wwPDB NMR Structure Validation Summary Report (i)

Jun 5, 2023 – 08:03 AM EDT

PDB ID	:	2LY8
BMRB ID	:	18713
Title	:	The budding yeast chaperone Scm3 recognizes the partially unfolded dimer of the centromere-specific Cse4/H4 histone variant
Authors	:	Hong, J.; Feng, H.; Zhou, Z.; Ghirlando, R.; Bai, Y.
Deposited on	:	2012-09-13

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

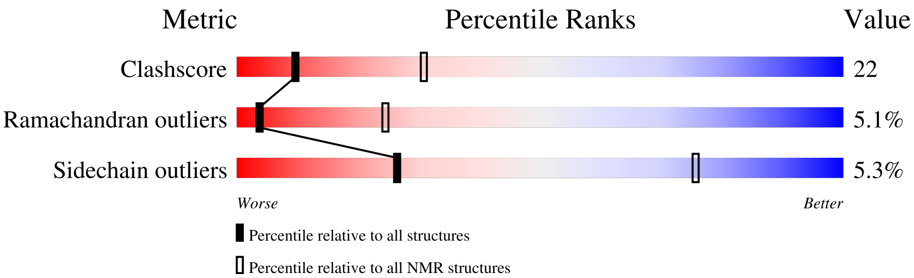
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

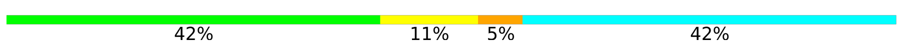
The overall completeness of chemical shifts assignment is 88%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 >=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 <=5%

Mol	Chain	Length	Quality of chain
1	A	121	

2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:7-A:41, A:75-A:109 (70)	0.18	10

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

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

The models can be grouped into 2 clusters and 4 single-model clusters were found.

Cluster number	Models
1	2, 5, 7, 10
2	3, 6
Single-model clusters	1; 4; 8; 9

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1971 atoms, of which 1005 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Budding yeast chaperone Scm3.

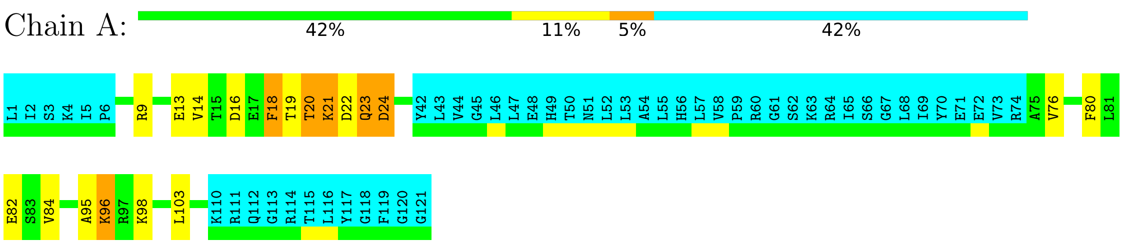
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	121	1971	618	1005	168	178	2	0

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.

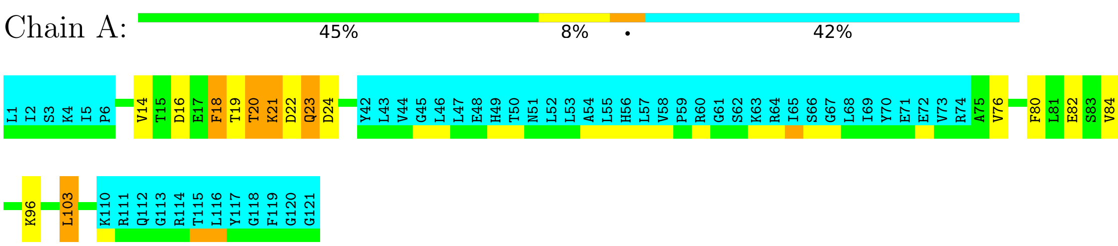
- Molecule 1: Budding yeast chaperone Scm3



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

The representative model is number 10. Colouring as in section 4.1 above.

- Molecule 1: Budding yeast chaperone Scm3



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 30 calculated structures, 10 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
X-PLOR NIH	structure solution	updated
ProcheckNMR	structure solution	updated
MOLMOL	structure solution	
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	1446
Number of shifts mapped to atoms	1446
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

6 Model quality (i)

6.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.72±0.00	0±0/568 (0.0± 0.0%)	0.83±0.00	1±0/769 (0.1± 0.0%)
All	All	0.72	0/5680 (0.0%)	0.83	9/7690 (0.1%)

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	18	PHE	CB-CG-CD2	-5.27	117.11	120.80	3	9

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	560	567	567	25±4
All	All	5600	5670	5670	250

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 22.

5 of 70 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:80:PHE:O	1:A:84:VAL:HG23	0.78	1.79	5	10

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:GLN:N	1:A:28:GLN:CD	0.73	2.42	8	1
1:A:88:SER:O	1:A:92:THR:HG23	0.72	1.84	9	5
1:A:31:ALA:O	1:A:34:ALA:HB3	0.69	1.87	4	5
1:A:15:THR:HG22	1:A:81:LEU:HD13	0.69	1.63	4	2

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	70/121 (58%)	64±1 (91±1%)	3±1 (4±1%)	4±1 (5±1%)	4	24
All	All	700/1210 (58%)	638 (91%)	26 (4%)	36 (5%)	4	24

All 5 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	20	THR	10
1	A	21	LYS	10
1	A	24	ASP	8
1	A	96	LYS	5
1	A	22	ASP	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	62/105 (59%)	59±1 (95±2%)	3±1 (5±2%)	26	75
All	All	620/1050 (59%)	587 (95%)	33 (5%)	26	75

5 of 8 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	23	GLN	10
1	A	96	LYS	9
1	A	76	VAL	4
1	A	98	LYS	4
1	A	103	LEU	3

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 monosaccharides 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 88% 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_chem_shift_list_1*

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	1446
Number of shifts mapped to atoms	1446
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	117	-0.37 ± 0.13	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	110	0.26 ± 0.06	None needed (< 0.5 ppm)
$^{13}C'$	111	0.06 ± 0.11	None needed (< 0.5 ppm)
^{15}N	111	0.20 ± 0.13	None needed (< 0.5 ppm)

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 88%, i.e. 862 atoms were assigned a chemical shift out of a possible 976. 0 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	343/350 (98%)	137/140 (98%)	139/140 (99%)	67/70 (96%)
Sidechain	495/559 (89%)	338/365 (93%)	154/174 (89%)	3/20 (15%)

Continued on next page...

