Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2KZ5
BMRB ID	:	16998
Title	:	Solution NMR Structure of Transcription factor NF-E2 subunit's DNA binding domain from Homo sapiens, Northeast Structural Genomics Consortium Target HR4653B
Authors	:	Liu, G.; Janjua, H.; Xiao, R.; Ciccosanti, C.; Shastry, R.; Acton, T.B.; Tong, S.; Everett, J.K.; Montelione, G.T.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2010-06-11

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *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 (i) 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 (i)) were used in the production of this report:

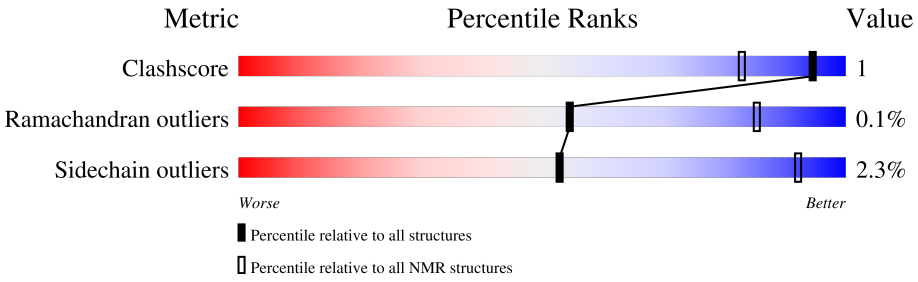
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal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

1 Overall quality at a glance

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

The overall completeness of chemical shifts assignment is 83%.

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	91	55% 45%

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 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:24-A:73 (50)	0.53	11

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 3 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 8, 11, 12, 13, 15, 16, 19, 20
2	7, 10
3	9, 17
Single-model clusters	14; 18

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1507 atoms, of which 765 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Transcription factor NF-E2 45 kDa subunit.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	91	1507	459	765	152	128	3	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q16621
A	2	GLY	-	expression tag	UNP Q16621
A	3	HIS	-	expression tag	UNP Q16621
A	4	HIS	-	expression tag	UNP Q16621
A	5	HIS	-	expression tag	UNP Q16621
A	6	HIS	-	expression tag	UNP Q16621
A	7	HIS	-	expression tag	UNP Q16621
A	8	HIS	-	expression tag	UNP Q16621
A	9	SER	-	expression tag	UNP Q16621
A	10	HIS	-	expression tag	UNP Q16621
A	11	MET	-	expression tag	UNP Q16621
A	81	TYR	CYS	conflict	UNP Q16621

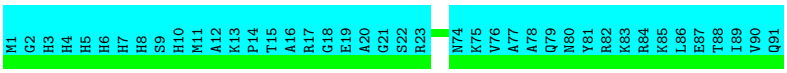
4 Residue-property plots

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: Transcription factor NF-E2 45 kDa subunit

Chain A:



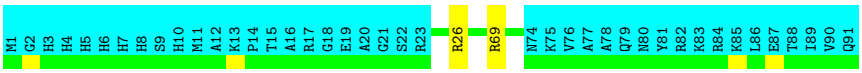
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

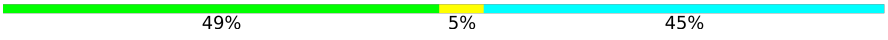
Chain A:

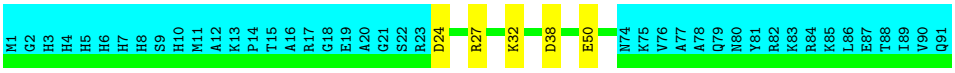


4.2.2 Score per residue for model 2

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

Chain A:

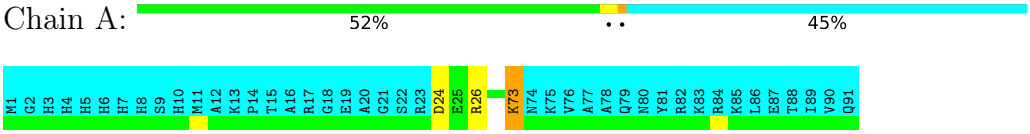




4.2.3 Score per residue for model 3

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

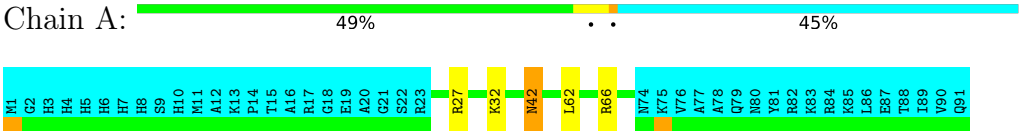
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

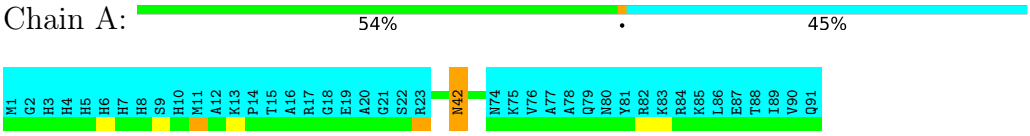
Chain A:



4.2.5 Score per residue for model 5

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

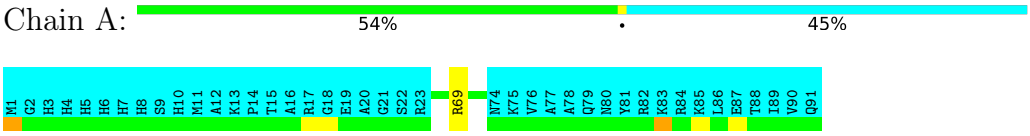
Chain A:



4.2.6 Score per residue for model 6

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

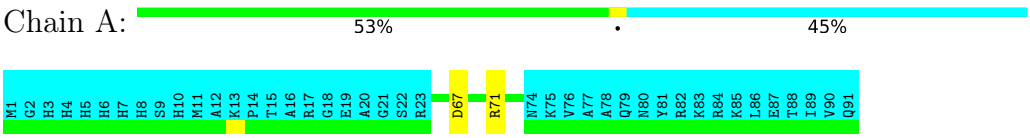
Chain A:



4.2.7 Score per residue for model 7

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

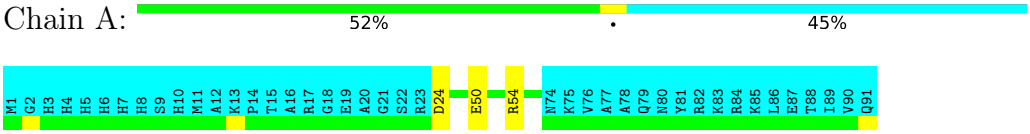
Chain A:



4.2.8 Score per residue for model 8

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

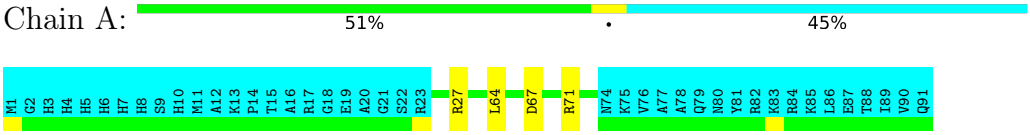
Chain A:



4.2.9 Score per residue for model 9

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

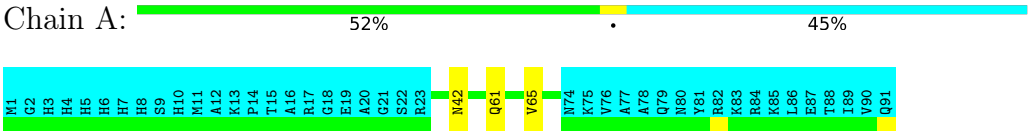
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

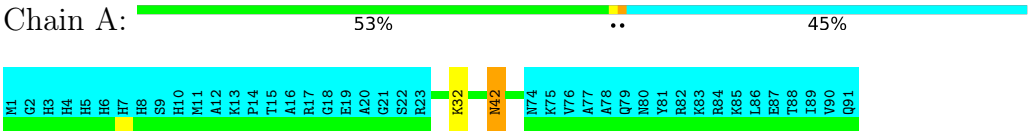
Chain A:



4.2.11 Score per residue for model 11 (medoid)

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

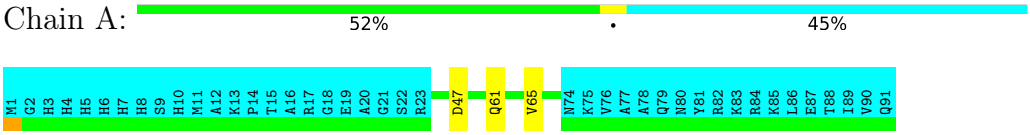
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

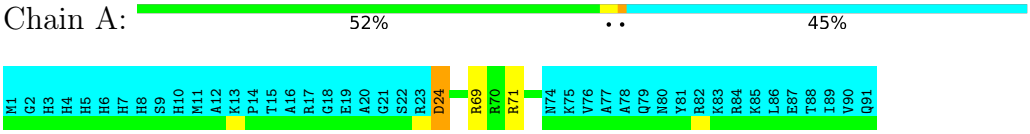
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

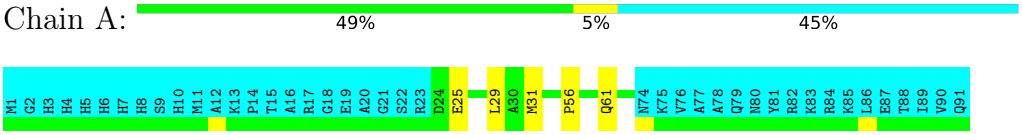
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

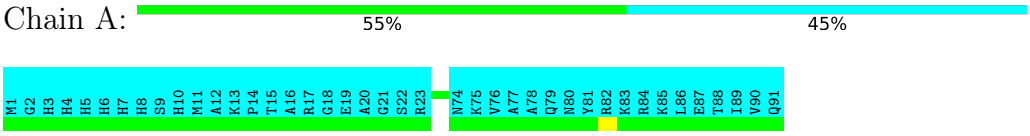
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

