



# Full wwPDB NMR Structure Validation Report ⓘ

Jun 25, 2025 – 04:50 pm BST

PDB ID : 9FSI / pdb\_00009fsi  
BMRB ID : 34922  
Title : NMR solution structure of synthetic hexapeptide  
Authors : Geyer, A.; Vazquez, O.  
Deposited on : 2024-06-21

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>.

---

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 1.8.4, CSD as541be (2020)  
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) : 2.44

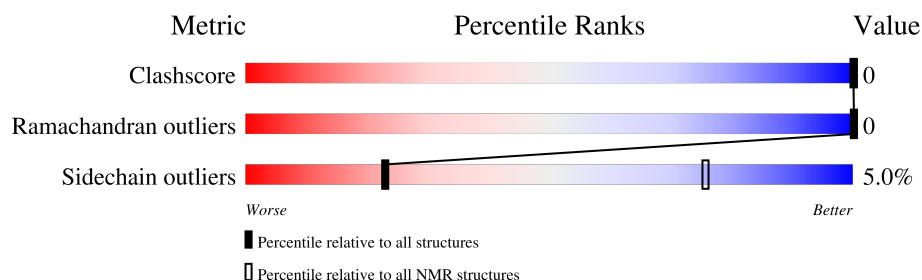
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 40%.

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	7	<div> <div>71%</div> <div>29%</div> </div>

## 2 Ensemble composition and analysis ⓘ

This entry contains 10 models.

Cyrange was unable to find well-defined residues.

Error message: The number of core atoms ( 4) was below the domain threshold value ( 8).

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust

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

There is only 1 type of molecule in this entry. The entry contains 224 atoms, of which 104 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called ACE-ARG-ARG-HDN-HDN-ARG-PHE.

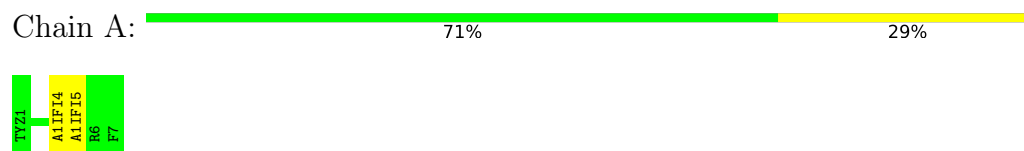
Mol	Chain	Residues	Atoms					Trace
1	A	7	Total	C	H	N	O	0
			224	92	104	20	8	

## 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: ACE-ARG-ARG-HDN-HDN-ARG-PHE

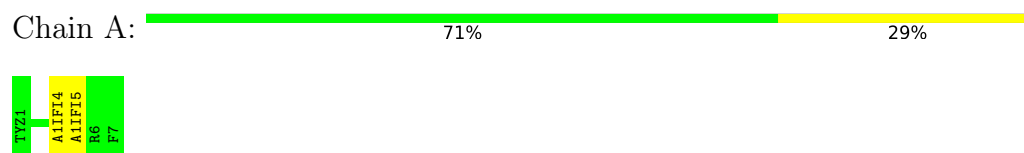


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

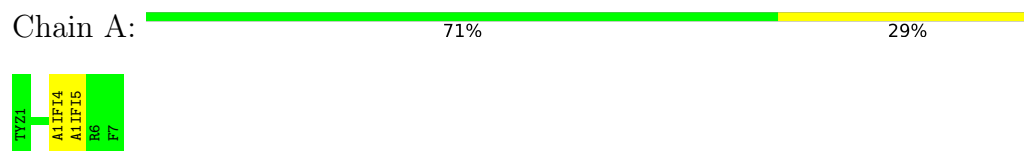
#### 4.2.1 Score per residue for model 1

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE



#### 4.2.2 Score per residue for model 2

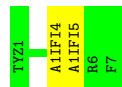
- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE



### 4.2.3 Score per residue for model 3

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

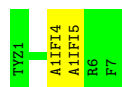
Chain A:  71% 29%



### 4.2.4 Score per residue for model 4

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

Chain A:  71% 29%



### 4.2.5 Score per residue for model 5

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

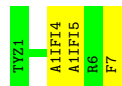
Chain A:  71% 29%



### 4.2.6 Score per residue for model 6

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

Chain A:  57% 43%



### 4.2.7 Score per residue for model 7

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

Chain A:  71% 29%

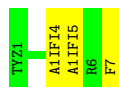




#### 4.2.8 Score per residue for model 8

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

Chain A:   
57% 43%



#### 4.2.9 Score per residue for model 9

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

Chain A:   
71% 29%



#### 4.2.10 Score per residue for model 10

- Molecule 1: ACE-ARG-ARG-HDN-HDN-ARG-PHE

Chain A:   
71% 29%



## 5 Refinement protocol and experimental data overview

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

Of the 10 calculated structures, 10 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
TopSpin	refinement	
HyperChem	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	1
Total number of shifts	50
Number of shifts mapped to atoms	35
Number of unparsed shifts	0
Number of shifts with mapping errors	15
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	40%



## 6 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: TYZ, A1IFI

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
All	All	1200	1040	550	-

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 [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	2/7 (29%)	2±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	20/70 (29%)	20 (100%)	0 (0%)	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	4/4 (100%)	4±0 (95±10%)	0±0 (5±10%)	23	76
All	All	40/40 (100%)	38 (95%)	2 (5%)	23	76

All 1 unique residues with a non-rotameric sidechain are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	7	PHE	2

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	TYZ	A	1	1	12,12,13	0.91±0.02	0±0 (0±0%)
1	A1IFI	A	5	1	34,36,37	1.42±0.01	4±0 (10±1%)
1	A1IFI	A	4	1	34,36,37	1.43±0.01	4±0 (10±1%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is

considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	TYZ	A	1	1	15,15,17	0.46±0.04	0±0 (0±0%)
1	A1IFI	A	5	1	42,50,52	1.08±0.03	3±0 (7±0%)
1	A1IFI	A	4	1	42,50,52	1.08±0.03	3±0 (7±0%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A1IFI	A	4	1	-	0±0,13,14,16	0±0,5,5,5
1	TYZ	A	1	1	-	0±0,6,6,8	0±0,1,1,1
1	A1IFI	A	5	1	-	0±0,13,14,16	0±0,5,5,5

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	4	A1IFI	CE1-ND1	5.03	1.38	1.33	1	10
1	A	5	A1IFI	CE1-ND1	4.87	1.38	1.33	4	10
1	A	4	A1IFI	CE1-NE2	2.79	1.38	1.33	5	10
1	A	5	A1IFI	CE1-NE2	2.76	1.38	1.33	1	10
1	A	5	A1IFI	C21-C20	2.11	1.41	1.36	7	8
1	A	4	A1IFI	C8-C7	2.11	1.41	1.36	7	7
1	A	4	A1IFI	C21-C20	2.10	1.41	1.36	3	8
1	A	5	A1IFI	C8-C7	2.08	1.41	1.36	9	8

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	5	A1IFI	ND1-CE1-NE2	4.78	112.05	108.76	3	10
1	A	4	A1IFI	ND1-CE1-NE2	4.49	111.86	108.76	9	10
1	A	5	A1IFI	CD2-NE2-CE1	3.09	105.28	108.22	6	10
1	A	4	A1IFI	CD2-NE2-CE1	3.07	105.30	108.22	9	10
1	A	5	A1IFI	CB-CG-CD2	2.63	122.74	127.82	10	10
1	A	4	A1IFI	CB-CG-CD2	2.60	122.81	127.82	1	10

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	5	A1IFI	C12-NE2-CD2	2.27	129.32	126.25	3	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 40% for the well-defined parts and 40% 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	50
Number of shifts mapped to atoms	35
Number of unparsed shifts	0
Number of shifts with mapping errors	15
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 15 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	ACE	H	10.15	0.000	1
1	A	1	ACE	QD	7.81	0.000	3
1	A	1	ACE	QE	7.6	0.000	3
1	A	4	HDN	H	8.38	0.000	1
1	A	4	HDN	HA	4.6	0.000	1
1	A	4	HDN	HB1	2.82	0.000	1
1	A	4	HDN	HB2	3.0	0.000	1
1	A	4	HDN	HD2	7.6	0.000	1
1	A	4	HDN	HE1	9.29	0.000	1
1	A	5	HDN	H	8.5	0.000	1
1	A	5	HDN	HA	4.66	0.000	1
1	A	5	HDN	HB1	2.81	0.000	1
1	A	5	HDN	HB2	3.02	0.000	1
1	A	5	HDN	HD2	7.41	0.000	1