Continued from previous page...

	Total	^{1}H	^{13}C	^{15}N
Aromatic	24/67 (36%)	24/33 (73%)	0/32 (0%)	0/2 (0%)
Overall	862/976 (88%)	499/538 (93%)	293/346 (85%)	70/92 (76%)

7.1.4 Statistically unusual chemical shifts (i)

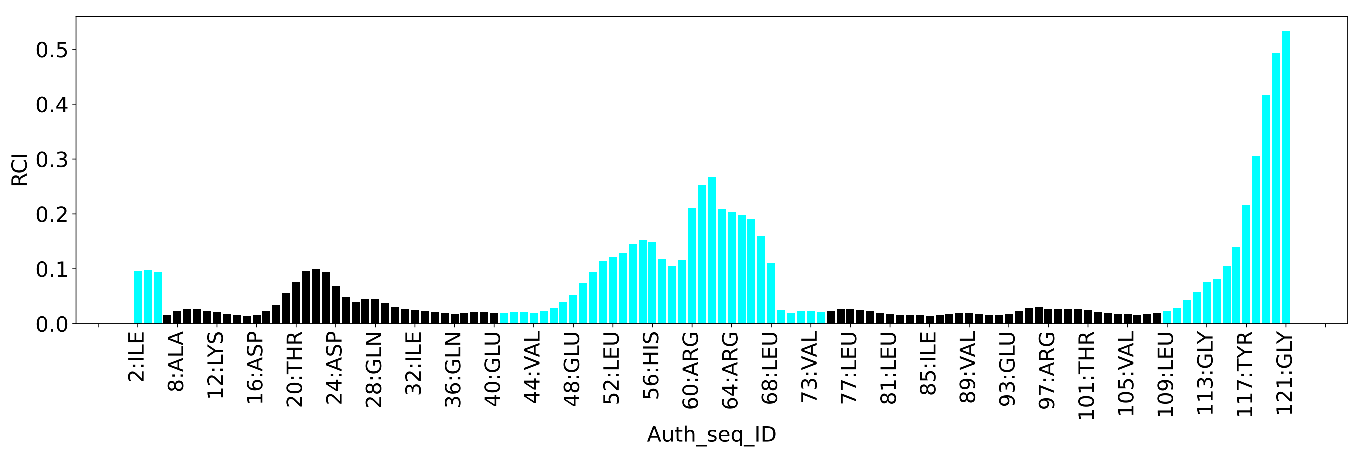
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	29	SER	HB2	2.59	2.61 – 5.13	-5.1

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	3334
Intra-residue (|i-j|=0)	779
Sequential (|i-j|=1)	850
Medium range (|i-j|>1 and |i-j|<5)	1150
Long range (|i-j|≥5)	437
Inter-chain	0
Hydrogen bond restraints	118
Disulfide bond restraints	0
Total dihedral-angle restraints	190
Number of unmapped restraints	0
Number of restraints per residue	29.1
Number of long range restraints per residue[1]	3.6

[1]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.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	168.7	0.2
0.2-0.5 (Medium)	123.0	0.49
>0.5 (Large)	5.1	3.64

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)	6.3	7.0
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis (i)

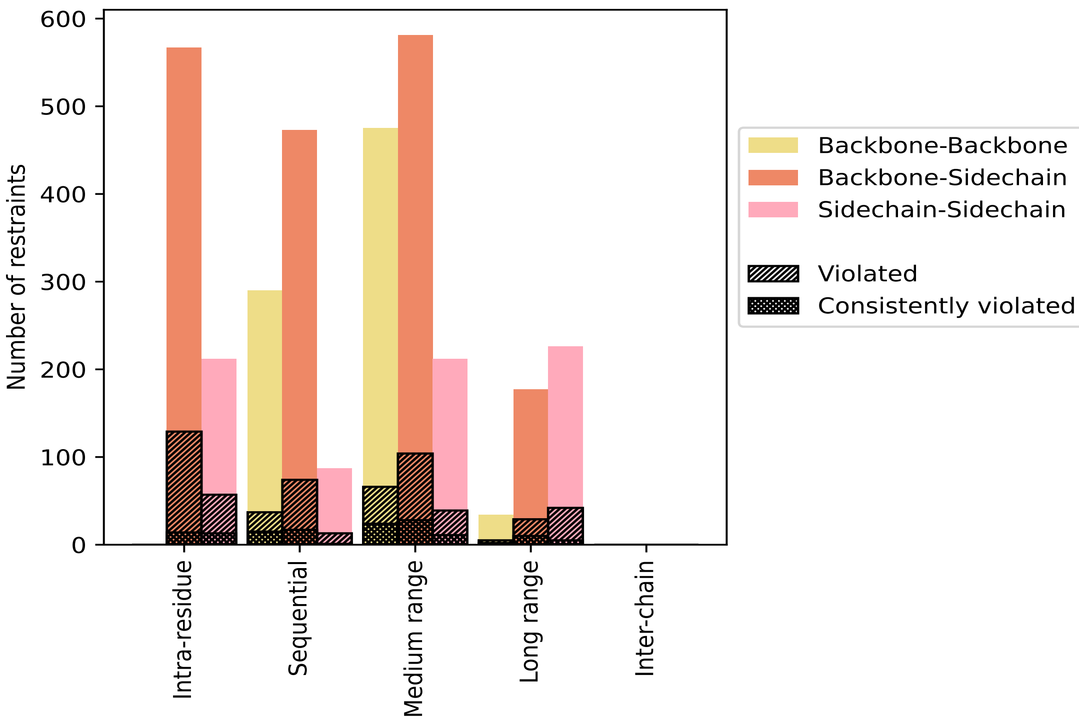
9.1 Summary of distance violations (i)

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.

