



# Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 03:33 AM UTC

PDB ID : 6D8S / pdb\_00006d8s  
BMRB ID : 30462  
Title : NMR solution structure of tamapin, mutant K27E  
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Deposited on : 2018-04-26

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

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<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  
BMRB Restraints Analysis : v1.2  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

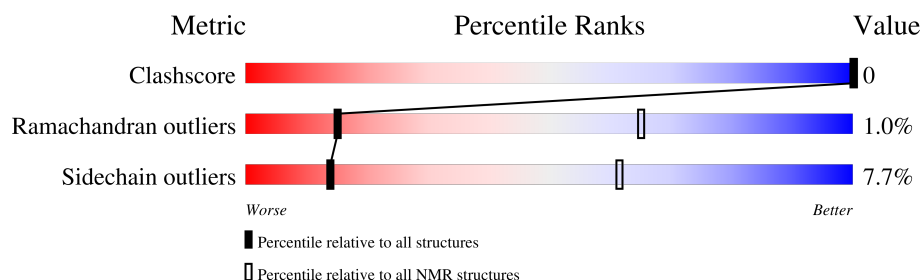
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 49%.

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     | 31     |                  |

## 2 Ensemble composition and analysis

This entry contains 20 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:5-A:31 (27)         | 0.69              | 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 2 clusters and 1 single-model cluster was found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 469 atoms, of which 232 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Potassium channel toxin alpha-KTx 5.4.

| Mol | Chain | Residues | Atoms |     |     |    |    |   | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|-------|
| 1   | A     | 31       | Total | C   | H   | N  | O  | S | 0     |
|     |       |          | 469   | 145 | 232 | 42 | 44 | 6 |       |

There is a discrepancy between the modelled and reference sequences:

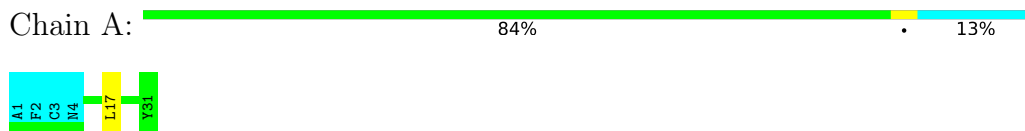
| Chain | Residue | Modelled | Actual | Comment             | Reference  |
|-------|---------|----------|--------|---------------------|------------|
| A     | 27      | GLU      | LYS    | engineered mutation | UNP P59869 |

## 4 Residue-property plots

### 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: Potassium channel toxin alpha-KTx 5.4

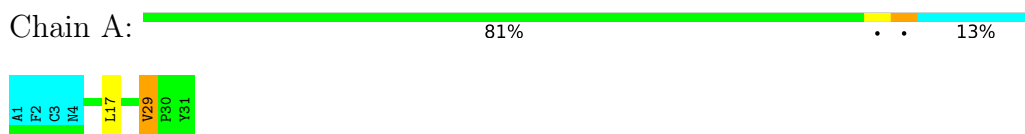


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

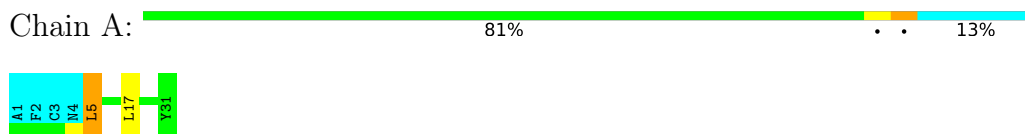
#### 4.2.1 Score per residue for model 1

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



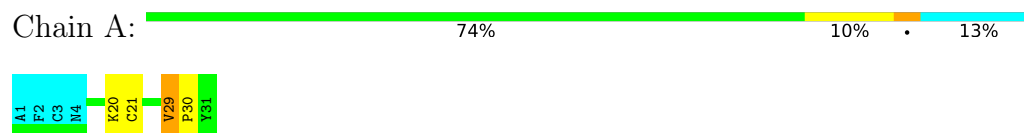
#### 4.2.2 Score per residue for model 2