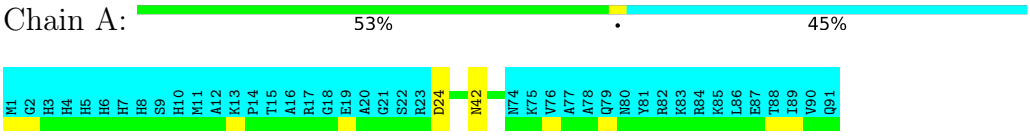
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

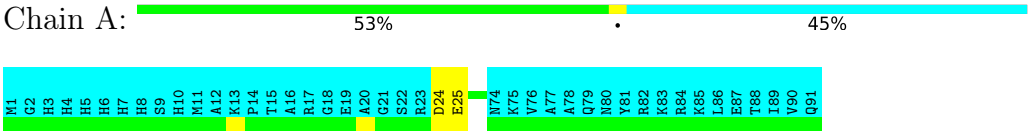
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

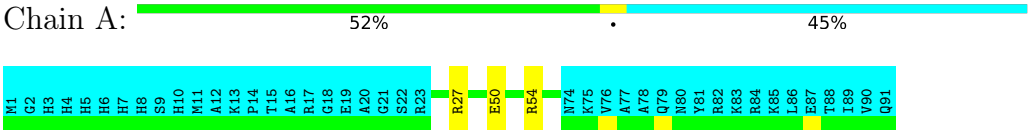
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

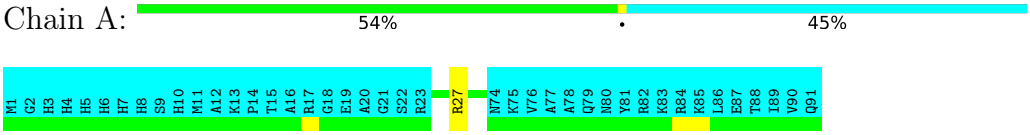
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

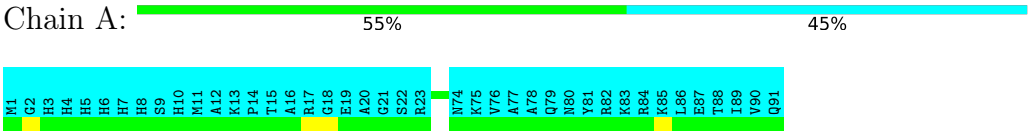
Chain A:



4.2.20 Score per residue for model 20

• Molecule 1: Transcription factor NF-E2 45 kDa subunit

Chain A:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry, simulated annealing, molecular dynamics, torsion angle dynamics.*

Of the 100 calculated structures, 20 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
CNS	refinement	
CNS	structure solution	
CNS	geometry optimization	
CYANA	refinement	3.0
CYANA	geometry optimization	3.0
CYANA	structure solution	3.0
TALOS+	geometry optimization	
PALES	geometry optimization	
REDCAT	geometry optimization	

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	956
Number of shifts mapped to atoms	956
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

6 Model quality

6.1 Standard geometry

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

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	411	431	431	1±1
All	All	8220	8620	8620	19

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:ASP:HB3	1:A:71:ARG:HH22	0.70	1.47	13	1
1:A:67:ASP:O	1:A:71:ARG:HG2	0.47	2.09	9	2
1:A:27:ARG:NE	1:A:27:ARG:HA	0.47	2.25	19	1
1:A:24:ASP:HA	1:A:27:ARG:HD3	0.45	1.87	2	1
1:A:32:LYS:HE2	1:A:32:LYS:HA	0.45	1.88	2	1
1:A:25:GLU:O	1:A:29:LEU:HG	0.45	2.11	14	1
1:A:73:LYS:HE2	1:A:73:LYS:HA	0.43	1.91	3	1
1:A:61:GLN:O	1:A:65:VAL:HG23	0.43	2.13	10	2
1:A:62:LEU:O	1:A:66:ARG:HG3	0.43	2.13	4	1
1:A:32:LYS:HB3	1:A:32:LYS:NZ	0.43	2.28	11	1
1:A:42:ASN:HD22	1:A:42:ASN:N	0.42	2.13	4	3
1:A:50:GLU:O	1:A:54:ARG:HG3	0.41	2.15	18	2
1:A:27:ARG:HB3	1:A:64:LEU:HD21	0.41	1.92	9	1
1:A:31:MET:HB3	1:A:61:GLN:HG2	0.41	1.91	14	1

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	50/91 (55%)	47±1 (94±2%)	3±1 (6±2%)	0±0 (0±0%)	54	85
All	All	1000/1820 (55%)	944 (94%)	55 (6%)	1 (0%)	54	85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	32	LYS	1

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	45/78 (58%)	44±1 (98±2%)	1±1 (2±2%)	53	92
All	All	900/1560 (58%)	879 (98%)	21 (2%)	53	92

