



# Full wwPDB NMR Structure Validation Report ⓘ

Sep 9, 2025 – 01:05 pm BST

PDB ID : 9HR9 / pdb\_00009hr9  
BMRB ID : 34971  
Title : SSNMR structure of amyloid fibrils formed by human RIPK1  
Authors : Polonio, P.; Escobedo-Gonzales, F.C.; Titau-Delgado, G.A.; Mompean, M.  
Deposited on : 2024-12-17

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 : **FAILED**  
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) : 2.45.1

## 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLID-STATE NMR*

The overall completeness of chemical shifts assignment is 43%.

There are no overall percentile quality scores available for this entry.

The sequence quality summary graphics cannot be shown.

## 2 Ensemble composition and analysis

This entry contains 10 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:538-A:549 (12)	0.29	3

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

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

The models can be grouped into 1 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 348 atoms, of which 172 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Receptor-interacting serine/threonine-protein kinase 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	22	348	115	172	26	34	1	0

## 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: Receptor-interacting serine/threonine-protein kinase 1



### 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: Receptor-interacting serine/threonine-protein kinase 1



#### 4.2.2 Score per residue for model 2

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



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

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



### 4.2.4 Score per residue for model 4

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



### 4.2.5 Score per residue for model 5

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



### 4.2.6 Score per residue for model 6

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



### 4.2.7 Score per residue for model 7

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



#### 4.2.8 Score per residue for model 8

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



#### 4.2.9 Score per residue for model 9

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



#### 4.2.10 Score per residue for model 10

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 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	
GROMACS	refinement	

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	117
Number of shifts mapped to atoms	117
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	43%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.



## 6 Model quality [i](#)

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

MolProbity failed to run properly - this section will have to be empty.

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

MolProbity failed to run properly - this section will have to be empty.

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

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

MolProbity failed to run properly - this section will have to be empty.

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

MolProbity failed to run properly - this section will have to be empty.

#### 6.3.3 RNA [i](#)

MolProbity failed to run properly - this section will have to be empty.

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

MolProbity failed to run properly - this section will have to be empty.

### 6.5 Carbohydrates [i](#)

MolProbity failed to run properly - this section will have to be empty.

### 6.6 Ligand geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

### 6.7 Other polymers [i](#)

MolProbity failed to run properly - this section will have to be empty.

## 6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 43% for the well-defined parts and 38% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *hRIPK1*

#### 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	117
Number of shifts mapped to atoms	117
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

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

#### 7.1.3 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 43%, i.e. 70 atoms were assigned a chemical shift out of a possible 163. 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	36/62 (58%)	0/26 (0%)	24/24 (100%)	12/12 (100%)
Sidechain	24/83 (29%)	0/55 (0%)	24/26 (92%)	0/2 (0%)
Aromatic	10/18 (56%)	0/8 (0%)	10/10 (100%)	0/0 (—%)
Overall	70/163 (43%)	0/89 (0%)	58/60 (97%)	12/14 (86%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

The following table shows the completeness of the chemical shift assignments for the full structure.

The overall completeness is 38%, i.e. 114 atoms were assigned a chemical shift out of a possible 299. 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	60/113 (53%)	0/47 (0%)	41/44 (93%)	19/22 (86%)
Sidechain	38/150 (25%)	0/99 (0%)	38/47 (81%)	0/4 (0%)
Aromatic	16/36 (44%)	0/16 (0%)	16/20 (80%)	0/0 (—%)
Overall	114/299 (38%)	0/162 (0%)	95/111 (86%)	19/26 (73%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

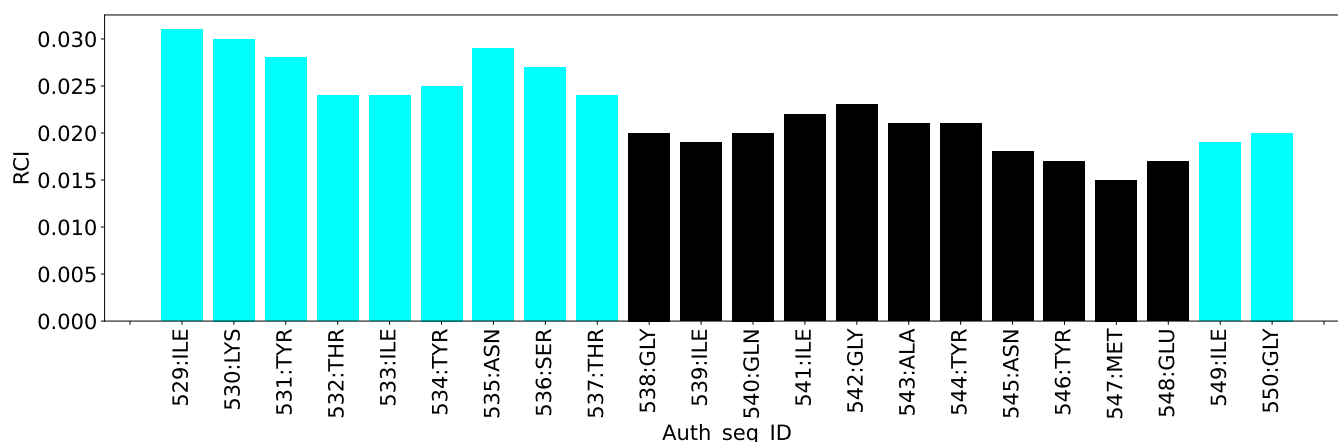
#### 7.1.4 Statistically unusual chemical shifts [i](#)

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

### 8.1 Conformationally restricting restraints

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	121
Intra-residue ( $ i-j =0$ )	4
Sequential ( $ i-j =1$ )	44
Medium range ( $ i-j >1$ and $ i-j <5$ )	48
Long range ( $ i-j \geq 5$ )	25
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	35
Number of unmapped restraints	0
Number of restraints per residue	7.1
Number of long range restraints per residue <sup>1</sup>	1.1

<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

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

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	0.6	0.2
0.2-0.5 (Medium)	1.1	0.48
>0.5 (Large)	0.6	1.39

### 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)	0.2	5.92
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

## 9 Distance violation analysis ⓘ

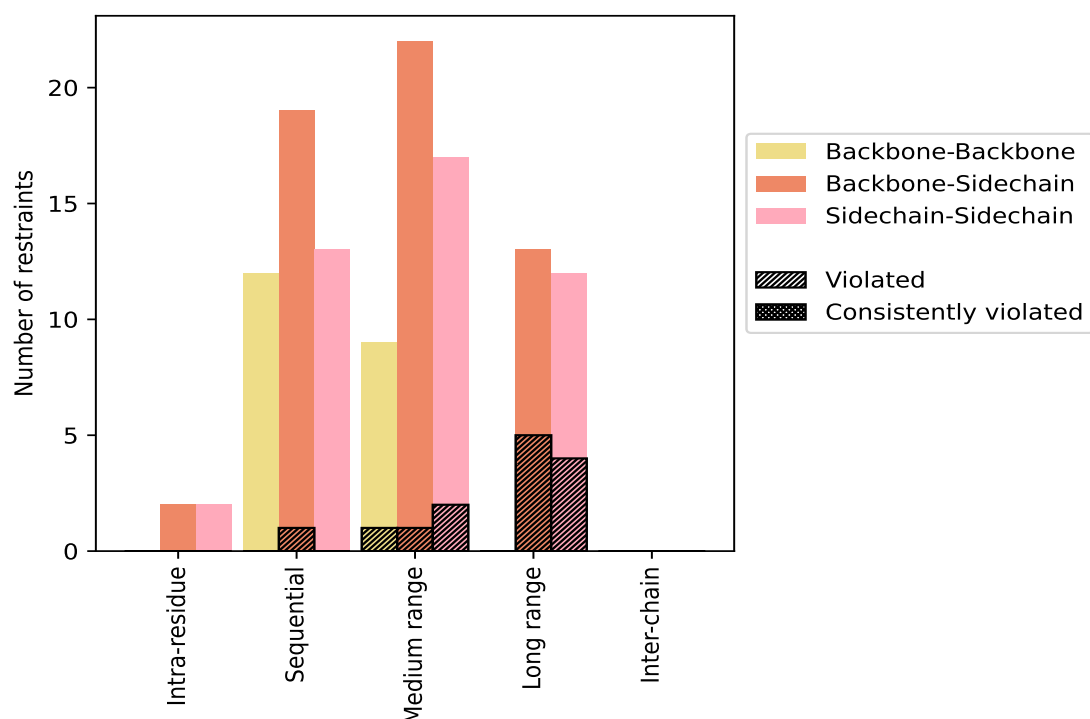
### 9.1 Summary of distance violations ⓘ

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>
Intra-residue ( $ i-j =0$ )	4	3.3	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	2	1.7	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	2	1.7	0	0.0	0.0	0	0.0	0.0
Sequential ( $ i-j =1$ )	44	36.4	1	2.3	0.8	0	0.0	0.0
Backbone-Backbone	12	9.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	19	15.7	1	5.3	0.8	0	0.0	0.0
Sidechain-Sidechain	13	10.7	0	0.0	0.0	0	0.0	0.0
Medium range ( $ i-j >1$ & $ i-j <5$ )	48	39.7	4	8.3	3.3	0	0.0	0.0
Backbone-Backbone	9	7.4	1	11.1	0.8	0	0.0	0.0
Backbone-Sidechain	22	18.2	1	4.5	0.8	0	0.0	0.0
Sidechain-Sidechain	17	14.0	2	11.8	1.7	0	0.0	0.0
Long range ( $ i-j \geq 5$ )	25	20.7	9	36.0	7.4	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	13	10.7	5	38.5	4.1	0	0.0	0.0
Sidechain-Sidechain	12	9.9	4	33.3	3.3	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
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
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	121	100.0	14	11.6	11.6	0	0.0	0.0
Backbone-Backbone	21	17.4	1	4.8	0.8	0	0.0	0.0
Backbone-Sidechain	56	46.3	7	12.5	5.8	0	0.0	0.0
Sidechain-Sidechain	44	36.4	6	13.6	5.0	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 disulfied bonds are counted in their appropriate category on the x-axis

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

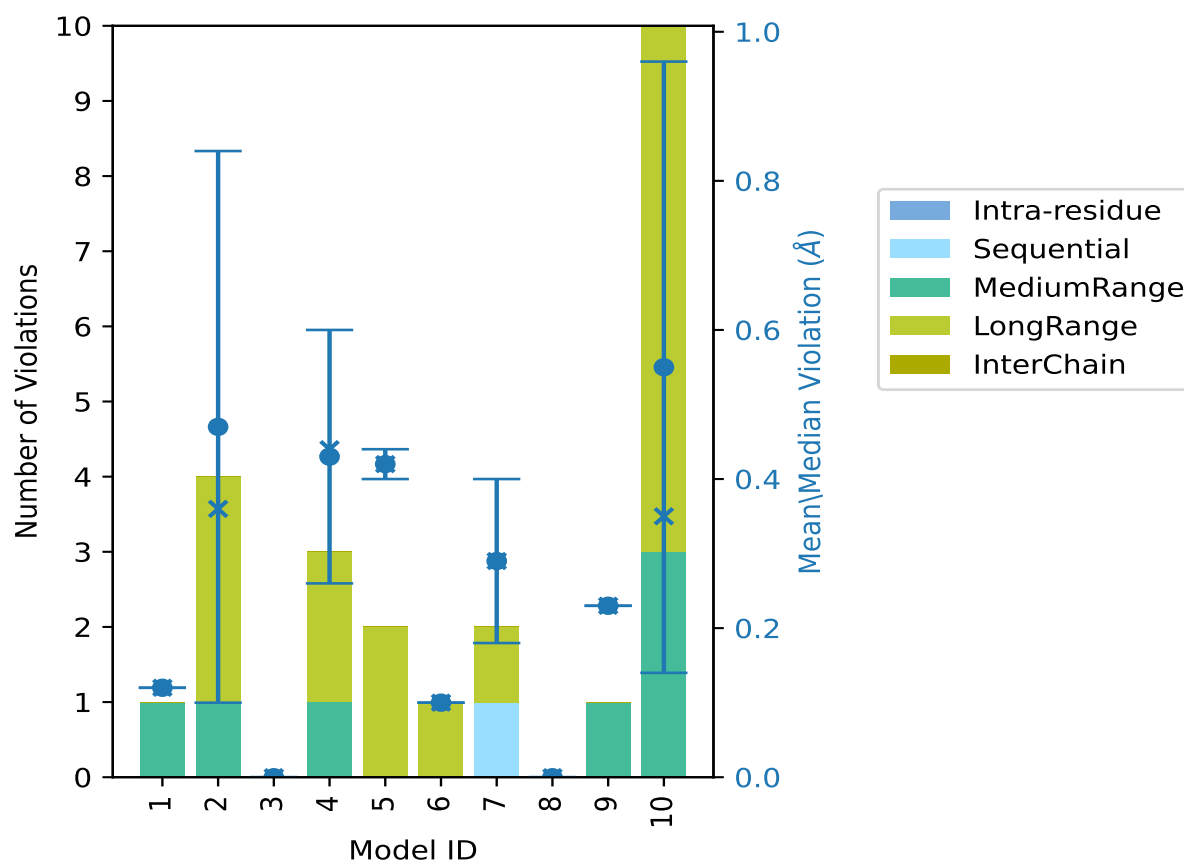
The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD <sup>6</sup> (Å)	Median (Å)
	IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total				
1	0	0	1	0	0	1	0.12	0.12	0.0	0.12
2	0	0	1	3	0	4	0.47	1.07	0.37	0.36
3	0	0	0	0	0	0	0.0	0.0	0.0	0.0
4	0	0	1	2	0	3	0.43	0.63	0.17	0.44
5	0	0	0	2	0	2	0.42	0.44	0.02	0.42
6	0	0	0	1	0	1	0.1	0.1	0.0	0.1
7	0	1	0	1	0	2	0.29	0.4	0.11	0.29
8	0	0	0	0	0	0	0.0	0.0	0.0	0.0
9	0	0	1	0	0	1	0.23	0.23	0.0	0.23
10	0	0	3	7	0	10	0.55	1.39	0.41	0.35



<sup>1</sup>Intra-residue restraints, <sup>2</sup>Sequential restraints, <sup>3</sup>Medium range restraints, <sup>4</sup>Long range restraints, <sup>5</sup>Inter-chain restraints, <sup>6</sup>Standard deviation

### 9.2.1 Bar graph : Distance 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

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

Violation analysis may find that some restraints are violated in 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 the ensemble. In total, 107(IR:4, SQ:43, MR:44, LR:16, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total	Count <sup>6</sup>	%
0	1	3	5	0	9	1	10.0
0	0	0	3	0	3	2	20.0
0	0	0	0	0	0	3	30.0

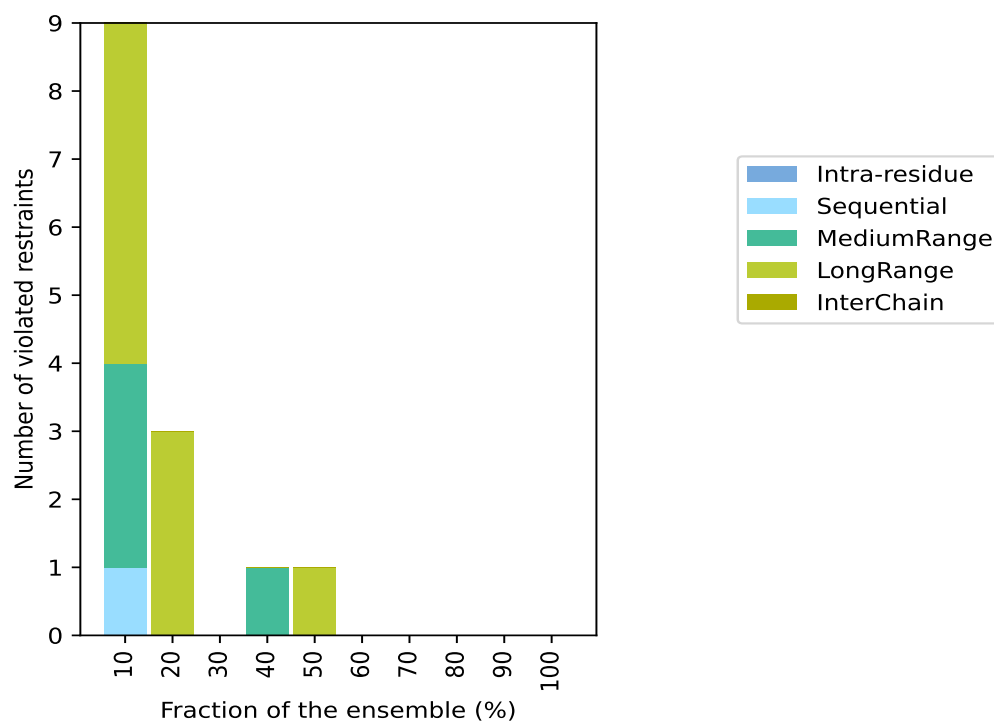
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Number of violated restraints						Fraction of the ensemble	
IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total	Count <sup>6</sup>	%
0	0	1	0	0	1	4	40.0
0	0	0	1	0	1	5	50.0
0	0	0	0	0	0	6	60.0
0	0	0	0	0	0	7	70.0
0	0	0	0	0	0	8	80.0
0	0	0	0	0	0	9	90.0
0	0	0	0	0	0	10	100.0

<sup>1</sup>Intra-residue restraints, <sup>2</sup>Sequential restraints, <sup>3</sup>Medium range restraints, <sup>4</sup>Long range restraints, <sup>5</sup>Inter-chain restraints, <sup>6</sup> Number of models with violations

### 9.3.1 Bar graph : Distance violation statistics for the ensemble ⓘ

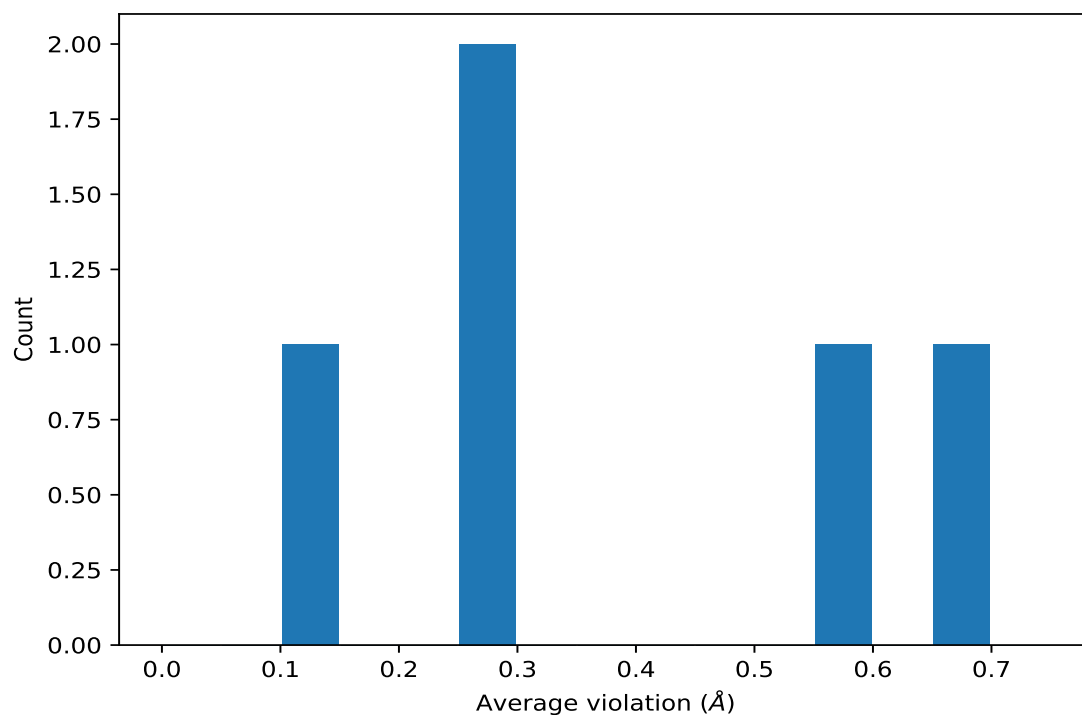


## 9.4 Most violated distance restraints in the ensemble ⓘ

### 9.4.1 Histogram : Distribution of mean distance violations ⓘ

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



#### 9.4.2 Table: Most violated distance 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. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

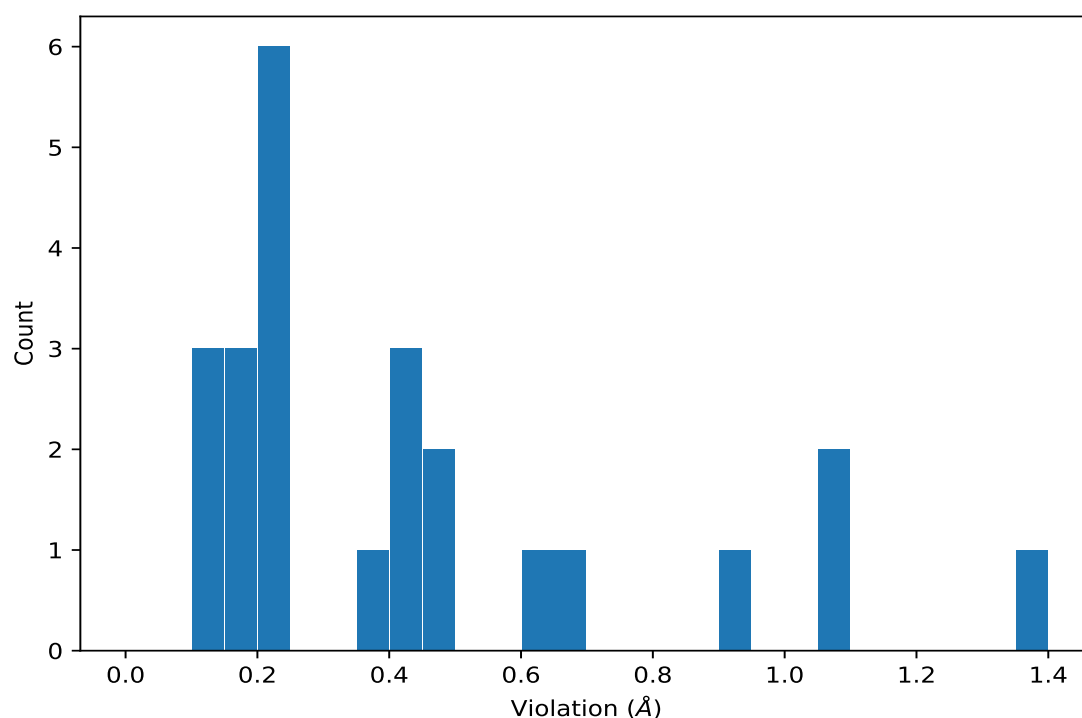
Key	Atom-1	Atom-2	Models <sup>1</sup>	Mean (Å)	SD <sup>1</sup> (Å)	Median (Å)
(1,14)	1:547:A:MET:CG	1:538:A:GLY:CA	5	0.7	0.45	0.44
(1,29)	1:539:A:ILE:CB	1:536:A:SER:CB	4	0.3	0.19	0.23
(1,15)	1:547:A:MET:CE	1:538:A:GLY:CA	2	0.57	0.09	0.57
(2,1)	1:547:A:MET:CE	1:538:A:GLY:C	2	0.29	0.18	0.29
(2,29)	1:540:A:GLN:CG	1:547:A:MET:CE	2	0.14	0.04	0.14

<sup>1</sup>Number of violated models, <sup>2</sup>Standard deviation

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

#### 9.5.1 Histogram : Distribution of distance violations [i](#)

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



### 9.5.2 Table : All distance violations [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. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,14)	1:547:A:MET:CG	1:538:A:GLY:CA	10	1.39
(1,14)	1:547:A:MET:CG	1:538:A:GLY:CA	2	1.07
(2,32)	1:540:A:GLN:CB	1:547:A:MET:CE	10	1.06
(2,30)	1:540:A:GLN:CA	1:547:A:MET:CE	10	0.91
(1,15)	1:547:A:MET:CE	1:538:A:GLY:CA	10	0.66
(1,29)	1:539:A:ILE:CB	1:536:A:SER:CB	4	0.63
(1,15)	1:547:A:MET:CE	1:538:A:GLY:CA	2	0.48
(2,1)	1:547:A:MET:CE	1:538:A:GLY:C	10	0.46
(1,19)	1:541:A:ILE:CD1	1:533:A:ILE:CG1	4	0.44
(1,14)	1:547:A:MET:CG	1:538:A:GLY:CA	5	0.44
(1,14)	1:547:A:MET:CG	1:538:A:GLY:CA	7	0.4
(1,1)	1:529:A:ILE:CD1	1:543:A:ALA:CB	5	0.39
(1,40)	1:542:A:GLY:CA	1:545:A:ASN:CA	10	0.24
(1,21)	1:545:A:ASN:CB	1:541:A:ILE:CA	10	0.24
(1,29)	1:539:A:ILE:CB	1:536:A:SER:CB	2	0.23
(1,29)	1:539:A:ILE:CB	1:536:A:SER:CB	9	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,14)	1:547:A:MET:CG	1:538:A:GLY:CA	4	0.21
(1,17)	1:547:A:MET:CG	1:539:A:ILE:CA	10	0.2
(2,29)	1:540:A:GLN:CG	1:547:A:MET:CE	10	0.18
(2,26)	1:537:A:THR:CG2	1:538:A:GLY:CA	7	0.18
(2,37)	1:547:A:MET:CB	1:549:A:ILE:CD1	10	0.16
(1,29)	1:539:A:ILE:CB	1:536:A:SER:CB	1	0.12
(2,1)	1:547:A:MET:CE	1:538:A:GLY:C	2	0.11
(2,29)	1:540:A:GLN:CG	1:547:A:MET:CE	6	0.1

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

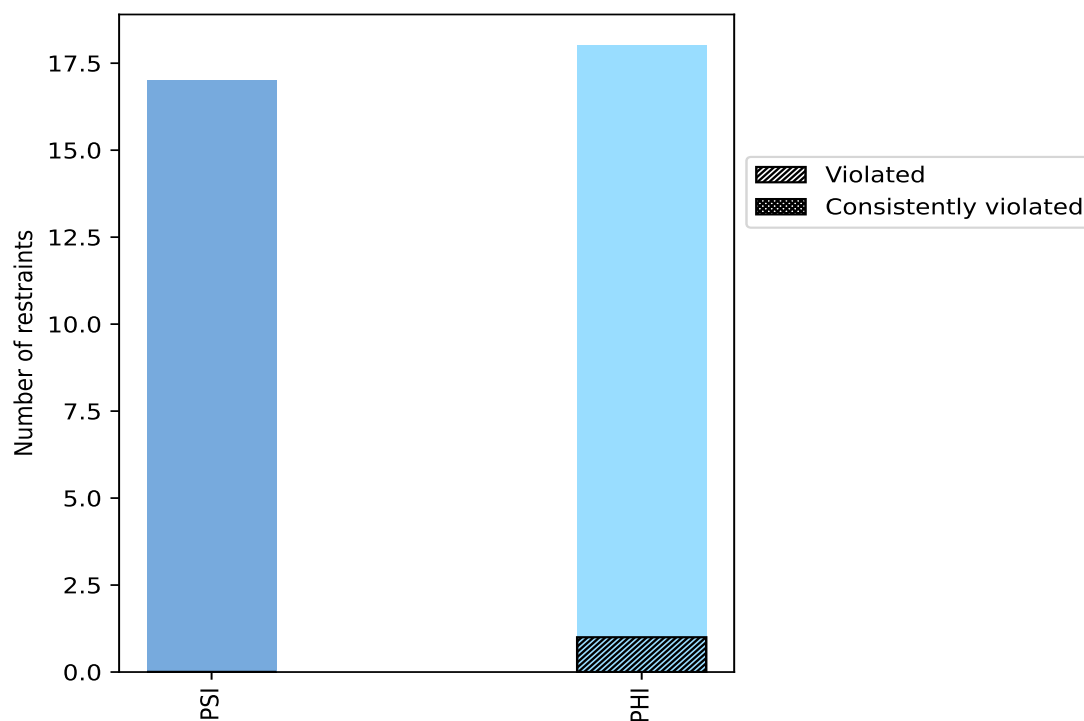
### 10.1 Summary of dihedral-angle violations [i](#)

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>
PSI	17	48.6	0	0.0	0.0	0	0.0	0.0
PHI	18	51.4	1	5.6	2.9	0	0.0	0.0
Total	35	100.0	1	2.9	2.9	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](#)



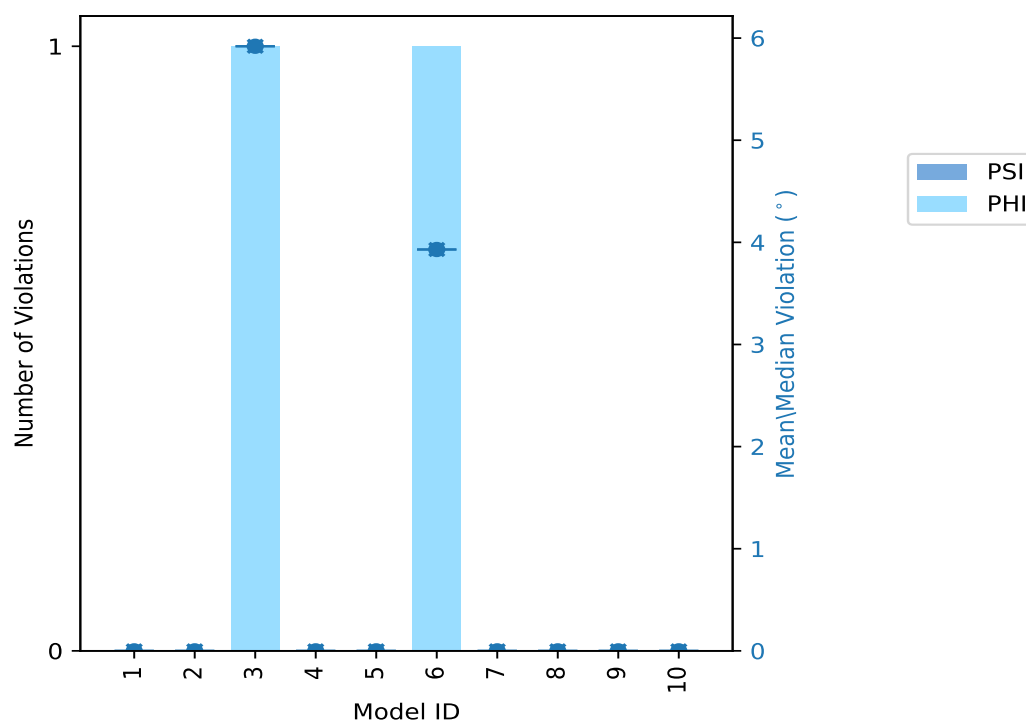
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

## 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 (°)
	PSI	PHI	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	1	1	5.92	5.92	0.0	5.92
4	0	0	0	0.0	0.0	0.0	0.0
5	0	0	0	0.0	0.0	0.0	0.0
6	0	1	1	3.93	3.93	0.0	3.93
7	0	0	0	0.0	0.0	0.0	0.0
8	0	0	0	0.0	0.0	0.0	0.0
9	0	0	0	0.0	0.0	0.0	0.0
10	0	0	0	0.0	0.0	0.0	0.0

### 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

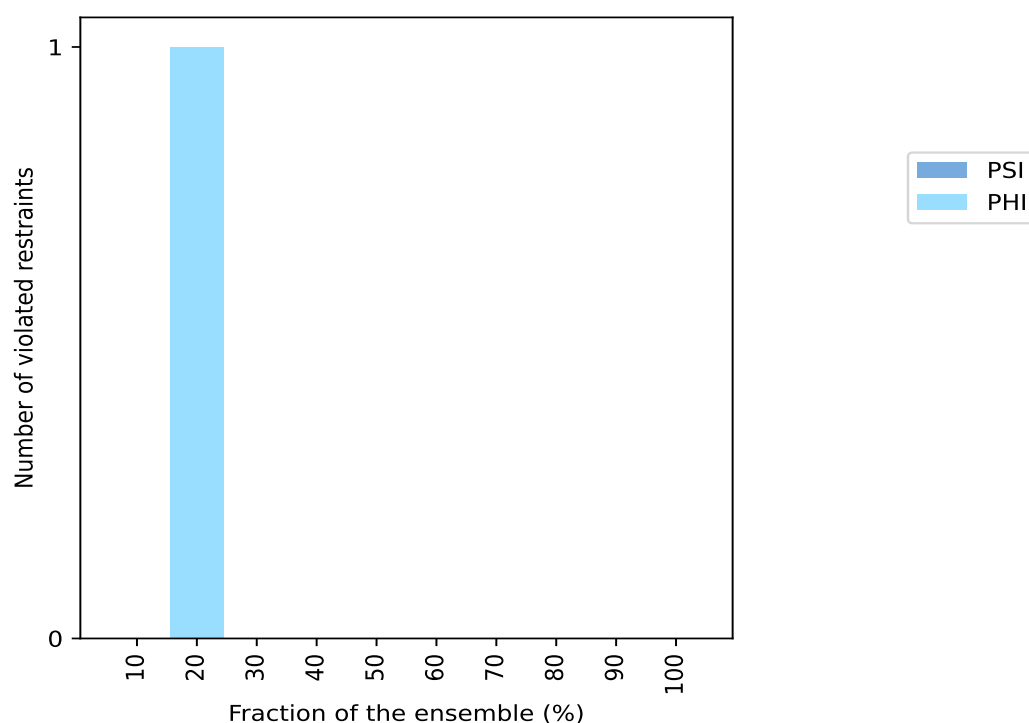
### 10.3 Dihedral-angle violation statistics for the ensemble [i](#)

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	
PSI	PHI	Total	Count <sup>1</sup>	%
0	0	0	1	10.0
0	1	1	2	20.0
0	0	0	3	30.0
0	0	0	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](#)

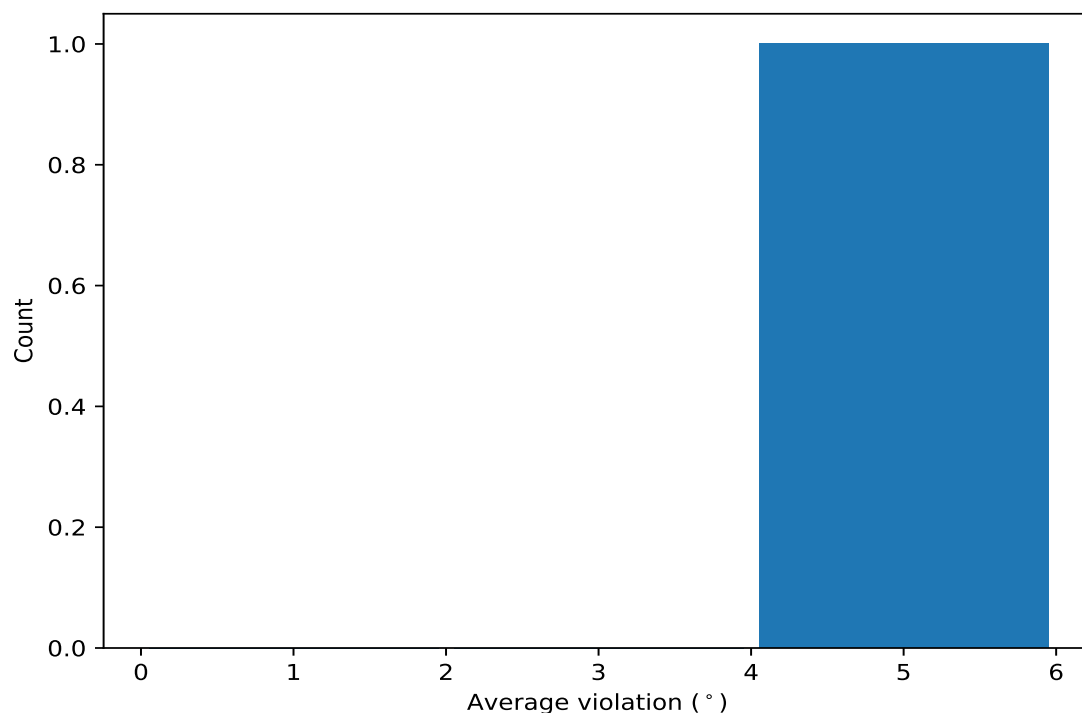




## 10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

### 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
(1,19)	1:541:A:ILE:C	1:542:A:GLY:N	1:542:A:GLY:CA	1:542:A:GLY:C	2	4.92	0.99	4.92

<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 (°)
(1,19)	1:541:A:ILE:C	1:542:A:GLY:N	1:542:A:GLY:CA	1:542:A:GLY:C	3	5.92
(1,19)	1:541:A:ILE:C	1:542:A:GLY:N	1:542:A:GLY:CA	1:542:A:GLY:C	6	3.93