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



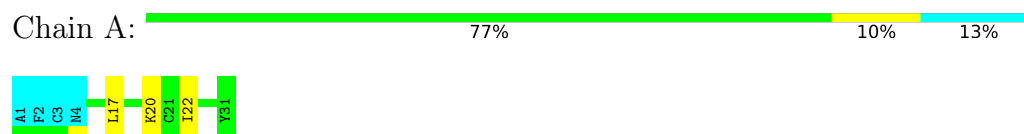
### 4.2.3 Score per residue for model 3

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



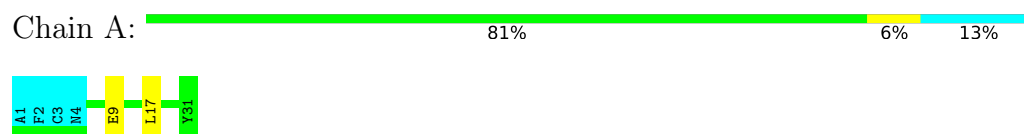
### 4.2.4 Score per residue for model 4

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



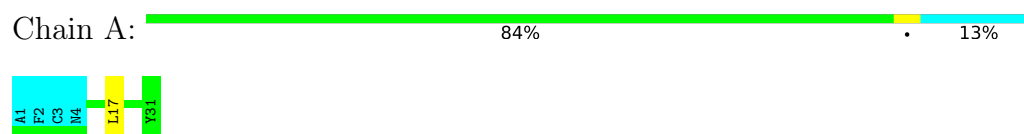
### 4.2.5 Score per residue for model 5

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



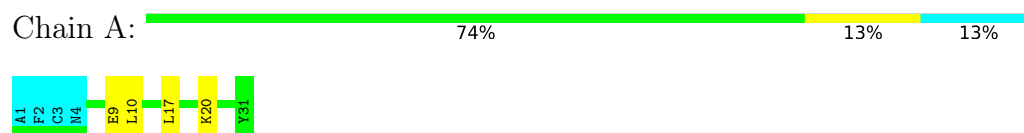
### 4.2.6 Score per residue for model 6

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



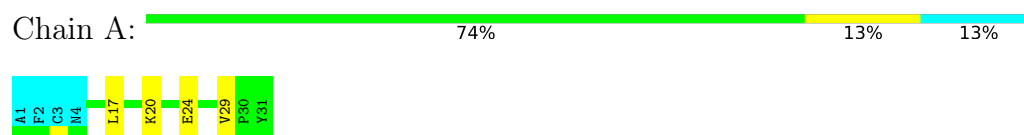
### 4.2.7 Score per residue for model 7

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



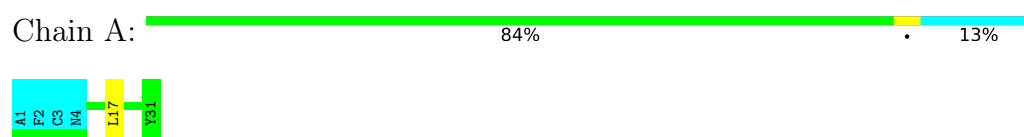
#### 4.2.8 Score per residue for model 8

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



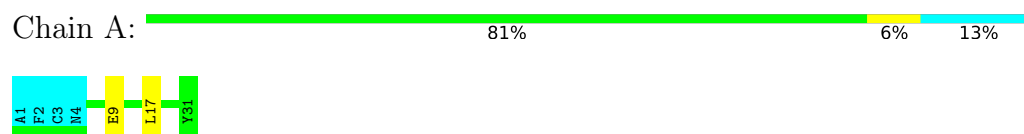
#### 4.2.9 Score per residue for model 9

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



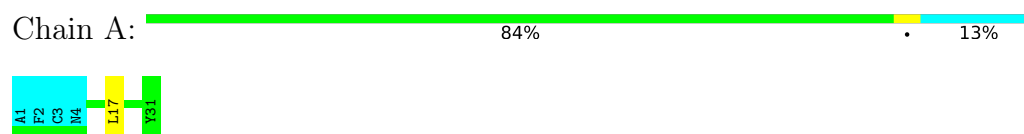
#### 4.2.10 Score per residue for model 10