*Continued on next page...*

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	5	HDN	HE1	9.32	0.000	1

### 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 40%, i.e. 35 atoms were assigned a chemical shift out of a possible 87. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	8/20 (40%)	8/8 (100%)	0/8 (0%)	0/4 (0%)
Sidechain	23/57 (40%)	23/35 (66%)	0/13 (0%)	0/9 (0%)
Aromatic	4/10 (40%)	4/5 (80%)	0/5 (0%)	0/0 (—%)
Overall	35/87 (40%)	35/48 (73%)	0/26 (0%)	0/13 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 40%, i.e. 35 atoms were assigned a chemical shift out of a possible 87. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	8/20 (40%)	8/8 (100%)	0/8 (0%)	0/4 (0%)
Sidechain	23/57 (40%)	23/35 (66%)	0/13 (0%)	0/9 (0%)
Aromatic	4/10 (40%)	4/5 (80%)	0/5 (0%)	0/0 (—%)
Overall	35/87 (40%)	35/48 (73%)	0/26 (0%)	0/13 (0%)

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

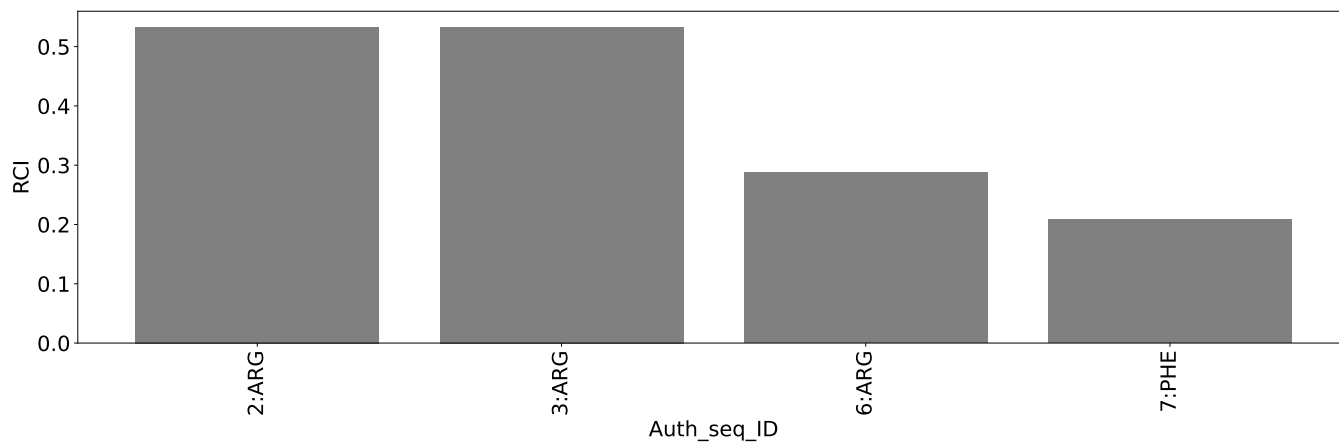
There are no statistically unusual chemical shifts.

### 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	5
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.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	0.3	4.55

*Continued on next page...*



*Continued from previous page...*

Bins (°)	Average number of violations per model	Max (°)
10.0-20.0 (Medium)	None	None
>20.0 (Large)	0.1	35.1