All 9 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	24	ASP	5
1	A	42	ASN	5
1	A	69	ARG	3
1	A	26	ARG	2
1	A	27	ARG	2
1	A	38	ASP	1
1	A	50	GLU	1
1	A	73	LYS	1
1	A	47	ASP	1

6.3.3 RNA

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates

There are no monosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

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 83% for the well-defined parts and 72% 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

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	956
Number of shifts mapped to atoms	956
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	81	-0.01 ± 0.07	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	78	0.35 ± 0.07	None needed (< 0.5 ppm)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	75	0.02 ± 0.28	None needed (< 0.5 ppm)

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 83%, i.e. 622 atoms were assigned a chemical shift out of a possible 748. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	193/243 (79%)	97/97 (100%)	50/100 (50%)	46/46 (100%)
Sidechain	401/476 (84%)	273/307 (89%)	124/142 (87%)	4/27 (15%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	28/29 (97%)	14/14 (100%)	14/15 (93%)	0/0 (—%)
Overall	622/748 (83%)	384/418 (92%)	188/257 (73%)	50/73 (68%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 72%, i.e. 956 atoms were assigned a chemical shift out of a possible 1328. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	315/449 (70%)	159/181 (88%)	81/182 (45%)	75/86 (87%)
Sidechain	605/785 (77%)	411/506 (81%)	187/232 (81%)	7/47 (15%)
Aromatic	36/94 (38%)	18/46 (39%)	18/34 (53%)	0/14 (0%)
Overall	956/1328 (72%)	588/733 (80%)	286/448 (64%)	82/147 (56%)

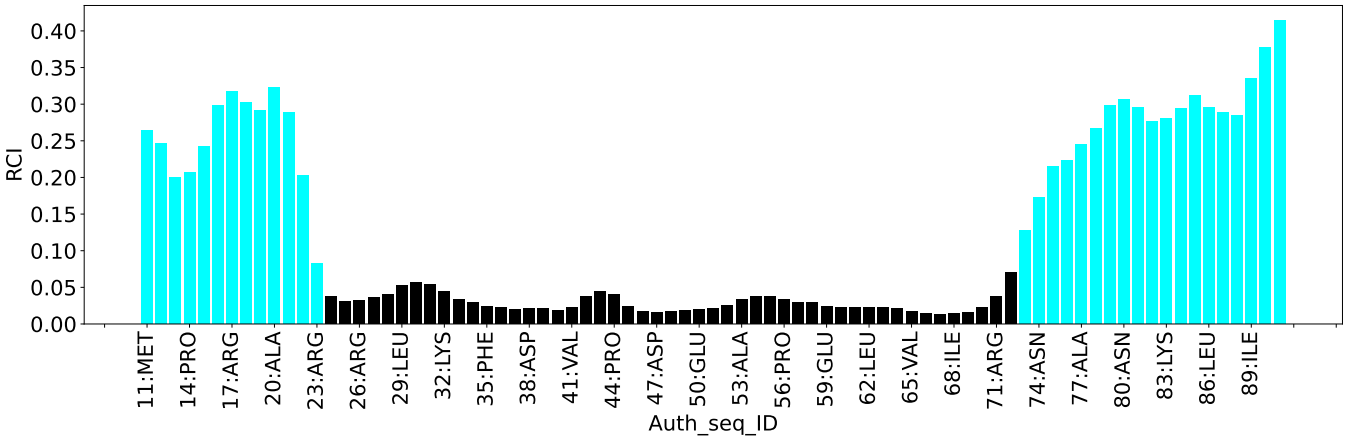
7.1.4 Statistically unusual chemical shifts (i)

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	2047
Intra-residue (|i-j|=0)	511
Sequential (|i-j|=1)	535
Medium range (|i-j|>1 and |i-j|<5)	579
Long range (|i-j|≥5)	422
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	78
Number of unmapped restraints	0
Number of restraints per residue	23.4
Number of long range restraints per residue[1]	4.6

[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

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)	0.1	0.13
0.2-0.5 (Medium)	None	None
>0.5 (Large)	None	None

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)	0.1	1.9
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis (i)