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



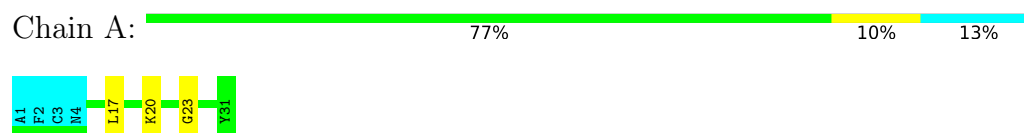
#### 4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



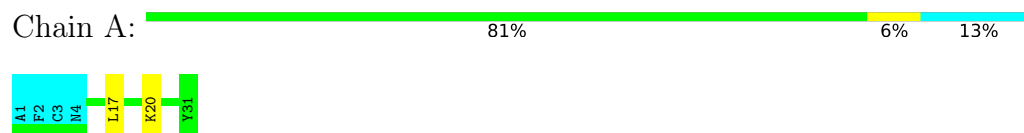
#### 4.2.12 Score per residue for model 12

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



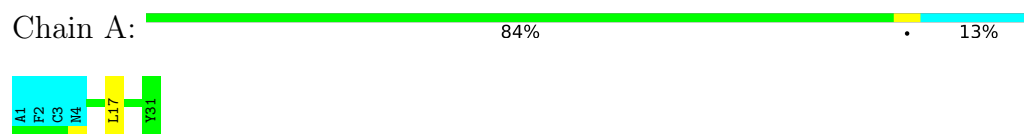
#### 4.2.13 Score per residue for model 13

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



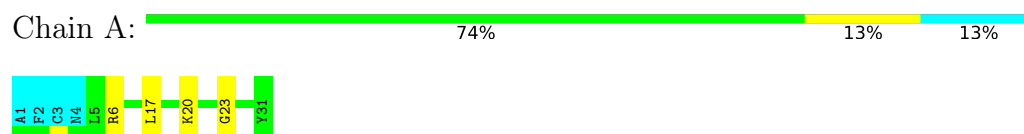
#### 4.2.14 Score per residue for model 14

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



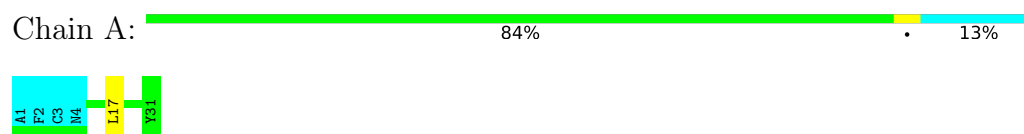
#### 4.2.15 Score per residue for model 15

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



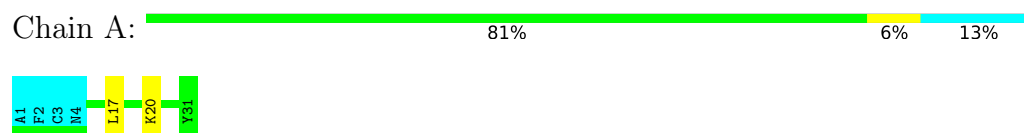
#### 4.2.16 Score per residue for model 16

- Molecule 1: Potassium channel toxin alpha-KTx 5.4



#### 4.2.17 Score per residue for model 17

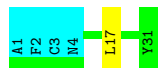
- Molecule 1: Potassium channel toxin alpha-KTx 5.4



#### 4.2.18 Score per residue for model 18

- Molecule 1: Potassium channel toxin alpha-KTx 5.4

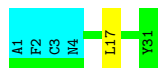
Chain A:  84% 13%



#### 4.2.19 Score per residue for model 19

- Molecule 1: Potassium channel toxin alpha-KTx 5.4

Chain A:  84% 13%



#### 4.2.20 Score per residue for model 20

- Molecule 1: Potassium channel toxin alpha-KTx 5.4

Chain A:  84% 13%



## 5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

| Software name | Classification        | Version |
|---------------|-----------------------|---------|
| Amber         | refinement            | 16      |
| CYANA         | structure calculation | 2.1     |

