



## Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 11:35 pm GMT

PDB ID : 2L1G  
Title : RDC refined solution structure of the THAP zinc finger of THAP1 in complex with its 16bp RRM1 DNA target  
Authors : Campagne, S.; Gervais, V.; Saurel, O.; Milon, A.  
Deposited on : 2010-07-28

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

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:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : trunk28760  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

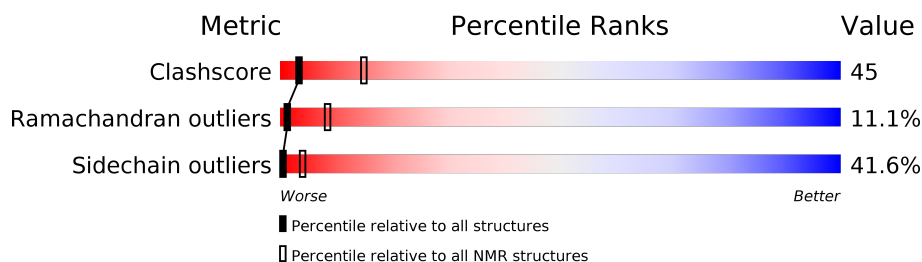
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment was not calculated.

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) | NMR archive<br>(#Entries) |
|-----------------------|-----------------------------|---------------------------|
| Clashscore            | 125131                      | 11601                     |
| Ramachandran outliers | 121729                      | 10391                     |
| Sidechain outliers    | 121581                      | 10367                     |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | A     | 87     |                  |
| 2   | B     | 16     |                  |
| 3   | C     | 16     |                  |

## 2 Ensemble composition and analysis

This entry contains 17 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

| Well-defined (core) protein residues |                       |                   |              |
|--------------------------------------|-----------------------|-------------------|--------------|
| Well-defined core                    | Residue range (total) | Backbone RMSD (Å) | Medoid model |
| 1                                    | A:3-A:82 (80)         | 0.14              | 11           |

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 1 clusters and 3 single-model clusters were found.

| Cluster number        | Models  |
|-----------------------|---|
| 1                     | 1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 13, 15, 17 |
| Single-model clusters | 10; 14; 16                                    |

### 3 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2447 atoms, of which 1078 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called THAP domain-containing protein 1.

| Mol | Chain | Residues | Atoms |     |     |     |     |   | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|-------|
| 1   | A     | 87       | Total | C   | H   | N   | O   | S | 0     |
|     |       |          | 1434  | 455 | 719 | 127 | 128 | 5 |       |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment             | Reference  |
|-------|---------|----------|--------|---------------------|------------|
| A     | 62      | SER      | CYS    | ENGINEERED MUTATION | UNP Q9NVV9 |
| A     | 67      | SER      | CYS    | ENGINEERED MUTATION | UNP Q9NVV9 |
| A     | 83      | GLU      | -      | EXPRESSION TAG      | UNP Q9NVV9 |
| A     | 84      | LEU      | -      | EXPRESSION TAG      | UNP Q9NVV9 |
| A     | 85      | VAL      | -      | EXPRESSION TAG      | UNP Q9NVV9 |
| A     | 86      | PRO      | -      | EXPRESSION TAG      | UNP Q9NVV9 |
| A     | 87      | ARG      | -      | EXPRESSION TAG      | UNP Q9NVV9 |

- Molecule 2 is a DNA chain called DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3').

| Mol | Chain | Residues | Atoms |     |     |    |    |    | Trace |
|-----|-------|----------|-------|-----|-----|----|----|----|-------|
| 2   | B     | 16       | Total | C   | H   | N  | O  | P  | 0     |
|     |       |          | 512   | 157 | 181 | 62 | 97 | 15 |       |

- Molecule 3 is a DNA chain called DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3').

| Mol | Chain | Residues | Atoms |     |     |    |    |    | Trace |
|-----|-------|----------|-------|-----|-----|----|----|----|-------|
| 3   | C     | 16       | Total | C   | H   | N  | O  | P  | 0     |
|     |       |          | 500   | 152 | 178 | 61 | 93 | 16 |       |

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

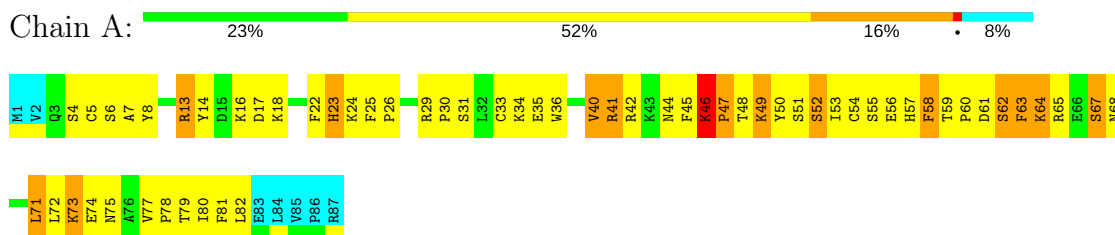
| Mol | Chain | Residues | Atoms |    |
|-----|-------|----------|-------|----|
| 4   | A     | 1        | Total | Zn |
|     |       |          | 1     | 1  |

## 4 Residue-property plots

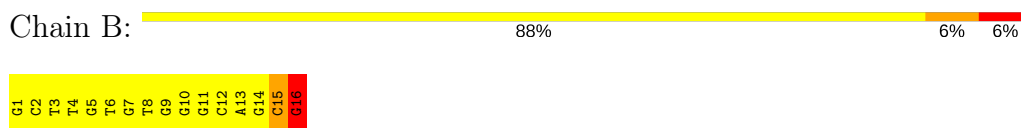
### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

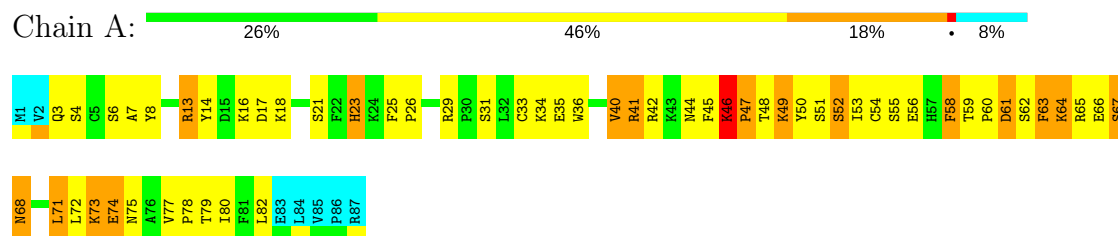


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

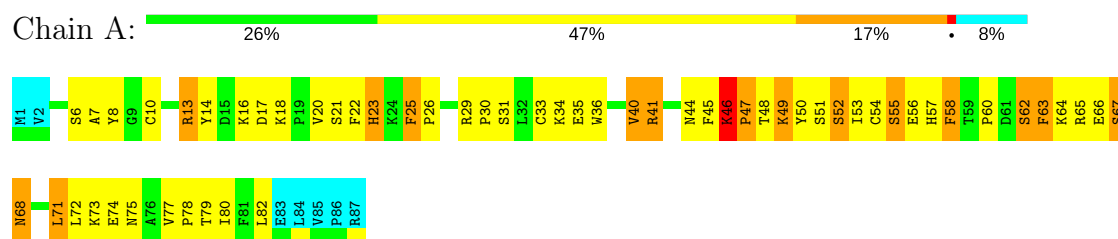


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

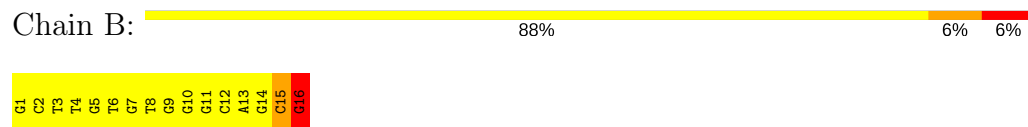


## 4.2.2 Score per residue for model 2

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



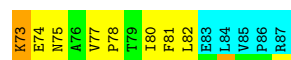
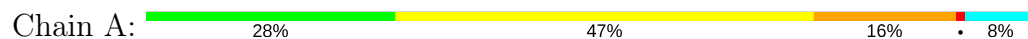
- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')