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	779	23.4	186	23.9	5.6	27	3.5	0.8
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	567	17.0	129	22.8	3.9	14	2.5	0.4
Sidechain-Sidechain	212	6.4	57	26.9	1.7	13	6.1	0.4
Sequential (|i-j|=1)	850	25.5	124	14.6	3.7	33	3.9	1.0
Backbone-Backbone	290	8.7	37	12.8	1.1	15	5.2	0.4
Backbone-Sidechain	473	14.2	74	15.6	2.2	17	3.6	0.5
Sidechain-Sidechain	87	2.6	13	14.9	0.4	1	1.1	0.0
Medium range (|i-j|>1 & |i-j|<5)	1150	34.5	195	17.0	5.8	62	5.4	1.9
Backbone-Backbone	357	10.7	52	14.6	1.6	23	6.4	0.7
Backbone-Sidechain	581	17.4	104	17.9	3.1	28	4.8	0.8
Sidechain-Sidechain	212	6.4	39	18.4	1.2	11	5.2	0.3
Long range (|i-j|≥5)	437	13.1	76	17.4	2.3	17	3.9	0.5
Backbone-Backbone	34	1.0	5	14.7	0.1	2	5.9	0.1
Backbone-Sidechain	177	5.3	29	16.4	0.9	10	5.6	0.3
Sidechain-Sidechain	226	6.8	42	18.6	1.3	5	2.2	0.1
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	118	3.5	14	11.9	0.4	1	0.8	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	3334	100.0	595	17.8	17.8	140	4.2	4.2
Backbone-Backbone	799	24.0	108	13.5	3.2	41	5.1	1.2
Backbone-Sidechain	1798	53.9	336	18.7	10.1	69	3.8	2.1
Sidechain-Sidechain	737	22.1	151	20.5	4.5	30	4.1	0.9

[1] percentage calculated with respect to the total number of distance restraints, [2] percentage calculated with respect to the number of restraints in a particular restraint category, [3] violated in at least one model, [4] 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)

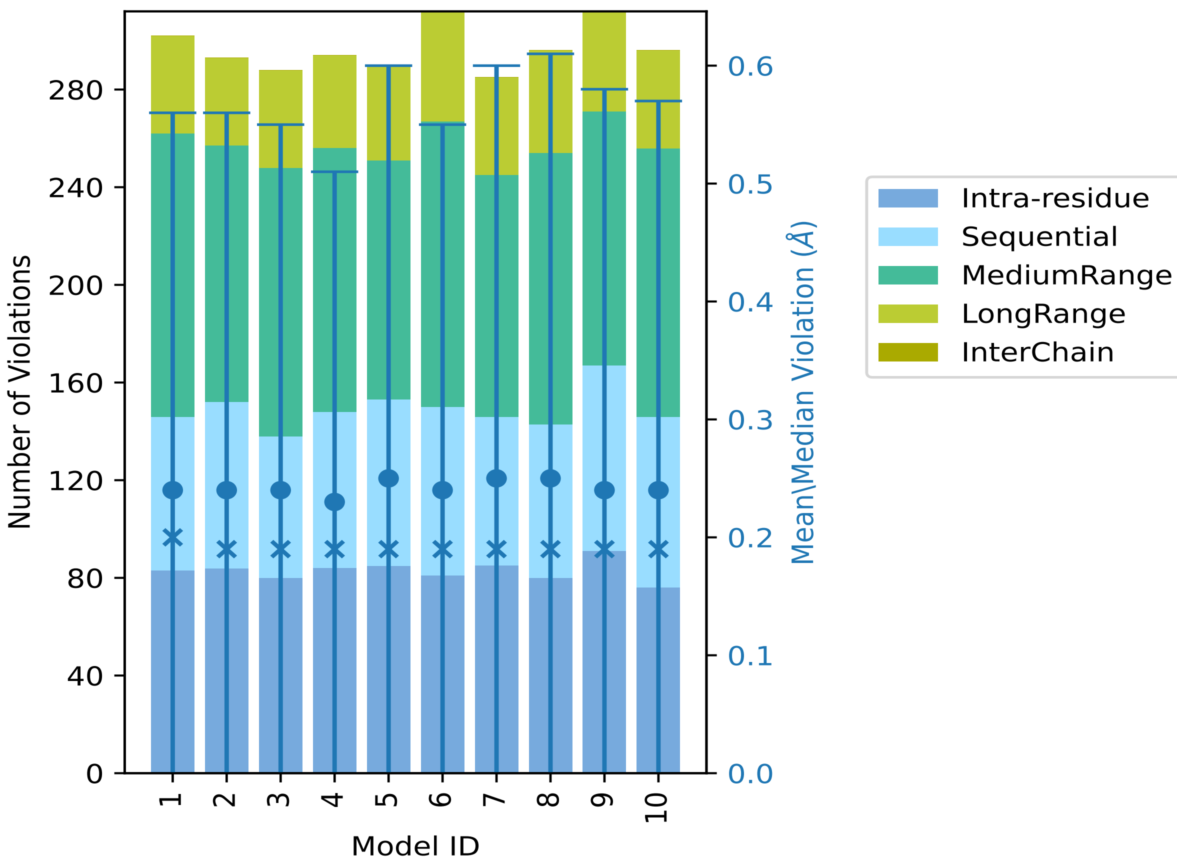
The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
1	83	63	116	40	0	302	0.24	3.2	0.32	0.2
2	84	68	105	36	0	293	0.24	3.31	0.32	0.19
3	80	58	110	40	0	288	0.24	3.03	0.31	0.19
4	84	64	108	38	0	294	0.23	2.89	0.28	0.19
5	85	68	98	39	0	290	0.25	3.58	0.35	0.19
6	81	69	117	45	0	312	0.24	3.16	0.31	0.19
7	85	61	99	40	0	285	0.25	3.47	0.35	0.19
8	80	63	111	42	0	296	0.25	3.64	0.36	0.19
9	91	76	104	41	0	312	0.24	3.52	0.34	0.19
10	76	70	110	40	0	296	0.24	3.34	0.33	0.19

