:121[B]:GLN:HE22 | 1.71                     | 0.56              |
| 1:E:143:LYS:HE3    | 1:E:184:GLN:HE22    | 1.70                     | 0.56              |
| 1:A:59[B]:ARG:HG2  | 1:A:116[B]:MET:SD   | 2.46                     | 0.55              |
| 1:B:143:LYS:HE3    | 1:B:184:GLN:NE2     | 2.21                     | 0.55              |
| 1:E:175:GLU:HB3    | 1:E:207[B]:ARG:NH1  | 2.21                     | 0.55              |
| 1:A:207:ARG:HG2    | 1:A:207:ARG:HH11    | 1.71                     | 0.55              |
| 1:C:94:SER:HB3     | 2:C:301:MLK:H121    | 1.88                     | 0.55              |
| 1:J:143:LYS:HZ2    | 1:J:184:GLN:HE22    | 1.54                     | 0.55              |
| 1:B:59[A]:ARG:HD2  | 1:B:116[A]:MET:CE   | 2.37                     | 0.55              |
| 1:B:59[B]:ARG:HH21 | 1:B:59[B]:ARG:CG    | 2.20                     | 0.55              |
| 1:F:169:TYR:CZ     | 1:F:171:SER:HB2     | 2.42                     | 0.55              |
| 1:B:50:VAL:CG2     | 1:B:127:CYS:SG      | 2.95                     | 0.55              |
| 1:C:143:LYS:NZ     | 1:C:184:GLN:HE22    | 2.05                     | 0.55              |
| 1:J:50:VAL:HG21    | 1:J:127:CYS:SG      | 2.47                     | 0.54              |
| 1:I:7:MET:SD       | 1:J:18:PRO:HB2      | 2.47                     | 0.54              |
| 2:E:301:MLK:O28    | 2:E:301:MLK:H31     | 2.06                     | 0.54              |
| 1:G:177:LEU:HB2    | 1:G:203:LYS:HG2     | 1.88                     | 0.54              |
| 1:D:94:SER:HB3     | 2:D:301:MLK:H121    | 1.88                     | 0.54              |
| 1:B:122:ARG:HD2    | 1:C:96:THR:O        | 2.08                     | 0.53              |
| 1:D:167:SER:HB2    | 2:E:301:MLK:H9C1    | 1.90                     | 0.53              |

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| Atom-1             | Atom-2              | Interatomic distance (Å) | Clash overlap (Å) |
|--------------------|---------------------|--------------------------|-------------------|
| 1:D:56:GLU:OE2     | 1:D:58:GLN:NE2      | 2.40                     | 0.53              |
| 1:A:18:PRO:HB2     | 1:E:7:MET:SD        | 2.48                     | 0.53              |
| 1:B:16:ARG:HH11    | 1:B:16:ARG:HG3      | 1.74                     | 0.52              |
| 1:A:208:ARG:CG     | 1:A:208:ARG:HH11    | 2.22                     | 0.52              |
| 1:D:37:LEU:HD11    | 1:D:52:LEU:CD1      | 2.35                     | 0.52              |
| 1:E:57:GLN:NE2     | 3:E:2022:HOH:O      | 2.29                     | 0.52              |
| 1:F:50:VAL:HG21    | 1:F:127:CYS:SG      | 2.51                     | 0.51              |
| 1:F:119:PRO:HB2    | 1:F:121[B]:GLN:NE2  | 2.25                     | 0.50              |
| 1:E:50:VAL:HG21    | 1:E:127:CYS:SG      | 2.51                     | 0.50              |
| 1:I:38[A]:GLN:HE21 | 2:J:301:MLK:H122    | 1.77                     | 0.50              |
| 1:E:175:GLU:HB3    | 1:E:207[B]:ARG:HH12 | 1.76                     | 0.50              |
| 2:B:301:MLK:H31    | 2:B:301:MLK:O28     | 2.10                     | 0.50              |
| 1:D:141:ALA:HB1    | 1:D:199:ASN:HD21    | 1.76                     | 0.50              |
| 1:D:56:GLU:CD      | 1:D:58:GLN:HE21     | 2.14                     | 0.49              |
| 1:G:94:SER:HB3     | 2:G:301:MLK:H121    | 1.94                     | 0.49              |
| 1:B:177:LEU:HD12   | 1:B:203[B]:LYS:HG2  | 1.95                     | 0.49              |
| 2:F:301:MLK:H123   | 1:J:38[B]:GLN:HE21  | 1.75                     | 0.49              |
| 1:H:122:ARG:HD2    | 1:I:96:THR:O        | 2.12                     | 0.49              |
| 2:I:301:MLK:H31    | 2:I:301:MLK:O28     | 2.12                     | 0.49              |
| 1:F:141:ALA:HB1    | 1:F:199:ASN:HD21    | 1.78                     | 0.49              |
| 1:A:50:VAL:HG21    | 1:A:127:CYS:SG      | 2.53                     | 0.49              |
| 2:J:301:MLK:O28    | 2:J:301:MLK:H31     | 2.13                     | 0.48              |
| 1:E:56:GLU:O       | 1:E:119:PRO:HD2     | 2.14                     | 0.48              |
| 1:F:171:SER:C      | 1:F:207[B]:ARG:HH12 | 2.17                     | 0.48              |
| 2:F:301:MLK:O28    | 2:F:301:MLK:H31     | 2.14                     | 0.48              |
| 1:C:167:SER:HB2    | 2:D:301:MLK:H9C1    | 1.94                     | 0.48              |
| 1:D:104:PRO:C      | 1:D:105[B]:GLN:HE21 | 2.17                     | 0.48              |
| 1:A:59[B]:ARG:HG3  | 1:A:116[B]:MET:SD   | 2.53                     | 0.48              |
| 1:C:56:GLU:O       | 1:C:119:PRO:HD2     | 2.13                     | 0.48              |
| 1:A:37:LEU:HD13    | 1:A:163:VAL:HG11    | 1.95                     | 0.48              |
| 2:G:301:MLK:O28    | 2:G:301:MLK:H31     | 2.13                     | 0.48              |
| 1:I:186:GLN:NE2    | 2:I:301:MLK:H4      | 2.29                     | 0.48              |
| 1:A:122:ARG:HD2    | 1:B:96:THR:O        | 2.14                     | 0.48              |
| 1:D:177:LEU:HD12   | 1:D:203:LYS:HG2     | 1.96                     | 0.48              |
| 1:E:59[A]:ARG:HG2  | 1:E:116[A]:MET:SD   | 2.53                     | 0.48              |
| 1:C:50:VAL:CG2     | 1:C:127:CYS:SG      | 3.01                     | 0.48              |
| 1:H:3:GLN:NE2      | 1:I:27:ASP:OD2      | 2.41                     | 0.48              |
| 1:H:38:GLN:NE2     | 1:H:38:GLN:HA       | 2.19                     | 0.47              |
| 1:J:38[A]:GLN:NE2  | 1:J:167:SER:OG      | 2.47                     | 0.47              |
| 1:F:105[B]:GLN:OE1 | 1:F:119:PRO:HB3     | 2.14                     | 0.47              |
| 2:A:301:MLK:C9     | 1:E:167:SER:HB2     | 2.43                     | 0.47              |