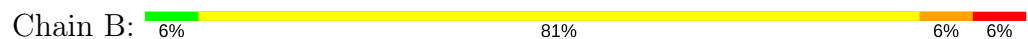


#### 4.2.3 Score per residue for model 3

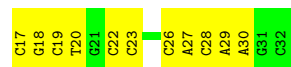
- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

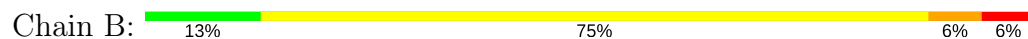


#### 4.2.4 Score per residue for model 4

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



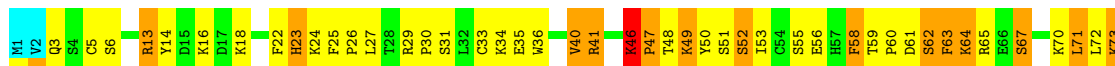
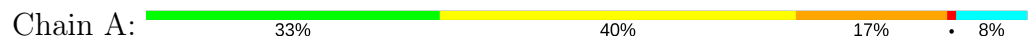


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

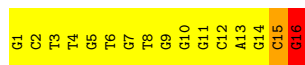
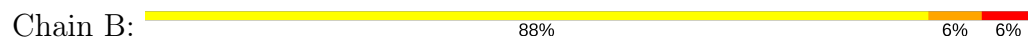


#### 4.2.5 Score per residue for model 5

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

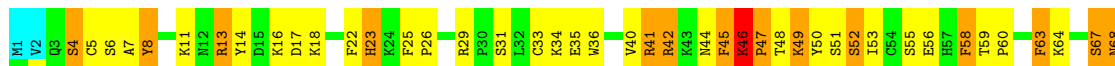


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')



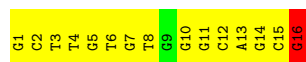
#### 4.2.6 Score per residue for model 6

- Molecule 1: THAP domain-containing protein 1





- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

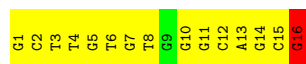


#### 4.2.7 Score per residue for model 7

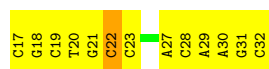
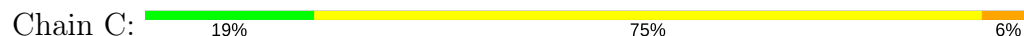
- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

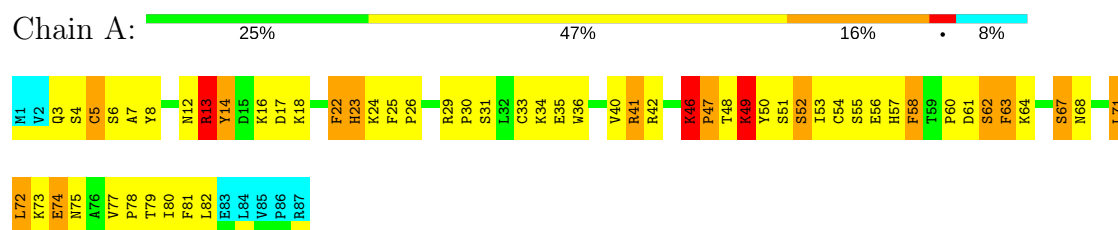


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

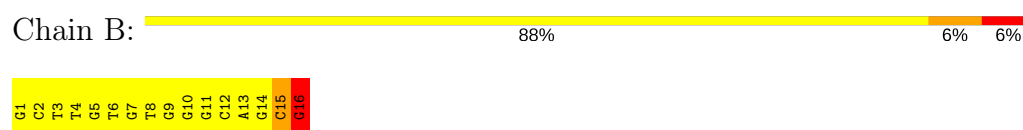


### 4.2.8 Score per residue for model 8

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

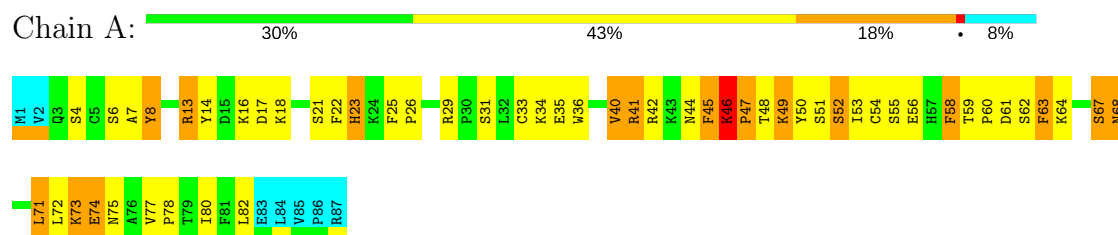


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

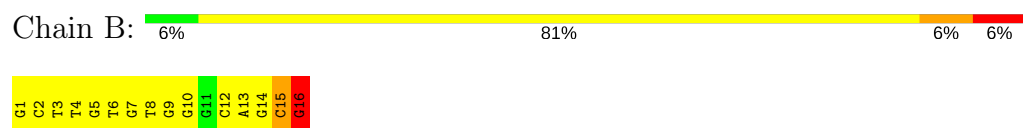


### 4.2.9 Score per residue for model 9

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

Chain C:  13% 81% 6%

C17  
G18  
C19  
T20  
C21  
C22  
C23  
C24  
A25  
C26  
A27  
C28  
A29  
A30  
G31  
C32

#### 4.2.10 Score per residue for model 10

- Molecule 1: THAP domain-containing protein 1

Chain A:  26% 45% 18% 8%

M1  
V2  
Q3  
S4  
C5  
S6  
A7  
Y8  
R13  
Y14  
D15  
K16  
D17  
K18  
F22  
H23  
K24  
F25  
P26  
L27  
T28  
R29  
P30  
S31  
L32  
C33  
K34  
E35  
W36  
V40  
R41  
R42  
K43  
N44  
F45  
K46  
P47  
T48  
K49  
Y50  
S51  
S52  
I53  
C54  
S55  
E56  
H57  
F58  
T59  
P60  
D61  
S62  
F63  
K64  
R65  
E66  
S67

N68  
R69  
K70  
L71  
L72  
K73  
E74  
N75  
A76  
V77  
P78  
T79  
I80  
F81  
L82  
E83  
L84  
V85  
P86  
R87

- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

Chain B:  94% 6%

G1  
C2  
T3  
T4  
G5  
T6  
G7  
T8  
G9  
G10  
G11  
G12  
A13  
G14  
C15  
G16

- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

Chain C:  6% 88% 6%

C17  
G18  
C19  
T20  
C21  
C22  
C23  
C24  
A25  
C26  
A27  
C28  
A29  
A30  
G31  
C32

#### 4.2.11 Score per residue for model 11 (medoid)

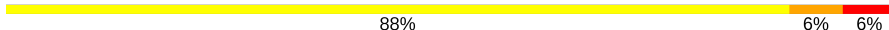
- Molecule 1: THAP domain-containing protein 1