[1]Intra-residue restraints, [2]Sequential restraints, [3]Medium range restraints, [4]Long range restraints,

[5]Inter-chain restraints, [6]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, 2635(IR:593, SQ:726, MR:955, LR:361, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total	Count[6]	%
56	27	51	22	0	156	1	10.0
26	17	21	8	0	72	2	20.0
15	14	18	1	0	48	3	30.0
12	5	9	3	0	29	4	40.0

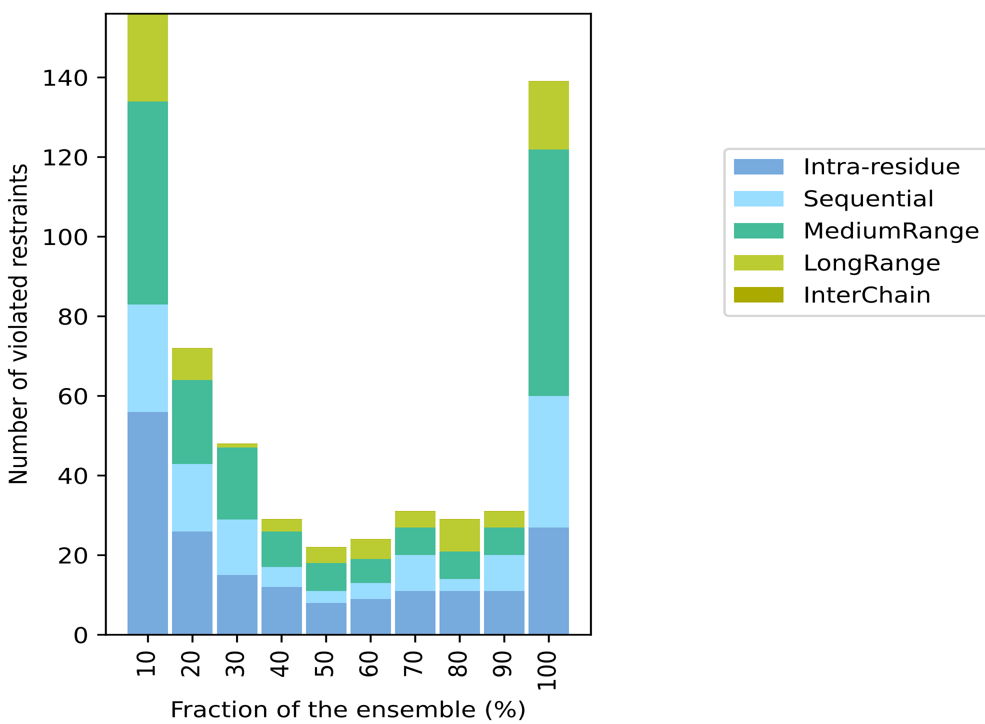
Continued on next page...

Continued from previous page...

Number of violated restraints						Fraction of the ensemble	
IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total	Count[6]	%
8	3	7	4	0	22	5	50.0
9	4	6	5	0	24	6	60.0
11	9	7	4	0	31	7	70.0
11	3	7	8	0	29	8	80.0
11	9	7	4	0	31	9	90.0
27	33	62	17	0	139	10	100.0

[1]Intra-residue restraints, [2]Sequential restraints, [3]Medium range restraints, [4]Long range restraints, [5]Inter-chain restraints, [6] Number of models with violations

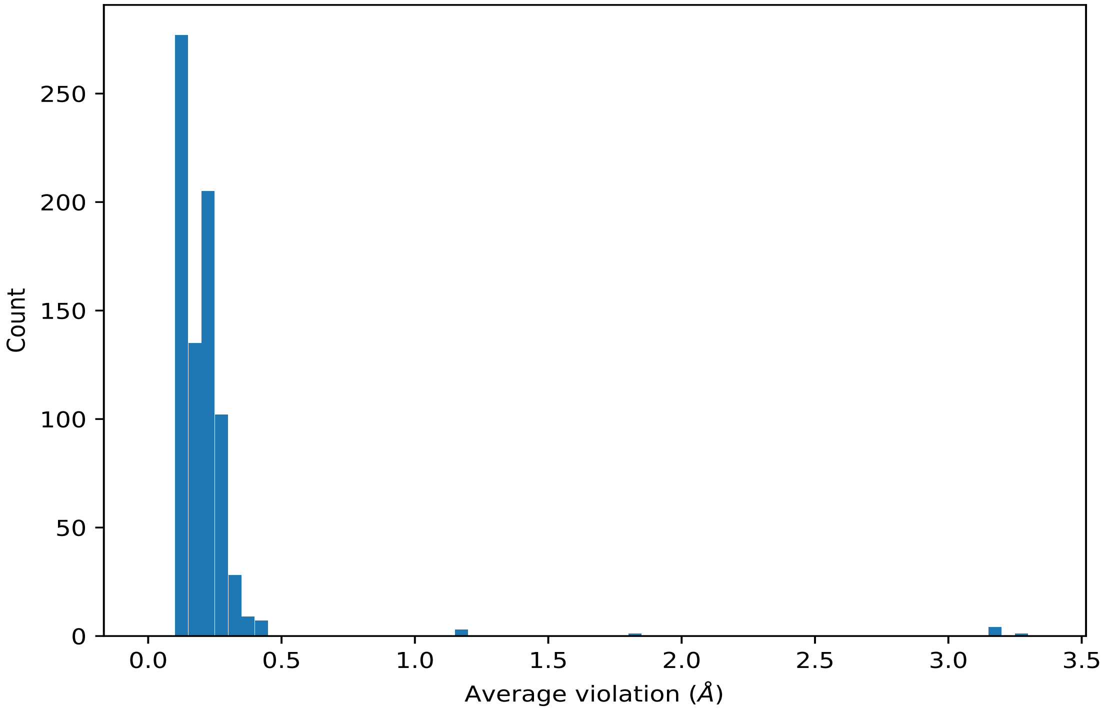
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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.

