



wwPDB NMR Structure Validation Summary Report ⓘ

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BMRB ID : 17827
Title : NMR structure for Kindle-2 N-terminus
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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>.

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

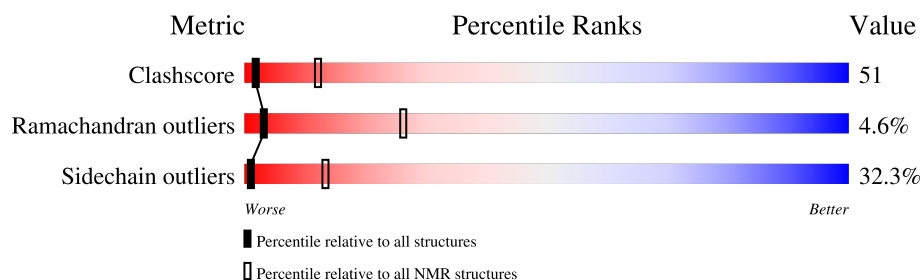
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 78%.

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 ≥ 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	112	

2 Ensemble composition and analysis

This entry contains 20 models. Model 9 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:18-A:51, A:61-A:94 (68)	0.34	9

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 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1529 atoms, of which 763 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Fermitin family homolog 2.

Mol	Chain	Residues	Atoms						Trace
1	A	94	Total	C	H	N	O	S	0
			1529	493	763	132	137	4	

There are 8 discrepancies between the modelled and reference sequences:

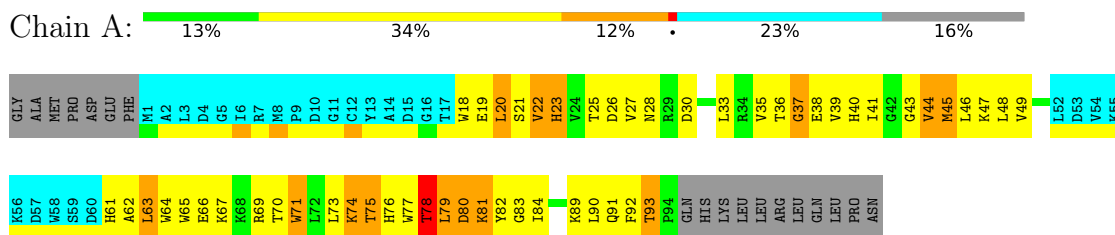
Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP Q96AC1
A	-5	ALA	-	expression tag	UNP Q96AC1
A	-4	MET	-	expression tag	UNP Q96AC1
A	-3	PRO	-	expression tag	UNP Q96AC1
A	-2	ASP	-	expression tag	UNP Q96AC1
A	-1	GLU	-	expression tag	UNP Q96AC1
A	0	PHE	-	expression tag	UNP Q96AC1
A	27	VAL	LEU	conflict	UNP Q96AC1

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.

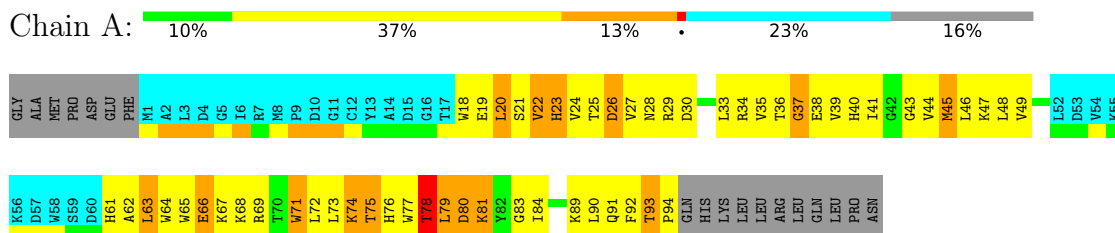
- Molecule 1: Fermitin family homolog 2



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

The representative model is number 9. Colouring as in section 4.1 above.