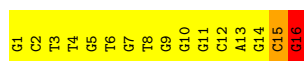
Chain A:  29% 44% 18% 8%

M1  
V2  
Q3  
S4  
C5  
S6  
A7  
N12  
R13  
I80  
Y14  
D15  
K16  
D17  
K18  
S21  
F22  
H23  
K24  
F25  
R29  
P30  
S31  
L32  
C33  
K34  
E35  
W36  
V40  
R41  
R42  
K43  
N44  
F45  
K46  
P47  
T48  
K49  
Y50  
S51  
S52  
I53  
C54  
S55  
E56  
H57  
F58  
T59  
P60  
D61  
S62  
F63  
K64  
S67  
N68

L71  
L72  
K73  
E74  
N75  
A76  
V77  
P78  
T79  
I80  
F81  
L82  
E83  
L84  
V85  
P86  
R87

- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

Chain B:  88% 6% 6%

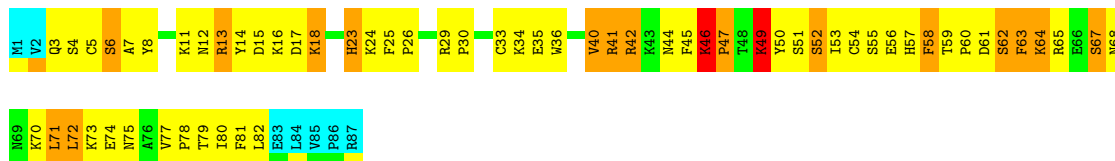
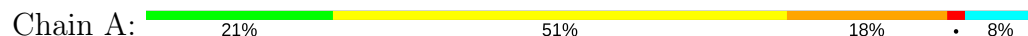


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

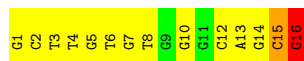


#### 4.2.12 Score per residue for model 12

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')



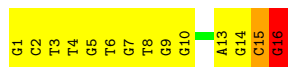
#### 4.2.13 Score per residue for model 13

- Molecule 1: THAP domain-containing protein 1





- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

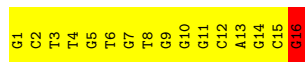


#### 4.2.14 Score per residue for model 14

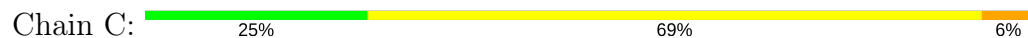
- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

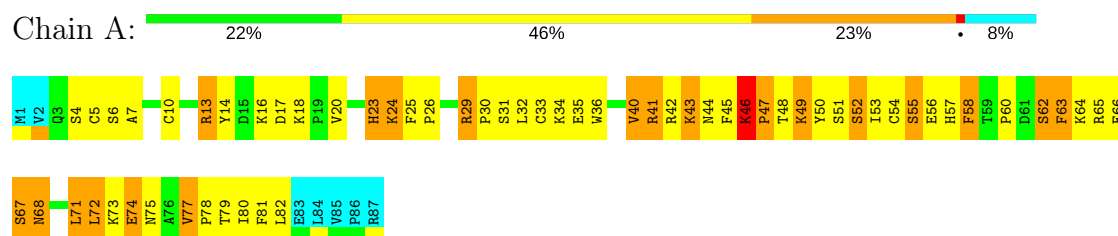


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')



### 4.2.15 Score per residue for model 15

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

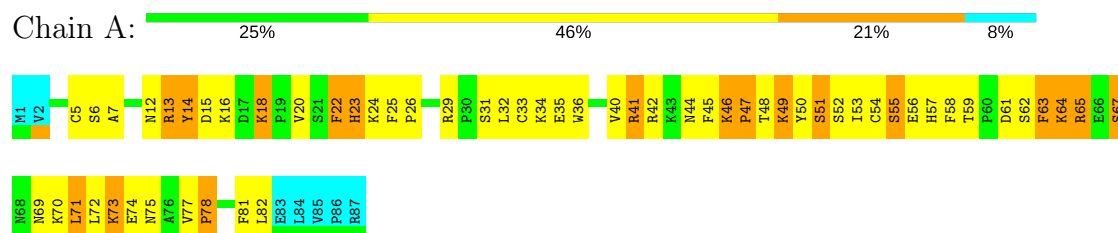


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')

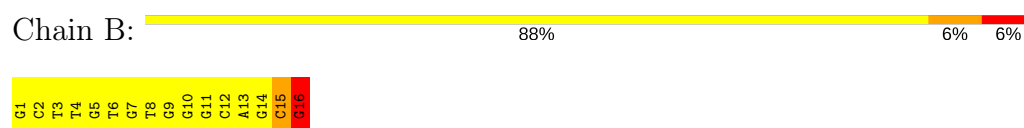


### 4.2.16 Score per residue for model 16

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')

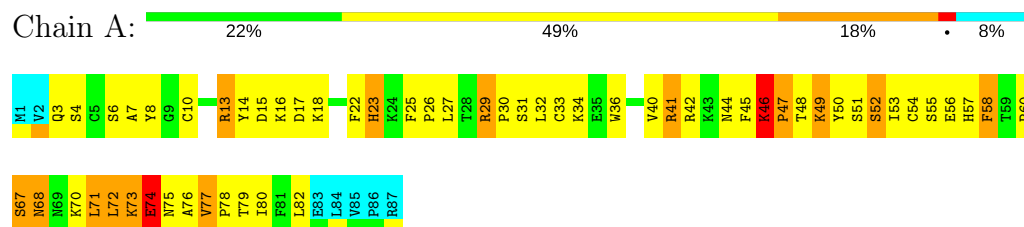


- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')



#### 4.2.17 Score per residue for model 17

- Molecule 1: THAP domain-containing protein 1



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*TP\*GP\*TP\*GP\*TP\*GP\*GP\*GP\*CP\*AP\*GP\*CP\*G)-3')



- Molecule 3: DNA (5'-D(P\*CP\*GP\*CP\*TP\*GP\*CP\*CP\*CP\*AP\*CP\*AP\*CP\*AP\*AP\*GP\*C)-3')



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *Rigid body docking, Semi flexible simulated annealing, Water refinement.*

Of the 200 calculated structures, 17 were deposited, based on the following criterion: *structures with the least restraint violations.*

The following table shows the software used for structure solution, optimisation and refinement.

| Software name | Classification | Version |
|---------------|----------------|---------|
| CNS           | refinement     | 1.21    |

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the (average) 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     | 0.50±0.02    | 0±0/676 (0.0±0.0%) | 0.78±0.02   | 0±0/910 (0.0±0.0%) |
| 2   | B     | 0.42±0.02    | 0±0/371 (0.0±0.0%) | 0.84±0.01   | 2±0/573 (0.3±0.0%) |
| 3   | C     | 0.31±0.02    | 0±0/360 (0.0±0.0%) | 0.69±0.01   | 0±0/551 (0.0±0.0%) |
| All | All   | 0.44         | 0/23919 (0.0%)     | 0.77        | 34/34578 (0.1%)    |

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 | Planarity |
|-----|-------|-----------|-----------|
| 2   | B     | 0.0±0.0   | 1.6±0.5   |
| 3   | C     | 0.0±0.0   | 0.8±0.5   |
| All | All   | 0         | 42        |