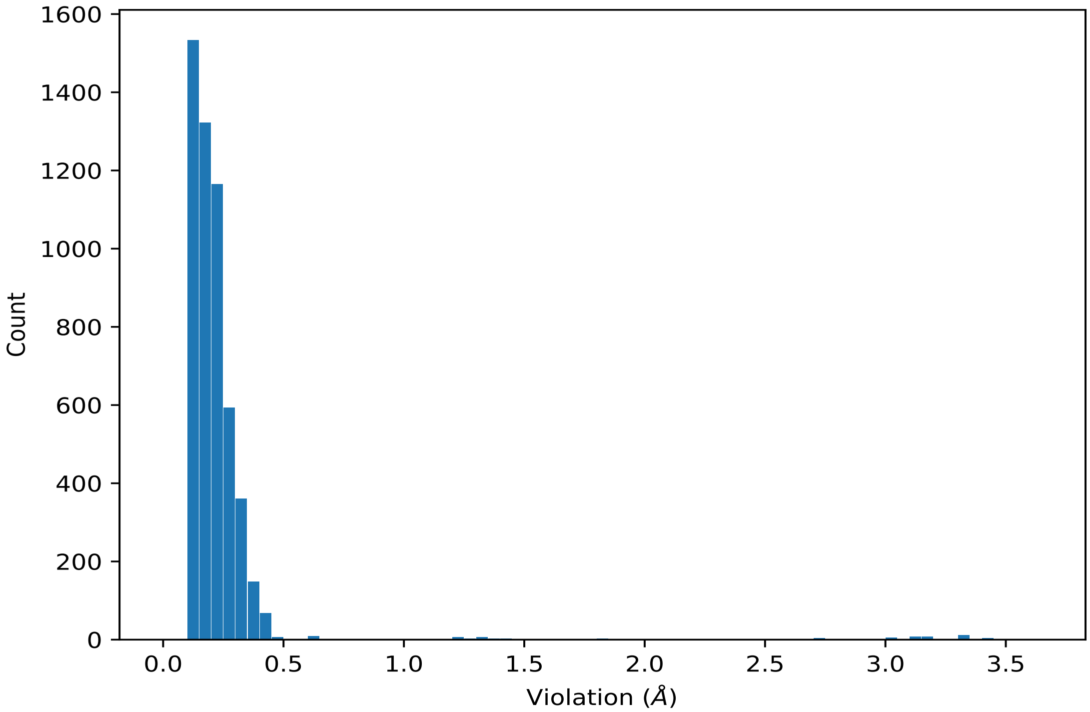
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,3206)	1:A:91:TYR:HE1	1:A:108:ALA:HA	10	3.3	0.26	3.32
(1,2643)	1:A:91:TYR:HE1	1:A:108:ALA:H	10	3.19	0.17	3.15
(1,3205)	1:A:91:TYR:HE1	1:A:108:ALA:HB1	10	3.17	0.18	3.18
(1,3205)	1:A:91:TYR:HE1	1:A:108:ALA:HB2	10	3.17	0.18	3.18
(1,3205)	1:A:91:TYR:HE1	1:A:108:ALA:HB3	10	3.17	0.18	3.18
(1,2642)	1:A:91:TYR:HD1	1:A:108:ALA:H	10	1.81	0.14	1.81
(1,2252)	1:A:74:ARG:H	1:A:77:LEU:H	10	0.4	0.04	0.4
(1,177)	1:A:22:ASP:HA	1:A:25:LEU:HB3	10	0.39	0.02	0.39
(1,2364)	1:A:80:PHE:HZ	1:A:81:LEU:H	10	0.38	0.02	0.38
(1,1613)	1:A:30:MET:HG2	1:A:31:ALA:H	10	0.38	0.03	0.36
(1,1613)	1:A:30:MET:HG3	1:A:31:ALA:H	10	0.38	0.03	0.36
(1,3129)	1:A:14:VAL:HG21	1:A:18:PHE:HD2	10	0.37	0.04	0.39
(1,3129)	1:A:14:VAL:HG22	1:A:18:PHE:HD2	10	0.37	0.04	0.39
(1,3129)	1:A:14:VAL:HG23	1:A:18:PHE:HD2	10	0.37	0.04	0.39
(1,2501)	1:A:85:ILE:H	1:A:87:ASP:H	10	0.34	0.02	0.35

[1]Number of violated models, [2]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)
(1,3206)	1:A:91:TYR:HE1	1:A:108:ALA:HA	8	3.64
(1,3206)	1:A:91:TYR:HE1	1:A:108:ALA:HA	5	3.58
(1,3206)	1:A:91:TYR:HE1	1:A:108:ALA:HA	9	3.52
(1,3206)	1:A:91:TYR:HE1	1:A:108:ALA:HA	7	3.47
(1,2643)	1:A:91:TYR:HE1	1:A:108:ALA:H	9	3.42
(1,3205)	1:A:91:TYR:HE1	1:A:108:ALA:HB1	8	3.41
(1,3205)	1:A:91:TYR:HE1	1:A:108:ALA:HB2	8	3.41
(1,3205)	1:A:91:TYR:HE1	1:A:108:ALA:HB3	8	3.41

