



# Full wwPDB NMR Structure Validation Report ⓘ

Mar 23, 2026 – 03:57 AM UTC

PDB ID : 2DLK / pdb\_00002dlk  
Title : Solution structure of the first and the second zf-C2H2 domains of zinc finger protein 692  
Authors : Zhang, H.P.; Nagashima, T.; Hayashi, F.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2006-04-20

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

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

|                                |   |                                                                  |
|--------------------------------|---|------------------------------------------------------------------|
| MolProbity                     | : | 4-5-2 with Phenix2.0                                             |
| Percentile statistics          | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| wwPDB-RCI                      | : | v_1n_11_5_13_A (Berjanski et al., 2005)                          |
| PANAV                          | : | Wang et al. (2010)                                               |
| wwPDB-ShiftChecker             | : | v1.2                                                             |
| Ideal geometry (proteins)      | : | Engh & Huber (2001)                                              |
| Ideal geometry (DNA, RNA)      | : | Parkinson et al. (1996)                                          |
| Validation Pipeline (wwPDB-VP) | : | 2.49                                                             |

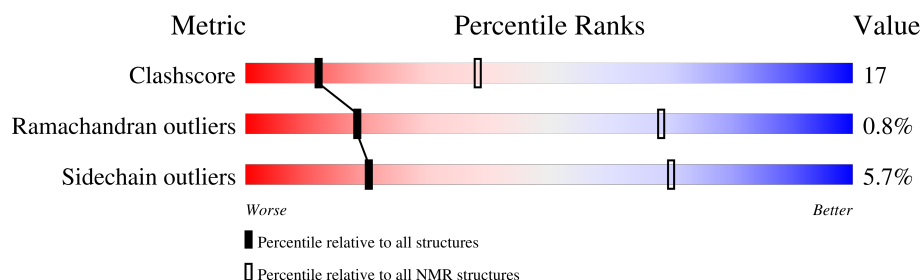
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*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            | 229148                      | 14424                     |
| Ramachandran outliers | 224038                      | 12848                     |
| Sidechain outliers    | 223484                      | 12823                     |

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     | 79     |                  |

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 3 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:7-A:33 (27)         | 0.42              | 3            |
| 2                                    | A:39-A:63 (25)        | 0.60              | 19           |

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 5 clusters. No single-model clusters were found.

| Cluster number | Models              |
|----------------|---------------------|
| 1              | 1, 2, 5, 10, 12, 13 |
| 2              | 3, 9, 11, 16, 20    |
| 3              | 6, 7, 15, 19        |
| 4              | 4, 8, 18            |
| 5              | 14, 17              |

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1207 atoms, of which 581 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called novel protein.

| Mol | Chain | Residues | Atoms |     |     |     |     |   | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|-------|
| 1   | A     | 79       | Total | C   | H   | N   | O   | S | 0     |
|     |       |          | 1205  | 388 | 581 | 116 | 113 | 7 |       |

There are 13 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment          | Reference  |
|-------|---------|----------|--------|------------------|------------|
| A     | 1       | GLY      | -      | cloning artifact | UNP Q9BU19 |
| A     | 2       | SER      | -      | cloning artifact | UNP Q9BU19 |
| A     | 3       | SER      | -      | cloning artifact | UNP Q9BU19 |
| A     | 4       | GLY      | -      | cloning artifact | UNP Q9BU19 |
| A     | 5       | SER      | -      | cloning artifact | UNP Q9BU19 |
| A     | 6       | SER      | -      | cloning artifact | UNP Q9BU19 |
| A     | 7       | GLY      | -      | cloning artifact | UNP Q9BU19 |
| A     | 74      | SER      | -      | cloning artifact | UNP Q9BU19 |
| A     | 75      | GLY      | -      | cloning artifact | UNP Q9BU19 |
| A     | 76      | PRO      | -      | cloning artifact | UNP Q9BU19 |
| A     | 77      | SER      | -      | cloning artifact | UNP Q9BU19 |
| A     | 78      | SER      | -      | cloning artifact | UNP Q9BU19 |
| A     | 79      | GLY      | -      | cloning artifact | UNP Q9BU19 |

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

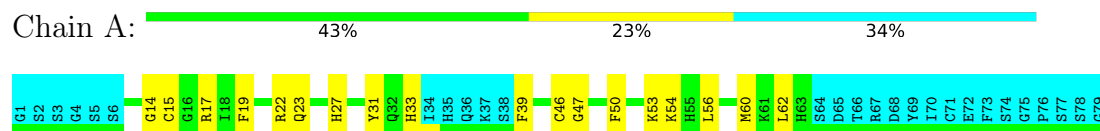
| Mol | Chain | Residues | Atoms |    |
|-----|-------|----------|-------|----|
| 2   | A     | 2        | Total | Zn |
|     |       |          | 2     | 2  |