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

| Mol | Chain | Res | Type | Atoms       | Z     | Observed(°) | Ideal(°) | Models |       |
|-----|-------|-----|------|-------------|-------|-------------|----------|--------|-------|
|     |       |     |      |             |       |             |          | Worst  | Total |
| 2   | B     | 16  | DG   | O4'-C4'-C3' | -6.70 | 101.82      | 104.50   | 1      | 17    |
| 2   | B     | 16  | DG   | O4'-C1'-N9  | 6.46  | 112.52      | 108.00   | 7      | 17    |

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type | Group     | Models (Total) |
|-----|-------|-----|------|-----------|----------------|
| 2   | B     | 16  | DG   | Sidechain | 17             |

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| Mol | Chain | Res | Type | Group     | Models (Total) |
|-----|-------|-----|------|-----------|----------------|
| 2   | B     | 15  | DC   | Sidechain | 11             |
| 3   | C     | 22  | DC   | Sidechain | 11             |
| 3   | C     | 23  | DC   | Sidechain | 3              |

## 6.2 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 each 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 averaged over the ensemble.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes |
|-----|-------|-------|----------|----------|---------|
| 1   | A     | 657   | 653      | 652      | 40±5    |
| 2   | B     | 331   | 181      | 182      | 47±2    |
| 3   | C     | 322   | 178      | 178      | 25±3    |
| All | All   | 22287 | 17204    | 17204    | 1781    |

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 45.

All unique clashes are listed below, sorted by their clash magnitude.

| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 2:B:15:DC:H1'   | 2:B:16:DG:N7    | 1.12     | 1.60        | 7      | 17    |
| 2:B:7:DG:C2'    | 2:B:8:DT:H71    | 0.94     | 1.91        | 5      | 10    |
| 2:B:14:DG:H2''  | 2:B:15:DC:C5    | 0.91     | 1.99        | 16     | 17    |
| 2:B:7:DG:H2'    | 2:B:8:DT:H72    | 0.91     | 1.41        | 6      | 7     |
| 1:A:25:PHE:HD2  | 1:A:33:CYS:HG   | 0.89     | 1.11        | 7      | 17    |
| 2:B:15:DC:C1'   | 2:B:16:DG:N7    | 0.88     | 2.35        | 12     | 17    |
| 2:B:1:DG:H2''   | 2:B:2:DC:C5     | 0.86     | 2.04        | 5      | 17    |
| 3:C:19:DC:C2'   | 3:C:20:DT:H72   | 0.84     | 2.03        | 11     | 7     |
| 3:C:19:DC:H2''  | 3:C:20:DT:C5    | 0.84     | 2.06        | 1      | 17    |
| 1:A:71:LEU:HD13 | 1:A:72:LEU:HD12 | 0.82     | 1.52        | 4      | 17    |
| 2:B:7:DG:H2'    | 2:B:8:DT:H71    | 0.82     | 1.50        | 15     | 10    |
| 3:C:18:DG:H2''  | 3:C:19:DC:C5    | 0.82     | 2.10        | 9      | 17    |
| 2:B:3:DT:H2''   | 2:B:4:DT:H71    | 0.81     | 1.50        | 9      | 17    |
| 2:B:7:DG:H2''   | 2:B:8:DT:H71    | 0.76     | 1.57        | 12     | 10    |
| 2:B:7:DG:C2'    | 2:B:8:DT:H72    | 0.76     | 2.09        | 9      | 7     |
| 1:A:67:SER:HB3  | 1:A:71:LEU:O    | 0.75     | 1.81        | 7      | 17    |
| 2:B:1:DG:H2''   | 2:B:2:DC:C6     | 0.75     | 2.15        | 5      | 17    |
| 2:B:11:DG:H2''  | 2:B:12:DC:C5    | 0.73     | 2.18        | 14     | 9     |

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| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 2:B:1:DG:C2'    | 2:B:2:DC:C5     | 0.73     | 2.72        | 5      | 17    |
| 3:C:27:DA:H2''  | 3:C:28:DC:C5    | 0.73     | 2.19        | 17     | 17    |
| 1:A:55:SER:HB3  | 1:A:63:PHE:CE1  | 0.72     | 2.19        | 14     | 1     |
| 3:C:19:DC:H2'   | 3:C:20:DT:H72   | 0.72     | 1.60        | 11     | 7     |
| 2:B:14:DG:C2'   | 2:B:15:DC:C5    | 0.72     | 2.71        | 16     | 17    |
| 1:A:62:SER:HA   | 1:A:73:LYS:CD   | 0.72     | 2.15        | 16     | 1     |
| 3:C:18:DG:H2''  | 3:C:19:DC:C6    | 0.71     | 2.21        | 9      | 17    |
| 2:B:6:DT:H1'    | 2:B:7:DG:C8     | 0.70     | 2.21        | 11     | 17    |
| 2:B:3:DT:H2''   | 2:B:4:DT:C7     | 0.70     | 2.17        | 9      | 17    |
| 2:B:2:DC:H2''   | 2:B:3:DT:H71    | 0.70     | 1.63        | 9      | 17    |
| 2:B:7:DG:C2'    | 2:B:8:DT:C7     | 0.69     | 2.69        | 13     | 17    |
| 2:B:5:DG:H2''   | 2:B:6:DT:C5     | 0.69     | 2.22        | 17     | 16    |
| 1:A:67:SER:OG   | 1:A:73:LYS:HD2  | 0.69     | 1.88        | 14     | 16    |
| 2:B:15:DC:C2'   | 2:B:16:DG:N7    | 0.69     | 2.55        | 1      | 17    |
| 2:B:5:DG:H2''   | 2:B:6:DT:C7     | 0.69     | 2.17        | 17     | 17    |
| 3:C:19:DC:H2''  | 3:C:20:DT:C7    | 0.69     | 2.18        | 5      | 17    |
| 2:B:5:DG:H2''   | 2:B:6:DT:H71    | 0.68     | 1.64        | 17     | 17    |
| 1:A:47:PRO:HB2  | 1:A:51:SER:OG   | 0.68     | 1.88        | 10     | 16    |
| 2:B:15:DC:H2''  | 2:B:16:DG:N7    | 0.68     | 2.02        | 1      | 17    |
| 2:B:3:DT:C2'    | 2:B:4:DT:H71    | 0.68     | 2.19        | 9      | 17    |
| 2:B:14:DG:H2''  | 2:B:15:DC:C6    | 0.68     | 2.24        | 7      | 17    |
| 2:B:16:DG:C8    | 2:B:16:DG:O5'   | 0.67     | 2.47        | 1      | 8     |
| 1:A:23:HIS:HE1  | 1:A:55:SER:N    | 0.67     | 1.88        | 15     | 17    |
| 1:A:25:PHE:CD1  | 1:A:53:ILE:HD11 | 0.66     | 2.26        | 16     | 15    |
| 2:B:7:DG:H2'    | 2:B:8:DT:C7     | 0.65     | 2.22        | 13     | 16    |
| 1:A:25:PHE:HD2  | 1:A:33:CYS:SG   | 0.65     | 2.14        | 12     | 17    |
| 1:A:24:LYS:HD3  | 2:B:8:DT:H72    | 0.65     | 1.67        | 5      | 4     |
| 2:B:15:DC:H1'   | 2:B:16:DG:C8    | 0.65     | 2.26        | 12     | 17    |
| 3:C:17:DC:H2''  | 3:C:18:DG:C8    | 0.64     | 2.26        | 2      | 17    |
| 3:C:18:DG:C2'   | 3:C:19:DC:C5    | 0.64     | 2.80        | 9      | 15    |
| 2:B:16:DG:O5'   | 2:B:16:DG:C8    | 0.64     | 2.50        | 12     | 9     |
| 3:C:19:DC:H2''  | 3:C:20:DT:H72   | 0.64     | 1.68        | 15     | 7     |
| 3:C:19:DC:C2'   | 3:C:20:DT:C7    | 0.63     | 2.75        | 5      | 16    |
| 3:C:26:DC:H2''  | 3:C:27:DA:C8    | 0.63     | 2.28        | 15     | 9     |
| 2:B:15:DC:C2    | 2:B:16:DG:O6    | 0.63     | 2.51        | 13     | 17    |
| 3:C:19:DC:H2''  | 3:C:20:DT:C6    | 0.62     | 2.29        | 5      | 15    |
| 1:A:50:TYR:CD2  | 3:C:22:DC:H2'   | 0.62     | 2.29        | 8      | 16    |
| 2:B:2:DC:C2'    | 2:B:3:DT:H71    | 0.62     | 2.24        | 8      | 17    |
| 1:A:50:TYR:HB2  | 3:C:22:DC:C5    | 0.62     | 2.29        | 12     | 17    |
| 1:A:48:THR:HG21 | 3:C:22:DC:OP2   | 0.62     | 1.95        | 1      | 14    |
| 1:A:36:TRP:O    | 1:A:40:VAL:HG23 | 0.61     | 1.95        | 14     | 17    |