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2643)	1:A:91:TYR:HE1	1:A:108:ALA:H	8	3.38
(1,2643)	1:A:91:TYR:HE1	1:A:108:ALA:H	5	3.37
(1,3206)	1:A:91:TYR:HE1	1:A:108:ALA:HA	10	3.34
(1,2643)	1:A:91:TYR:HE1	1:A:108:ALA:H	7	3.34

10 Dihedral-angle violation analysis

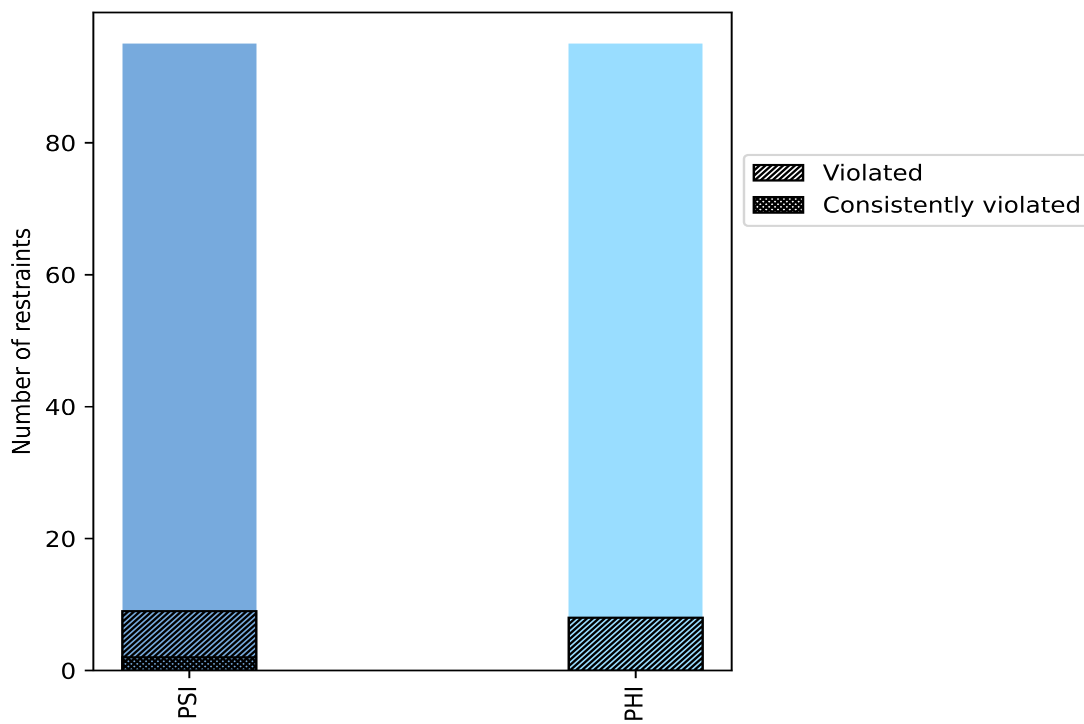
10.1 Summary of dihedral-angle violations

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	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
PSI	95	50.0	9	9.5	4.7	2	2.1	1.1
PHI	95	50.0	8	8.4	4.2	0	0.0	0.0
Total	190	100.0	17	8.9	8.9	2	1.1	1.1

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

10.1.1 Bar chart : Distribution of dihedral-angles and violations



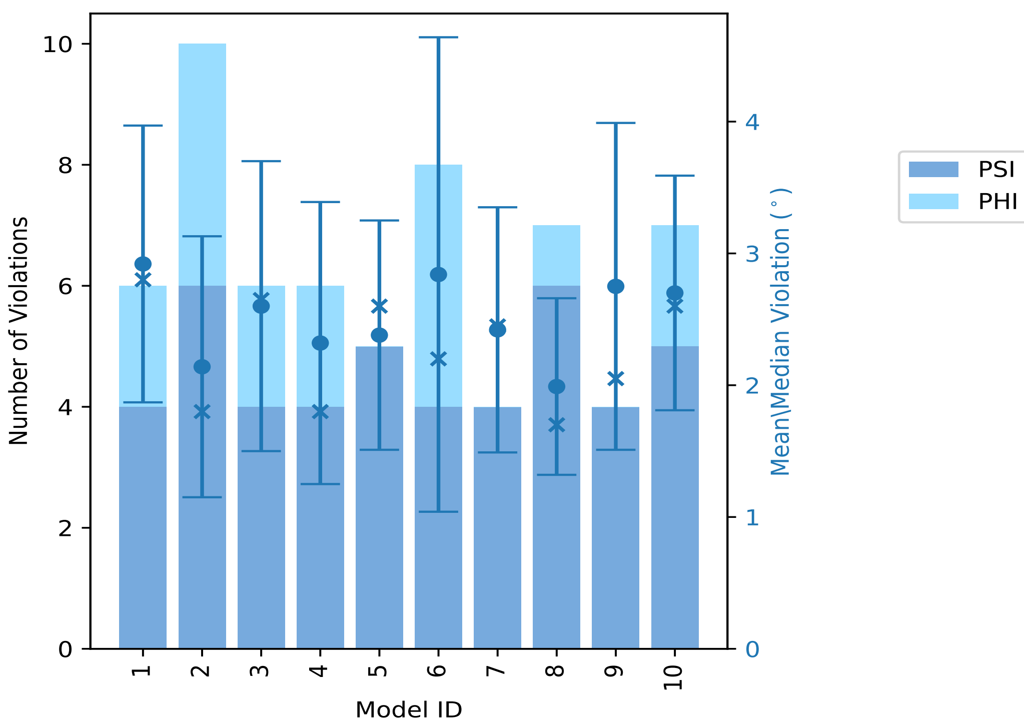
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	4	2	6	2.92	4.4	1.05	2.8
2	6	4	10	2.14	4.2	0.99	1.8
3	4	2	6	2.6	4.1	1.1	2.65
4	4	2	6	2.32	4.2	1.07	1.8
5	5	0	5	2.38	3.5	0.87	2.6
6	4	4	8	2.84	7.0	1.8	2.2
7	4	0	4	2.42	3.6	0.93	2.45
8	6	1	7	1.99	3.2	0.67	1.7
9	4	0	4	2.75	4.9	1.24	2.05
10	5	2	7	2.7	4.0	0.89	2.6