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

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

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: novel protein

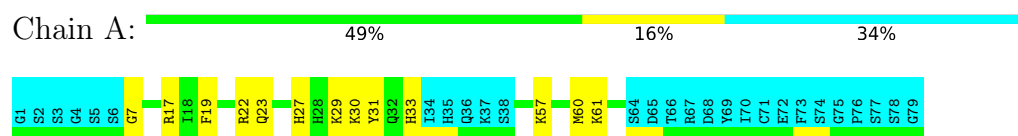


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

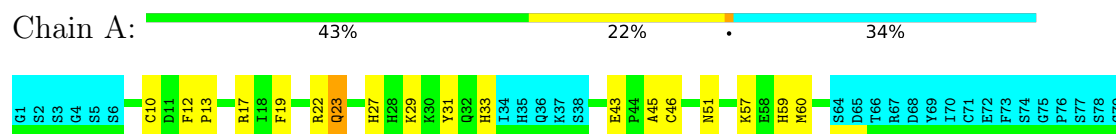
#### 4.2.1 Score per residue for model 1

- Molecule 1: novel protein



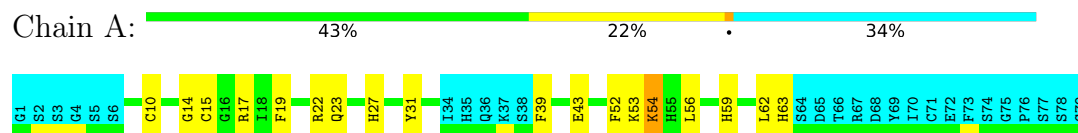
#### 4.2.2 Score per residue for model 2

- Molecule 1: novel protein



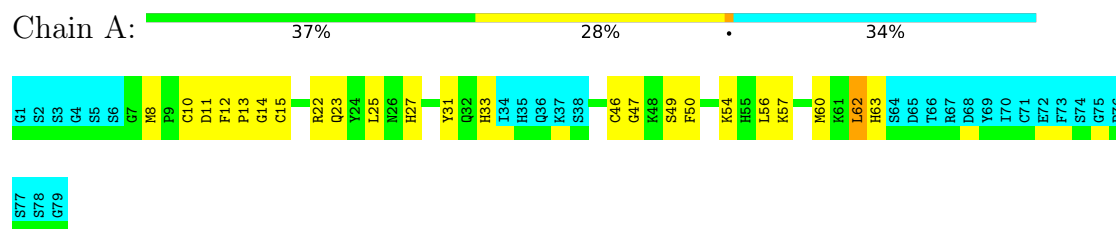
### 4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: novel protein