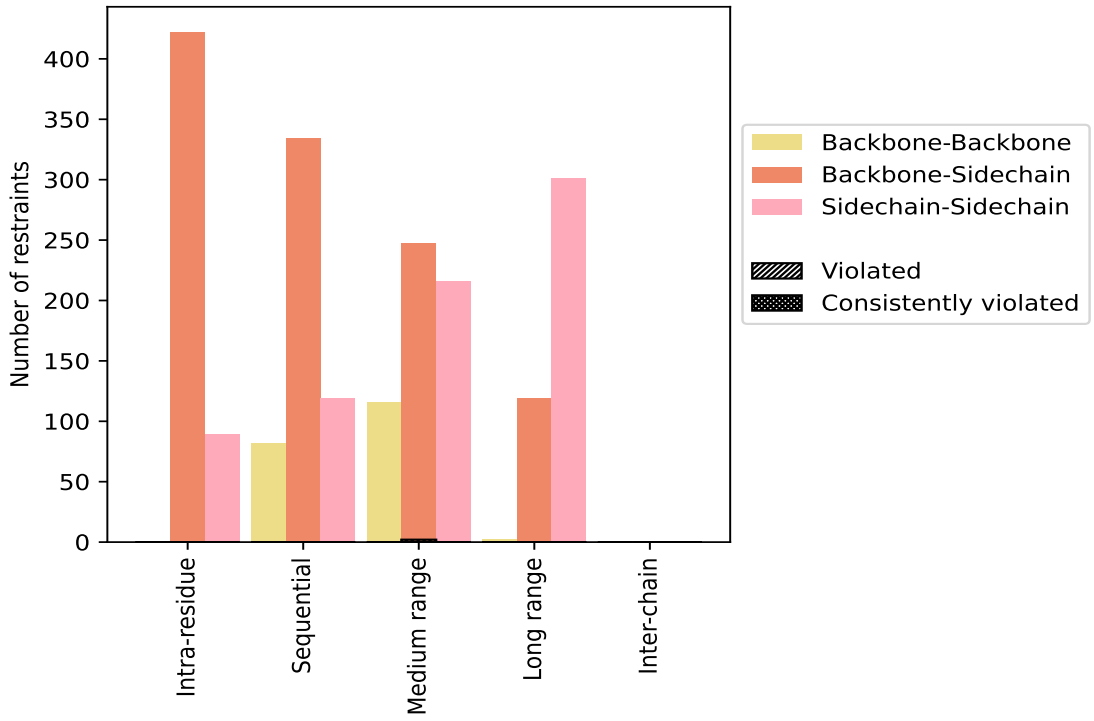
9.1 Summary of distance violations (i)

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)	511	25.0	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	422	20.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	89	4.3	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	535	26.1	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	82	4.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	334	16.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	119	5.8	0	0.0	0.0	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	579	28.3	2	0.3	0.1	0	0.0	0.0
Backbone-Backbone	116	5.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	247	12.1	2	0.8	0.1	0	0.0	0.0
Sidechain-Sidechain	216	10.6	0	0.0	0.0	0	0.0	0.0
Long range (|i-j|≥5)	422	20.6	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	2	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	119	5.8	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	301	14.7	0	0.0	0.0	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	2047	100.0	2	0.1	0.1	0	0.0	0.0
Backbone-Backbone	200	9.8	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	1122	54.8	2	0.2	0.1	0	0.0	0.0
Sidechain-Sidechain	725	35.4	0	0.0	0.0	0	0.0	0.0

[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



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

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	0	0	0	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0	0	0	0.0	0.0	0.0	0.0
3	0	0	0	0	0	0	0.0	0.0	0.0	0.0
4	0	0	1	0	0	1	0.13	0.13	0.0	0.13
5	0	0	0	0	0	0	0.0	0.0	0.0	0.0
6	0	0	0	0	0	0	0.0	0.0	0.0	0.0
7	0	0	0	0	0	0	0.0	0.0	0.0	0.0
8	0	0	0	0	0	0	0.0	0.0	0.0	0.0
9	0	0	0	0	0	0	0.0	0.0	0.0	0.0
10	0	0	0	0	0	0	0.0	0.0	0.0	0.0
11	0	0	0	0	0	0	0.0	0.0	0.0	0.0