## 9 Distance violation analysis

No distance restraints data found

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

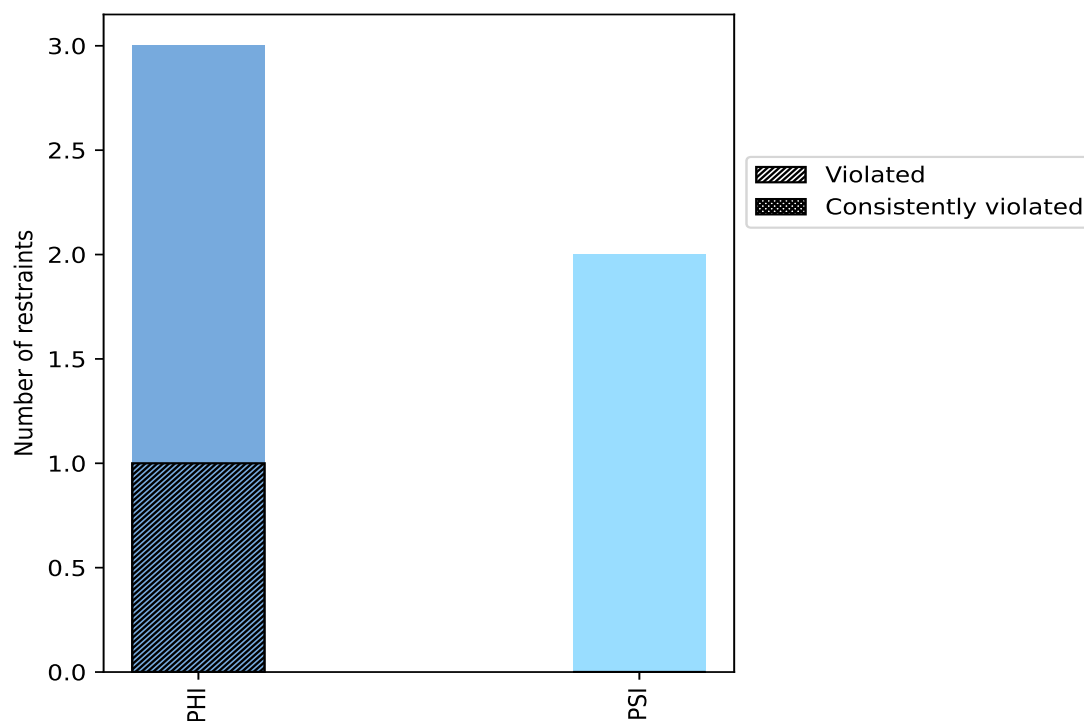
### 10.1 Summary of dihedral-angle violations [i](#)

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>
PHI	3	60.0	1	33.3	20.0	0	0.0	0.0
PSI	2	40.0	0	0.0	0.0	0	0.0	0.0
Total	5	100.0	1	20.0	20.0	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](#)



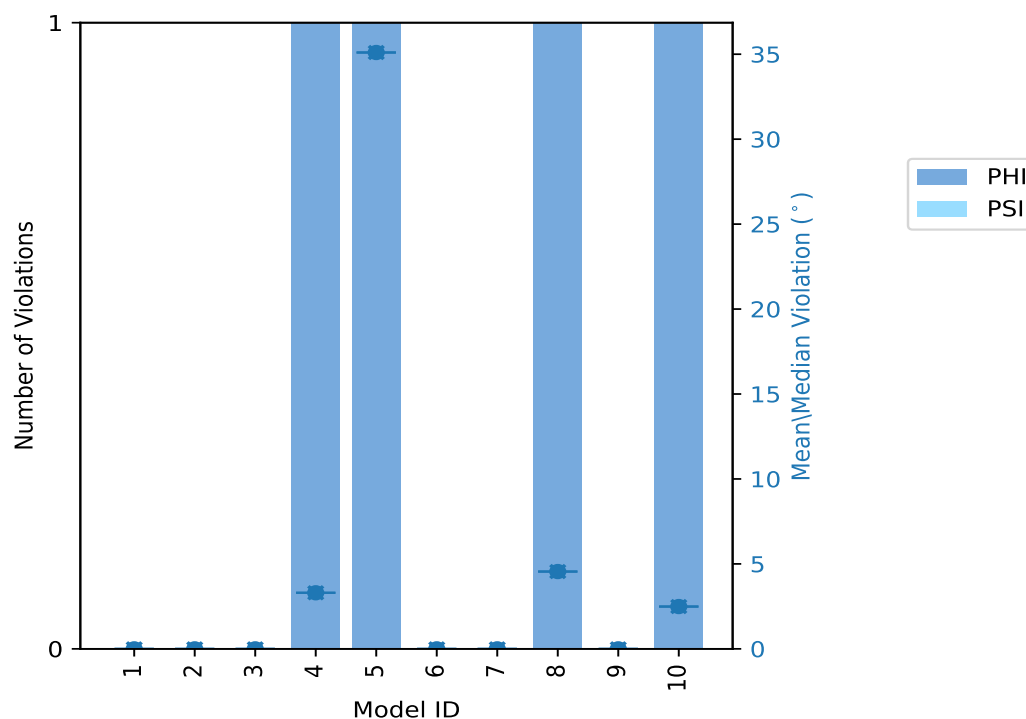
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0.0	0.0	0.0	0.0
3	0	0	0	0.0	0.0	0.0	0.0
4	1	0	1	3.3	3.3	0.0	3.3
5	1	0	1	35.1	35.1	0.0	35.1
6	0	0	0	0.0	0.0	0.0	0.0
7	0	0	0	0.0	0.0	0.0	0.0
8	1	0	1	4.55	4.55	0.0	4.55
9	0	0	0	0.0	0.0	0.0	0.0
10	1	0	1	2.49	2.49	0.0	2.49