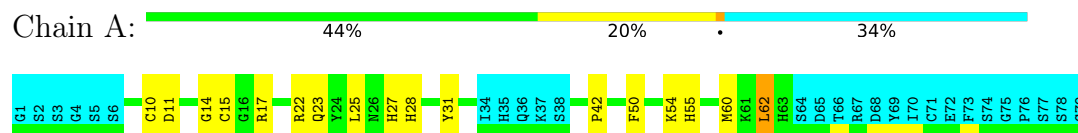
### 4.2.4 Score per residue for model 4

- Molecule 1: novel protein



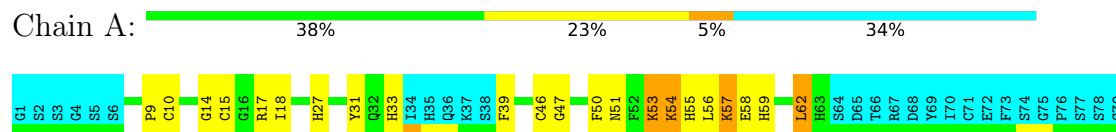
### 4.2.5 Score per residue for model 5

- Molecule 1: novel protein



### 4.2.6 Score per residue for model 6

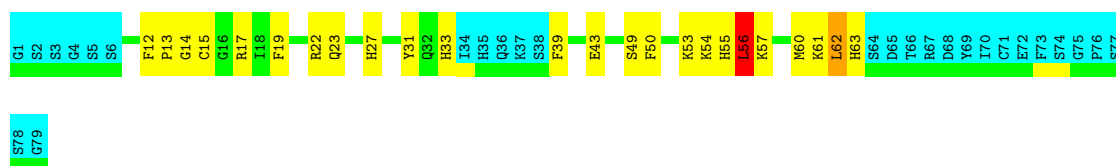
- Molecule 1: novel protein



### 4.2.7 Score per residue for model 7

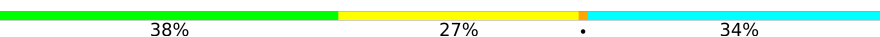
- Molecule 1: novel protein

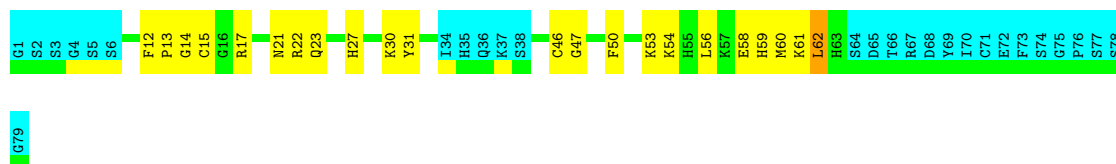




#### 4.2.8 Score per residue for model 8

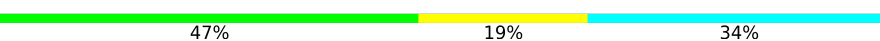
- Molecule 1: novel protein

Chain A: 



#### 4.2.9 Score per residue for model 9

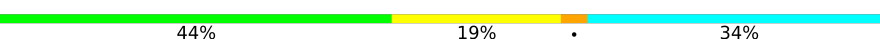
- Molecule 1: novel protein

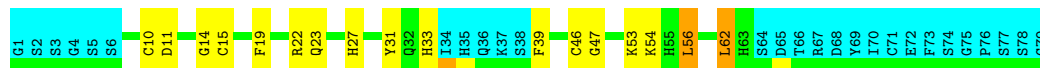
Chain A: 



#### 4.2.10 Score per residue for model 10

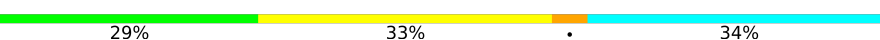
- Molecule 1: novel protein

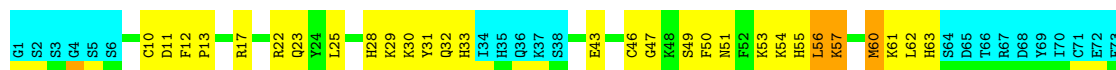
Chain A: 



#### 4.2.11 Score per residue for model 11

- Molecule 1: novel protein

Chain A: 



S74  
G75  
P76  
S77  
S78  
G79

#### 4.2.12 Score per residue for model 12

- Molecule 1: novel protein

Chain A: 52% 14% 34%

G1 S2 S3 S4 S5 S6 D11 G14 C15 H27 Y31 I34 H35 Q36 K37 S38 F39 K53 K54 H55 L56 M60 K61 S64 D65 T66 R67 D68 Y69 I70 C71 E72 F73 S74 G75 P76 S77 S78 G79

#### 4.2.13 Score per residue for model 13

- Molecule 1: novel protein

Chain A: 52% 13% 34%

G1 S2 S3 S4 S5 S6 F19 R22 Q23 H27 Y31 I34 H35 Q36 K37 S38 F39 C46 G47 K53 E58 L62 H63 S64 D65 T66 R67 D68 Y69 I70 C71 E72 F73 S74 G75 P76 S77 S78 G79

#### 4.2.14 Score per residue for model 14

- Molecule 1: novel protein

Chain A: 37% 28% 34%

G1 S2 S3 S4 S5 S6 C10 G14 G16 R17 I18 F19 R22 Q23 H27 Y31 Q32 H33 I34 H36 Q36 K37 S38 F39 C46 G47 K48 S49 F50 H51 F52 K53 K54 H55 L56 H59 L62 H63 S64 D65 T66 R67 D68 Y69 I70 C71 E72 F73 S74 G75 P76

S77  
S78  
G79

#### 4.2.15 Score per residue for model 15

- Molecule 1: novel protein

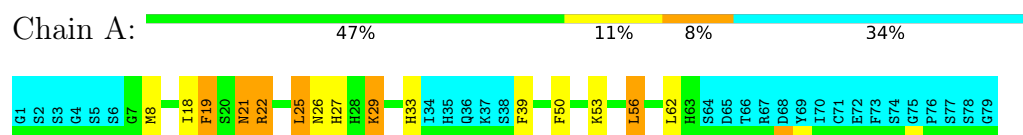
Chain A: 39% 23% 34%

G1 S2 S3 S4 S5 S6 F12 P13 G14 C15 G16 R17 I18 F19 R22 Q23 Y24 L25 H27 Y31 Q32 H33 I34 H35 Q36 K37 S38 F39 C46 G47 K48 S49 F50 K53 L56 H59 L62 H63 S64 D65 T66 R67 D68 Y69 I70 C71 E72 F73 S74 G75 P76