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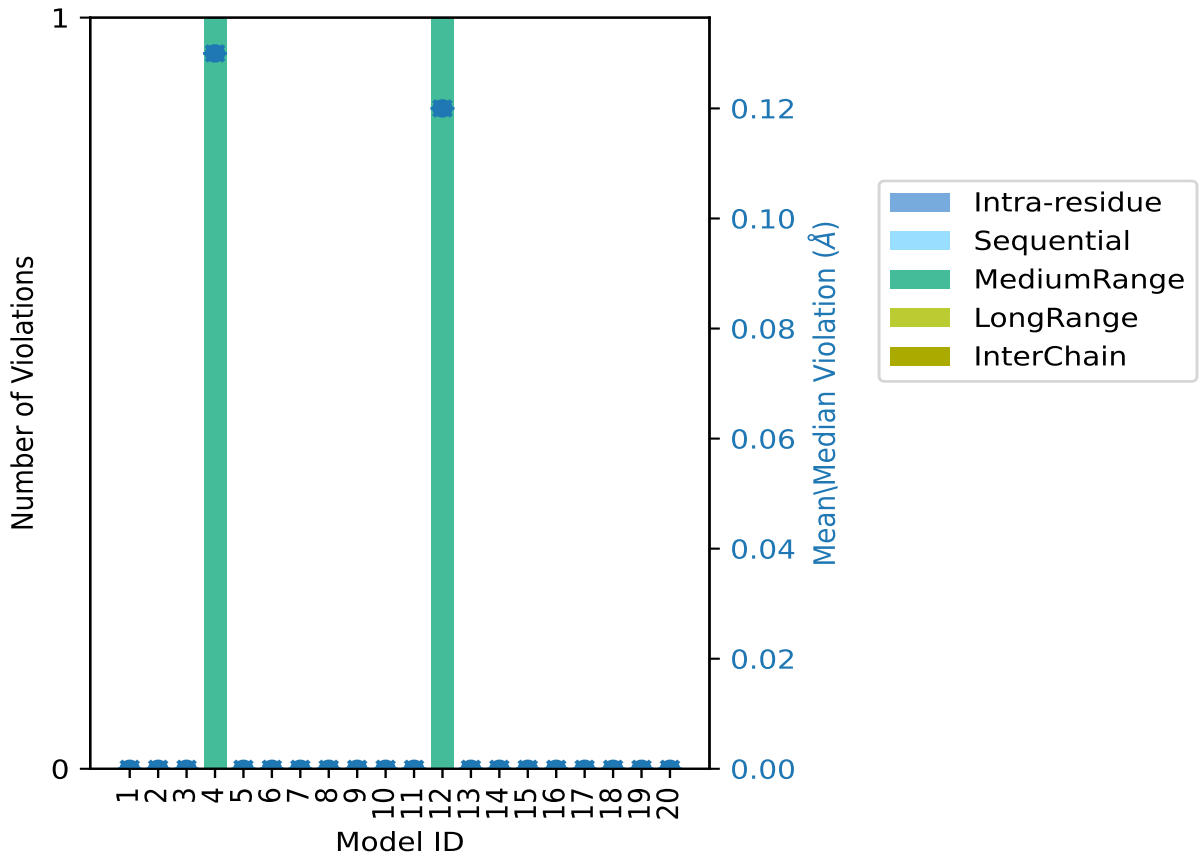
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	0	0	1	0	0	1	0.12	0.12	0.0	0.12
13	0	0	0	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	0	0	0	0.0	0.0	0.0	0.0
15	0	0	0	0	0	0	0.0	0.0	0.0	0.0
16	0	0	0	0	0	0	0.0	0.0	0.0	0.0
17	0	0	0	0	0	0	0.0	0.0	0.0	0.0
18	0	0	0	0	0	0	0.0	0.0	0.0	0.0
19	0	0	0	0	0	0	0.0	0.0	0.0	0.0
20	0	0	0	0	0	0	0.0	0.0	0.0	0.0

[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



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

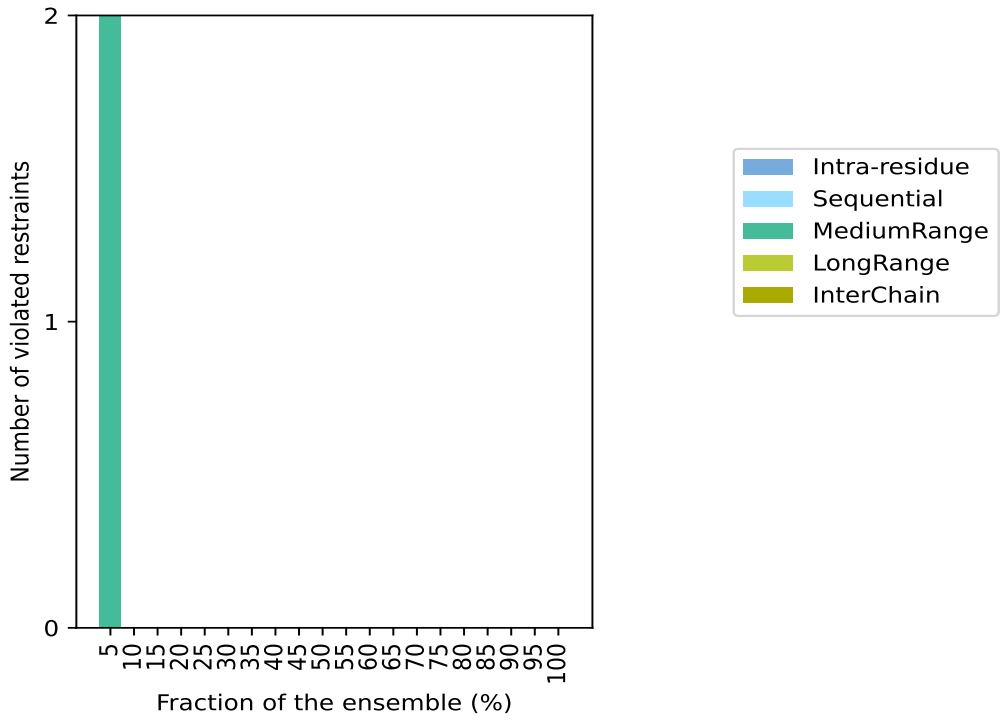
9.3 Distance violation statistics for the ensemble (i)

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, 2045(IR:511, SQ:535, MR:577, LR:422, 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]	%
0	0	2	0	0	2	1	5.0
0	0	0	0	0	0	2	10.0
0	0	0	0	0	0	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	7	35.0
0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	20	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