- Molecule 1: Fermitin family homolog 2



5 Refinement protocol and experimental data overview

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

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
X-PLOR NIH	structure solution	
TALOS	geometry optimization	
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	1088
Number of shifts mapped to atoms	1004
Number of unparsed shifts	0
Number of shifts with mapping errors	84
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

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	1.49±0.01	0±0/584 (0.0± 0.0%)	1.27±0.01	0±0/794 (0.0± 0.0%)
All	All	1.49	1/11680 (0.0%)	1.27	3/15880 (0.0%)

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	92	PHE	C-N	-5.61	1.26	1.33	19	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	42	GLY	N-CA-C	-6.57	107.17	115.31	13	2
1	A	83	GLY	N-CA-C	-5.37	107.12	115.67	8	1

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	568	578	578	58±6
All	All	11360	11560	11560	1165

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 51.

5 of 196 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:HIS:O	1:A:92:PHE:N	0.90	2.05	14	20
1:A:79:LEU:HD22	1:A:79:LEU:H	0.87	1.29	11	4
1:A:41:ILE:HD11	1:A:77:TRP:O	0.83	1.74	6	20
1:A:41:ILE:HD12	1:A:74:LYS:O	0.82	1.75	17	20
1:A:45:MET:O	1:A:49:VAL:HG23	0.81	1.76	9	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	67/112 (60%)	55±1 (83±2%)	9±1 (13±1%)	3±1 (5±1%)	3	26
All	All	1340/2240 (60%)	1107 (83%)	172 (13%)	61 (5%)	3	26

5 of 8 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	37	GLY	17
1	A	78	THR	16
1	A	76	HIS	12
1	A	26	ASP	5
1	A	35	VAL	4

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	61/98 (62%)	41±2 (68±4%)	20±2 (32±4%)	1	13
All	All	1220/1960 (62%)	826 (68%)	394 (32%)	1	13

5 of 39 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	20	LEU	20
1	A	22	VAL	20
1	A	23	HIS	20
1	A	30	ASP	20
1	A	45	MET	20

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

The completeness of assignment taking into account all chemical shift lists is 78% for the well-defined parts and 76% 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	1088
Number of shifts mapped to atoms	1004
Number of unparsed shifts	0
Number of shifts with mapping errors	84
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	8