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| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 2:B:5:DG:C2'    | 2:B:6:DT:H71    | 0.61     | 2.25        | 14     | 17    |
| 2:B:2:DC:H2''   | 2:B:3:DT:C7     | 0.61     | 2.26        | 6      | 17    |
| 2:B:7:DG:H2''   | 2:B:8:DT:C6     | 0.61     | 2.31        | 13     | 17    |
| 1:A:40:VAL:HG22 | 1:A:81:PHE:HE2  | 0.60     | 1.56        | 16     | 2     |
| 2:B:16:DG:H8    | 2:B:16:DG:O5'   | 0.60     | 1.79        | 3      | 4     |
| 1:A:60:PRO:HA   | 1:A:63:PHE:CD2  | 0.60     | 2.30        | 7      | 12    |
| 3:C:27:DA:H2''  | 3:C:28:DC:C6    | 0.60     | 2.31        | 15     | 17    |
| 1:A:62:SER:O    | 1:A:72:LEU:HD23 | 0.60     | 1.97        | 13     | 12    |
| 1:A:55:SER:HB2  | 1:A:63:PHE:CE1  | 0.60     | 2.31        | 5      | 10    |
| 1:A:6:SER:HA    | 1:A:46:LYS:CB   | 0.60     | 2.27        | 9      | 14    |
| 1:A:23:HIS:CE1  | 1:A:58:PHE:HE2  | 0.59     | 2.15        | 14     | 4     |
| 3:C:19:DC:H2''  | 3:C:20:DT:H71   | 0.59     | 1.74        | 6      | 10    |
| 1:A:50:TYR:CD1  | 3:C:23:DC:H5    | 0.59     | 2.15        | 13     | 16    |
| 2:B:6:DT:H2''   | 2:B:7:DG:C8     | 0.59     | 2.31        | 11     | 17    |
| 2:B:16:DG:O5'   | 2:B:16:DG:H8    | 0.59     | 1.78        | 1      | 13    |
| 2:B:12:DC:H2''  | 2:B:13:DA:C8    | 0.59     | 2.31        | 6      | 11    |
| 2:B:3:DT:C2'    | 2:B:4:DT:C7     | 0.59     | 2.80        | 9      | 15    |
| 1:A:42:ARG:HG3  | 1:A:43:LYS:O    | 0.59     | 1.97        | 14     | 2     |
| 2:B:6:DT:C1'    | 2:B:7:DG:C8     | 0.58     | 2.86        | 11     | 17    |
| 3:C:28:DC:H2''  | 3:C:29:DA:C8    | 0.58     | 2.33        | 13     | 13    |
| 1:A:5:CYS:O     | 1:A:46:LYS:HD3  | 0.58     | 1.98        | 15     | 4     |
| 1:A:64:LYS:O    | 1:A:67:SER:HB3  | 0.58     | 1.99        | 14     | 2     |
| 1:A:52:SER:C    | 1:A:53:ILE:HD12 | 0.57     | 2.20        | 6      | 16    |
| 2:B:6:DT:C2     | 2:B:7:DG:C5     | 0.57     | 2.92        | 11     | 17    |
| 1:A:24:LYS:HG3  | 2:B:8:DT:H72    | 0.57     | 1.74        | 16     | 1     |
| 2:B:5:DG:C2'    | 2:B:6:DT:C7     | 0.57     | 2.82        | 17     | 16    |
| 1:A:26:PRO:HB3  | 1:A:72:LEU:CD1  | 0.57     | 2.29        | 8      | 12    |
| 3:C:19:DC:C2'   | 3:C:20:DT:C5    | 0.57     | 2.86        | 1      | 10    |
| 1:A:43:LYS:HG2  | 1:A:44:ASN:N    | 0.57     | 2.14        | 7      | 2     |
| 3:C:29:DA:H2''  | 3:C:30:DA:C8    | 0.56     | 2.36        | 5      | 10    |
| 2:B:13:DA:H2''  | 2:B:14:DG:C8    | 0.56     | 2.36        | 6      | 14    |
| 2:B:7:DG:H2''   | 2:B:8:DT:C7     | 0.55     | 2.29        | 7      | 12    |
| 3:C:27:DA:C2'   | 3:C:28:DC:C5    | 0.55     | 2.89        | 16     | 15    |
| 2:B:2:DC:C2'    | 2:B:3:DT:C7     | 0.55     | 2.84        | 8      | 17    |
| 1:A:61:ASP:O    | 1:A:73:LYS:HD3  | 0.55     | 2.01        | 7      | 6     |
| 1:A:49:LYS:H    | 1:A:49:LYS:HD2  | 0.55     | 1.62        | 14     | 1     |
| 1:A:47:PRO:HB2  | 1:A:51:SER:CB   | 0.55     | 2.31        | 8      | 2     |
| 1:A:3:GLN:NE2   | 3:C:20:DT:H71   | 0.55     | 2.17        | 12     | 3     |
| 3:C:19:DC:C2'   | 3:C:20:DT:H71   | 0.54     | 2.32        | 5      | 4     |
| 1:A:36:TRP:CE2  | 1:A:78:PRO:HD2  | 0.54     | 2.38        | 17     | 17    |
| 1:A:23:HIS:HE1  | 1:A:54:CYS:C    | 0.54     | 2.05        | 17     | 13    |