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| Atom-1             | Atom-2             | Interatomic distance (Å) | Clash overlap (Å) |
|--------------------|--------------------|--------------------------|-------------------|
| 1:B:167:SER:HB2    | 2:C:301:MLK:H9C1   | 1.96                     | 0.47              |
| 3:F:2002:HOH:O     | 1:J:3:GLN:HG2      | 2.13                     | 0.47              |
| 1:E:30:THR:CG2     | 1:E:157:LYS:HG3    | 2.45                     | 0.47              |
| 1:E:38:GLN:HE21    | 1:E:38:GLN:HA      | 1.80                     | 0.47              |
| 1:H:38:GLN:OE1     | 1:H:55:TYR:CE1     | 2.68                     | 0.47              |
| 2:A:301:MLK:O28    | 2:A:301:MLK:H31    | 2.15                     | 0.47              |
| 1:E:59[A]:ARG:HD3  | 1:E:116[A]:MET:HE1 | 1.96                     | 0.47              |
| 1:H:175:GLU:HB3    | 1:H:207:ARG:HG3    | 1.96                     | 0.47              |
| 1:E:52:LEU:HG      | 1:E:125:PHE:HE2    | 1.80                     | 0.46              |
| 1:A:94:SER:HB3     | 2:A:301:MLK:H121   | 1.96                     | 0.46              |
| 1:I:59[B]:ARG:NE   | 1:I:116[B]:MET:HE1 | 2.30                     | 0.46              |
| 1:E:59[A]:ARG:HD3  | 1:E:116[A]:MET:CE  | 2.46                     | 0.46              |
| 1:D:7:MET:SD       | 1:E:18:PRO:HB2     | 2.55                     | 0.46              |
| 1:G:56:GLU:OE2     | 1:G:58:GLN:NE2     | 2.38                     | 0.46              |
| 1:A:207:ARG:HD3    | 3:A:2095:HOH:O     | 2.15                     | 0.46              |
| 1:B:59[B]:ARG:CZ   | 1:B:114[B]:SER:HB2 | 2.46                     | 0.46              |
| 1:F:119:PRO:HG2    | 1:F:121[B]:GLN:NE2 | 2.30                     | 0.46              |
| 1:B:94:SER:HB3     | 2:B:301:MLK:H121   | 1.99                     | 0.45              |
| 1:A:177:LEU:HB2    | 1:A:203[B]:LYS:HG2 | 1.98                     | 0.45              |
| 1:A:96:THR:O       | 1:E:122:ARG:HD2    | 2.16                     | 0.45              |
| 1:G:37:LEU:C       | 1:G:38[A]:GLN:HE21 | 2.20                     | 0.45              |
| 1:C:116:MET:SD     | 1:C:118:ILE:HD11   | 2.57                     | 0.45              |
| 1:I:195:TYR:HE1    | 2:I:301:MLK:H222   | 1.82                     | 0.45              |
| 1:C:97[B]:ARG:HH11 | 1:C:97[B]:ARG:CG   | 2.27                     | 0.45              |
| 1:E:38:GLN:NE2     | 1:E:38:GLN:HA      | 2.31                     | 0.45              |
| 1:E:25:LYS:NZ      | 3:E:2004:HOH:O     | 2.46                     | 0.44              |
| 1:F:19:MET:HG3     | 1:F:20:TYR:N       | 2.32                     | 0.44              |
| 1:A:59[A]:ARG:NH2  | 1:A:61:LYS:HB2     | 2.31                     | 0.44              |
| 1:A:139:THR:OG1    | 1:A:203[A]:LYS:HD2 | 2.18                     | 0.44              |
| 1:H:149:TYR:CD2    | 1:H:154:ILE:HD12   | 2.52                     | 0.44              |
| 1:I:122:ARG:HD2    | 1:J:96:THR:O       | 2.18                     | 0.44              |
| 1:G:38[B]:GLN:CD   | 2:H:301:MLK:H122   | 2.37                     | 0.44              |
| 1:J:50:VAL:CG2     | 1:J:127:CYS:SG     | 3.06                     | 0.44              |
| 1:G:56:GLU:O       | 1:G:119:PRO:HD2    | 2.18                     | 0.44              |
| 1:B:16:ARG:HH11    | 1:B:16:ARG:CG      | 2.30                     | 0.44              |
| 1:F:33[A]:LEU:HD21 | 1:F:35:PHE:CZ      | 2.52                     | 0.44              |
| 1:F:33[A]:LEU:HD23 | 1:F:34:GLY:N       | 2.33                     | 0.43              |
| 1:I:56:GLU:OE2     | 1:I:58:GLN:NE2     | 2.43                     | 0.43              |
| 1:I:59[A]:ARG:HE   | 1:I:116[A]:MET:HE2 | 1.83                     | 0.43              |
| 2:H:301:MLK:O28    | 2:H:301:MLK:H31    | 2.19                     | 0.43              |
| 1:F:207[A]:ARG:NH2 | 1:F:207[A]:ARG:HG2 | 2.14                     | 0.43              |

