



# Full wwPDB NMR Structure Validation Report ⓘ

Nov 18, 2025 – 12:15 pm GMT

PDB ID : 9G7T / pdb\_00009g7t  
BMRB ID : 52491  
Title : Solution NMR structure of a peptide encompassing residues 967-991 of the human formin INF2  
Authors : Jimenez, M.A.; Morales, P.; Correas, I.; Alonso, M.A.  
Deposited on : 2024-07-22

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 : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.46

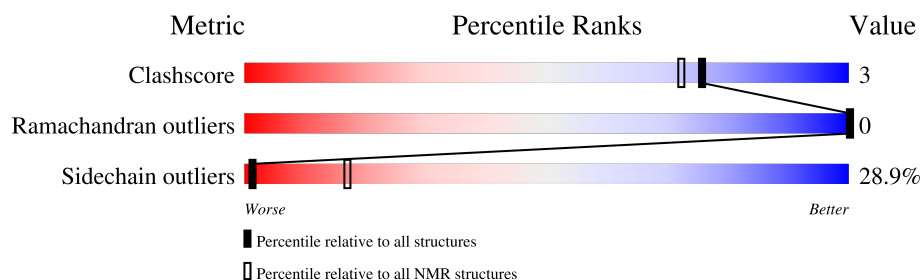
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 85%.

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 (#Entries)	NMR archive (#Entries)
Clashscore	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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	27	<div> <div style="width: 63%; background-color: green;"></div> <div style="width: 22%; background-color: yellow;"></div> <div style="width: 7%; background-color: cyan;"></div> <div style="width: 7%; background-color: grey;"></div> </div> <div>63% 22% 7% 7%</div>

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 9 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:25 (23)	0.89	9

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

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

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 413 atoms, of which 213 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Inverted formin-2.

Mol	Chain	Residues	Atoms					Trace
1	A	25	Total	C	H	N	O	0
			413	125	213	38	37	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	expression tag	UNP Q27J81
A	5	SER	CYS	conflict	UNP Q27J81
A	26	NH2	-	expression tag	UNP Q27J81

## 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: Inverted formin-2



### 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: Inverted formin-2



#### 4.2.2 Score per residue for model 2

- Molecule 1: Inverted formin-2



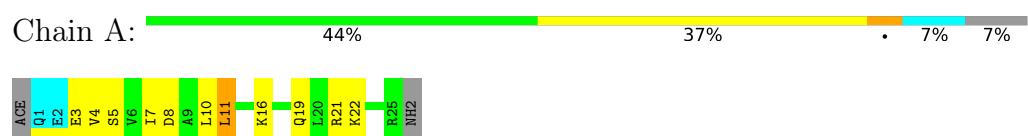
### 4.2.3 Score per residue for model 3

- Molecule 1: Inverted formin-2



### 4.2.4 Score per residue for model 4

- Molecule 1: Inverted formin-2



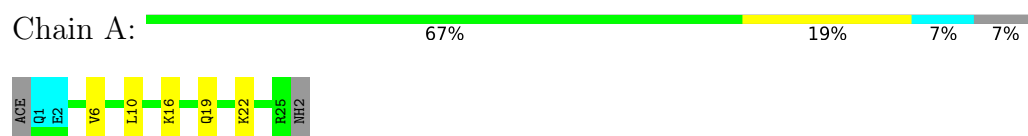
### 4.2.5 Score per residue for model 5

- Molecule 1: Inverted formin-2



### 4.2.6 Score per residue for model 6

- Molecule 1: Inverted formin-2



### 4.2.7 Score per residue for model 7

- Molecule 1: Inverted formin-2



### 4.2.8 Score per residue for model 8

- Molecule 1: Inverted formin-2

Chain A:  63% 22% 7% 7%



### 4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: Inverted formin-2

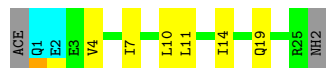
Chain A:  56% 30% 7% 7%



### 4.2.10 Score per residue for model 10

- Molecule 1: Inverted formin-2

Chain A:  63% 22% 7% 7%



### 4.2.11 Score per residue for model 11

- Molecule 1: Inverted formin-2

Chain A:  70% 15% 7% 7%



### 4.2.12 Score per residue for model 12

- Molecule 1: Inverted formin-2

Chain A:  48% 33% 7% 7%



### 4.2.13 Score per residue for model 13

- Molecule 1: Inverted formin-2



### 4.2.14 Score per residue for model 14

- Molecule 1: Inverted formin-2



### 4.2.15 Score per residue for model 15

- Molecule 1: Inverted formin-2



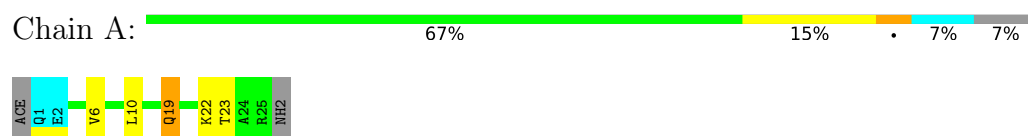
### 4.2.16 Score per residue for model 16

- Molecule 1: Inverted formin-2



### 4.2.17 Score per residue for model 17


- Molecule 1: Inverted formin-2





#### 4.2.18 Score per residue for model 18

- Molecule 1: Inverted formin-2

Chain A:  63% 22% 7% 7%



#### 4.2.19 Score per residue for model 19

- Molecule 1: Inverted formin-2

Chain A:  70% 15% 7% 7%



#### 4.2.20 Score per residue for model 20

- Molecule 1: Inverted formin-2

Chain A:  52% 33% 7% 7%



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure calculation	

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	2
Total number of shifts	560
Number of shifts mapped to atoms	549
Number of unparsed shifts	0
Number of shifts with mapping errors	11
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

## 6 Model quality [i](#)

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

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 [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
1	A	182	199	199	1±1
All	All	3640	3980	3980	22

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:LEU:HD13	1:A:14:ILE:HD12	0.64	1.69	15	2
1:A:7:ILE:HG22	1:A:11:LEU:HD23	0.59	1.74	2	11
1:A:6:VAL:O	1:A:10:LEU:HD23	0.58	1.99	6	2
1:A:10:LEU:HD12	1:A:10:LEU:O	0.47	2.10	14	4
1:A:10:LEU:O	1:A:14:ILE:HD12	0.42	2.14	10	1
1:A:19:GLN:O	1:A:23:THR:HG23	0.41	2.16	17	1
1:A:19:GLN:O	1:A:23:THR:HG22	0.40	2.17	12	1

### 6.3 Torsion angles [i](#)

#### 6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	22/27 (81%)	22±0 (99±2%)	0±0 (1±2%)	0±0 (0±0%)	100	100
All	All	440/540 (81%)	437 (99%)	3 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

### 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	19/21 (90%)	14±2 (71±11%)	6±2 (29±11%)	1	17
All	All	380/420 (90%)	270 (71%)	110 (29%)	1	17

All 14 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	19	GLN	18
1	A	20	LEU	13
1	A	5	SER	11
1	A	16	LYS	11
1	A	11	LEU	9
1	A	3	GLU	8
1	A	8	ASP	7
1	A	22	LYS	7
1	A	15	ARG	6
1	A	18	PHE	6
1	A	13	ASP	5
1	A	21	ARG	5
1	A	25	ARG	2
1	A	10	LEU	2

### 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 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

The completeness of assignment taking into account all chemical shift lists is 85% for the well-defined parts and 84% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shifts\_1*

#### 7.1.1 Bookkeeping

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	312
Number of shifts mapped to atoms	305
Number of unparsed shifts	0
Number of shifts with mapping errors	7
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 7 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	0	ACE	H1	2.112	0.000	1
1	A	0	ACE	H2	2.112	0.000	1
1	A	0	ACE	H3	2.112	0.000	1
1	A	0	ACE	C	24.366	0.000	1
1	A	26	NH2	HN1	7.026	0.001	2
1	A	26	NH2	HN2	7.371	0.001	2
1	A	26	NH2	N	106.248	0.007	1

#### 7.1.2 Chemical shift referencing

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 83%, i.e. 283 atoms were assigned a chemical shift out of a possible 340. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	88/116 (76%)	47/47 (100%)	18/46 (39%)	23/23 (100%)
Sidechain	187/214 (87%)	127/139 (91%)	56/63 (89%)	4/12 (33%)
Aromatic	8/10 (80%)	5/5 (100%)	3/5 (60%)	0/0 (—%)
Overall	283/340 (83%)	179/191 (94%)	77/114 (68%)	27/35 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 83%, i.e. 305 atoms were assigned a chemical shift out of a possible 367. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	95/126 (75%)	51/51 (100%)	20/50 (40%)	24/25 (96%)
Sidechain	202/231 (87%)	137/149 (92%)	60/69 (87%)	5/13 (38%)
Aromatic	8/10 (80%)	5/5 (100%)	3/5 (60%)	0/0 (—%)
Overall	305/367 (83%)	193/205 (94%)	83/124 (67%)	29/38 (76%)

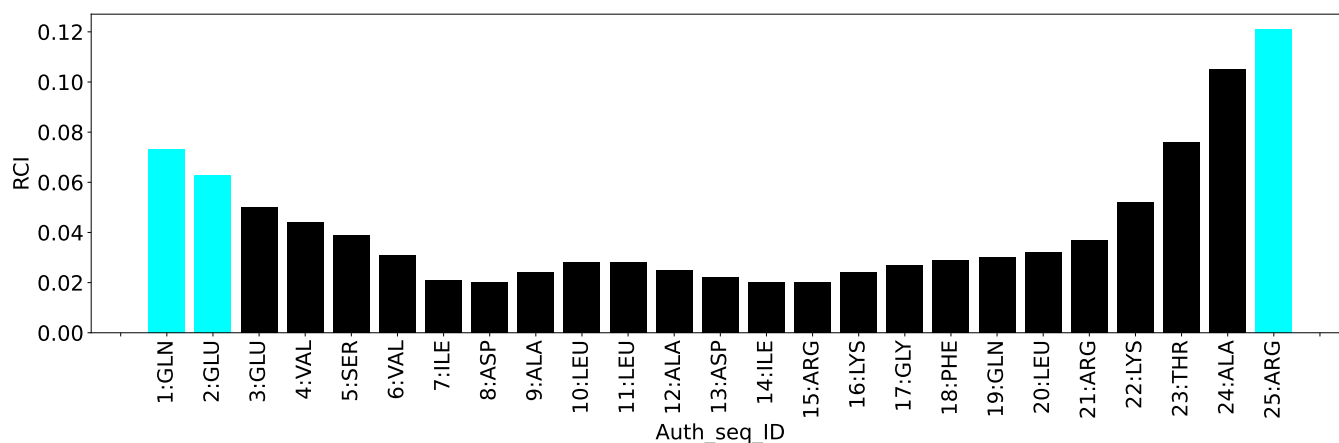
### 7.1.4 Statistically unusual chemical shifts [i](#)

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:



## 7.2 Chemical shift list 2

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shifts\_2*

### 7.2.1 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	248
Number of shifts mapped to atoms	244
Number of unparsed shifts	0
Number of shifts with mapping errors	4
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 4 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
2	A	0	ACE	H1	2.096	0.000	1
2	A	0	ACE	H2	2.096	0.000	1
2	A	0	ACE	H3	2.096	0.000	1
2	A	0	ACE	C	24.312	0.000	1



## 7.2.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	25	$-0.79 \pm 0.10$	Should be checked
$^{13}\text{C}_\beta$	24	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
$^{15}\text{N}$	0	—	None (insufficient data)

## 7.2.3 Completeness of resonance assignments ⓘ

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 67%, i.e. 228 atoms were assigned a chemical shift out of a possible 340. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	47/116 (41%)	24/47 (51%)	23/46 (50%)	0/23 (0%)
Sidechain	178/214 (83%)	122/139 (88%)	56/63 (89%)	0/12 (0%)
Aromatic	3/10 (30%)	3/5 (60%)	0/5 (0%)	0/0 (—%)
Overall	228/340 (67%)	149/191 (78%)	79/114 (69%)	0/35 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 66%, i.e. 244 atoms were assigned a chemical shift out of a possible 367. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	51/126 (40%)	26/51 (51%)	25/50 (50%)	0/25 (0%)
Sidechain	190/231 (82%)	130/149 (87%)	60/69 (87%)	0/13 (0%)
Aromatic	3/10 (30%)	3/5 (60%)	0/5 (0%)	0/0 (—%)
Overall	244/367 (66%)	159/205 (78%)	85/124 (69%)	0/38 (0%)

## 7.2.4 Statistically unusual chemical shifts ⓘ

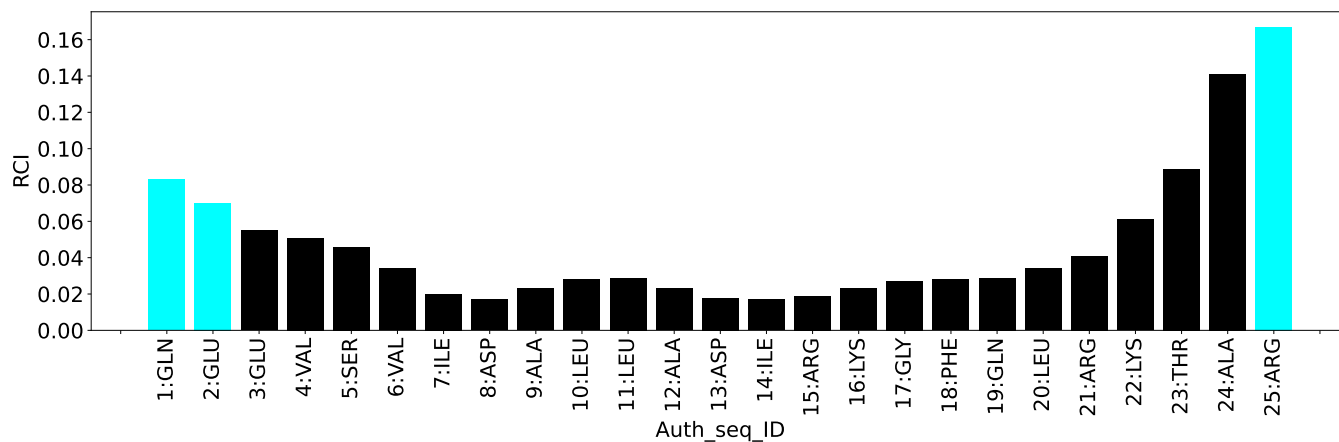
There are no statistically unusual chemical shifts.

## 7.2.5 Random Coil Index (RCI) plots ⓘ

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	235
Intra-residue ( $ i-j =0$ )	110
Sequential ( $ i-j =1$ )	63
Medium range ( $ i-j >1$ and $ i-j <5$ )	62
Long range ( $ i-j \geq 5$ )	0
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	46
Number of unmapped restraints	0
Number of restraints per residue	11.2
Number of long range restraints per residue <sup>1</sup>	0.0

<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 violations

#### 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 [i](#)

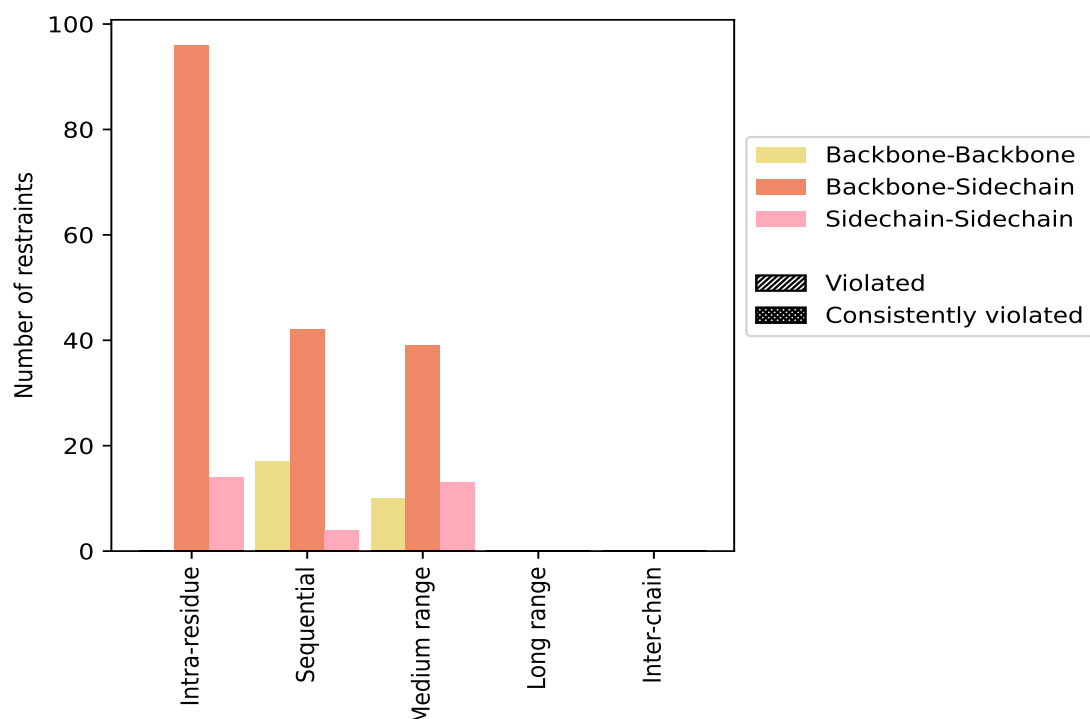
### 9.1 Summary of distance violations [i](#)

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains 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>
<b>Intra-residue (<math> i-j =0</math>)</b>	<b>110</b>	<b>46.8</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	96	40.9	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	14	6.0	0	0.0	0.0	0	0.0	0.0
<b>Sequential (<math> i-j =1</math>)</b>	<b>63</b>	<b>26.8</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	17	7.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	42	17.9	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	4	1.7	0	0.0	0.0	0	0.0	0.0
<b>Medium range (<math> i-j &gt;1</math> &amp; <math> i-j &lt;5</math>)</b>	<b>62</b>	<b>26.4</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	10	4.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	39	16.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	13	5.5	0	0.0	0.0	0	0.0	0.0
<b>Long range (<math> i-j \geq 5</math>)</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
<b>Inter-chain</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
<b>Hydrogen bond</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
<b>Disulfide bond</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
<b>Total</b>	<b>235</b>	<b>100.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	27	11.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	177	75.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	31	13.2	0	0.0	0.0	0	0.0	0.0

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

### 9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfide bonds are counted in their appropriate category on the x-axis

## 9.2 Distance violation statistics for each model [i](#)

No violations found

## 9.3 Distance violation statistics for the ensemble [i](#)

No violations found

## 9.4 Most violated distance restraints in the ensemble [i](#)

No violations found

## 9.5 All violated distance restraints [i](#)

No violations found

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

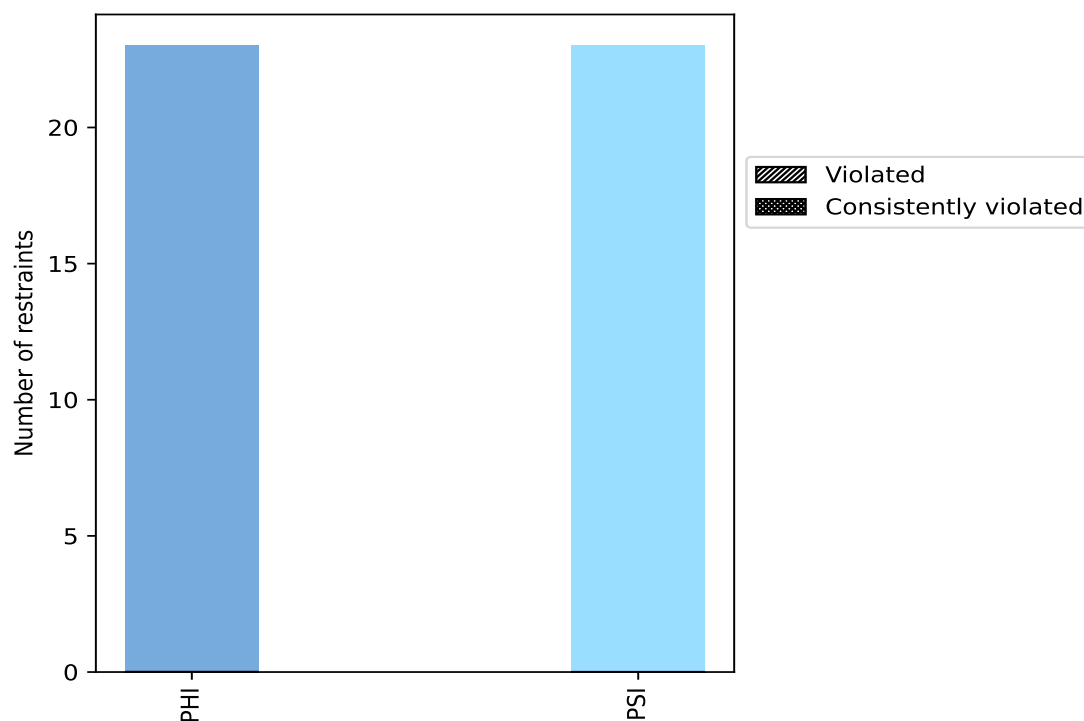
### 10.1 Summary of dihedral-angle violations [i](#)

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>
PHI	23	50.0	0	0.0	0.0	0	0.0	0.0
PSI	23	50.0	0	0.0	0.0	0	0.0	0.0
Total	46	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