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

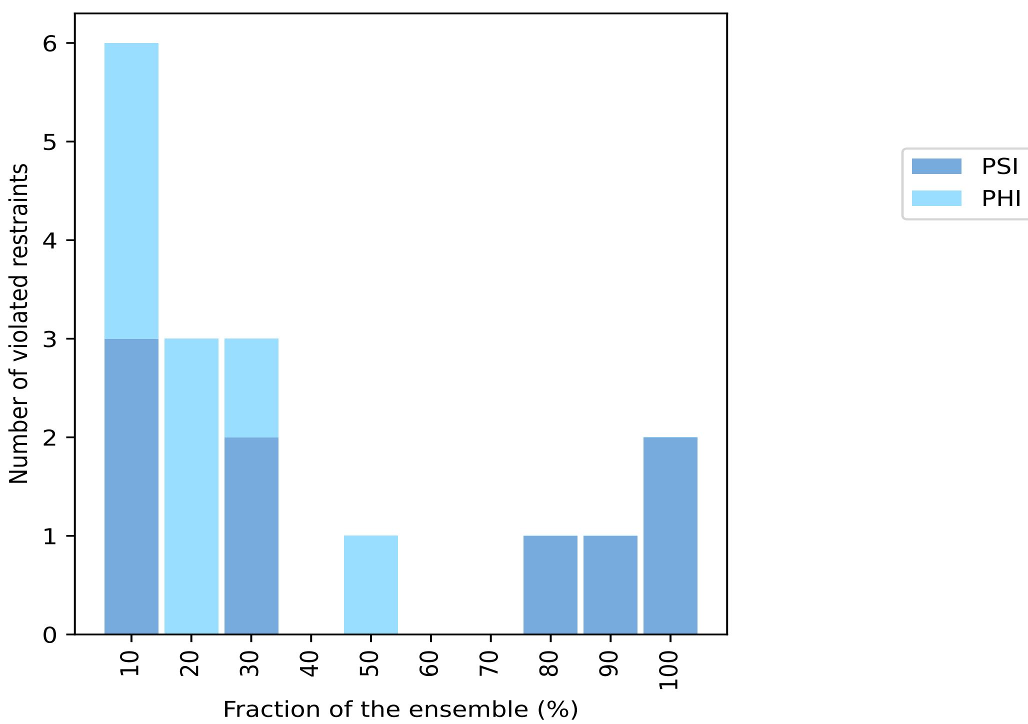
10.3 Dihedral-angle violation statistics for the ensemble (i)

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[1]	%
3	3	6	1	10.0
0	3	3	2	20.0
2	1	3	3	30.0
0	0	0	4	40.0
0	1	1	5	50.0
0	0	0	6	60.0
0	0	0	7	70.0
1	0	1	8	80.0
1	0	1	9	90.0
2	0	2	10	100.0

[1] Number of models with violations

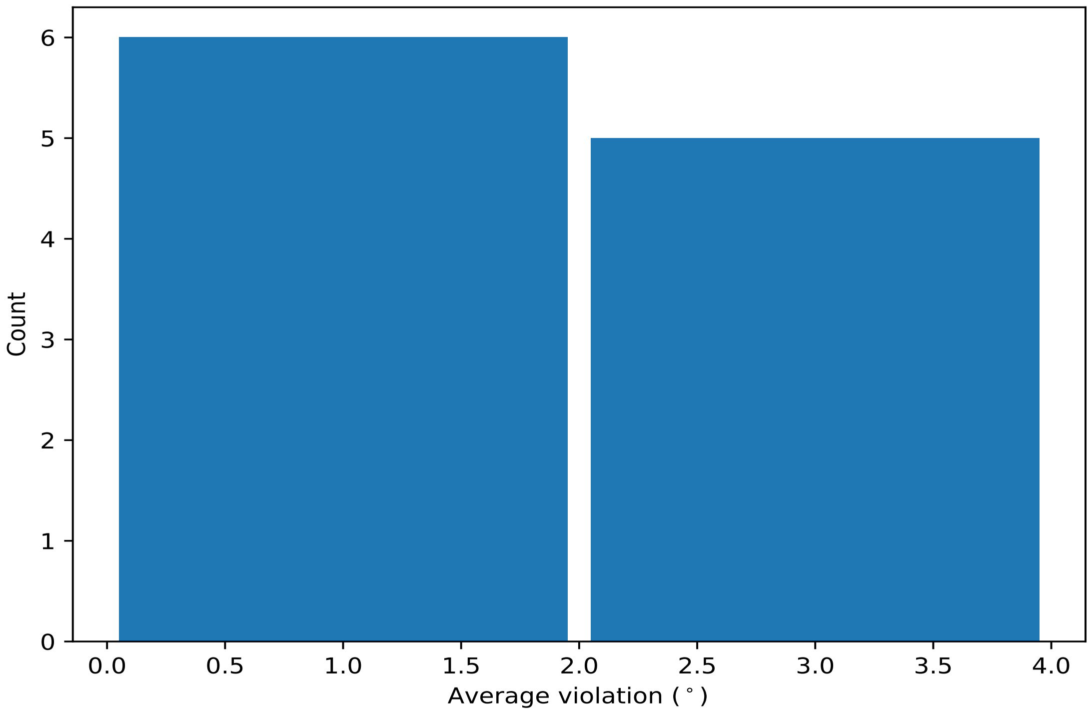
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble (i)



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.