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| Atom-1            | Atom-2              | Interatomic distance (Å) | Clash overlap (Å) |
|-------------------|---------------------|--------------------------|-------------------|
| 1:B:199:ASN:ND2   | 3:B:2059:HOH:O      | 2.51                     | 0.43              |
| 1:F:122:ARG:HD2   | 1:G:96:THR:O        | 2.19                     | 0.43              |
| 1:H:33:LEU:HD12   | 1:H:156:LEU:HD22    | 1.99                     | 0.43              |
| 1:F:56:GLU:O      | 1:F:119:PRO:HD2     | 2.19                     | 0.43              |
| 1:A:169:TYR:CZ    | 1:A:171:SER:HB2     | 2.54                     | 0.43              |
| 1:I:59[A]:ARG:NH1 | 1:I:116[A]:MET:HE1  | 2.27                     | 0.43              |
| 1:H:141:ALA:HA    | 1:H:200:LEU:O       | 2.18                     | 0.43              |
| 1:H:40:ILE:HG12   | 1:H:52:LEU:HD22     | 2.01                     | 0.42              |
| 1:A:14:PHE:C      | 1:A:15:ASN:HD22     | 2.23                     | 0.42              |
| 1:F:143:LYS:HD2   | 2:F:301:MLK:C5      | 2.49                     | 0.42              |
| 1:C:7:MET:HG2     | 3:D:2003:HOH:O      | 2.20                     | 0.42              |
| 2:E:301:MLK:C31   | 2:E:301:MLK:O28     | 2.68                     | 0.42              |
| 1:B:190:CYS:SG    | 2:B:301:MLK:H393    | 2.59                     | 0.42              |
| 1:I:173:LYS:HE3   | 1:J:45:SER:O        | 2.19                     | 0.42              |
| 1:A:56:GLU:O      | 1:A:119:PRO:HD2     | 2.20                     | 0.42              |
| 1:B:38[B]:GLN:OE1 | 1:B:55:TYR:CE2      | 2.73                     | 0.42              |
| 1:F:172:SER:O     | 1:F:207[B]:ARG:CZ   | 2.68                     | 0.41              |
| 1:H:143:LYS:HD2   | 2:H:301:MLK:O11     | 2.19                     | 0.41              |
| 1:B:56:GLU:O      | 1:B:119:PRO:HD2     | 2.20                     | 0.41              |
| 1:H:169:TYR:CZ    | 1:H:171:SER:HB2     | 2.55                     | 0.41              |
| 1:B:1:HIS:C       | 1:B:3:GLN:N         | 2.73                     | 0.41              |
| 1:J:143:LYS:HZ1   | 1:J:184:GLN:HE22    | 1.66                     | 0.41              |
| 1:I:18:PRO:C      | 3:I:2003:HOH:O      | 2.58                     | 0.41              |
| 2:E:301:MLK:H242  | 2:E:301:MLK:O27     | 2.19                     | 0.41              |
| 1:F:175:GLU:HB3   | 1:F:207[B]:ARG:HD3  | 1.99                     | 0.41              |
| 1:B:59[B]:ARG:NH2 | 1:B:59[B]:ARG:CG    | 2.82                     | 0.41              |
| 1:E:94:SER:HB3    | 2:E:301:MLK:H121    | 2.03                     | 0.41              |
| 2:F:301:MLK:H9C1  | 1:J:167:SER:HB2     | 2.02                     | 0.41              |
| 2:I:301:MLK:H242  | 2:I:301:MLK:O27     | 2.20                     | 0.41              |
| 1:D:56:GLU:HB3    | 1:D:121[B]:GLN:HE22 | 1.85                     | 0.41              |
| 1:I:127:CYS:O     | 1:I:129:PRO:HD3     | 2.20                     | 0.41              |
| 1:G:191:CYS:HA    | 1:G:192:PRO:HD3     | 1.95                     | 0.41              |
| 2:C:301:MLK:H31   | 2:C:301:MLK:O28     | 2.21                     | 0.41              |
| 1:F:99:VAL:HG13   | 1:F:121[A]:GLN:HB3  | 2.02                     | 0.41              |
| 1:J:195:TYR:CE1   | 2:J:301:MLK:H222    | 2.55                     | 0.41              |
| 1:C:59[A]:ARG:NH1 | 1:C:159:ASP:OD1     | 2.53                     | 0.41              |
| 1:D:20:TYR:HA     | 1:D:21:PRO:HD3      | 1.95                     | 0.41              |
| 1:F:148:VAL:HG21  | 1:J:106:ILE:HG21    | 2.02                     | 0.41              |
| 1:D:37:LEU:HD12   | 1:D:37:LEU:HA       | 1.94                     | 0.40              |
| 1:A:59[B]:ARG:NH1 | 1:A:159:ASP:OD1     | 2.55                     | 0.40              |
| 2:D:301:MLK:H31   | 2:D:301:MLK:O28     | 2.21                     | 0.40              |

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| Atom-1            | Atom-2          | Interatomic distance (Å) | Clash overlap (Å) |
|-------------------|-----------------|--------------------------|-------------------|
| 1:I:50:VAL:HG21   | 1:I:127:CYS:SG  | 2.62                     | 0.40              |
| 1:A:97[A]:ARG:HD3 | 3:E:2045:HOH:O  | 2.20                     | 0.40              |
| 1:E:101:VAL:HG11  | 1:E:105:GLN:NE2 | 2.36                     | 0.40              |

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     | 218/227 (96%)   | 213 (98%)  | 5 (2%)  | 0        | 100         | 100 |
| 1   | B     | 216/227 (95%)   | 211 (98%)  | 4 (2%)  | 1 (0%)   | 34          | 41  |
| 1   | C     | 211/227 (93%)   | 206 (98%)  | 5 (2%)  | 0        | 100         | 100 |
| 1   | D     | 215/227 (95%)   | 209 (97%)  | 4 (2%)  | 2 (1%)   | 21          | 25  |
| 1   | E     | 216/227 (95%)   | 211 (98%)  | 5 (2%)  | 0        | 100         | 100 |
| 1   | F     | 213/227 (94%)   | 206 (97%)  | 7 (3%)  | 0        | 100         | 100 |
| 1   | G     | 204/227 (90%)   | 201 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 1   | H     | 201/227 (88%)   | 194 (96%)  | 7 (4%)  | 0        | 100         | 100 |
| 1   | I     | 213/227 (94%)   | 206 (97%)  | 7 (3%)  | 0        | 100         | 100 |
| 1   | J     | 215/227 (95%)   | 211 (98%)  | 4 (2%)  | 0        | 100         | 100 |
| All | All   | 2122/2270 (94%) | 2068 (98%) | 51 (2%) | 3 (0%)   | 56          | 71  |

All (3) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | B     | 18  | PRO  |
| 1   | D     | 19  | MET  |
| 1   | D     | 18  | PRO  |

### 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     | 201/205 (98%)   | 188 (94%)  | 13 (6%)  | 21          | 28 |
| 1   | B     | 198/205 (97%)   | 193 (98%)  | 5 (2%)   | 55          | 72 |
| 1   | C     | 195/205 (95%)   | 188 (96%)  | 7 (4%)   | 42          | 58 |
| 1   | D     | 198/205 (97%)   | 196 (99%)  | 2 (1%)   | 82          | 89 |
| 1   | E     | 199/205 (97%)   | 195 (98%)  | 4 (2%)   | 63          | 78 |
| 1   | F     | 196/205 (96%)   | 189 (96%)  | 7 (4%)   | 42          | 58 |
| 1   | G     | 187/205 (91%)   | 181 (97%)  | 6 (3%)   | 46          | 63 |
| 1   | H     | 186/205 (91%)   | 176 (95%)  | 10 (5%)  | 27          | 38 |
| 1   | I     | 198/205 (97%)   | 192 (97%)  | 6 (3%)   | 48          | 65 |
| 1   | J     | 198/205 (97%)   | 195 (98%)  | 3 (2%)   | 72          | 84 |
| All | All   | 1956/2050 (95%) | 1893 (97%) | 63 (3%)  | 50          | 63 |