S77  
S78  
G79

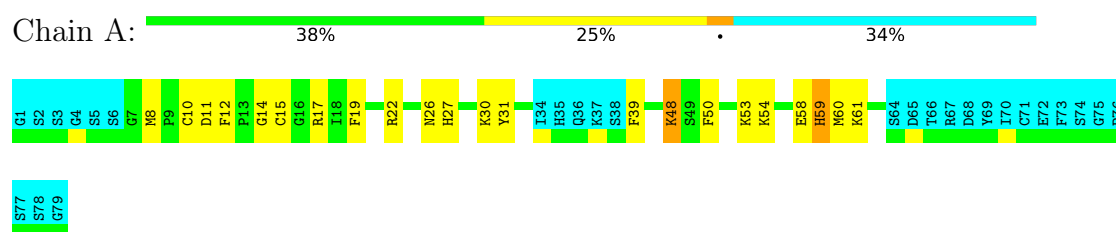
#### 4.2.16 Score per residue for model 16

- Molecule 1: novel protein



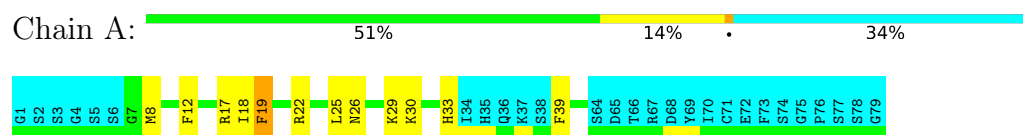
#### 4.2.17 Score per residue for model 17

- Molecule 1: novel protein



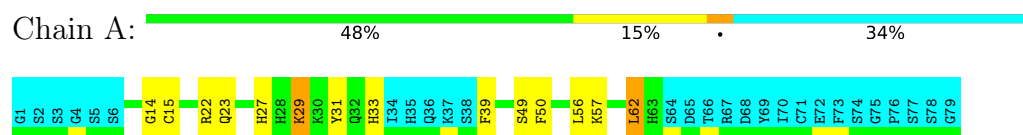
#### 4.2.18 Score per residue for model 18

- Molecule 1: novel protein



#### 4.2.19 Score per residue for model 19

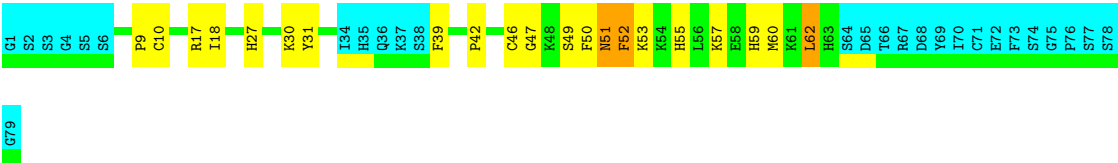
- Molecule 1: novel protein



#### 4.2.20 Score per residue for model 20

- Molecule 1: novel protein





## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function, structures with the lowest energy, structures with the least restraint violations*.

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

| Software name | Classification     | Version |
|---------------|--------------------|---------|
| CYANA         | structure solution | 2.0.17  |
| CYANA         | refinement         | 2.0.17  |

No chemical shift data was provided.

## 6 Model quality

### 6.1 Standard geometry

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

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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     | 431   | 410      | 410      | 15±5    |
| All | All   | 8660  | 8200     | 8200     | 291     |

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 17.

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

| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 1:A:25:LEU:HD13 | 1:A:26:ASN:N    | 0.88     | 1.82        | 16     | 2     |
| 1:A:27:HIS:CE1  | 1:A:31:TYR:CE1  | 0.75     | 2.75        | 20     | 9     |
| 1:A:8:MET:HE1   | 1:A:22:ARG:HG2  | 0.74     | 1.59        | 4      | 3     |
| 1:A:56:LEU:HD13 | 1:A:56:LEU:O    | 0.74     | 1.82        | 11     | 2     |
| 1:A:27:HIS:CE1  | 1:A:31:TYR:CZ   | 0.73     | 2.76        | 13     | 13    |
| 1:A:25:LEU:HD13 | 1:A:25:LEU:C    | 0.72     | 2.10        | 16     | 2     |
| 1:A:39:PHE:CD2  | 1:A:56:LEU:HD13 | 0.71     | 2.20        | 16     | 2     |
| 1:A:62:LEU:C    | 1:A:62:LEU:HD12 | 0.70     | 2.11        | 20     | 4     |
| 1:A:12:PHE:CG   | 1:A:33:HIS:CE1  | 0.69     | 2.80        | 11     | 2     |
| 1:A:62:LEU:HD12 | 1:A:62:LEU:C    | 0.68     | 2.13        | 5      | 4     |
| 1:A:49:SER:C    | 1:A:50:PHE:CD1  | 0.67     | 2.72        | 20     | 7     |
| 1:A:25:LEU:HD11 | 1:A:29:LYS:HD3  | 0.65     | 1.67        | 16     | 1     |