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| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 1:A:50:TYR:CE2  | 3:C:22:DC:H2'   | 0.54     | 2.38        | 8      | 11    |
| 3:C:31:DG:H2''  | 3:C:32:DC:C5    | 0.54     | 2.38        | 2      | 14    |
| 1:A:64:LYS:HD3  | 2:B:8:DT:OP1    | 0.54     | 2.02        | 7      | 4     |
| 1:A:23:HIS:CE1  | 1:A:55:SER:N    | 0.54     | 2.75        | 15     | 17    |
| 1:A:50:TYR:CD2  | 3:C:23:DC:H5    | 0.53     | 2.21        | 14     | 1     |
| 1:A:27:LEU:HD21 | 1:A:49:LYS:HG3  | 0.53     | 1.79        | 5      | 6     |
| 1:A:45:PHE:HD1  | 1:A:46:LYS:O    | 0.53     | 1.87        | 14     | 15    |
| 2:B:2:DC:H2''   | 2:B:3:DT:C5     | 0.53     | 2.39        | 2      | 16    |
| 1:A:26:PRO:HB3  | 1:A:72:LEU:HD13 | 0.53     | 1.81        | 2      | 12    |
| 1:A:25:PHE:CD2  | 1:A:49:LYS:HB3  | 0.53     | 2.39        | 9      | 9     |
| 2:B:15:DC:C2    | 2:B:16:DG:C6    | 0.52     | 2.97        | 1      | 17    |
| 2:B:2:DC:H2''   | 2:B:3:DT:C6     | 0.52     | 2.39        | 16     | 12    |
| 1:A:15:ASP:OD2  | 1:A:17:ASP:HB2  | 0.52     | 2.05        | 17     | 1     |
| 3:C:31:DG:H2''  | 3:C:32:DC:C6    | 0.52     | 2.40        | 17     | 9     |
| 1:A:67:SER:HB2  | 1:A:73:LYS:CE   | 0.52     | 2.34        | 16     | 1     |
| 3:C:17:DC:C5    | 3:C:17:DC:OP2   | 0.52     | 2.63        | 16     | 2     |
| 2:B:3:DT:H2''   | 2:B:4:DT:C5     | 0.51     | 2.40        | 5      | 8     |
| 2:B:9:DG:H2''   | 2:B:10:DG:OP2   | 0.51     | 2.05        | 8      | 13    |
| 1:A:60:PRO:O    | 1:A:63:PHE:HB2  | 0.51     | 2.04        | 10     | 2     |
| 1:A:15:ASP:O    | 1:A:18:LYS:HG2  | 0.51     | 2.04        | 12     | 3     |
| 1:A:57:HIS:O    | 1:A:78:PRO:HA   | 0.51     | 2.06        | 15     | 11    |
| 3:C:20:DT:OP2   | 3:C:20:DT:H71   | 0.51     | 2.05        | 16     | 3     |
| 1:A:61:ASP:O    | 1:A:67:SER:HA   | 0.50     | 2.07        | 14     | 1     |
| 1:A:30:PRO:O    | 1:A:33:CYS:HB3  | 0.50     | 2.07        | 2      | 12    |
| 3:C:17:DC:C6    | 3:C:17:DC:OP2   | 0.49     | 2.65        | 16     | 1     |
| 2:B:11:DG:H2''  | 2:B:12:DC:C6    | 0.49     | 2.42        | 14     | 1     |
| 2:B:11:DG:C2'   | 2:B:12:DC:C5    | 0.49     | 2.93        | 14     | 2     |
| 2:B:5:DG:H2''   | 2:B:6:DT:C6     | 0.49     | 2.41        | 17     | 8     |
| 2:B:12:DC:H2''  | 2:B:13:DA:N7    | 0.49     | 2.22        | 6      | 2     |
| 3:C:28:DC:C4    | 3:C:29:DA:N6    | 0.49     | 2.80        | 1      | 9     |
| 1:A:33:CYS:SG   | 1:A:49:LYS:HD3  | 0.49     | 2.47        | 15     | 2     |
| 3:C:17:DC:H2''  | 3:C:18:DG:N7    | 0.49     | 2.22        | 6      | 5     |
| 1:A:15:ASP:OD1  | 1:A:17:ASP:HB2  | 0.49     | 2.07        | 3      | 2     |
| 1:A:24:LYS:HB2  | 2:B:8:DT:H72    | 0.49     | 1.84        | 15     | 3     |
| 1:A:32:LEU:HD21 | 1:A:76:ALA:O    | 0.49     | 2.07        | 17     | 1     |
| 3:C:20:DT:H2''  | 3:C:21:DG:C8    | 0.49     | 2.43        | 12     | 1     |
| 1:A:8:TYR:CE1   | 1:A:42:ARG:HD3  | 0.49     | 2.43        | 6      | 2     |
| 2:B:14:DG:C4    | 2:B:15:DC:C4    | 0.48     | 3.01        | 13     | 6     |
| 1:A:67:SER:OG   | 1:A:68:ASN:N    | 0.48     | 2.47        | 13     | 14    |
| 1:A:8:TYR:CE1   | 1:A:82:LEU:HB2  | 0.48     | 2.44        | 10     | 1     |
| 1:A:65:ARG:HA   | 1:A:70:LYS:C    | 0.48     | 2.27        | 10     | 2     |

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| Atom-1         | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|----------------|-----------------|----------|-------------|--------|-------|
|                |                 |          |             | Worst  | Total |
| 1:A:78:PRO:HB2 | 1:A:81:PHE:CE1  | 0.48     | 2.44        | 14     | 5     |
| 2:B:6:DT:C2'   | 2:B:7:DG:C8     | 0.48     | 2.96        | 11     | 7     |
| 1:A:23:HIS:CE1 | 1:A:58:PHE:CE2  | 0.48     | 3.02        | 1      | 3     |
| 1:A:65:ARG:HA  | 1:A:70:LYS:O    | 0.48     | 2.09        | 14     | 1     |
| 2:B:5:DG:C2'   | 2:B:6:DT:C5     | 0.48     | 2.96        | 17     | 2     |
| 1:A:4:SER:HB2  | 1:A:11:LYS:HA   | 0.47     | 1.86        | 7      | 3     |
| 1:A:23:HIS:HB3 | 2:B:8:DT:OP1    | 0.47     | 2.09        | 7      | 4     |
| 1:A:64:LYS:HG2 | 1:A:65:ARG:N    | 0.47     | 2.24        | 14     | 2     |
| 1:A:62:SER:OG  | 1:A:73:LYS:HG2  | 0.47     | 2.09        | 17     | 4     |
| 1:A:25:PHE:HD1 | 1:A:53:ILE:HD11 | 0.47     | 1.68        | 16     | 1     |
| 1:A:64:LYS:HG3 | 1:A:66:GLU:OE1  | 0.47     | 2.08        | 1      | 1     |
| 1:A:23:HIS:CE1 | 1:A:58:PHE:HE1  | 0.47     | 2.27        | 9      | 9     |
| 1:A:62:SER:HA  | 1:A:73:LYS:HD3  | 0.47     | 1.87        | 16     | 1     |
| 1:A:47:PRO:HA  | 3:C:21:DG:OP2   | 0.47     | 2.09        | 16     | 2     |
| 1:A:46:LYS:HG3 | 3:C:20:DT:OP1   | 0.47     | 2.10        | 7      | 2     |
| 1:A:61:ASP:C   | 1:A:73:LYS:HD3  | 0.47     | 2.30        | 12     | 5     |
| 1:A:29:ARG:HG2 | 1:A:32:LEU:CB   | 0.47     | 2.40        | 10     | 3     |
| 1:A:6:SER:HA   | 1:A:46:LYS:HB3  | 0.47     | 1.85        | 16     | 1     |
| 2:B:10:DG:H2'' | 2:B:11:DG:OP2   | 0.47     | 2.10        | 6      | 2     |
| 1:A:25:PHE:CE1 | 1:A:53:ILE:HD11 | 0.46     | 2.45        | 17     | 6     |
| 1:A:20:VAL:HB  | 1:A:55:SER:OG   | 0.46     | 2.10        | 14     | 5     |
| 1:A:23:HIS:CE1 | 1:A:58:PHE:CE1  | 0.46     | 3.03        | 13     | 10    |
| 1:A:62:SER:CB  | 1:A:73:LYS:HG2  | 0.46     | 2.40        | 1      | 3     |
| 1:A:25:PHE:CD1 | 1:A:49:LYS:HA   | 0.46     | 2.45        | 10     | 7     |
| 3:C:20:DT:H71  | 3:C:20:DT:OP2   | 0.46     | 2.10        | 14     | 1     |
| 3:C:27:DA:C4   | 3:C:28:DC:C4    | 0.46     | 3.04        | 6      | 2     |
| 1:A:18:LYS:HZ2 | 1:A:20:VAL:HG22 | 0.46     | 1.71        | 14     | 1     |
| 1:A:49:LYS:N   | 1:A:49:LYS:HD2  | 0.46     | 2.25        | 14     | 1     |
| 1:A:10:CYS:SG  | 1:A:10:CYS:O    | 0.46     | 2.73        | 15     | 3     |
| 3:C:25:DA:H2'' | 3:C:26:DC:OP2   | 0.46     | 2.11        | 6      | 9     |
| 1:A:25:PHE:CD2 | 1:A:33:CYS:SG   | 0.46     | 3.08        | 13     | 5     |
| 1:A:40:VAL:O   | 1:A:40:VAL:HG12 | 0.46     | 2.10        | 3      | 1     |
| 1:A:49:LYS:CD  | 1:A:49:LYS:H    | 0.45     | 2.22        | 14     | 1     |
| 1:A:8:TYR:CE2  | 1:A:42:ARG:HD3  | 0.45     | 2.45        | 12     | 1     |
| 1:A:6:SER:O    | 1:A:40:VAL:HG13 | 0.45     | 2.11        | 2      | 3     |
| 2:B:1:DG:H8    | 2:B:1:DG:HO5'   | 0.45     | 1.53        | 15     | 1     |
| 1:A:72:LEU:H   | 1:A:72:LEU:HD12 | 0.45     | 1.71        | 12     | 5     |
| 1:A:62:SER:HA  | 1:A:73:LYS:HD2  | 0.45     | 1.88        | 16     | 1     |
| 1:A:23:HIS:O   | 1:A:53:ILE:N    | 0.45     | 2.46        | 8      | 2     |
| 1:A:14:TYR:CD2 | 1:A:22:PHE:HD2  | 0.45     | 2.30        | 16     | 2     |
| 2:B:6:DT:H2''  | 2:B:7:DG:OP2    | 0.45     | 2.12        | 9      | 5     |