9.4 Most violated distance restraints in the ensemble

No violations found

9.5 All violated distance restraints

9.5.1 Histogram : Distribution of distance violations

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

9.5.2 Table : All distance violations

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)
(1,1120)	1:A:67:ASP:HA	1:A:70:ARG:HB2	4	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,609)	1:A:44:PRO:HG3	1:A:47:ASP:H	12	0.12

10 Dihedral-angle violation analysis

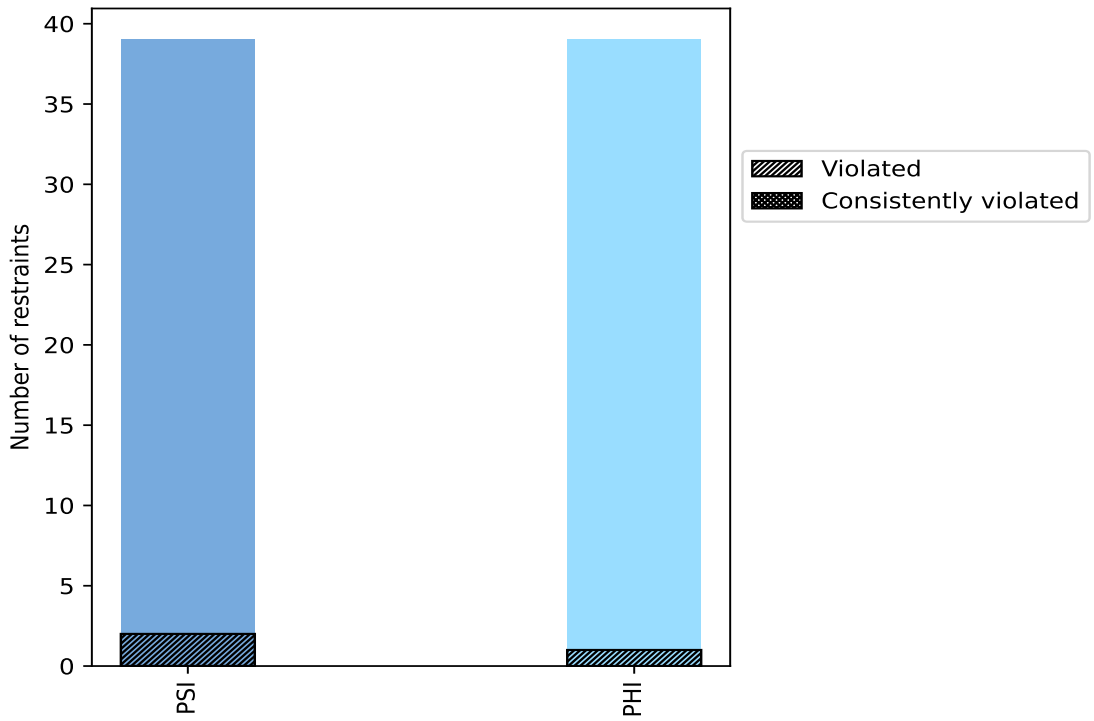
10.1 Summary of dihedral-angle violations

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	39	50.0	2	5.1	2.6	0	0.0	0.0
PHI	39	50.0	1	2.6	1.3	0	0.0	0.0
Total	78	100.0	3	3.8	3.8	0	0.0	0.0

[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



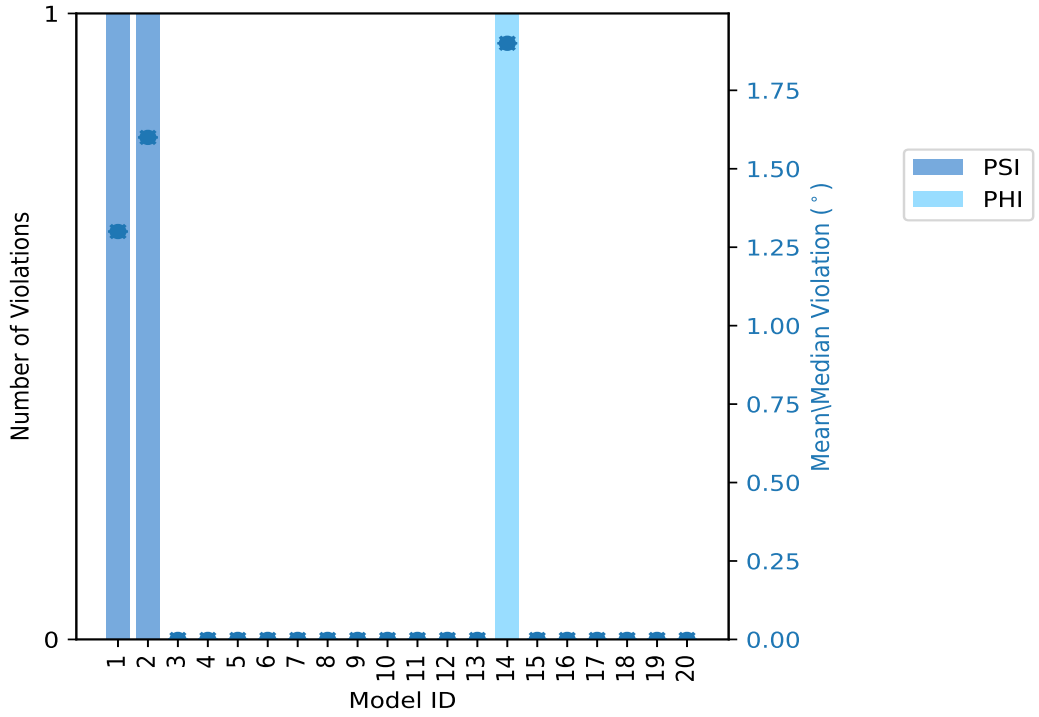
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	1	0	1	1.3	1.3	0.0	1.3
2	1	0	1	1.6	1.6	0.0	1.6
3	0	0	0	0.0	0.0	0.0	0.0
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	0	0	0.0	0.0	0.0	0.0
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
11	0	0	0	0.0	0.0	0.0	0.0
12	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0.0	0.0	0.0	0.0
14	0	1	1	1.9	1.9	0.0	1.9
15	0	0	0	0.0	0.0	0.0	0.0
16	0	0	0	0.0	0.0	0.0	0.0
17	0	0	0	0.0	0.0	0.0	0.0
18	0	0	0	0.0	0.0	0.0	0.0
19	0	0	0	0.0	0.0	0.0	0.0
20	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[1]	%
2	1	3	1	5.0
0	0	0	2	10.0
0	0	0	3	15.0
0	0	0	4	20.0
0	0	0	5	25.0
0	0	0	6	30.0
0	0	0	7	35.0
0	0	0	8	40.0
0	0	0	9	45.0
0	0	0	10	50.0
0	0	0	11	55.0

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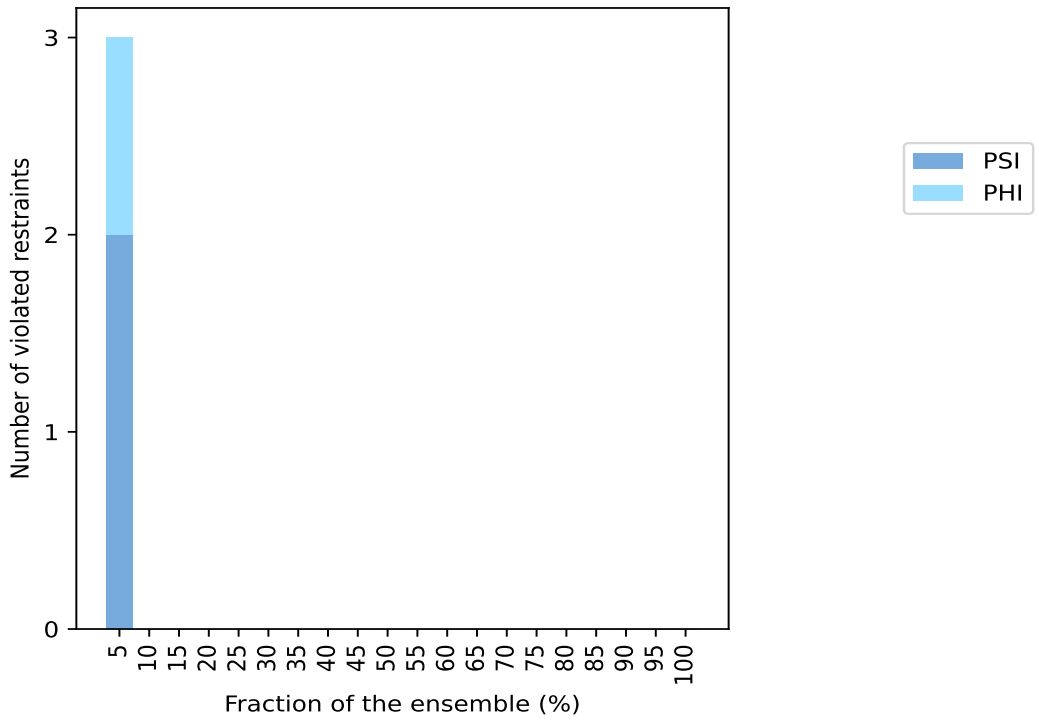
Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count[1]	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

[1] Number of models with violations

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



10.4 Most violated dihedral-angle restraints in the ensemble

No violations found

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 (°)
(1,47)	1:A:52:LEU:C	1:A:53:ALA:N	1:A:53:ALA:CA	1:A:53:ALA:C	14	1.9
(1,34)	1:A:46:ASP:N	1:A:46:ASP:CA	1:A:46:ASP:C	1:A:47:ASP:N	2	1.6
(1,16)	1:A:30:ALA:N	1:A:30:ALA:CA	1:A:30:ALA:C	1:A:31:MET:N	1	1.3