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| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 1:A:10:CYS:HA   | 1:A:25:LEU:HD11 | 0.65     | 1.68        | 11     | 1     |
| 1:A:12:PHE:CD2  | 1:A:33:HIS:CE1  | 0.63     | 2.87        | 9      | 3     |
| 1:A:25:LEU:CD1  | 1:A:26:ASN:N    | 0.63     | 2.61        | 16     | 1     |
| 1:A:27:HIS:NE2  | 1:A:31:TYR:CE1  | 0.62     | 2.67        | 8      | 10    |
| 1:A:12:PHE:CD2  | 1:A:33:HIS:ND1  | 0.62     | 2.67        | 9      | 4     |
| 1:A:39:PHE:HD2  | 1:A:56:LEU:HD13 | 0.61     | 1.55        | 7      | 2     |
| 1:A:62:LEU:H    | 1:A:62:LEU:HD13 | 0.61     | 1.55        | 14     | 1     |
| 1:A:27:HIS:CE1  | 1:A:31:TYR:CE2  | 0.60     | 2.89        | 13     | 2     |
| 1:A:27:HIS:NE2  | 1:A:31:TYR:CZ   | 0.59     | 2.70        | 17     | 9     |
| 1:A:19:PHE:N    | 1:A:19:PHE:CD1  | 0.58     | 2.71        | 18     | 5     |
| 1:A:27:HIS:NE2  | 1:A:31:TYR:CD2  | 0.58     | 2.71        | 15     | 2     |
| 1:A:39:PHE:HB3  | 1:A:56:LEU:HD22 | 0.58     | 1.74        | 19     | 2     |
| 1:A:56:LEU:HD13 | 1:A:56:LEU:C    | 0.57     | 2.25        | 8      | 3     |
| 1:A:25:LEU:HD21 | 1:A:29:LYS:HD3  | 0.56     | 1.77        | 16     | 1     |
| 1:A:27:HIS:CE1  | 1:A:31:TYR:CG   | 0.53     | 2.97        | 5      | 1     |
| 1:A:49:SER:O    | 1:A:50:PHE:CD1  | 0.52     | 2.61        | 20     | 1     |
| 1:A:39:PHE:CB   | 1:A:56:LEU:HD22 | 0.52     | 2.35        | 14     | 2     |
| 1:A:27:HIS:CE1  | 1:A:31:TYR:CD2  | 0.52     | 2.97        | 5      | 1     |
| 1:A:25:LEU:HD11 | 1:A:29:LYS:CD   | 0.52     | 2.34        | 16     | 1     |
| 1:A:62:LEU:CD2  | 1:A:62:LEU:C    | 0.52     | 2.83        | 14     | 1     |
| 1:A:27:HIS:CE1  | 1:A:31:TYR:CD1  | 0.51     | 2.98        | 8      | 1     |
| 1:A:51:ASN:ND2  | 1:A:51:ASN:H    | 0.51     | 2.04        | 20     | 1     |
| 1:A:27:HIS:CD2  | 1:A:27:HIS:C    | 0.50     | 2.88        | 6      | 4     |
| 1:A:10:CYS:N    | 1:A:17:ARG:O    | 0.50     | 2.43        | 6      | 6     |
| 1:A:9:PRO:CA    | 1:A:18:ILE:HD13 | 0.50     | 2.37        | 6      | 2     |
| 1:A:39:PHE:CZ   | 1:A:53:LYS:HG2  | 0.50     | 2.42        | 17     | 1     |
| 1:A:58:GLU:O    | 1:A:60:MET:N    | 0.50     | 2.44        | 17     | 1     |
| 1:A:55:HIS:O    | 1:A:57:LYS:N    | 0.50     | 2.45        | 7      | 2     |
| 1:A:25:LEU:HD13 | 1:A:26:ASN:CA   | 0.50     | 2.36        | 16     | 1     |
| 1:A:58:GLU:O    | 1:A:61:LYS:N    | 0.50     | 2.45        | 8      | 1     |
| 1:A:31:TYR:O    | 1:A:32:GLN:C    | 0.50     | 2.54        | 11     | 1     |
| 1:A:46:CYS:O    | 1:A:47:GLY:C    | 0.50     | 2.54        | 11     | 9     |
| 1:A:42:PRO:HD2  | 1:A:60:MET:HE1  | 0.50     | 1.82        | 5      | 1     |
| 1:A:60:MET:O    | 1:A:63:HIS:N    | 0.50     | 2.45        | 11     | 2     |
| 1:A:39:PHE:CD1  | 1:A:56:LEU:HD22 | 0.50     | 2.41        | 15     | 1     |
| 1:A:50:PHE:CD1  | 1:A:56:LEU:HG   | 0.49     | 2.42        | 16     | 1     |
| 1:A:10:CYS:O    | 1:A:11:ASP:C    | 0.49     | 2.55        | 10     | 5     |
| 1:A:56:LEU:C    | 1:A:56:LEU:CD1  | 0.49     | 2.85        | 8      | 2     |
| 1:A:62:LEU:CD2  | 1:A:62:LEU:N    | 0.49     | 2.75        | 15     | 1     |
| 1:A:27:HIS:CD2  | 1:A:31:TYR:CE1  | 0.49     | 3.00        | 14     | 2     |
| 1:A:55:HIS:O    | 1:A:56:LEU:C    | 0.49     | 2.55        | 11     | 3     |