### 10.2.1 Bar graph : Dihedral violation statistics for each model [i](#)



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

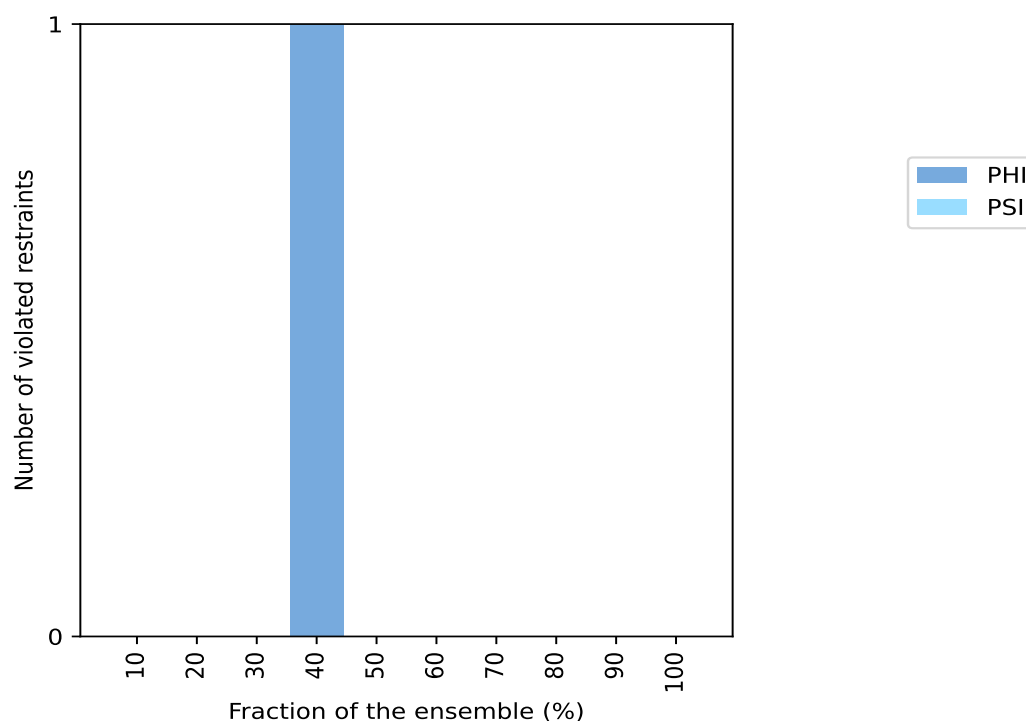
### 10.3 Dihedral-angle violation statistics for the ensemble [i](#)

Violation analysis may find that some restraints are violated in very few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of ensemble.

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count <sup>1</sup>	%
0	0	0	1	10.0
0	0	0	2	20.0
0	0	0	3	30.0
1	0	1	4	40.0
0	0	0	5	50.0
0	0	0	6	60.0
0	0	0	7	70.0
0	0	0	8	80.0
0	0	0	9	90.0
0	0	0	10	100.0

<sup>1</sup> Number of models with violations

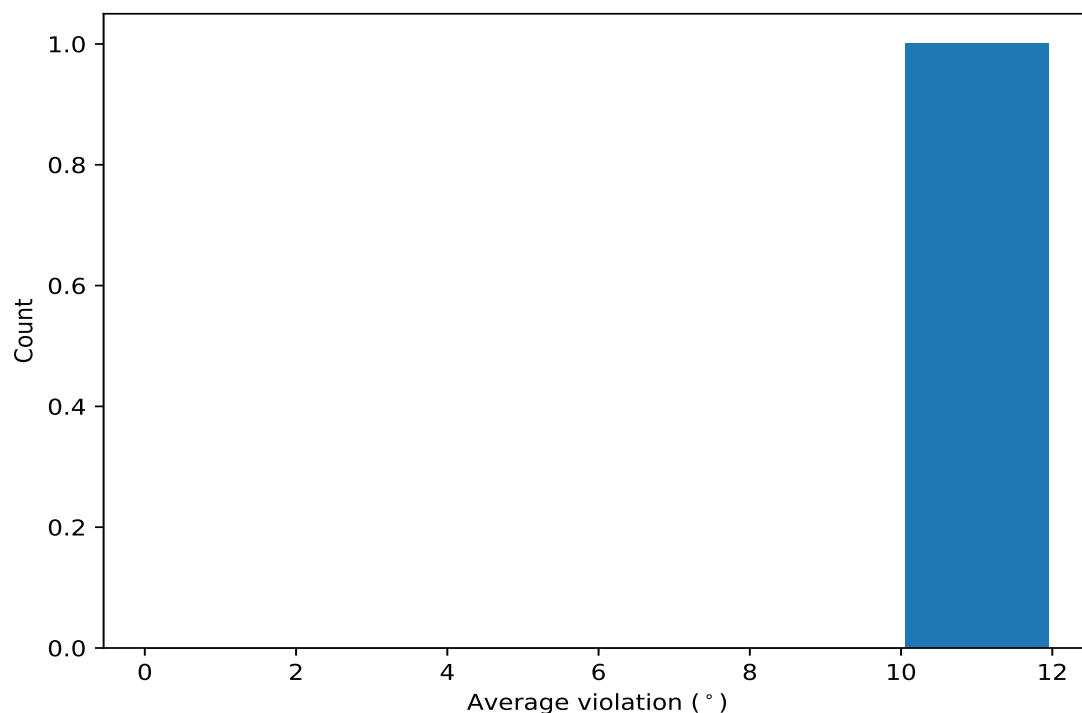
#### 10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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

### 10.4.1 Histogram : Distribution of mean dihedral-angle violations [i](#)

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models in the ensemble



### 10.4.2 Table: Most violated dihedral-angle restraints [i](#)

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Models <sup>1</sup>	Mean	SD <sup>2</sup>	Median
(1,5)	1:6:A:ARG:C	1:7:A:PHE:N	1:7:A:PHE:CA	1:7:A:PHE:C	4	11.36	13.73	3.92

<sup>1</sup> Number of violated models, <sup>2</sup>Standard deviation, All angle values are in degree (°)

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

### 10.5.1 Histogram : Distribution of violations [i](#)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.

Data insufficient to plot histogram

### 10.5.2 Table: All violated dihedral-angle restraints [i](#)

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,5)	1:6:A:ARG:C	1:7:A:PHE:N	1:7:A:PHE:CA	1:7:A:PHE:C	5	35.1
(1,5)	1:6:A:ARG:C	1:7:A:PHE:N	1:7:A:PHE:CA	1:7:A:PHE:C	8	4.55
(1,5)	1:6:A:ARG:C	1:7:A:PHE:N	1:7:A:PHE:CA	1:7:A:PHE:C	4	3.3
(1,5)	1:6:A:ARG:C	1:7:A:PHE:N	1:7:A:PHE:CA	1:7:A:PHE:C	10	2.49