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

| Chemical shift file(s)                       | working_cs.cif |
|----------------------------------------------|----------------|
| Number of chemical shift lists               | 1              |
| Total number of shifts                       | 200            |
| Number of shifts mapped to atoms             | 200            |
| Number of unparsed shifts                    | 0              |
| Number of shifts with mapping errors         | 0              |
| Number of shifts with mapping warnings       | 0              |
| Assignment completeness (well-defined parts) | 49%            |

## 6 Model quality [i](#)

### 6.1 Standard geometry [i](#)

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     | 0.87±0.02    | 0±0/208 ( 0.0± 0.0%) | 1.39±0.05   | 0±1/275 ( 0.1± 0.2%) |
| All | All   | 0.87         | 0/4160 ( 0.0%)       | 1.39        | 5/5500 ( 0.1%)       |

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 |
| 1   | A     | 29  | VAL  | CA-C-N | 6.35 | 126.89      | 120.04   | 1      | 1     |
| 1   | A     | 29  | VAL  | C-N-CA | 6.35 | 126.89      | 120.04   | 1      | 1     |
| 1   | A     | 5   | LEU  | CA-C-N | 5.26 | 127.76      | 120.29   | 2      | 1     |
| 1   | A     | 5   | LEU  | C-N-CA | 5.26 | 127.76      | 120.29   | 2      | 1     |
| 1   | A     | 29  | VAL  | N-CA-C | 5.03 | 113.31      | 109.19   | 8      | 1     |

There are no chirality outliers.

There are no planarity outliers.

### 6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in 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 |
|-----|-------|-------|----------|----------|---------|
| All | All   | 4140  | 4120     | 4120     | -       |

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 -.

There are no clashes.

## 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     | 26/31 (84%)   | 25±1 (97±3%) | 1±1 (2±3%) | 0±1 (1±2%) | 15          | 65 |
| All | All   | 520/620 (84%) | 504 (97%)    | 11 (2%)    | 5 (1%)     | 15          | 65 |

All 4 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     | 23  | GLY  | 2              |
| 1   | A     | 5   | LEU  | 1              |
| 1   | A     | 29  | VAL  | 1              |
| 1   | A     | 30  | PRO  | 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     | 24/27 (89%)   | 22±1 (92±4%) | 2±1 (8±4%) | 14          | 61 |
| All | All   | 480/540 (89%) | 443 (92%)    | 37 (8%)    | 14          | 61 |

All 9 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     | 17  | LEU  | 19             |
| 1   | A     | 20  | LYS  | 8              |
| 1   | A     | 9   | GLU  | 3              |
| 1   | A     | 29  | VAL  | 2              |
| 1   | A     | 21  | CYS  | 1              |
| 1   | A     | 22  | ILE  | 1              |

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| Mol | Chain | Res | Type | Models (Total) |
|-----|-------|-----|------|----------------|
| 1   | A     | 10  | LEU  | 1              |
| 1   | A     | 24  | GLU  | 1              |
| 1   | A     | 6   | ARG  | 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](#)

There are no ligands in this entry.

## 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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 49% for the well-defined parts and 49% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *depositok27e.str*

#### 7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

|                                         |     |
|-----------------------------------------|-----|
| Total number of shifts                  | 200 |
| Number of shifts mapped to atoms        | 200 |
| Number of unparsed shifts               | 0   |
| Number of shifts with mapping errors    | 0   |
| Number of shifts with mapping warnings  | 0   |
| Number of shift outliers (ShiftChecker) | 0   |

#### 7.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

#### 7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 49%, i.e. 178 atoms were assigned a chemical shift out of a possible 361. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

|           | Total         | <sup>1</sup> H | <sup>13</sup> C | <sup>15</sup> N |
|-----------|---------------|----------------|-----------------|-----------------|
| Backbone  | 56/136 (41%)  | 56/56 (100%)   | 0/54 (0%)       | 0/26 (0%)       |
| Sidechain | 118/216 (55%) | 118/140 (84%)  | 0/66 (0%)       | 0/10 (0%)       |
| Aromatic  | 4/9 (44%)     | 4/4 (100%)     | 0/5 (0%)        | 0/0 (—%)        |
| Overall   | 178/361 (49%) | 178/200 (89%)  | 0/125 (0%)      | 0/36 (0%)       |

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 49%, i.e. 200 atoms were assigned a chemical shift out of a possible 408. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

|           | Total         | $^1\text{H}$  | $^{13}\text{C}$ | $^{15}\text{N}$ |
|-----------|---------------|---------------|-----------------|-----------------|
| Backbone  | 63/156 (40%)  | 63/64 (98%)   | 0/62 (0%)       | 0/30 (0%)       |
| Sidechain | 129/233 (55%) | 129/151 (85%) | 0/71 (0%)       | 0/11 (0%)       |
| Aromatic  | 8/19 (42%)    | 8/9 (89%)     | 0/10 (0%)       | 0/0 (—%)        |
| Overall   | 200/408 (49%) | 200/224 (89%) | 0/143 (0%)      | 0/41 (0%)       |

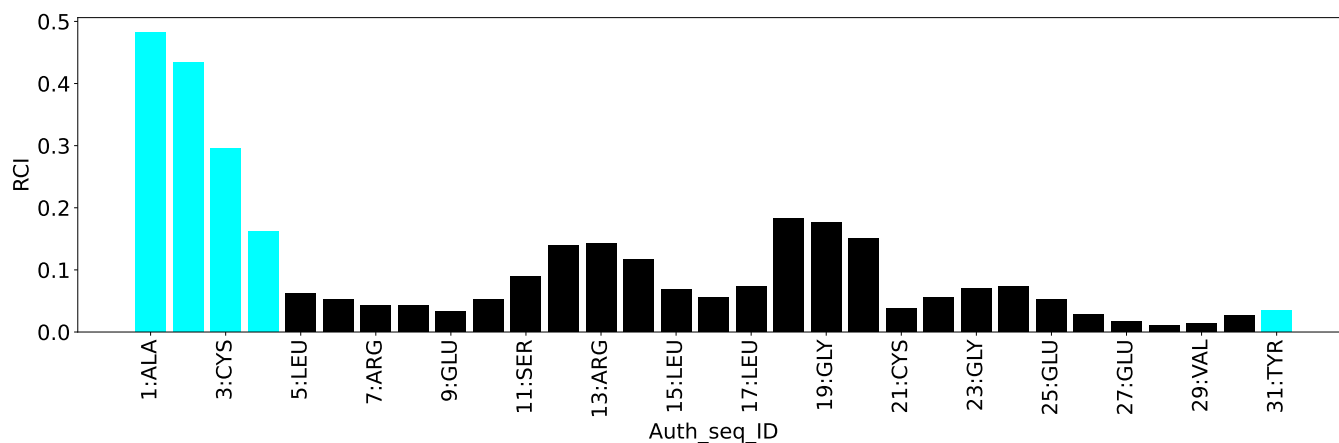
#### 7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



## 8 NMR restraints analysis [i](#)

### 8.1 Conformationally restricting restraints [i](#)

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

| Description                                              | Value |
|----------------------------------------------------------|-------|
| Total distance restraints                                | 0     |
| Intra-residue ( $ i-j =0$ )                              | 0     |
| Sequential ( $ i-j =1$ )                                 | 0     |
| Medium range ( $ i-j >1$ and $ i-j <5$ )                 | 0     |
| Long range ( $ i-j \geq 5$ )                             | 0     |
| Inter-chain                                              | 0     |
| Hydrogen bond restraints                                 | 0     |
| Disulfide bond restraints                                | 0     |
| Total dihedral-angle restraints                          | 95    |
| Number of unmapped restraints                            | 0     |
| Number of restraints per residue                         | 0     |
| Number of long range restraints per residue <sup>1</sup> | 0     |

<sup>1</sup>Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

### 8.2 Residual restraint violations [i](#)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

#### 8.2.1 Average number of distance violations per model [i](#)

Distance violations less than 0.1 Å are not included in the calculation. There are no distance restraints

#### 8.2.2 Average number of dihedral-angle violations per model [i](#)

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

## 9 Distance violation analysis ⓘ

No distance restraints data found

## 10 Dihedral-angle violation analysis [i](#)

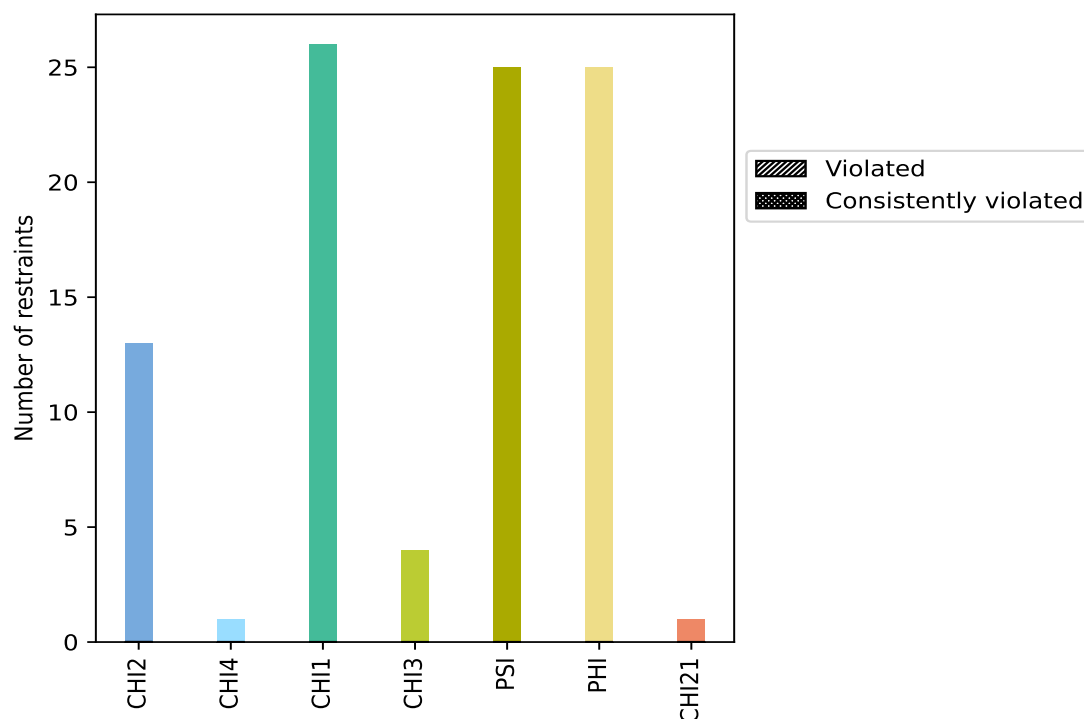
### 10.1 Summary of dihedral-angle violations [i](#)

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

| Angle type | Count | % <sup>1</sup> | Violated <sup>3</sup> |                |                | Consistently Violated <sup>4</sup> |                |                |
|------------|-------|----------------|-----------------------|----------------|----------------|------------------------------------|----------------|----------------|
|            |       |                | Count                 | % <sup>2</sup> | % <sup>1</sup> | Count                              | % <sup>2</sup> | % <sup>1</sup> |
| CHI2       | 13    | 13.7           | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |
| CHI4       | 1     | 1.1            | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |
| CHI1       | 26    | 27.4           | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |
| CHI3       | 4     | 4.2            | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |
| PSI        | 25    | 26.3           | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |
| PHI        | 25    | 26.3           | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |
| CHI21      | 1     | 1.1            | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |
| Total      | 95    | 100.0          | 0                     | 0.0            | 0.0            | 0                                  | 0.0            | 0.0            |

<sup>1</sup> percentage calculated with respect to total number of dihedral-angle restraints, <sup>2</sup> percentage calculated with respect to number of restraints in a particular dihedral-angle type, <sup>3</sup> violated in at least one model, <sup>4</sup> violated in all the models

#### 10.1.1 Bar chart : Distribution of dihedral-angles and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

## 10.2 Dihedral-angle violation statistics for each model [i](#)

No violations found

## 10.3 Dihedral-angle violation statistics for the ensemble [i](#)

No violations found

## 10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

No violations found

## 10.5 All violated dihedral-angle restraints [i](#)

No violations found