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| Atom-1         | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|----------------|-----------------|----------|-------------|--------|-------|
|                |                 |          |             | Worst  | Total |
| 1:A:14:GLY:O   | 1:A:15:CYS:C    | 0.49     | 2.56        | 12     | 13    |
| 1:A:58:GLU:OE1 | 1:A:58:GLU:C    | 0.49     | 2.55        | 13     | 1     |
| 1:A:32:GLN:NE2 | 1:A:32:GLN:N    | 0.49     | 2.61        | 15     | 1     |
| 1:A:22:ARG:O   | 1:A:25:LEU:N    | 0.49     | 2.46        | 5      | 3     |
| 1:A:52:PHE:CD1 | 1:A:55:HIS:HB2  | 0.49     | 2.43        | 20     | 1     |
| 1:A:12:PHE:CD1 | 1:A:13:PRO:HD2  | 0.48     | 2.43        | 11     | 6     |
| 1:A:60:MET:O   | 1:A:61:LYS:C    | 0.48     | 2.55        | 12     | 5     |
| 1:A:39:PHE:CZ  | 1:A:53:LYS:HE2  | 0.48     | 2.43        | 9      | 1     |
| 1:A:59:HIS:O   | 1:A:62:LEU:HD21 | 0.48     | 2.07        | 14     | 1     |
| 1:A:53:LYS:HD3 | 1:A:56:LEU:HD23 | 0.48     | 1.85        | 9      | 1     |
| 1:A:39:PHE:CE2 | 1:A:53:LYS:HG2  | 0.48     | 2.42        | 17     | 1     |
| 1:A:52:PHE:O   | 1:A:53:LYS:C    | 0.48     | 2.57        | 14     | 2     |
| 1:A:58:GLU:O   | 1:A:59:HIS:C    | 0.48     | 2.57        | 17     | 3     |
| 1:A:62:LEU:H   | 1:A:62:LEU:HD23 | 0.48     | 1.68        | 8      | 2     |
| 1:A:17:ARG:HB3 | 1:A:19:PHE:CZ   | 0.47     | 2.44        | 1      | 4     |
| 1:A:53:LYS:O   | 1:A:54:LYS:C    | 0.47     | 2.56        | 11     | 8     |
| 1:A:23:GLN:CD  | 1:A:23:GLN:C    | 0.47     | 2.82        | 2      | 1     |
| 1:A:43:GLU:HG3 | 1:A:63:HIS:CD2  | 0.47     | 2.44        | 7      | 1     |
| 1:A:27:HIS:CD2 | 1:A:31:TYR:CD1  | 0.47     | 3.02        | 20     | 2     |
| 1:A:62:LEU:C   | 1:A:62:LEU:CD1  | 0.47     | 2.82        | 20     | 2     |
| 1:A:21:ASN:OD1 | 1:A:21:ASN:N    | 0.47     | 2.48        | 16     | 1     |
| 1:A:22:ARG:O   | 1:A:23:GLN:C    | 0.47     | 2.58        | 4      | 13    |
| 1:A:56:LEU:O   | 1:A:57:LYS:C    | 0.47     | 2.58        | 6      | 2     |
| 1:A:25:LEU:C   | 1:A:25:LEU:CD1  | 0.47     | 2.82        | 16     | 1     |
| 1:A:12:PHE:CB  | 1:A:33:HIS:CE1  | 0.47     | 2.98        | 11     | 1     |
| 1:A:58:GLU:C   | 1:A:60:MET:N    | 0.47     | 2.72        | 17     | 1     |
| 1:A:50:PHE:CD2 | 1:A:55:HIS:ND1  | 0.46     | 2.83        | 5      | 1     |
| 1:A:8:MET:HE2  | 1:A:22:ARG:HG2  | 0.46     | 1.86        | 16     | 1     |
| 1:A:27:HIS:NE2 | 1:A:31:TYR:CE2  | 0.46     | 2.84        | 15     | 2     |
| 1:A:59:HIS:CE1 | 1:A:62:LEU:HD21 | 0.46     | 2.46        | 6      | 1     |
| 1:A:50:PHE:CD1 | 1:A:50:PHE:N    | 0.46     | 2.83        | 5      | 1     |
| 1:A:55:HIS:C   | 1:A:57:LYS:N    | 0.46     | 2.72        | 7      | 2     |
| 1:A:39:PHE:CZ  | 1:A:53:LYS:HB3  | 0.46     | 2.46        | 12     | 1     |
| 1:A:43:GLU:HG3 | 1:A:63:HIS:CE1  | 0.45     | 2.46        | 3      | 2     |
| 1:A:53:LYS:O   | 1:A:55:HIS:N    | 0.45     | 2.50        | 6      | 1     |
| 1:A:50:PHE:CZ  | 1:A:59:HIS:CG   | 0.45     | 3.05        | 8      | 2     |
| 1:A:60:MET:C   | 1:A:62:LEU:N    | 0.45     | 2.74        | 4      | 1     |
| 1:A:27:HIS:NE2 | 1:A:31:TYR:CG   | 0.45     | 2.85        | 15     | 1     |
| 1:A:9:PRO:N    | 1:A:18:ILE:HD13 | 0.45     | 2.27        | 6      | 2     |
| 1:A:39:PHE:CD1 | 1:A:56:LEU:HG   | 0.45     | 2.47        | 6      | 1     |
| 1:A:50:PHE:O   | 1:A:51:ASN:C    | 0.44     | 2.61        | 6      | 1     |

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| Atom-1          | Atom-2          | Clash(Å) | Distance(Å) | Models |       |
|-----------------|-----------------|----------|-------------|--------|-------|
|                 |                 |          |             | Worst  | Total |
| 1:A:18:ILE:C    | 1:A:19:PHE:CD1  | 0.44     | 2.95        | 18     | 2     |
| 1:A:17:ARG:HD2  | 1:A:28:HIS:CE1  | 0.44     | 2.47        | 5      | 1     |
| 1:A:59:HIS:O    | 1:A:62:LEU:CD2  | 0.44     | 2.66        | 14     | 1     |
| 1:A:17:ARG:HB3  | 1:A:19:PHE:CE1  | 0.44     | 2.47        | 17     | 2     |
| 1:A:15:CYS:SG   | 1:A:17:ARG:CG   | 0.44     | 3.06        | 8      | 2     |
| 1:A:62:LEU:HD22 | 1:A:63:HIS:N    | 0.44     | 2.28        | 14     | 1     |
| 1:A:59:HIS:O    | 1:A:60:MET:C    | 0.43     | 2.62        | 2      | 1     |
| 1:A:28:HIS:CD2  | 1:A:29:LYS:N    | 0.43     | 2.85        | 11     | 1     |
| 1:A:53:LYS:O    | 1:A:56:LEU:N    | 0.43     | 2.52        | 6      | 2     |
| 1:A:53:LYS:C    | 1:A:55:HIS:N    | 0.43     | 2.74        | 6      | 1     |
| 1:A:49:SER:C    | 1:A:50:PHE:CG   | 0.43     | 2.96        | 4      | 3     |
| 1:A:25:LEU:CD2  | 1:A:29:LYS:HD2  | 0.43     | 2.43        | 18     | 1     |
| 1:A:48:LYS:HB3  | 1:A:50:PHE:CZ   | 0.43     | 2.48        | 17     | 1     |
| 1:A:39:PHE:CE2  | 1:A:53:LYS:HB2  | 0.43     | 2.49        | 9      | 1     |
| 1:A:39:PHE:HB3  | 1:A:56:LEU:HD13 | 0.43     | 1.89        | 10     | 1     |
| 1:A:39:PHE:CE2  | 1:A:53:LYS:HE2  | 0.42     | 2.49        | 9      | 1     |
| 1:A:25:LEU:CD1  | 1:A:29:LYS:HD3  | 0.42     | 2.41        | 16     | 1     |
| 1:A:27:HIS:CD2  | 1:A:31:TYR:CG   | 0.42     | 3.07        | 15     | 1     |
| 1:A:59:HIS:CD2  | 1:A:59:HIS:C    | 0.42     | 2.96        | 20     | 1     |
| 1:A:45:ALA:O    | 1:A:46:CYS:C    | 0.42     | 2.62        | 2      | 1     |
| 1:A:39:PHE:CD1  | 1:A:53:LYS:HD3  | 0.42     | 2.50        | 20     | 1     |
| 1:A:59:HIS:HA   | 1:A:62:LEU:CD1  | 0.42     | 2.45        | 3      | 1     |
| 1:A:59:HIS:HA   | 1:A:62:LEU:HD12 | 0.42     | 1.91        | 9      | 1     |
| 1:A:42:PRO:CG   | 1:A:60:MET:HE1  | 0.42     | 2.44        | 20     | 1     |
| 1:A:29:LYS:O    | 1:A:33:HIS:O    | 0.41     | 2.38        | 2      | 3     |
| 1:A:26:ASN:O    | 1:A:27:HIS:C    | 0.41     | 2.63        | 16     | 1     |
| 1:A:19:PHE:CD1  | 1:A:25:LEU:HD23 | 0.41     | 2.50        | 16     | 1     |
| 1:A:19:PHE:CE1  | 1:A:25:LEU:HD23 | 0.41     | 2.50        | 16     | 1     |
| 1:A:39:PHE:HB2  | 1:A:56:LEU:HD22 | 0.41     | 1.92        | 14     | 1     |
| 1:A:10:CYS:O    | 1:A:12:PHE:N    | 0.41     | 2.54        | 17     | 1     |
| 1:A:19:PHE:CD1  | 1:A:19:PHE:N    | 0.40     | 2.89        | 10     | 2     |
| 1:A:27:HIS:CD2  | 1:A:27:HIS:O    | 0.40     | 2.74        | 6      | 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     | 52/79 (66%)     | 45±2 (86±3%) | 7±2 (13±3%) | 0±0 (1±1%) | 18          | 68 |
| All | All   | 1040/1580 (66%) | 893 (86%)    | 139 (13%)   | 8 (1%)     | 18          | 68 |