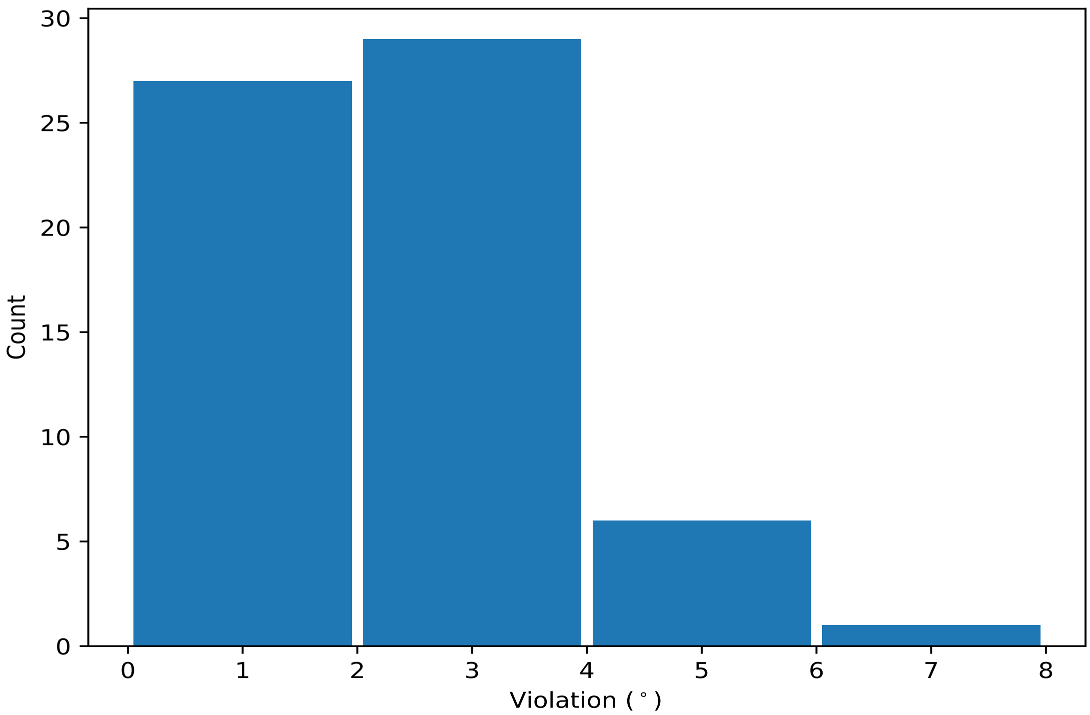
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,136)	1:A:47:LEU:N	1:A:47:LEU:CA	1:A:47:LEU:C	1:A:48:GLU:N	10	3.28	0.79	3.3
(1,110)	1:A:19:THR:N	1:A:19:THR:CA	1:A:19:THR:C	1:A:20:THR:N	10	3.0	0.79	3.45
(1,144)	1:A:58:VAL:N	1:A:58:VAL:CA	1:A:58:VAL:C	1:A:59:PRO:N	9	3.09	1.79	2.5
(1,175)	1:A:98:LYS:N	1:A:98:LYS:CA	1:A:98:LYS:C	1:A:99:THR:N	8	1.88	0.44	1.8
(1,78)	1:A:95:ALA:C	1:A:96:LYS:N	1:A:96:LYS:CA	1:A:96:LYS:C	5	2.94	1.08	3.3
(1,43)	1:A:48:GLU:C	1:A:49:HIS:N	1:A:49:HIS:CA	1:A:49:HIS:C	3	2.3	0.64	1.9
(1,112)	1:A:21:LYS:N	1:A:21:LYS:CA	1:A:21:LYS:C	1:A:22:ASP:N	3	1.93	0.62	2.1
(1,178)	1:A:101:THR:N	1:A:101:THR:CA	1:A:101:THR:C	1:A:102:SER:N	3	1.6	0.33	1.6
(1,18)	1:A:22:ASP:C	1:A:23:GLN:N	1:A:23:GLN:CA	1:A:23:GLN:C	2	1.55	0.05	1.55
(1,81)	1:A:98:LYS:C	1:A:99:THR:N	1:A:99:THR:CA	1:A:99:THR:C	2	1.25	0.05	1.25

[1] Number of violated models, [2]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 violationsfor 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 (°)
(1,144)	1:A:58:VAL:N	1:A:58:VAL:CA	1:A:58:VAL:C	1:A:59:PRO:N	6	7.0
(1,144)	1:A:58:VAL:N	1:A:58:VAL:CA	1:A:58:VAL:C	1:A:59:PRO:N	9	4.9
(1,78)	1:A:95:ALA:C	1:A:96:LYS:N	1:A:96:LYS:CA	1:A:96:LYS:C	1	4.4
(1,136)	1:A:47:LEU:N	1:A:47:LEU:CA	1:A:47:LEU:C	1:A:48:GLU:N	2	4.2
(1,136)	1:A:47:LEU:N	1:A:47:LEU:CA	1:A:47:LEU:C	1:A:48:GLU:N	4	4.2
(1,136)	1:A:47:LEU:N	1:A:47:LEU:CA	1:A:47:LEU:C	1:A:48:GLU:N	3	4.1
(1,144)	1:A:58:VAL:N	1:A:58:VAL:CA	1:A:58:VAL:C	1:A:59:PRO:N	10	4.0
(1,136)	1:A:47:LEU:N	1:A:47:LEU:CA	1:A:47:LEU:C	1:A:48:GLU:N	1	3.9
(1,110)	1:A:19:THR:N	1:A:19:THR:CA	1:A:19:THR:C	1:A:20:THR:N	2	3.7
(1,136)	1:A:47:LEU:N	1:A:47:LEU:CA	1:A:47:LEU:C	1:A:48:GLU:N	6	3.6