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| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 1:A:25:PHE:CG   | 1:A:49:LYS:HB3  | 0.44     | 2.47        | 3      | 5     |
| 2:B:6:DT:C1'    | 2:B:7:DG:N7     | 0.44     | 2.81        | 2      | 7     |
| 1:A:29:ARG:HG2  | 1:A:32:LEU:HB3  | 0.44     | 1.89        | 10     | 1     |
| 2:B:7:DG:H2''   | 2:B:8:DT:C5     | 0.44     | 2.47        | 13     | 3     |
| 1:A:64:LYS:HG2  | 1:A:65:ARG:H    | 0.44     | 1.72        | 14     | 1     |
| 1:A:50:TYR:CD2  | 3:C:22:DC:C6    | 0.43     | 3.06        | 6      | 4     |
| 1:A:60:PRO:HA   | 1:A:63:PHE:CE2  | 0.43     | 2.47        | 7      | 1     |
| 1:A:62:SER:HA   | 1:A:73:LYS:NZ   | 0.43     | 2.28        | 16     | 1     |
| 1:A:59:THR:O    | 1:A:62:SER:N    | 0.43     | 2.51        | 16     | 2     |
| 1:A:60:PRO:HA   | 1:A:63:PHE:CG   | 0.43     | 2.48        | 11     | 4     |
| 3:C:30:DA:H2''  | 3:C:31:DG:C8    | 0.43     | 2.49        | 16     | 4     |
| 1:A:3:GLN:HE22  | 3:C:20:DT:H73   | 0.43     | 1.73        | 5      | 1     |
| 1:A:71:LEU:CD1  | 1:A:72:LEU:HD12 | 0.43     | 2.40        | 13     | 1     |
| 1:A:65:ARG:HD2  | 2:B:7:DG:H4'    | 0.43     | 1.88        | 16     | 2     |
| 1:A:46:LYS:HG3  | 3:C:20:DT:P     | 0.43     | 2.53        | 2      | 2     |
| 1:A:46:LYS:CB   | 1:A:47:PRO:CD   | 0.43     | 2.97        | 3      | 17    |
| 1:A:3:GLN:NE2   | 3:C:20:DT:H73   | 0.42     | 2.29        | 7      | 3     |
| 3:C:21:DG:H2''  | 3:C:22:DC:C6    | 0.42     | 2.48        | 10     | 2     |
| 3:C:26:DC:C4    | 3:C:27:DA:N6    | 0.42     | 2.87        | 15     | 1     |
| 1:A:25:PHE:CD1  | 1:A:53:ILE:CD1  | 0.42     | 3.02        | 13     | 2     |
| 1:A:69:ASN:CG   | 1:A:70:LYS:N    | 0.42     | 2.72        | 16     | 1     |
| 1:A:48:THR:O    | 1:A:50:TYR:N    | 0.42     | 2.52        | 10     | 2     |
| 1:A:60:PRO:HA   | 1:A:63:PHE:CD1  | 0.42     | 2.50        | 17     | 1     |
| 1:A:23:HIS:HB3  | 2:B:8:DT:P      | 0.42     | 2.54        | 15     | 1     |
| 2:B:15:DC:N3    | 2:B:16:DG:O6    | 0.42     | 2.51        | 9      | 1     |
| 1:A:72:LEU:HD12 | 1:A:72:LEU:H    | 0.42     | 1.74        | 17     | 2     |
| 1:A:48:THR:HG23 | 3:C:21:DG:H2'   | 0.42     | 1.92        | 9      | 1     |
| 1:A:81:PHE:O    | 1:A:82:LEU:HG   | 0.42     | 2.15        | 10     | 1     |
| 1:A:50:TYR:HB3  | 3:C:23:DC:H41   | 0.41     | 1.75        | 16     | 1     |
| 1:A:77:VAL:O    | 1:A:79:THR:HG23 | 0.41     | 2.15        | 17     | 1     |
| 1:A:50:TYR:O    | 3:C:23:DC:N4    | 0.41     | 2.52        | 12     | 1     |
| 1:A:29:ARG:HD3  | 1:A:32:LEU:CB   | 0.41     | 2.45        | 15     | 1     |
| 1:A:47:PRO:HB2  | 1:A:51:SER:HB2  | 0.41     | 1.91        | 16     | 1     |
| 1:A:45:PHE:O    | 3:C:20:DT:H3'   | 0.41     | 2.15        | 10     | 1     |
| 3:C:19:DC:H2'   | 3:C:20:DT:C7    | 0.41     | 2.45        | 5      | 1     |
| 1:A:47:PRO:HB3  | 3:C:22:DC:N4    | 0.41     | 2.30        | 8      | 1     |
| 1:A:26:PRO:HB3  | 1:A:72:LEU:HD11 | 0.41     | 1.92        | 8      | 1     |
| 1:A:29:ARG:HD2  | 1:A:74:GLU:HB2  | 0.41     | 1.92        | 17     | 1     |
| 1:A:8:TYR:CZ    | 1:A:42:ARG:HD3  | 0.41     | 2.49        | 9      | 1     |
| 2:B:6:DT:C2     | 2:B:7:DG:N7     | 0.41     | 2.89        | 16     | 1     |
| 2:B:3:DT:H2''   | 2:B:4:DT:C6     | 0.41     | 2.50        | 11     | 3     |