All 6 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     | 56  | LEU  | 2              |
| 1   | A     | 47  | GLY  | 2              |
| 1   | A     | 7   | GLY  | 1              |
| 1   | A     | 54  | LYS  | 1              |
| 1   | A     | 39  | PHE  | 1              |
| 1   | A     | 59  | HIS  | 1              |

### 6.3.2 Protein sidechains [i](#)

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     | 47/70 (67%)    | 44±1 (94±3%) | 3±1 (6±3%) | 20          | 70 |
| All | All   | 940/1400 (67%) | 886 (94%)    | 54 (6%)    | 20          | 70 |

All 22 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     | 62  | LEU  | 10             |
| 1   | A     | 57  | LYS  | 6              |
| 1   | A     | 54  | LYS  | 5              |
| 1   | A     | 53  | LYS  | 5              |
| 1   | A     | 51  | ASN  | 4              |
| 1   | A     | 29  | LYS  | 3              |
| 1   | A     | 56  | LEU  | 3              |
| 1   | A     | 43  | GLU  | 2              |
| 1   | A     | 21  | ASN  | 2              |
| 1   | A     | 19  | PHE  | 2              |
| 1   | A     | 23  | GLN  | 1              |
| 1   | A     | 60  | MET  | 1              |

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| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1   | A     | 11  | ASP  | 1              |
| 1   | A     | 46  | CYS  | 1              |
| 1   | A     | 32  | GLN  | 1              |
| 1   | A     | 22  | ARG  | 1              |
| 1   | A     | 25  | LEU  | 1              |
| 1   | A     | 26  | ASN  | 1              |
| 1   | A     | 48  | LYS  | 1              |
| 1   | A     | 61  | LYS  | 1              |
| 1   | A     | 30  | LYS  | 1              |
| 1   | A     | 52  | PHE  | 1              |

### 6.3.3 RNA [i](#)

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 oligosaccharides in this entry.

## 6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are 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