All (63) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res    | Type |
|-----|-------|--------|------|
| 1   | A     | -3     | ASP  |
| 1   | A     | 16     | ARG  |
| 1   | A     | 37     | LEU  |
| 1   | A     | 52     | LEU  |
| 1   | A     | 59[A]  | ARG  |
| 1   | A     | 59[B]  | ARG  |
| 1   | A     | 101    | VAL  |
| 1   | A     | 116[A] | MET  |
| 1   | A     | 116[B] | MET  |
| 1   | A     | 142    | VAL  |
| 1   | A     | 186    | GLN  |
| 1   | A     | 207    | ARG  |
| 1   | A     | 208    | ARG  |
| 1   | B     | 38[A]  | GLN  |
| 1   | B     | 38[B]  | GLN  |
| 1   | B     | 121[A] | GLN  |

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| Mol | Chain | Res    | Type |
|-----|-------|--------|------|
| 1   | B     | 121[B] | GLN  |
| 1   | B     | 135    | GLU  |
| 1   | C     | 8      | ARG  |
| 1   | C     | 11     | SER  |
| 1   | C     | 19     | MET  |
| 1   | C     | 33[A]  | LEU  |
| 1   | C     | 33[B]  | LEU  |
| 1   | C     | 116    | MET  |
| 1   | C     | 193    | GLU  |
| 1   | D     | 33     | LEU  |
| 1   | D     | 186    | GLN  |
| 1   | E     | -3     | ASP  |
| 1   | E     | 25     | LYS  |
| 1   | E     | 70     | ASN  |
| 1   | E     | 208    | ARG  |
| 1   | F     | 17     | SER  |
| 1   | F     | 38[A]  | GLN  |
| 1   | F     | 38[B]  | GLN  |
| 1   | F     | 52     | LEU  |
| 1   | F     | 156    | LEU  |
| 1   | F     | 207[A] | ARG  |
| 1   | F     | 207[B] | ARG  |
| 1   | G     | 16     | ARG  |
| 1   | G     | 33     | LEU  |
| 1   | G     | 157    | LYS  |
| 1   | G     | 186    | GLN  |
| 1   | G     | 200    | LEU  |
| 1   | G     | 203    | LYS  |
| 1   | H     | 33     | LEU  |
| 1   | H     | 38     | GLN  |
| 1   | H     | 79     | ARG  |
| 1   | H     | 105    | GLN  |
| 1   | H     | 160    | THR  |
| 1   | H     | 167    | SER  |
| 1   | H     | 175    | GLU  |
| 1   | H     | 185    | VAL  |
| 1   | H     | 193    | GLU  |
| 1   | H     | 205    | ARG  |
| 1   | I     | -5     | ASP  |
| 1   | I     | 0      | LEU  |
| 1   | I     | 52     | LEU  |
| 1   | I     | 94     | SER  |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | I     | 157 | LYS  |
| 1   | I     | 203 | LYS  |
| 1   | J     | 17  | SER  |
| 1   | J     | 19  | MET  |
| 1   | J     | 207 | ARG  |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 3   | GLN  |
| 1   | A     | 15  | ASN  |
| 1   | A     | 70  | ASN  |
| 1   | A     | 199 | ASN  |
| 1   | B     | 63  | ASN  |
| 1   | B     | 105 | GLN  |
| 1   | B     | 184 | GLN  |
| 1   | B     | 199 | ASN  |
| 1   | C     | 38  | GLN  |
| 1   | C     | 74  | ASN  |
| 1   | C     | 184 | GLN  |
| 1   | D     | 186 | GLN  |
| 1   | D     | 199 | ASN  |
| 1   | E     | 38  | GLN  |
| 1   | E     | 105 | GLN  |
| 1   | E     | 184 | GLN  |
| 1   | F     | 5   | ASN  |
| 1   | F     | 199 | ASN  |
| 1   | G     | 15  | ASN  |
| 1   | G     | 105 | GLN  |
| 1   | G     | 111 | HIS  |
| 1   | G     | 186 | GLN  |
| 1   | H     | 38  | GLN  |
| 1   | H     | 121 | GLN  |
| 1   | H     | 162 | GLN  |
| 1   | H     | 184 | GLN  |
| 1   | I     | 184 | GLN  |
| 1   | I     | 186 | GLN  |
| 1   | J     | 184 | GLN  |
| 1   | J     | 199 | ASN  |



### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

10 ligands 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$ |
| 2   | MLK  | A     | 301 | -    | 55,56,56     | 1.45 | 7 (12%)     | 74,92,92    | 1.39 | 10 (13%)    |
| 2   | MLK  | B     | 301 | -    | 55,56,56     | 1.58 | 7 (12%)     | 74,92,92    | 1.22 | 8 (10%)     |
| 2   | MLK  | C     | 301 | -    | 55,56,56     | 1.51 | 7 (12%)     | 74,92,92    | 1.27 | 9 (12%)     |
| 2   | MLK  | D     | 301 | -    | 55,56,56     | 1.54 | 6 (10%)     | 74,92,92    | 1.35 | 11 (14%)    |
| 2   | MLK  | E     | 301 | -    | 55,56,56     | 1.46 | 7 (12%)     | 74,92,92    | 1.34 | 10 (13%)    |
| 2   | MLK  | F     | 301 | -    | 55,56,56     | 1.55 | 6 (10%)     | 74,92,92    | 1.15 | 9 (12%)     |
| 2   | MLK  | G     | 301 | -    | 55,56,56     | 1.50 | 7 (12%)     | 74,92,92    | 1.22 | 8 (10%)     |
| 2   | MLK  | H     | 301 | -    | 55,56,56     | 1.41 | 6 (10%)     | 74,92,92    | 1.50 | 11 (14%)    |
| 2   | MLK  | I     | 301 | -    | 55,56,56     | 1.47 | 7 (12%)     | 74,92,92    | 1.30 | 9 (12%)     |
| 2   | MLK  | J     | 301 | -    | 55,56,56     | 1.40 | 7 (12%)     | 74,92,92    | 1.39 | 10 (13%)    |

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

| Mol | Type | Chain | Res | Link | Chirals | Torsions     | Rings   |
|-----|------|-------|-----|------|---------|--------------|---------|
| 2   | MLK  | A     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | B     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | C     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | D     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | E     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | F     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | G     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | H     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | I     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |
| 2   | MLK  | J     | 301 | -    | -       | 0/24/141/141 | 0/2/8/8 |

All (67) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms   | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 2   | B     | 301 | MLK  | C11-N7  | -5.29 | 1.32        | 1.39     |
| 2   | F     | 301 | MLK  | C8-N7   | -5.15 | 1.33        | 1.40     |
| 2   | C     | 301 | MLK  | C8-N7   | -5.08 | 1.33        | 1.40     |
| 2   | D     | 301 | MLK  | C8-N7   | -5.02 | 1.33        | 1.40     |
| 2   | F     | 301 | MLK  | C11-N7  | -4.99 | 1.32        | 1.39     |
| 2   | G     | 301 | MLK  | C8-N7   | -4.93 | 1.33        | 1.40     |
| 2   | B     | 301 | MLK  | C8-N7   | -4.90 | 1.33        | 1.40     |
| 2   | D     | 301 | MLK  | C11-N7  | -4.59 | 1.33        | 1.39     |
| 2   | C     | 301 | MLK  | C11-N7  | -4.54 | 1.33        | 1.39     |
| 2   | H     | 301 | MLK  | C8-N7   | -4.45 | 1.34        | 1.40     |
| 2   | I     | 301 | MLK  | C8-N7   | -4.42 | 1.34        | 1.40     |
| 2   | A     | 301 | MLK  | C11-N7  | -4.26 | 1.33        | 1.39     |
| 2   | A     | 301 | MLK  | C8-N7   | -4.25 | 1.34        | 1.40     |
| 2   | I     | 301 | MLK  | C11-N7  | -4.22 | 1.33        | 1.39     |
| 2   | E     | 301 | MLK  | C11-N7  | -4.20 | 1.33        | 1.39     |
| 2   | J     | 301 | MLK  | C11-N7  | -4.13 | 1.33        | 1.39     |
| 2   | E     | 301 | MLK  | C8-N7   | -4.10 | 1.34        | 1.40     |
| 2   | J     | 301 | MLK  | C8-N7   | -3.94 | 1.35        | 1.40     |
| 2   | G     | 301 | MLK  | C11-N7  | -3.90 | 1.34        | 1.39     |
| 2   | H     | 301 | MLK  | C11-N7  | -3.69 | 1.34        | 1.39     |
| 2   | B     | 301 | MLK  | C6-N7   | -3.55 | 1.39        | 1.44     |
| 2   | G     | 301 | MLK  | C6-N7   | -3.20 | 1.40        | 1.44     |
| 2   | C     | 301 | MLK  | C6-N7   | -3.19 | 1.40        | 1.44     |
| 2   | F     | 301 | MLK  | C6-N7   | -3.11 | 1.40        | 1.44     |
| 2   | D     | 301 | MLK  | C6-N7   | -2.95 | 1.40        | 1.44     |
| 2   | A     | 301 | MLK  | C6-N7   | -2.93 | 1.40        | 1.44     |
| 2   | B     | 301 | MLK  | C18-C17 | -2.67 | 1.53        | 1.56     |
| 2   | G     | 301 | MLK  | C32-C27 | -2.59 | 1.53        | 1.56     |
| 2   | E     | 301 | MLK  | C6-N7   | -2.56 | 1.41        | 1.44     |

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| Mol | Chain | Res | Type | Atoms   | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 2   | D     | 301 | MLK  | C18-C17 | -2.50 | 1.53        | 1.56     |
| 2   | E     | 301 | MLK  | C18-C17 | -2.50 | 1.53        | 1.56     |
| 2   | B     | 301 | MLK  | C32-C27 | -2.48 | 1.53        | 1.56     |
| 2   | A     | 301 | MLK  | C32-C27 | -2.47 | 1.53        | 1.56     |
| 2   | G     | 301 | MLK  | C18-C17 | -2.40 | 1.53        | 1.56     |
| 2   | F     | 301 | MLK  | C18-C17 | -2.37 | 1.53        | 1.56     |
| 2   | J     | 301 | MLK  | C6-N7   | -2.34 | 1.41        | 1.44     |
| 2   | C     | 301 | MLK  | C18-C17 | -2.32 | 1.53        | 1.56     |
| 2   | I     | 301 | MLK  | C6-N7   | -2.30 | 1.41        | 1.44     |
| 2   | A     | 301 | MLK  | C18-C17 | -2.24 | 1.53        | 1.56     |
| 2   | J     | 301 | MLK  | C18-C17 | -2.24 | 1.53        | 1.56     |
| 2   | H     | 301 | MLK  | C18-C17 | -2.22 | 1.53        | 1.56     |
| 2   | C     | 301 | MLK  | C32-C27 | -2.22 | 1.53        | 1.56     |
| 2   | H     | 301 | MLK  | C6-N7   | -2.21 | 1.41        | 1.44     |
| 2   | J     | 301 | MLK  | C32-C27 | -2.18 | 1.53        | 1.56     |
| 2   | I     | 301 | MLK  | C18-C17 | -2.07 | 1.53        | 1.56     |
| 2   | E     | 301 | MLK  | O14-C15 | -2.03 | 1.41        | 1.45     |
| 2   | I     | 301 | MLK  | C32-C27 | -2.02 | 1.54        | 1.56     |
| 2   | E     | 301 | MLK  | O14-C13 | 4.16  | 1.43        | 1.33     |
| 2   | B     | 301 | MLK  | O14-C13 | 4.18  | 1.43        | 1.33     |
| 2   | C     | 301 | MLK  | O14-C13 | 4.38  | 1.44        | 1.33     |
| 2   | J     | 301 | MLK  | O14-C13 | 4.39  | 1.44        | 1.33     |
| 2   | F     | 301 | MLK  | O14-C13 | 4.46  | 1.44        | 1.33     |
| 2   | A     | 301 | MLK  | C1-C6   | 4.49  | 1.48        | 1.41     |
| 2   | B     | 301 | MLK  | C1-C6   | 4.52  | 1.48        | 1.41     |
| 2   | F     | 301 | MLK  | C1-C6   | 4.66  | 1.48        | 1.41     |
| 2   | A     | 301 | MLK  | O14-C13 | 4.71  | 1.44        | 1.33     |
| 2   | J     | 301 | MLK  | C1-C6   | 4.73  | 1.48        | 1.41     |
| 2   | G     | 301 | MLK  | O14-C13 | 4.77  | 1.44        | 1.33     |
| 2   | G     | 301 | MLK  | C1-C6   | 4.80  | 1.48        | 1.41     |
| 2   | H     | 301 | MLK  | C1-C6   | 4.82  | 1.48        | 1.41     |
| 2   | H     | 301 | MLK  | O14-C13 | 4.92  | 1.45        | 1.33     |
| 2   | I     | 301 | MLK  | O14-C13 | 4.94  | 1.45        | 1.33     |
| 2   | C     | 301 | MLK  | C1-C6   | 4.99  | 1.49        | 1.41     |
| 2   | D     | 301 | MLK  | O14-C13 | 5.00  | 1.45        | 1.33     |
| 2   | D     | 301 | MLK  | C1-C6   | 5.09  | 1.49        | 1.41     |
| 2   | E     | 301 | MLK  | C1-C6   | 5.14  | 1.49        | 1.41     |
| 2   | I     | 301 | MLK  | C1-C6   | 5.32  | 1.49        | 1.41     |

All (95) bond angle outliers are listed below:

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| Mol | Chain | Res | Type | Atoms       | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|-------|-------------|----------|
| 2   | J     | 301 | MLK  | C21-C16-C23 | -3.94 | 107.47      | 111.47   |
| 2   | J     | 301 | MLK  | O8-C8-C9    | -3.93 | 122.12      | 127.41   |
| 2   | H     | 301 | MLK  | C21-C16-C23 | -3.86 | 107.54      | 111.47   |
| 2   | A     | 301 | MLK  | C21-C16-C23 | -3.65 | 107.75      | 111.47   |
| 2   | E     | 301 | MLK  | O8-C8-C9    | -3.57 | 122.61      | 127.41   |
| 2   | H     | 301 | MLK  | O8-C8-C9    | -3.48 | 122.74      | 127.41   |
| 2   | H     | 301 | MLK  | O11-C11-C10 | -3.18 | 120.95      | 126.70   |
| 2   | B     | 301 | MLK  | O8-C8-C9    | -3.15 | 123.18      | 127.41   |
| 2   | A     | 301 | MLK  | O8-C8-C9    | -3.10 | 123.24      | 127.41   |
| 2   | D     | 301 | MLK  | O8-C8-C9    | -3.09 | 123.25      | 127.41   |
| 2   | I     | 301 | MLK  | O8-C8-C9    | -3.04 | 123.33      | 127.41   |
| 2   | C     | 301 | MLK  | C21-C16-C23 | -3.04 | 108.38      | 111.47   |
| 2   | D     | 301 | MLK  | C21-C16-C23 | -2.80 | 108.62      | 111.47   |
| 2   | G     | 301 | MLK  | O8-C8-C9    | -2.76 | 123.71      | 127.41   |
| 2   | F     | 301 | MLK  | O8-C8-C9    | -2.42 | 124.16      | 127.41   |
| 2   | E     | 301 | MLK  | C21-C16-C23 | -2.42 | 109.01      | 111.47   |
| 2   | C     | 301 | MLK  | O8-C8-C9    | -2.42 | 124.16      | 127.41   |
| 2   | C     | 301 | MLK  | O14-C13-O13 | -2.38 | 119.28      | 123.66   |
| 2   | F     | 301 | MLK  | O14-C13-O13 | -2.37 | 119.31      | 123.66   |
| 2   | D     | 301 | MLK  | O14-C13-O13 | -2.36 | 119.32      | 123.66   |
| 2   | I     | 301 | MLK  | C21-C16-C23 | -2.36 | 109.07      | 111.47   |
| 2   | A     | 301 | MLK  | O11-C11-C10 | -2.29 | 122.56      | 126.70   |
| 2   | A     | 301 | MLK  | O14-C13-O13 | -2.25 | 119.53      | 123.66   |
| 2   | E     | 301 | MLK  | O11-C11-C10 | -2.20 | 122.72      | 126.70   |
| 2   | E     | 301 | MLK  | C23-N23-C24 | -2.20 | 108.26      | 111.19   |
| 2   | I     | 301 | MLK  | O11-C11-C10 | -2.17 | 122.78      | 126.70   |
| 2   | B     | 301 | MLK  | C21-C16-C23 | -2.15 | 109.28      | 111.47   |
| 2   | D     | 301 | MLK  | C23-N23-C24 | -2.12 | 108.37      | 111.19   |
| 2   | I     | 301 | MLK  | O14-C13-O13 | -2.05 | 119.89      | 123.66   |
| 2   | F     | 301 | MLK  | C9-C8-N7    | 2.01  | 109.70      | 108.07   |
| 2   | F     | 301 | MLK  | C23-C16-C17 | 2.02  | 110.08      | 108.22   |
| 2   | H     | 301 | MLK  | C18-C17-C28 | 2.05  | 105.80      | 102.98   |
| 2   | J     | 301 | MLK  | C9-C8-N7    | 2.05  | 109.74      | 108.07   |
| 2   | J     | 301 | MLK  | C18-C17-C28 | 2.06  | 105.81      | 102.98   |
| 2   | D     | 301 | MLK  | C18-C30-C31 | 2.09  | 119.73      | 117.24   |
| 2   | E     | 301 | MLK  | C23-C16-C17 | 2.10  | 110.15      | 108.22   |
| 2   | G     | 301 | MLK  | C21-C16-C17 | 2.11  | 112.75      | 110.05   |
| 2   | C     | 301 | MLK  | O11-C11-N7  | 2.13  | 126.52      | 124.33   |
| 2   | B     | 301 | MLK  | O14-C13-C1  | 2.14  | 116.05      | 112.16   |
| 2   | H     | 301 | MLK  | C21-C16-C17 | 2.14  | 112.79      | 110.05   |
| 2   | J     | 301 | MLK  | C21-C16-C17 | 2.15  | 112.80      | 110.05   |

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| Mol | Chain | Res | Type | Atoms       | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|------|-------------|----------|
| 2   | F     | 301 | MLK  | O11-C11-N7  | 2.16 | 126.55      | 124.33   |
| 2   | D     | 301 | MLK  | O11-C11-N7  | 2.19 | 126.57      | 124.33   |
| 2   | J     | 301 | MLK  | O11-C11-N7  | 2.21 | 126.59      | 124.33   |
| 2   | C     | 301 | MLK  | C18-C17-C28 | 2.23 | 106.04      | 102.98   |
| 2   | F     | 301 | MLK  | O8-C8-N7    | 2.29 | 126.14      | 123.94   |
| 2   | A     | 301 | MLK  | C15-O14-C13 | 2.31 | 121.65      | 116.64   |
| 2   | B     | 301 | MLK  | C18-C17-C28 | 2.40 | 106.27      | 102.98   |
| 2   | B     | 301 | MLK  | C6-N7-C8    | 2.40 | 125.56      | 122.76   |
| 2   | B     | 301 | MLK  | C9-C8-N7    | 2.41 | 110.02      | 108.07   |
| 2   | A     | 301 | MLK  | O11-C11-N7  | 2.44 | 126.83      | 124.33   |
| 2   | G     | 301 | MLK  | C18-C17-C28 | 2.45 | 106.34      | 102.98   |
| 2   | I     | 301 | MLK  | C9-C8-N7    | 2.47 | 110.07      | 108.07   |
| 2   | D     | 301 | MLK  | O38-C38-C31 | 2.47 | 119.39      | 112.66   |
| 2   | E     | 301 | MLK  | O11-C11-N7  | 2.51 | 126.91      | 124.33   |
| 2   | F     | 301 | MLK  | C18-C17-C28 | 2.52 | 106.43      | 102.98   |
| 2   | A     | 301 | MLK  | C21-C16-C17 | 2.52 | 113.28      | 110.05   |
| 2   | H     | 301 | MLK  | O14-C13-C1  | 2.56 | 116.83      | 112.16   |
| 2   | I     | 301 | MLK  | C18-C17-C28 | 2.59 | 106.53      | 102.98   |
| 2   | G     | 301 | MLK  | C15-O14-C13 | 2.62 | 122.31      | 116.64   |
| 2   | J     | 301 | MLK  | O14-C13-C1  | 2.65 | 116.98      | 112.16   |
| 2   | E     | 301 | MLK  | C6-N7-C8    | 2.67 | 125.87      | 122.76   |
| 2   | E     | 301 | MLK  | O14-C13-C1  | 2.67 | 117.03      | 112.16   |
| 2   | G     | 301 | MLK  | O14-C13-C1  | 2.71 | 117.09      | 112.16   |
| 2   | D     | 301 | MLK  | C15-O14-C13 | 2.72 | 122.54      | 116.64   |
| 2   | G     | 301 | MLK  | O11-C11-N7  | 2.73 | 127.13      | 124.33   |
| 2   | F     | 301 | MLK  | O14-C13-C1  | 2.75 | 117.16      | 112.16   |
| 2   | J     | 301 | MLK  | C6-N7-C8    | 2.75 | 125.96      | 122.76   |
| 2   | I     | 301 | MLK  | O8-C8-N7    | 2.76 | 126.59      | 123.94   |
| 2   | G     | 301 | MLK  | C10-C11-N7  | 2.79 | 109.59      | 108.06   |
| 2   | H     | 301 | MLK  | C15-O14-C13 | 2.83 | 122.77      | 116.64   |
| 2   | C     | 301 | MLK  | C15-O14-C13 | 2.84 | 122.78      | 116.64   |
| 2   | C     | 301 | MLK  | O8-C8-N7    | 2.87 | 126.69      | 123.94   |
| 2   | G     | 301 | MLK  | O8-C8-N7    | 2.90 | 126.73      | 123.94   |
| 2   | F     | 301 | MLK  | C10-C11-N7  | 2.97 | 109.70      | 108.06   |
| 2   | B     | 301 | MLK  | O8-C8-N7    | 2.97 | 126.80      | 123.94   |
| 2   | C     | 301 | MLK  | O14-C13-C1  | 3.09 | 117.78      | 112.16   |
| 2   | H     | 301 | MLK  | O11-C11-N7  | 3.29 | 127.71      | 124.33   |
| 2   | D     | 301 | MLK  | O14-C13-C1  | 3.36 | 118.27      | 112.16   |
| 2   | I     | 301 | MLK  | O14-C13-C1  | 3.38 | 118.31      | 112.16   |
| 2   | H     | 301 | MLK  | C6-N7-C8    | 3.40 | 126.72      | 122.76   |
| 2   | A     | 301 | MLK  | O14-C13-C1  | 3.40 | 118.35      | 112.16   |
| 2   | B     | 301 | MLK  | C10-C11-N7  | 3.45 | 109.96      | 108.06   |

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| Mol | Chain | Res | Type | Atoms      | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|------------|------|-------------|----------|
| 2   | J     | 301 | MLK  | C10-C11-N7 | 3.62 | 110.05      | 108.06   |
| 2   | A     | 301 | MLK  | O8-C8-N7   | 3.65 | 127.45      | 123.94   |
| 2   | D     | 301 | MLK  | C10-C11-N7 | 3.74 | 110.12      | 108.06   |
| 2   | C     | 301 | MLK  | C10-C11-N7 | 4.02 | 110.28      | 108.06   |
| 2   | E     | 301 | MLK  | C10-C11-N7 | 4.03 | 110.28      | 108.06   |
| 2   | D     | 301 | MLK  | O8-C8-N7   | 4.14 | 127.92      | 123.94   |
| 2   | E     | 301 | MLK  | O8-C8-N7   | 4.16 | 127.94      | 123.94   |
| 2   | H     | 301 | MLK  | O8-C8-N7   | 4.18 | 127.96      | 123.94   |
| 2   | J     | 301 | MLK  | O8-C8-N7   | 4.37 | 128.14      | 123.94   |
| 2   | A     | 301 | MLK  | C10-C11-N7 | 4.49 | 110.53      | 108.06   |
| 2   | H     | 301 | MLK  | C10-C11-N7 | 5.22 | 110.94      | 108.06   |
| 2   | I     | 301 | MLK  | C10-C11-N7 | 5.23 | 110.94      | 108.06   |

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 45 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 2   | A     | 301 | MLK  | 4       | 0            |
| 2   | B     | 301 | MLK  | 3       | 0            |
| 2   | C     | 301 | MLK  | 3       | 0            |
| 2   | D     | 301 | MLK  | 3       | 0            |
| 2   | E     | 301 | MLK  | 7       | 0            |
| 2   | F     | 301 | MLK  | 6       | 0            |
| 2   | G     | 301 | MLK  | 4       | 0            |
| 2   | H     | 301 | MLK  | 6       | 0            |
| 2   | I     | 301 | MLK  | 6       | 0            |
| 2   | J     | 301 | MLK  | 3       | 0            |

## 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.

## 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<sup>th</sup> 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 <sup>2</sup> ) | Q<0.9 |
|-----|-------|-----------------|--------|---------------|-----------------------|-------|
| 1   | A     | 213/227 (93%)   | 0.16   | 3 (1%) 78 80  | 15, 28, 56, 77        | 0     |
| 1   | B     | 210/227 (92%)   | 0.11   | 2 (0%) 84 86  | 14, 31, 62, 78        | 0     |
| 1   | C     | 210/227 (92%)   | 0.11   | 5 (2%) 62 65  | 20, 38, 67, 96        | 0     |
| 1   | D     | 211/227 (92%)   | 0.23   | 6 (2%) 56 60  | 22, 39, 74, 85        | 0     |
| 1   | E     | 214/227 (94%)   | 0.12   | 4 (1%) 70 72  | 18, 30, 65, 92        | 0     |
| 1   | F     | 209/227 (92%)   | 0.45   | 7 (3%) 50 53  | 29, 48, 75, 92        | 0     |
| 1   | G     | 205/227 (90%)   | 0.43   | 7 (3%) 49 52  | 33, 55, 85, 95        | 0     |
| 1   | H     | 204/227 (89%)   | 1.15   | 32 (15%) 3 2  | 45, 65, 95, 106       | 0     |
| 1   | I     | 213/227 (93%)   | 0.45   | 11 (5%) 31 34 | 32, 51, 92, 100       | 0     |
| 1   | J     | 212/227 (93%)   | 0.12   | 3 (1%) 78 80  | 22, 39, 69, 99        | 0     |
| All | All   | 2101/2270 (92%) | 0.33   | 80 (3%) 44 48 | 14, 43, 81, 106       | 0     |

All (80) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1   | B     | 209 | ALA  | 5.6  |
| 1   | H     | 16  | ARG  | 5.4  |
| 1   | I     | 190 | CYS  | 5.3  |
| 1   | H     | 1   | HIS  | 4.8  |
| 1   | F     | 19  | MET  | 4.6  |
| 1   | H     | 33  | LEU  | 4.6  |
| 1   | D     | 0   | LEU  | 4.5  |
| 1   | H     | 14  | PHE  | 4.5  |
| 1   | F     | 0   | LEU  | 4.2  |
| 1   | H     | 200 | LEU  | 4.0  |
| 1   | G     | 7   | MET  | 3.8  |
| 1   | D     | 19  | MET  | 3.7  |
| 1   | G     | 19  | MET  | 3.6  |

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| Mol | Chain | Res   | Type | RSRZ |
|-----|-------|-------|------|------|
| 1   | H     | 35    | PHE  | 3.5  |
| 1   | B     | 1     | HIS  | 3.3  |
| 1   | F     | 15    | ASN  | 3.3  |
| 1   | F     | 18    | PRO  | 3.3  |
| 1   | H     | 6     | LEU  | 3.3  |
| 1   | G     | 6     | LEU  | 3.2  |
| 1   | E     | -3    | ASP  | 3.2  |
| 1   | H     | 2     | SER  | 3.2  |
| 1   | H     | 15    | ASN  | 3.1  |
| 1   | C     | -2    | ASP  | 3.1  |
| 1   | C     | 0     | LEU  | 3.0  |
| 1   | C     | 208   | ARG  | 3.0  |
| 1   | E     | 16    | ARG  | 2.9  |
| 1   | D     | 17    | SER  | 2.9  |
| 1   | I     | 189   | SER  | 2.9  |
| 1   | I     | 18    | PRO  | 2.9  |
| 1   | H     | 65    | LEU  | 2.9  |
| 1   | H     | 74    | ASN  | 2.9  |
| 1   | H     | 156   | LEU  | 2.9  |
| 1   | G     | 18    | PRO  | 2.9  |
| 1   | J     | 1     | HIS  | 2.8  |
| 1   | H     | 125   | PHE  | 2.8  |
| 1   | D     | 15    | ASN  | 2.7  |
| 1   | H     | 71    | GLU  | 2.7  |
| 1   | H     | 70    | ASN  | 2.7  |
| 1   | H     | 157   | LYS  | 2.7  |
| 1   | H     | 154   | ILE  | 2.7  |
| 1   | A     | 0     | LEU  | 2.7  |
| 1   | I     | 22    | GLY  | 2.7  |
| 1   | J     | 38[A] | GLN  | 2.6  |
| 1   | H     | 194   | PRO  | 2.6  |
| 1   | I     | 25    | LYS  | 2.6  |
| 1   | J     | -3    | ASP  | 2.5  |
| 1   | E     | 18    | PRO  | 2.5  |
| 1   | I     | 0     | LEU  | 2.4  |
| 1   | I     | 1     | HIS  | 2.4  |
| 1   | G     | 13    | LEU  | 2.4  |
| 1   | F     | 16    | ARG  | 2.4  |
| 1   | A     | 17    | SER  | 2.4  |
| 1   | C     | 16    | ARG  | 2.4  |
| 1   | I     | 26    | ASP  | 2.4  |
| 1   | H     | 108   | VAL  | 2.4  |

*Continued on next page...*



*Continued from previous page...*

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1   | A     | -4  | ASP  | 2.4  |
| 1   | H     | 138 | ALA  | 2.4  |
| 1   | H     | 37  | LEU  | 2.3  |
| 1   | D     | 16  | ARG  | 2.3  |
| 1   | D     | 18  | PRO  | 2.3  |
| 1   | H     | 152 | PHE  | 2.3  |
| 1   | H     | 20  | TYR  | 2.3  |
| 1   | F     | 75  | ILE  | 2.2  |
| 1   | H     | 135 | GLU  | 2.2  |
| 1   | H     | 57  | GLN  | 2.2  |
| 1   | H     | 201 | VAL  | 2.1  |
| 1   | H     | 140 | CYS  | 2.1  |
| 1   | I     | 15  | ASN  | 2.1  |
| 1   | H     | 161 | ASP  | 2.1  |
| 1   | G     | 3   | GLN  | 2.1  |
| 1   | F     | 1   | HIS  | 2.1  |
| 1   | I     | 17  | SER  | 2.1  |
| 1   | E     | 70  | ASN  | 2.1  |
| 1   | H     | 55  | TYR  | 2.1  |
| 1   | H     | 185 | VAL  | 2.0  |
| 1   | I     | 27  | ASP  | 2.0  |
| 1   | H     | 142 | VAL  | 2.0  |
| 1   | C     | 7   | MET  | 2.0  |
| 1   | H     | 72  | TYR  | 2.0  |
| 1   | G     | 5   | ASN  | 2.0  |

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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  | LLDF  | B-factors( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|-----|-------|------|------|-------|-----------------------------|-------|
| 2   | MLK  | D     | 301 | 49/49 | 0.93 | 0.17 | 0.09  | 39,40,45,45                 | 0     |
| 2   | MLK  | G     | 301 | 49/49 | 0.90 | 0.18 | 0.05  | 45,46,56,56                 | 0     |
| 2   | MLK  | F     | 301 | 49/49 | 0.93 | 0.18 | -0.12 | 43,44,48,48                 | 0     |
| 2   | MLK  | J     | 301 | 49/49 | 0.95 | 0.15 | -0.27 | 30,33,39,39                 | 0     |
| 2   | MLK  | E     | 301 | 49/49 | 0.95 | 0.16 | -0.31 | 27,28,37,38                 | 0     |
| 2   | MLK  | I     | 301 | 49/49 | 0.88 | 0.21 | -0.39 | 49,52,56,57                 | 0     |
| 2   | MLK  | A     | 301 | 49/49 | 0.93 | 0.14 | -0.47 | 28,30,40,40                 | 0     |
| 2   | MLK  | B     | 301 | 49/49 | 0.96 | 0.14 | -0.49 | 23,25,31,32                 | 0     |
| 2   | MLK  | H     | 301 | 49/49 | 0.89 | 0.17 | -0.53 | 51,52,59,59                 | 0     |
| 2   | MLK  | C     | 301 | 49/49 | 0.95 | 0.14 | -0.55 | 30,32,40,40                 | 0     |

## 6.5 Other polymers [i](#)

There are no such residues in this entry.