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| Atom-1          | Atom-2         | Clash(Å) | Distance(Å) | Models |       |
|-----------------|----------------|----------|-------------|--------|-------|
|                 |                |          |             | Worst  | Total |
| 1:A:36:TRP:CE2  | 1:A:78:PRO:CD  | 0.41     | 3.03        | 17     | 1     |
| 1:A:71:LEU:HD23 | 1:A:71:LEU:HA  | 0.41     | 1.77        | 6      | 2     |
| 1:A:64:LYS:HD2  | 2:B:8:DT:OP1   | 0.41     | 2.16        | 5      | 1     |
| 1:A:29:ARG:N    | 1:A:30:PRO:CD  | 0.41     | 2.83        | 15     | 2     |
| 1:A:67:SER:OG   | 1:A:73:LYS:HE3 | 0.41     | 2.14        | 16     | 1     |
| 1:A:77:VAL:HG23 | 1:A:78:PRO:HD2 | 0.41     | 1.92        | 15     | 1     |
| 1:A:46:LYS:HG3  | 3:C:20:DT:OP2  | 0.41     | 2.15        | 13     | 1     |
| 3:C:21:DG:H2''  | 3:C:22:DC:C5   | 0.41     | 2.51        | 10     | 1     |
| 1:A:67:SER:CB   | 1:A:71:LEU:O   | 0.41     | 2.63        | 16     | 1     |
| 3:C:17:DC:C6    | 3:C:17:DC:O5'  | 0.41     | 2.74        | 16     | 1     |
| 1:A:57:HIS:HD1  | 1:A:81:PHE:HA  | 0.40     | 1.75        | 8      | 1     |
| 1:A:50:TYR:CZ   | 3:C:23:DC:OP2  | 0.40     | 2.73        | 11     | 1     |
| 1:A:40:VAL:HG12 | 1:A:40:VAL:O   | 0.40     | 2.15        | 7      | 1     |
| 1:A:8:TYR:CD1   | 1:A:42:ARG:HG2 | 0.40     | 2.51        | 12     | 1     |
| 1:A:45:PHE:CD1  | 1:A:46:LYS:O   | 0.40     | 2.72        | 11     | 3     |
| 2:B:6:DT:C4     | 2:B:7:DG:O6    | 0.40     | 2.75        | 2      | 1     |
| 1:A:67:SER:HB2  | 1:A:73:LYS:HZ1 | 0.40     | 1.76        | 16     | 1     |
| 1:A:50:TYR:CD1  | 3:C:23:DC:C5   | 0.40     | 3.04        | 13     | 1     |
| 1:A:50:TYR:CD2  | 3:C:22:DC:C2'  | 0.40     | 3.04        | 8      | 1     |
| 1:A:55:SER:HA   | 1:A:58:PHE:CE1 | 0.40     | 2.52        | 17     | 1     |

## 6.3 Torsion angles ⓘ

### 6.3.1 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 NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

| Mol | Chain | Analysed        | Favoured     | Allowed      | Outliers    | Percentiles |   |
|-----|-------|-----------------|--------------|--------------|-------------|-------------|---|
| 1   | A     | 80/87 (92%)     | 57±2 (71±2%) | 14±2 (18±2%) | 9±1 (11±1%) | 1           | 8 |
| All | All   | 1360/1479 (92%) | 970 (71%)    | 239 (18%)    | 151 (11%)   | 1           | 8 |

All 12 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1   | A     | 46  | LYS  | 17             |
| 1   | A     | 64  | LYS  | 17             |

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| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1   | A     | 67  | SER  | 17             |
| 1   | A     | 41  | ARG  | 17             |
| 1   | A     | 47  | PRO  | 17             |
| 1   | A     | 13  | ARG  | 16             |
| 1   | A     | 7   | ALA  | 15             |
| 1   | A     | 74  | GLU  | 14             |
| 1   | A     | 40  | VAL  | 11             |
| 1   | A     | 72  | LEU  | 6              |
| 1   | A     | 49  | LYS  | 3              |
| 1   | A     | 63  | PHE  | 1              |

### 6.3.2 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 NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

| Mol | Chain | Analysed        | Rotameric    | Outliers     | Percentiles |   |
|-----|-------|-----------------|--------------|--------------|-------------|---|
| 1   | A     | 75/82 (91%)     | 44±2 (58±3%) | 31±2 (42±3%) | 0           | 4 |
| All | All   | 1275/1394 (91%) | 744 (58%)    | 531 (42%)    | 0           | 4 |

All 53 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1   | A     | 34  | LYS  | 17             |
| 1   | A     | 49  | LYS  | 17             |
| 1   | A     | 71  | LEU  | 17             |
| 1   | A     | 56  | GLU  | 17             |
| 1   | A     | 77  | VAL  | 17             |
| 1   | A     | 52  | SER  | 17             |
| 1   | A     | 75  | ASN  | 17             |
| 1   | A     | 14  | TYR  | 17             |
| 1   | A     | 58  | PHE  | 17             |
| 1   | A     | 16  | LYS  | 17             |
| 1   | A     | 13  | ARG  | 17             |
| 1   | A     | 23  | HIS  | 17             |
| 1   | A     | 41  | ARG  | 17             |
| 1   | A     | 63  | PHE  | 16             |
| 1   | A     | 35  | GLU  | 16             |

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| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1   | A     | 18  | LYS  | 16             |
| 1   | A     | 80  | ILE  | 15             |
| 1   | A     | 82  | LEU  | 15             |
| 1   | A     | 46  | LYS  | 15             |
| 1   | A     | 29  | ARG  | 14             |
| 1   | A     | 44  | ASN  | 13             |
| 1   | A     | 31  | SER  | 13             |
| 1   | A     | 62  | SER  | 12             |
| 1   | A     | 22  | PHE  | 12             |
| 1   | A     | 42  | ARG  | 11             |
| 1   | A     | 74  | GLU  | 10             |
| 1   | A     | 68  | ASN  | 10             |
| 1   | A     | 8   | TYR  | 9              |
| 1   | A     | 17  | ASP  | 9              |
| 1   | A     | 73  | LYS  | 9              |
| 1   | A     | 4   | SER  | 9              |
| 1   | A     | 5   | CYS  | 8              |
| 1   | A     | 65  | ARG  | 8              |
| 1   | A     | 79  | THR  | 8              |
| 1   | A     | 21  | SER  | 8              |
| 1   | A     | 61  | ASP  | 7              |
| 1   | A     | 59  | THR  | 7              |
| 1   | A     | 12  | ASN  | 7              |
| 1   | A     | 55  | SER  | 4              |
| 1   | A     | 70  | LYS  | 4              |
| 1   | A     | 25  | PHE  | 3              |
| 1   | A     | 45  | PHE  | 3              |
| 1   | A     | 64  | LYS  | 3              |
| 1   | A     | 66  | GLU  | 2              |
| 1   | A     | 20  | VAL  | 2              |
| 1   | A     | 43  | LYS  | 2              |
| 1   | A     | 24  | LYS  | 2              |
| 1   | A     | 81  | PHE  | 2              |
| 1   | A     | 6   | SER  | 2              |
| 1   | A     | 72  | LEU  | 1              |
| 1   | A     | 51  | SER  | 1              |
| 1   | A     | 15  | ASP  | 1              |
| 1   | A     | 78  | PRO  | 1              |

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

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

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided