



# wwPDB NMR Structure Validation Summary Report ⓘ

Mar 24, 2026 – 07:17 AM UTC

PDB ID : 7CLV / pdb\_00007clv  
BMRB ID : 36365  
Title : Solution structure of mitochondrial Tim23 channel in complex with a signaling peptide  
Authors : Zhou, S.; Ruan, M.S.; Li, Y.Y.; Yang, J.; Richter, C.; Schwalbe, H.; Shen, B.; Wang, J.F.  
Deposited on : 2020-07-22

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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

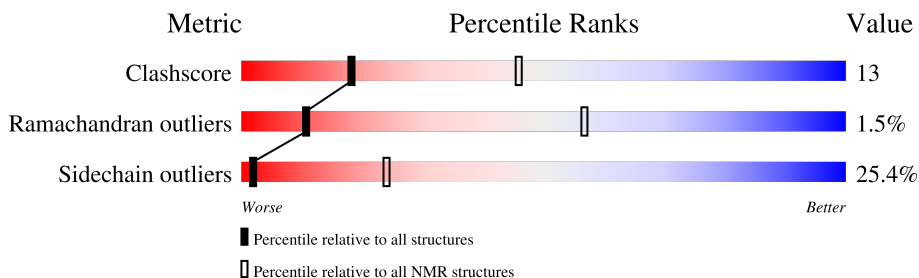
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 35%.

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	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	222	
1	B	222	
2	C	25	

## 2 Ensemble composition and analysis

This entry contains 15 models. Model 5 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:64-A:75, A:91-A:124, A:151-A:216, B:64-B:79, B:91-B:122, B:150-B:216 (227)	1.36	5

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 5, 6, 8, 9, 11, 12, 13, 14, 15
2	3, 4, 7, 10

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6985 atoms, of which 3514 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called TIM23 isoform 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	222	3274	1026	1643	281	315	9	0
1	B	222	3274	1026	1643	281	315	9	0

- Molecule 2 is a protein called COX4 isoform 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	C	25	437	134	228	39	34	2	0

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

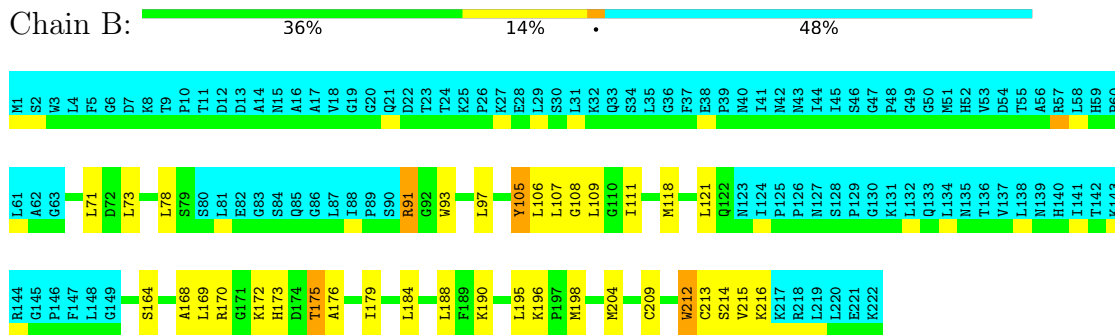
### 4.1 Average score per residue in the NMR ensemble

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.

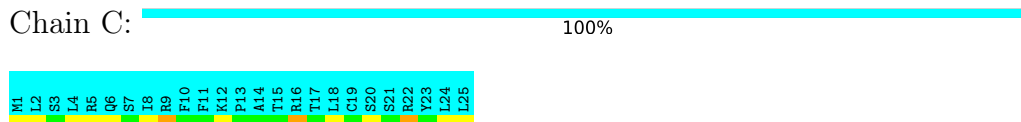
- Molecule 1: TIM23 isoform 1



- Molecule 1: TIM23 isoform 1



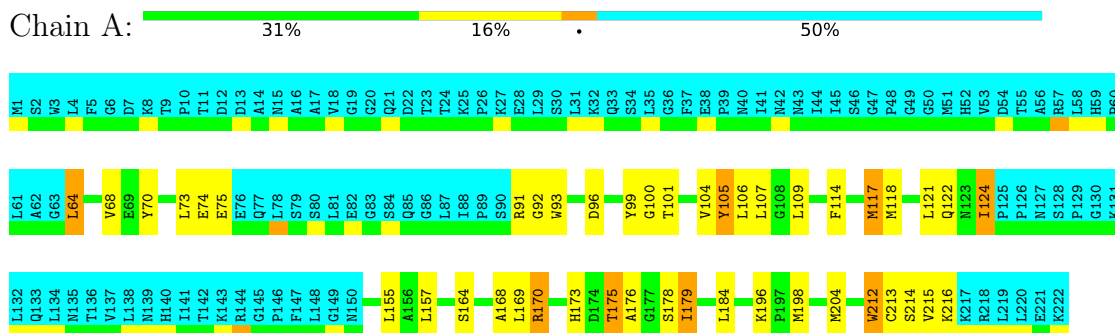
- Molecule 2: COX4 isoform 1



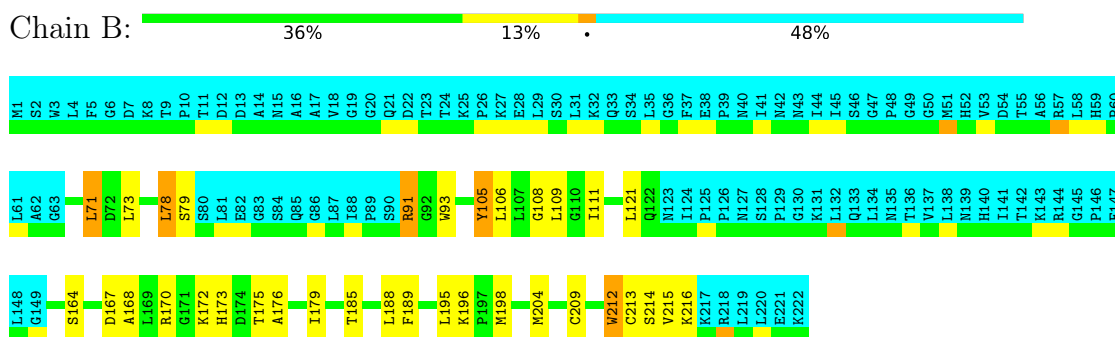
## 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 5. Colouring as in section 4.1 above.

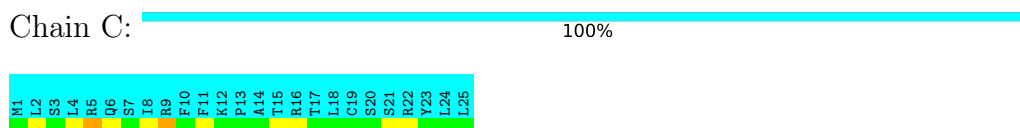
- Molecule 1: TIM23 isoform 1



- Molecule 1: TIM23 isoform 1



- Molecule 2: COX4 isoform 1



## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 15 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
X-PLOR NIH	structure calculation	
X-PLOR NIH	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	1891
Number of shifts mapped to atoms	1891
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	35%

## 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	1.51±0.00	0±0/820 ( 0.0± 0.0%)	1.48±0.01	0±0/1108 ( 0.0± 0.0%)
1	B	1.50±0.00	0±0/844 ( 0.0± 0.0%)	1.47±0.01	0±0/1139 ( 0.0± 0.0%)
All	All	1.51	0/24960 ( 0.0%)	1.47	11/33705 ( 0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.9±0.2
1	B	0.0±0.0	2.0±0.0
All	All	0	59

There are no bond-length outliers.

5 of 7 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( $^{\circ}$ )	Ideal( $^{\circ}$ )	Models	
								Worst	Total
1	A	124	ILE	N-CA-CB	-6.02	105.17	111.61	12	3
1	A	94	THR	N-CA-CB	-5.71	104.93	111.79	13	1
1	A	101	THR	N-CA-CB	-5.68	104.97	111.79	2	1
1	B	94	THR	N-CA-CB	-5.62	105.05	111.79	3	1
1	A	104	VAL	N-CA-CB	-5.58	104.77	110.62	6	2

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	170	ARG	Sidechain	15

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Mol	Chain	Res	Type	Group	Models (Total)
1	B	91	ARG	Sidechain	15
1	B	170	ARG	Sidechain	15
1	A	91	ARG	Sidechain	14

## 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	807	809	809	25±6
1	B	831	828	828	24±4
2	C	0	0	0	0±0
All	All	24570	24555	24555	649

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 13.

5 of 271 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:93:TRP:CD1	1:B:105:TYR:HH	1.08	1.67	1	15
1:A:93:TRP:CD1	1:A:105:TYR:HH	1.06	1.67	14	15
1:A:175:THR:HG21	1:A:212:TRP:CD1	0.86	2.05	14	2
1:A:175:THR:HG23	1:B:105:TYR:CZ	0.85	2.07	2	9
1:A:105:TYR:CZ	1:B:175:THR:HG23	0.81	2.10	13	9

## 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	112/222 (50%)	101±3 (90±2%)	10±3 (9±2%)	2±1 (1±1%)	<b>11</b> 58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	115/222 (52%)	103±2 (89±2%)	11±2 (9±2%)	2±1 (2±1%)	11 57
2	C	0	-	-	-	-
All	All	3405/7035 (48%)	3049 (90%)	306 (9%)	50 (1%)	11 57

5 of 12 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	175	THR	12
1	B	175	THR	12
1	A	214	SER	8
1	B	214	SER	5
1	B	216	LYS	3

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

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	81/173 (47%)	61±4 (75±6%)	20±4 (25±6%)	2 24
1	B	84/173 (49%)	63±3 (74±4%)	21±3 (26±4%)	2 23
2	C	0	-	-	-
All	All	2475/5550 (45%)	1847 (75%)	628 (25%)	2 24

5 of 123 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	212	TRP	15
1	B	212	TRP	15
1	B	172	LYS	14
1	A	172	LYS	12
1	A	105	TYR	11

### 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 35% for the well-defined parts and 31% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list*

#### 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	1891
Number of shifts mapped to atoms	1891
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](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	211	$0.40 \pm 0.15$	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	178	$0.72 \pm 0.04$	Should be checked
$^{13}\text{C}'$	197	$0.11 \pm 0.12$	None needed (< 0.5 ppm)
$^{15}\text{N}$	198	$0.71 \pm 0.20$	Should be applied

#### 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 35%, i.e. 1005 atoms were assigned a chemical shift out of a possible 2833. 0 out of 39 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	519/1167 (44%)	207/488 (42%)	209/454 (46%)	103/225 (46%)
Sidechain	463/1474 (31%)	328/978 (34%)	135/459 (29%)	0/37 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	23/192 (12%)	21/92 (23%)	0/94 (0%)	2/6 (33%)
Overall	1005/2833 (35%)	556/1558 (36%)	344/1007 (34%)	105/268 (39%)

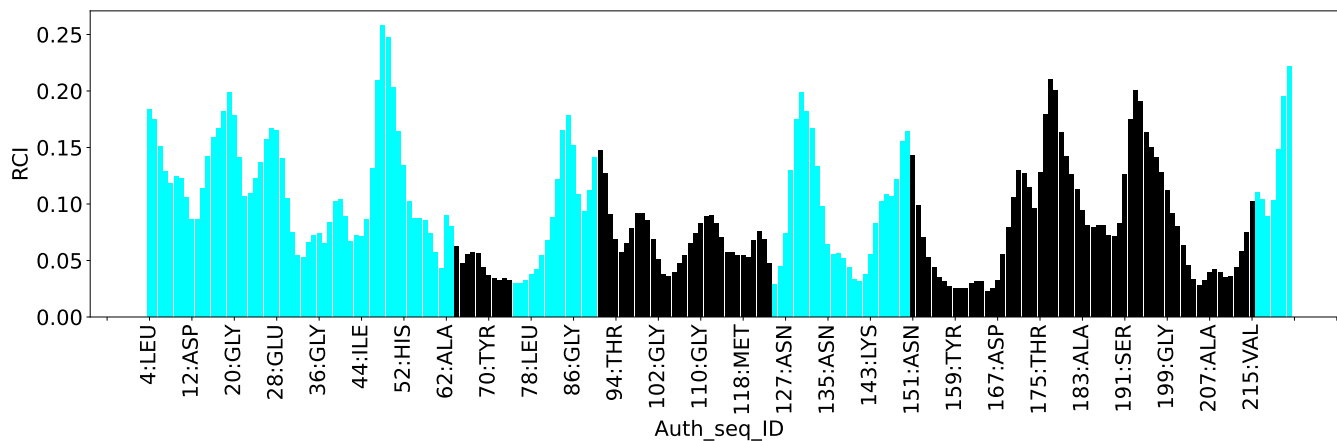
#### 7.1.4 Statistically unusual chemical shifts [i](#)

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	3104
Intra-residue ( $ i-j =0$ )	954
Sequential ( $ i-j =1$ )	960
Medium range ( $ i-j >1$ and $ i-j <5$ )	368
Long range ( $ i-j \geq 5$ )	228
Inter-chain	594
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	752
Number of unmapped restraints	0
Number of restraints per residue	8.2
Number of long range restraints per residue <sup>1</sup>	0.5

<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)	216.5	0.2
0.2-0.5 (Medium)	209.1	0.5
>0.5 (Large)	487.9	20.64

### 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)	25.3	10.0
10.0-20.0 (Medium)	10.1	19.77
>20.0 (Large)	66.1	157.17

## 9 Distance violation analysis i

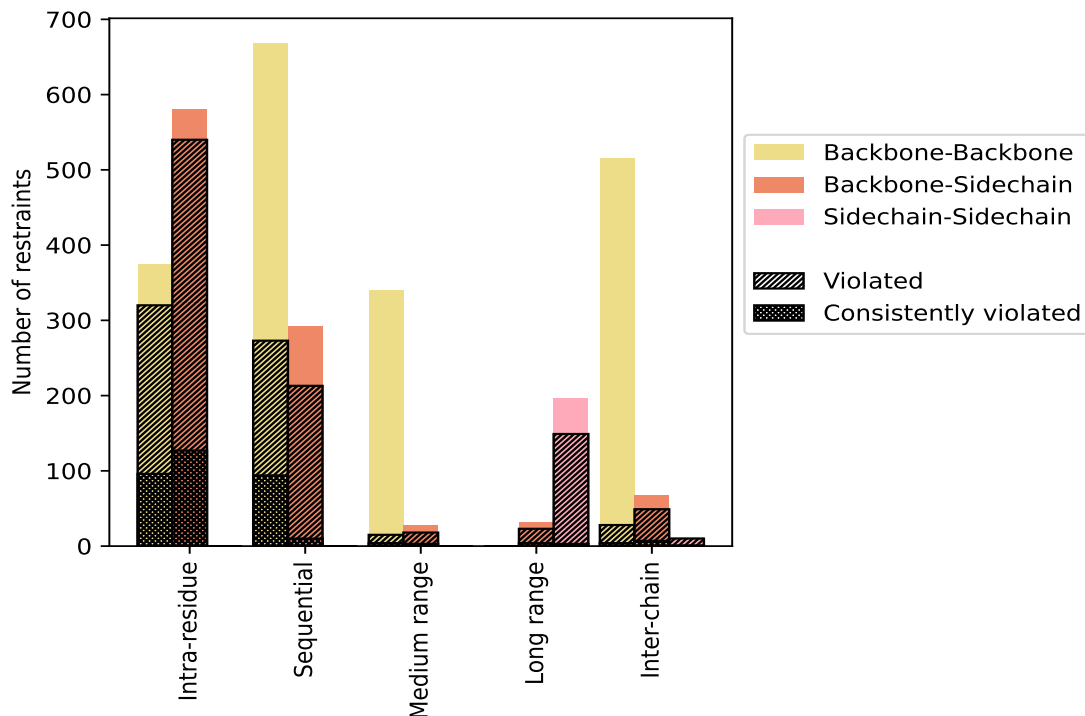
### 9.1 Summary of distance violations i

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>954</b>	<b>30.7</b>	<b>860</b>	<b>90.1</b>	<b>27.7</b>	<b>223</b>	<b>23.4</b>	<b>7.2</b>
Backbone-Backbone	374	12.0	320	85.6	10.3	96	25.7	3.1
Backbone-Sidechain	580	18.7	540	93.1	17.4	127	21.9	4.1
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
<b>Sequential (<math> i-j =1</math>)</b>	<b>960</b>	<b>30.9</b>	<b>486</b>	<b>50.6</b>	<b>15.7</b>	<b>104</b>	<b>10.8</b>	<b>3.4</b>
Backbone-Backbone	668	21.5	273	40.9	8.8	94	14.1	3.0
Backbone-Sidechain	292	9.4	213	72.9	6.9	10	3.4	0.3
Sidechain-Sidechain	0	0.0	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>368</b>	<b>11.9</b>	<b>33</b>	<b>9.0</b>	<b>1.1</b>	<b>7</b>	<b>1.9</b>	<b>0.2</b>
Backbone-Backbone	340	11.0	15	4.4	0.5	4	1.2	0.1
Backbone-Sidechain	28	0.9	18	64.3	0.6	3	10.7	0.1
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
<b>Long range (<math> i-j \geq 5</math>)</b>	<b>228</b>	<b>7.3</b>	<b>172</b>	<b>75.4</b>	<b>5.5</b>	<b>7</b>	<b>3.1</b>	<b>0.2</b>
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	32	1.0	23	71.9	0.7	4	12.5	0.1
Sidechain-Sidechain	196	6.3	149	76.0	4.8	3	1.5	0.1
<b>Inter-chain</b>	<b>594</b>	<b>19.1</b>	<b>87</b>	<b>14.6</b>	<b>2.8</b>	<b>12</b>	<b>2.0</b>	<b>0.4</b>
Backbone-Backbone	515	16.6	28	5.4	0.9	4	0.8	0.1
Backbone-Sidechain	67	2.2	49	73.1	1.6	7	10.4	0.2
Sidechain-Sidechain	12	0.4	10	83.3	0.3	1	8.3	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
<b>Total</b>	<b>3104</b>	<b>100.0</b>	<b>1638</b>	<b>52.8</b>	<b>52.8</b>	<b>353</b>	<b>11.4</b>	<b>11.4</b>
Backbone-Backbone	1897	61.1	636	33.5	20.5	198	10.4	6.4
Backbone-Sidechain	999	32.2	843	84.4	27.2	151	15.1	4.9
Sidechain-Sidechain	208	6.7	159	76.4	5.1	4	1.9	0.1

<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 disulfid 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	557	247	18	69	45	936	0.72	20.28	1.44	0.53
2	542	242	22	70	49	925	0.74	20.34	1.45	0.56
3	546	242	16	57	38	899	0.7	20.42	1.43	0.54
4	554	243	18	66	44	925	0.72	20.31	1.43	0.54
5	559	250	19	74	37	939	0.7	20.12	1.4	0.53
6	547	245	25	54	46	917	0.75	20.17	1.45	0.54
7	530	245	18	59	40	892	0.71	20.64	1.44	0.54
8	549	249	21	75	37	931	0.7	20.3	1.41	0.53
9	568	254	19	66	42	949	0.69	20.13	1.38	0.52
10	536	253	20	63	40	912	0.71	20.16	1.43	0.53

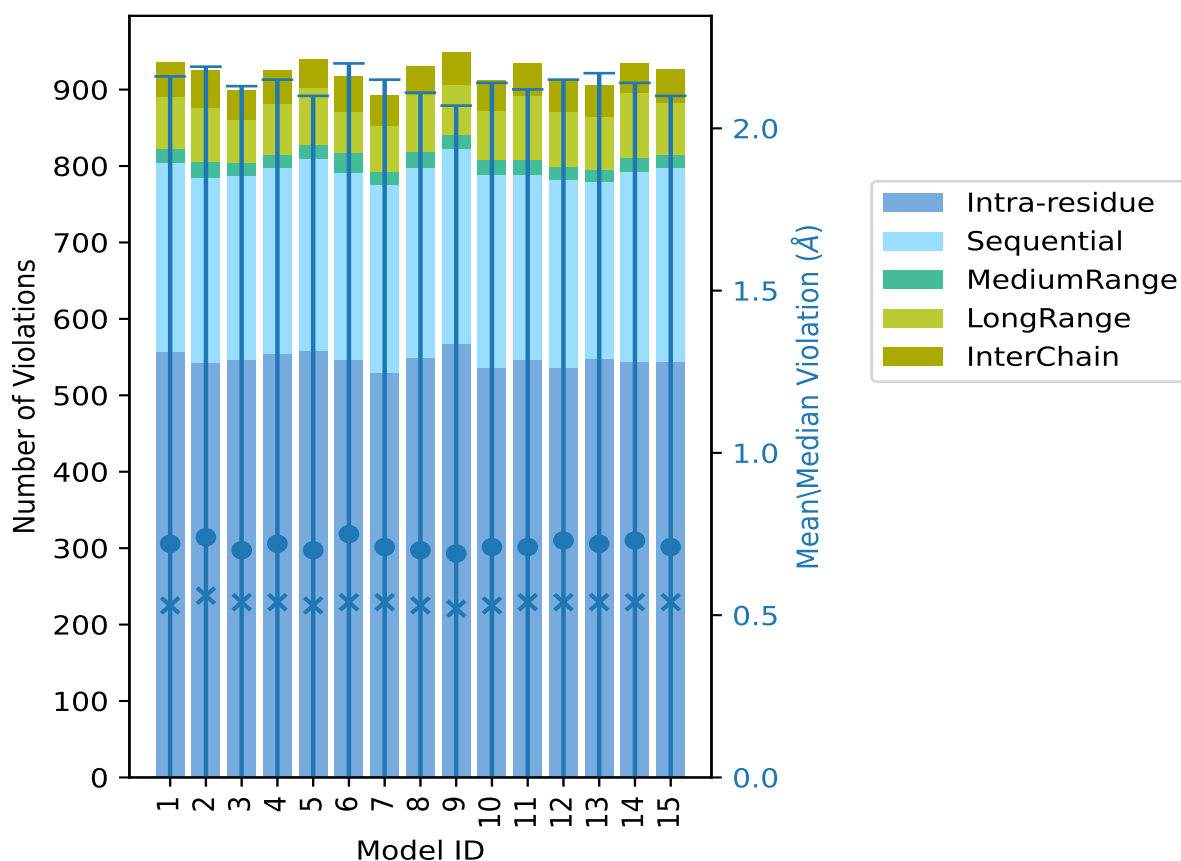
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD <sup>6</sup> (Å)	Median (Å)
	IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total				
11	546	243	19	84	43	935	0.71	20.13	1.41	0.54
12	536	246	17	72	40	911	0.73	20.14	1.42	0.54
13	548	231	16	69	41	905	0.72	20.54	1.45	0.54
14	544	248	19	85	38	934	0.73	20.3	1.41	0.54
15	544	253	18	68	44	927	0.71	19.81	1.39	0.54

<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



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

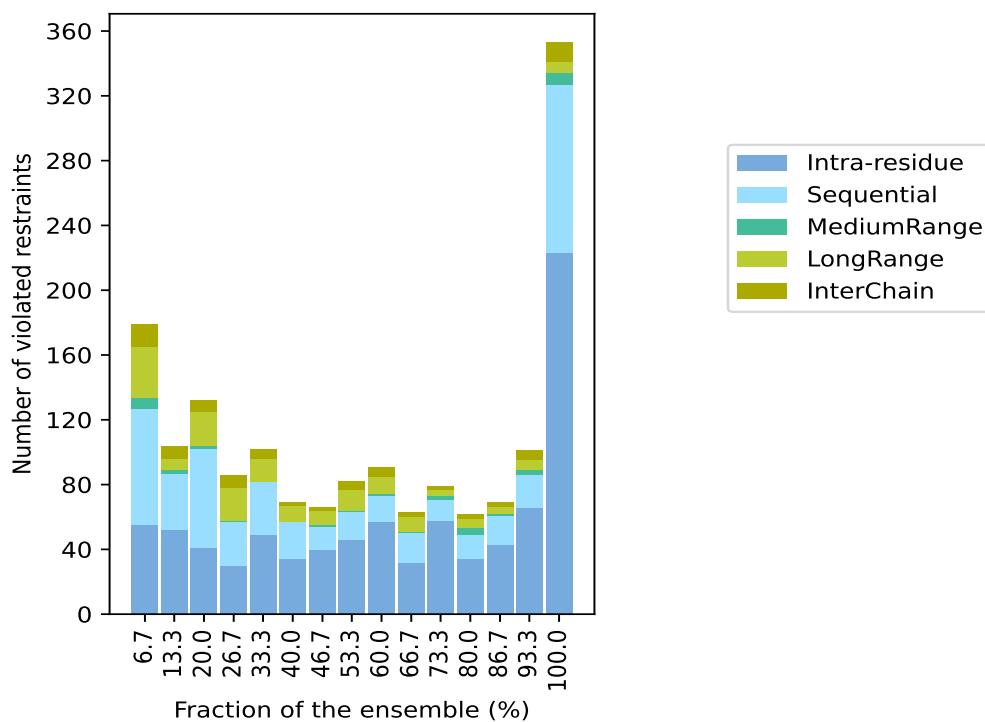
### 9.3 Distance violation statistics for the ensemble

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, 1466(IR:94, SQ:474, MR:335, LR:56, IC:507) 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>	%
55	72	7	31	14	179	1	6.7
52	35	2	7	8	104	2	13.3
41	61	2	21	7	132	3	20.0
30	27	1	20	8	86	4	26.7
49	33	0	14	6	102	5	33.3
34	23	0	10	2	69	6	40.0
40	14	1	9	2	66	7	46.7
46	17	1	13	5	82	8	53.3
57	16	1	11	6	91	9	60.0
32	18	1	9	3	63	10	66.7
58	13	2	4	2	79	11	73.3
34	15	4	6	3	62	12	80.0
43	18	1	4	3	69	13	86.7
66	20	3	6	6	101	14	93.3
223	104	7	7	12	353	15	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

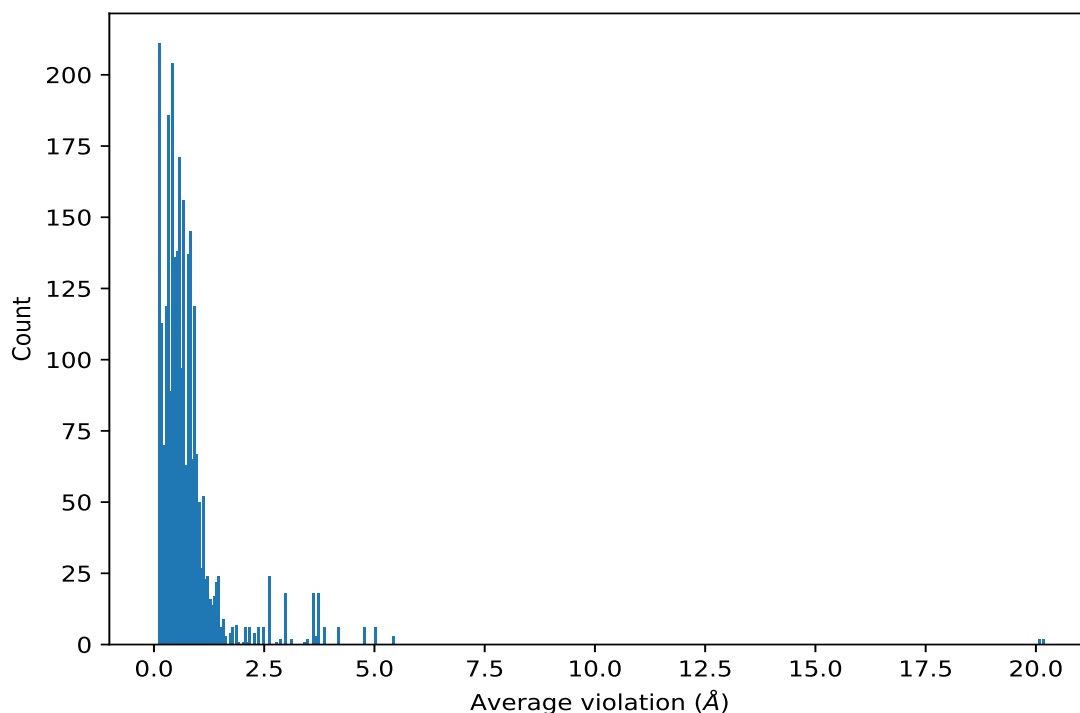
### 9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

### 9.4.1 Histogram : Distribution of mean distance 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



#### 9.4.2 Table: Most violated distance restraints [i](#)

The following table provides the mean and the standard deviation of the violations for the 10 worst performing restraints, sorted by number of violated models and the mean violation 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)
(1,662)	1:119:A:GLN:H	1:189:A:PHE:HB2	15	20.17	0.26	20.14
(1,663)	1:119:A:GLN:H	1:189:A:PHE:HB2	15	20.17	0.26	20.14
(1,1906)	1:119:B:GLN:H	1:189:B:PHE:HB2	15	20.05	0.25	20.1
(1,1907)	1:119:B:GLN:H	1:189:B:PHE:HB2	15	20.05	0.25	20.1
(1,2457)	1:211:B:VAL:HG23	1:173:B:HIS:HD1	15	5.02	2.54	5.26
(1,2457)	1:211:B:VAL:HG21	1:173:B:HIS:HD1	15	5.02	2.54	5.26
(1,2457)	1:211:B:VAL:HG22	1:173:B:HIS:HD2	15	5.02	2.54	5.26
(1,2457)	1:211:B:VAL:HG23	1:173:B:HIS:HD2	15	5.02	2.54	5.26
(1,2457)	1:211:B:VAL:HG22	1:173:B:HIS:HD1	15	5.02	2.54	5.26
(1,2457)	1:211:B:VAL:HG21	1:173:B:HIS:HD2	15	5.02	2.54	5.26
(1,1213)	1:211:A:VAL:HG22	1:173:A:HIS:HD2	15	4.8	2.48	5.15
(1,1213)	1:211:A:VAL:HG23	1:173:A:HIS:HD2	15	4.8	2.48	5.15
(1,1213)	1:211:A:VAL:HG22	1:173:A:HIS:HD1	15	4.8	2.48	5.15
(1,1213)	1:211:A:VAL:HG21	1:173:A:HIS:HD2	15	4.8	2.48	5.15
(1,1213)	1:211:A:VAL:HG23	1:173:A:HIS:HD1	15	4.8	2.48	5.15
(1,1213)	1:211:A:VAL:HG21	1:173:A:HIS:HD1	15	4.8	2.48	5.15

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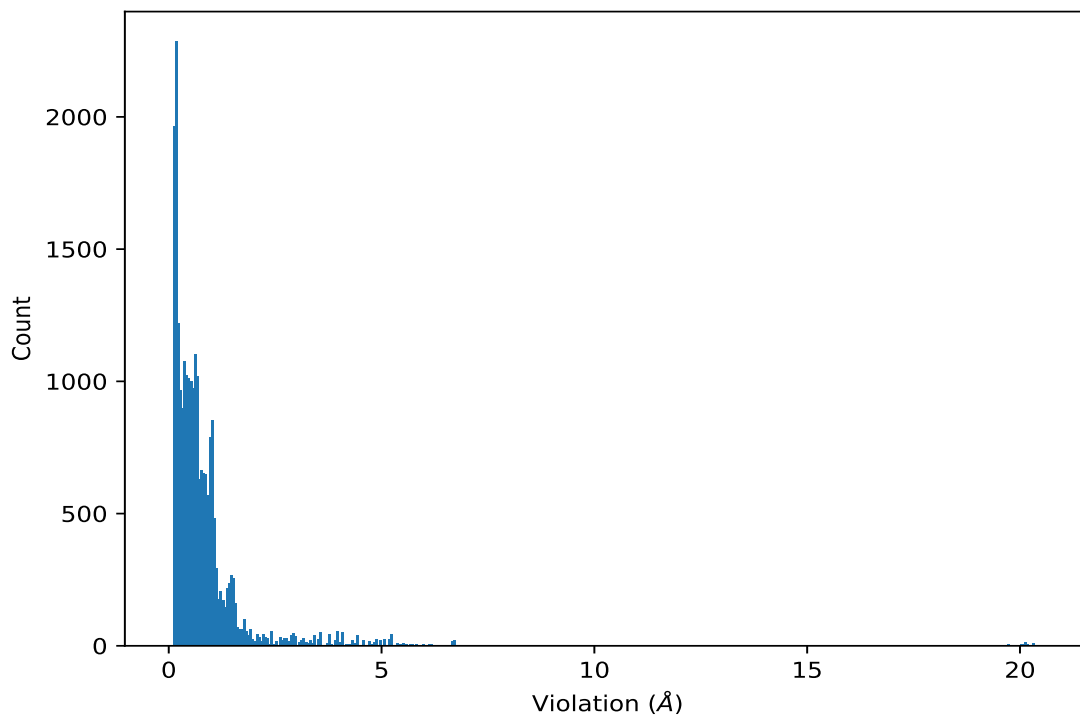
Key	Atom-1	Atom-2	Models <sup>1</sup>	Mean (Å)	SD <sup>1</sup> (Å)	Median (Å)
(1,2569)	1:88:B:ILE:HD11	1:95:A:ASP:HB2	15	3.85	1.08	3.75
(1,2569)	1:88:B:ILE:HD11	1:95:A:ASP:HB3	15	3.85	1.08	3.75
(1,2569)	1:88:B:ILE:HD12	1:95:A:ASP:HB2	15	3.85	1.08	3.75
(1,2569)	1:88:B:ILE:HD12	1:95:A:ASP:HB3	15	3.85	1.08	3.75
(1,2569)	1:88:B:ILE:HD13	1:95:A:ASP:HB2	15	3.85	1.08	3.75
(1,2569)	1:88:B:ILE:HD13	1:95:A:ASP:HB3	15	3.85	1.08	3.75
(1,2570)	1:88:B:ILE:HD11	1:95:A:ASP:HA	15	3.68	1.44	3.21
(1,2570)	1:88:B:ILE:HD12	1:95:A:ASP:HA	15	3.68	1.44	3.21
(1,2570)	1:88:B:ILE:HD13	1:95:A:ASP:HA	15	3.68	1.44	3.21
(1,2610)	2:25:C:LEU:HG	1:66:A:LYS:H	15	3.43	1.16	3.44
(1,2596)	2:21:C:SER:H	1:68:A:VAL:HG12	15	2.25	0.84	2.39

<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 provides the 10 worst performing restraints, sorted by the violation 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)
(1,663)	1:119:A:GLN:H	1:189:A:PHE:HB2	7	20.64
(1,662)	1:119:A:GLN:H	1:189:A:PHE:HB2	7	20.64
(1,663)	1:119:A:GLN:H	1:189:A:PHE:HB2	13	20.54
(1,662)	1:119:A:GLN:H	1:189:A:PHE:HB2	13	20.54
(1,1907)	1:119:B:GLN:H	1:189:B:PHE:HB2	7	20.48
(1,1906)	1:119:B:GLN:H	1:189:B:PHE:HB2	7	20.48
(1,663)	1:119:A:GLN:H	1:189:A:PHE:HB2	3	20.42
(1,662)	1:119:A:GLN:H	1:189:A:PHE:HB2	3	20.42
(1,663)	1:119:A:GLN:H	1:189:A:PHE:HB2	2	20.34
(1,662)	1:119:A:GLN:H	1:189:A:PHE:HB2	2	20.34

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

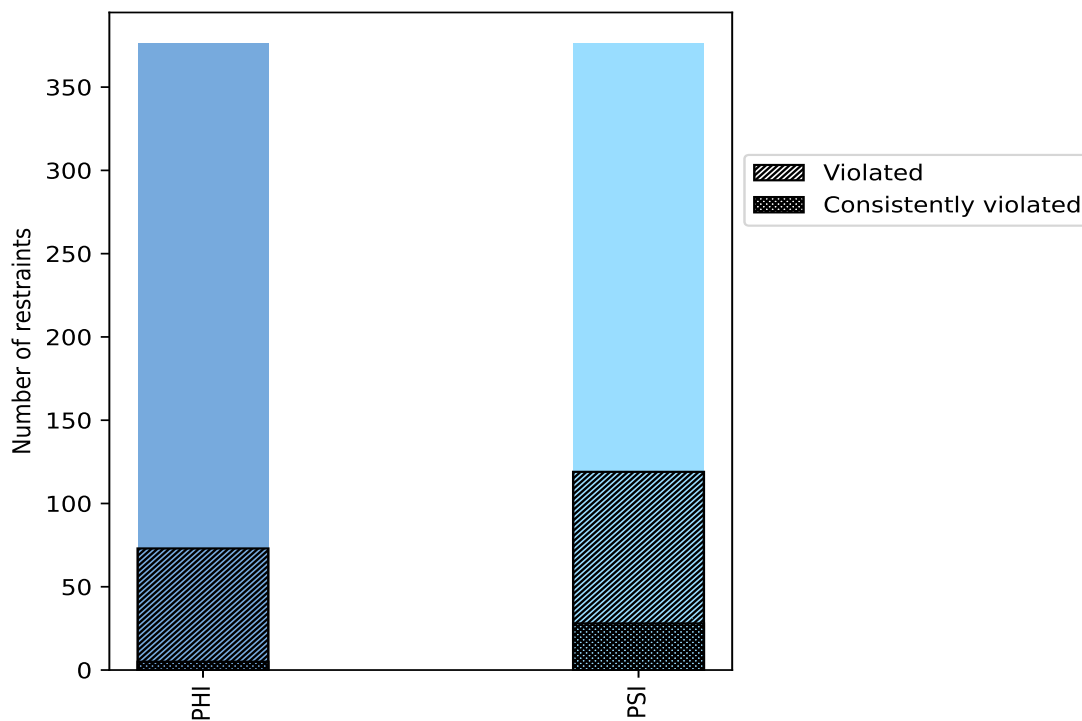
### 10.1 Summary of dihedral-angle violations [i](#)

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	376	50.0	73	19.4	9.7	5	1.3	0.7
PSI	376	50.0	119	31.6	15.8	28	7.4	3.7
Total	752	100.0	192	25.5	25.5	33	4.4	4.4

<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](#)



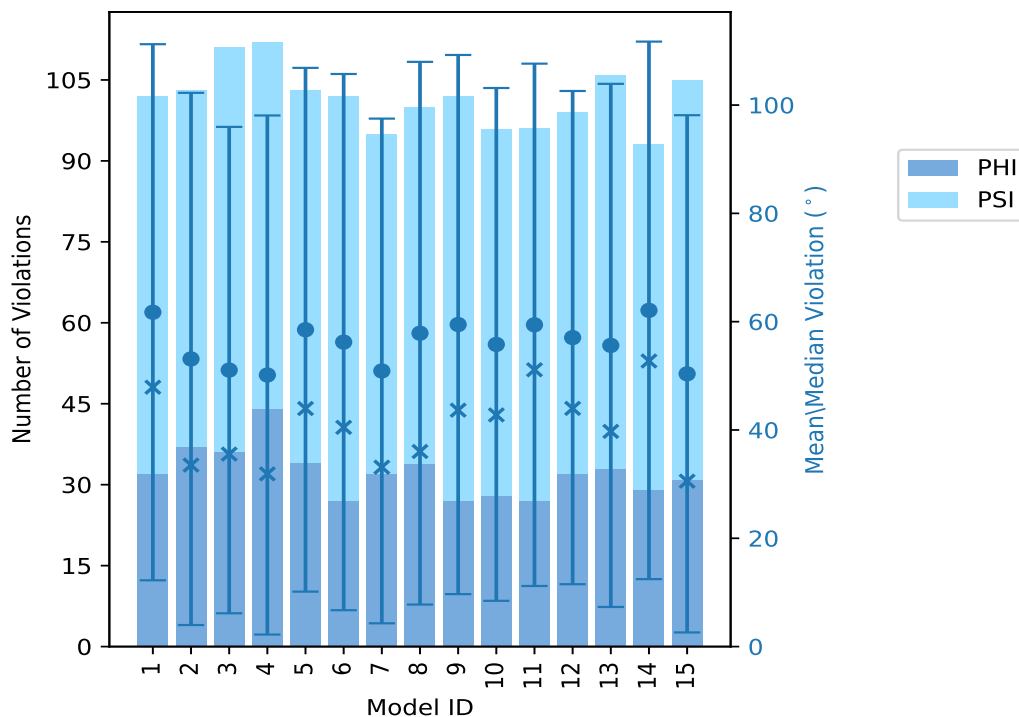
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

## 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	32	70	102	61.74	157.17	49.5	47.9
2	37	66	103	53.12	146.77	49.14	33.52
3	36	75	111	51.06	152.33	44.91	35.55
4	44	68	112	50.15	153.93	47.93	31.89
5	34	69	103	58.51	152.21	48.36	43.96
6	27	75	102	56.23	143.96	49.51	40.49
7	32	63	95	50.9	148.09	46.6	33.13
8	34	66	100	57.87	151.28	50.11	36.03
9	27	75	102	59.47	154.27	49.78	43.66
10	28	68	96	55.8	151.8	47.35	42.78
11	27	69	96	59.42	149.88	48.23	51.12
12	32	67	99	57.06	148.73	45.54	43.99
13	33	73	106	55.62	148.31	48.3	39.74
14	29	64	93	62.09	149.27	49.63	52.74
15	31	74	105	50.37	149.21	47.76	30.55

### 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

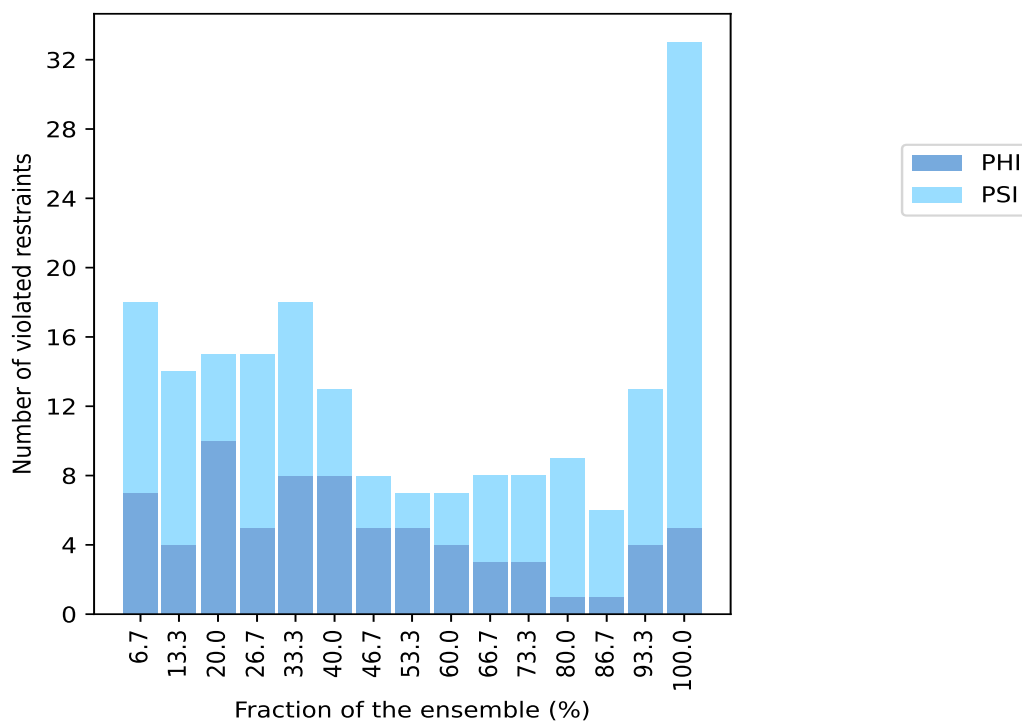
### 10.3 Dihedral-angle violation statistics for the ensemble

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>	%
7	11	18	1	6.7
4	10	14	2	13.3
10	5	15	3	20.0
5	10	15	4	26.7
8	10	18	5	33.3
8	5	13	6	40.0
5	3	8	7	46.7
5	2	7	8	53.3
4	3	7	9	60.0
3	5	8	10	66.7
3	5	8	11	73.3
1	8	9	12	80.0
1	5	6	13	86.7
4	9	13	14	93.3
5	28	33	15	100.0

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

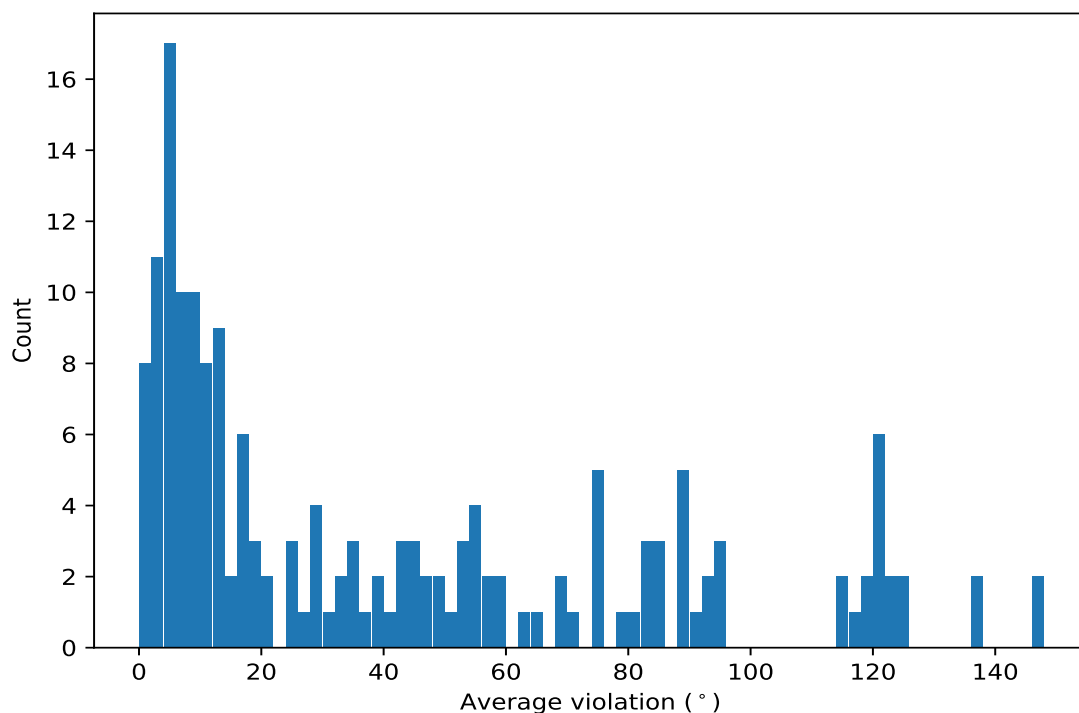
### 10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



## 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 violations for the 10 worst performing restraints, sorted by number of violated models and the mean violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

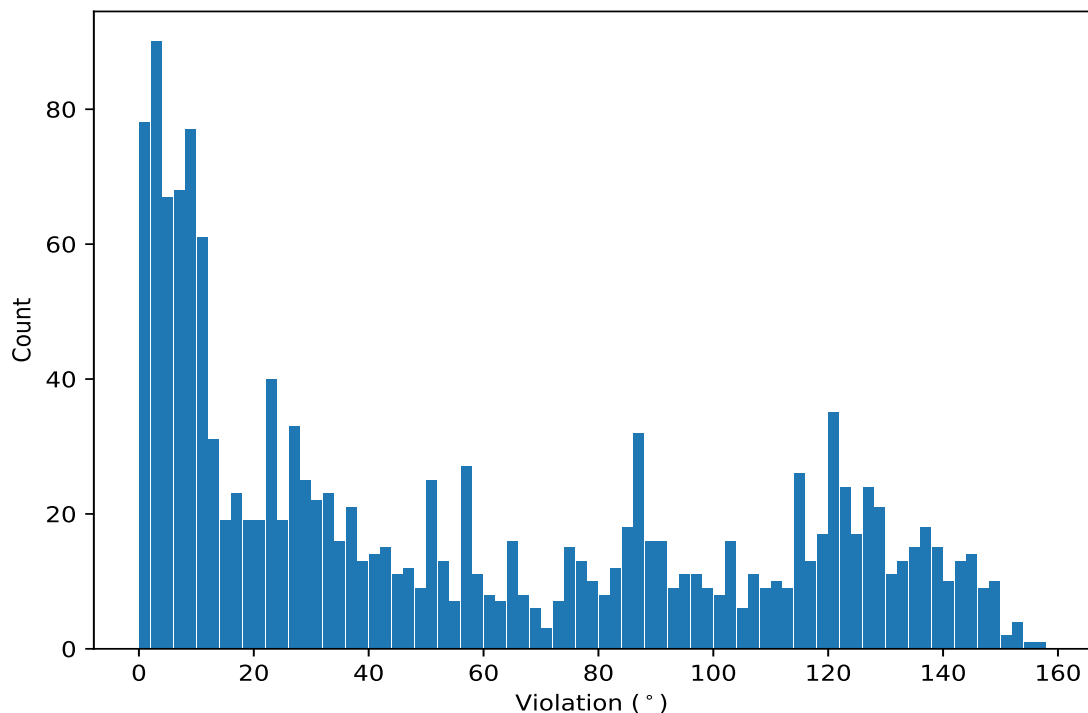
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models <sup>1</sup>	Mean	SD <sup>2</sup>	Median
(1,38)	1:26:A:PRO:N	1:26:A:PRO:CA	1:26:A:PRO:C	1:27:A:LYS:N	15	147.08	3.62	146.72
(1,414)	1:26:B:PRO:N	1:26:B:PRO:CA	1:26:B:PRO:C	1:27:B:LYS:N	15	146.7	4.62	148.73
(1,438)	1:39:B:PRO:N	1:39:B:PRO:CA	1:39:B:PRO:C	1:40:B:ASN:N	15	136.65	8.25	137.4
(1,62)	1:39:A:PRO:N	1:39:A:PRO:CA	1:39:A:PRO:C	1:40:A:ASN:N	15	136.28	10.77	137.79
(1,470)	1:60:B:PRO:N	1:60:B:PRO:CA	1:60:B:PRO:C	1:61:B:LEU:N	15	124.23	11.9	126.55
(1,584)	1:123:B:ASN:N	1:123:B:ASN:CA	1:123:B:ASN:C	1:124:B:ILE:N	15	123.29	4.74	124.86
(1,94)	1:60:A:PRO:N	1:60:A:PRO:CA	1:60:A:PRO:C	1:61:A:LEU:N	15	122.54	9.58	124.55
(1,336)	1:198:A:MET:N	1:198:A:MET:CA	1:198:A:MET:C	1:199:A:GLY:N	15	121.32	1.42	120.77
(1,614)	1:141:B:ILE:N	1:141:B:ILE:CA	1:141:B:ILE:C	1:142:B:THR:N	15	121.2	14.54	122.12
(1,712)	1:198:B:MET:N	1:198:B:MET:CA	1:198:B:MET:C	1:199:B:GLY:N	15	121.09	0.72	120.84

<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.



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

The following table provides the list of violations for the 10 worst performing restraints, sorted by the violation 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 (°)
(1,62)	1:39:A:PRO:N	1:39:A:PRO:CA	1:39:A:PRO:C	1:40:A:ASN:N	1	157.17
(1,438)	1:39:B:PRO:N	1:39:B:PRO:CA	1:39:B:PRO:C	1:40:B:ASN:N	9	154.27
(1,38)	1:26:A:PRO:N	1:26:A:PRO:CA	1:26:A:PRO:C	1:27:A:LYS:N	4	153.93
(1,414)	1:26:B:PRO:N	1:26:B:PRO:CA	1:26:B:PRO:C	1:27:B:LYS:N	4	153.11
(1,38)	1:26:A:PRO:N	1:26:A:PRO:CA	1:26:A:PRO:C	1:27:A:LYS:N	3	152.33
(1,414)	1:26:B:PRO:N	1:26:B:PRO:CA	1:26:B:PRO:C	1:27:B:LYS:N	5	152.21
(1,38)	1:26:A:PRO:N	1:26:A:PRO:CA	1:26:A:PRO:C	1:27:A:LYS:N	10	151.8
(1,414)	1:26:B:PRO:N	1:26:B:PRO:CA	1:26:B:PRO:C	1:27:B:LYS:N	8	151.28
(1,414)	1:26:B:PRO:N	1:26:B:PRO:CA	1:26:B:PRO:C	1:27:B:LYS:N	11	149.88
(1,414)	1:26:B:PRO:N	1:26:B:PRO:CA	1:26:B:PRO:C	1:27:B:LYS:N	9	149.5