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. First 5 (of 84) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	96	HIS	HA	4.358	0.03	1
1	A	96	HIS	HB2	2.984	0.03	1
1	A	96	HIS	C	174.808	0.50	1
1	A	96	HIS	CA	56.595	0.50	1
1	A	96	HIS	CB	29.646	0.50	1
1	A	97	LYS	H	7.985	0.03	1
1	A	97	LYS	C	176.22	0.50	1
1	A	97	LYS	CA	56.386	0.50	1
1	A	97	LYS	CB	32.442	0.50	1
1	A	97	LYS	CD	28.488	0.50	1
1	A	97	LYS	CE	41.584	0.50	1
1	A	97	LYS	CG	24.241	0.50	1
1	A	97	LYS	N	120.773	0.25	1
1	A	98	LEU	H	8.062	0.03	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	98	LEU	C	176.953	0.50	1
1	A	98	LEU	CA	55.061	0.50	1
1	A	98	LEU	CB	43.761	0.50	1
1	A	98	LEU	N	122.256	0.25	1
1	A	99	LEU	H	8.013	0.03	1
1	A	99	LEU	HA	4.206	0.03	1
1	A	99	LEU	HB2	1.46	0.03	1
1	A	99	LEU	HB3	1.51	0.03	1
1	A	99	LEU	HD11	0.72	0.03	1
1	A	99	LEU	HD12	0.72	0.03	1
1	A	99	LEU	HD13	0.72	0.03	1
1	A	99	LEU	HG	1.45	0.03	1
1	A	99	LEU	C	176.94	0.50	1
1	A	99	LEU	CA	54.95	0.50	1
1	A	99	LEU	CB	42.04	0.50	1
1	A	99	LEU	CD1	23.47	0.50	1
1	A	99	LEU	CG	26.77	0.50	1
1	A	99	LEU	N	123.01	0.25	1
1	A	100	ARG	H	8.091	0.03	1
1	A	100	ARG	HA	4.205	0.03	1
1	A	100	ARG	HB2	1.65	0.03	1
1	A	100	ARG	HB3	1.723	0.03	1
1	A	100	ARG	HD2	3.065	0.03	1
1	A	100	ARG	C	175.772	0.50	1
1	A	100	ARG	CA	55.62	0.50	1
1	A	100	ARG	CB	30.1	0.50	1
1	A	100	ARG	CD	43.15	0.50	1
1	A	100	ARG	N	121.353	0.25	1
1	A	101	LEU	H	8.032	0.03	1
1	A	101	LEU	HA	4.21	0.03	1
1	A	101	LEU	HB2	1.5	0.03	1
1	A	101	LEU	HB3	1.45	0.03	1
1	A	101	LEU	HD11	0.83	0.03	1
1	A	101	LEU	HD12	0.83	0.03	1
1	A	101	LEU	HD13	0.83	0.03	1
1	A	101	LEU	HD21	0.83	0.03	1
1	A	101	LEU	HD22	0.83	0.03	1
1	A	101	LEU	HD23	0.83	0.03	1
1	A	101	LEU	HG	1.45	0.03	1
1	A	101	LEU	C	176.744	0.50	1
1	A	101	LEU	CA	55.18	0.50	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	101	LEU	CB	42.03	0.50	1
1	A	101	LEU	CD1	23.13	0.50	1
1	A	101	LEU	CD2	24.52	0.50	1
1	A	101	LEU	CG	26.74	0.50	1
1	A	101	LEU	N	122.712	0.25	1
1	A	102	GLN	H	8.21	0.03	1
1	A	102	GLN	HA	4.28	0.03	1
1	A	102	GLN	HB2	1.9	0.03	1
1	A	102	GLN	HB3	2.0	0.03	1
1	A	102	GLN	HG2	2.255	0.03	1
1	A	102	GLN	C	175.167	0.50	1
1	A	102	GLN	CA	55.31	0.50	1
1	A	102	GLN	CB	29.2	0.50	1
1	A	102	GLN	CG	33.46	0.50	1
1	A	102	GLN	N	121.063	0.25	1
1	A	103	LEU	H	8.183	0.03	1
1	A	103	LEU	HA	4.54	0.03	1
1	A	103	LEU	HB2	1.57	0.03	1
1	A	103	LEU	HD11	0.85	0.03	1
1	A	103	LEU	HD12	0.85	0.03	1
1	A	103	LEU	HD13	0.85	0.03	1
1	A	103	LEU	HD21	0.85	0.03	1
1	A	103	LEU	HD22	0.85	0.03	1
1	A	103	LEU	HD23	0.85	0.03	1
1	A	103	LEU	C	174.815	0.50	1
1	A	103	LEU	CA	52.8	0.50	1
1	A	103	LEU	CB	41.55	0.50	1
1	A	103	LEU	CD2	22.86	0.50	1
1	A	103	LEU	N	125.202	0.25	1

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	93	0.19 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	91	0.36 ± 0.22	None needed (< 0.5 ppm)
$^{13}\text{C}'$	96	0.13 ± 0.22	None needed (< 0.5 ppm)
^{15}N	95	0.38 ± 0.31	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 78%, i.e. 781 atoms were assigned a chemical shift out of a possible 997. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	325/342 (95%)	132/139 (95%)	127/136 (93%)	66/67 (99%)
Sidechain	444/548 (81%)	291/358 (81%)	151/171 (88%)	2/19 (11%)
Aromatic	12/107 (11%)	7/55 (13%)	0/43 (0%)	5/9 (56%)
Overall	781/997 (78%)	430/552 (78%)	278/350 (79%)	73/95 (77%)

7.1.4 Statistically unusual chemical shifts [i](#)

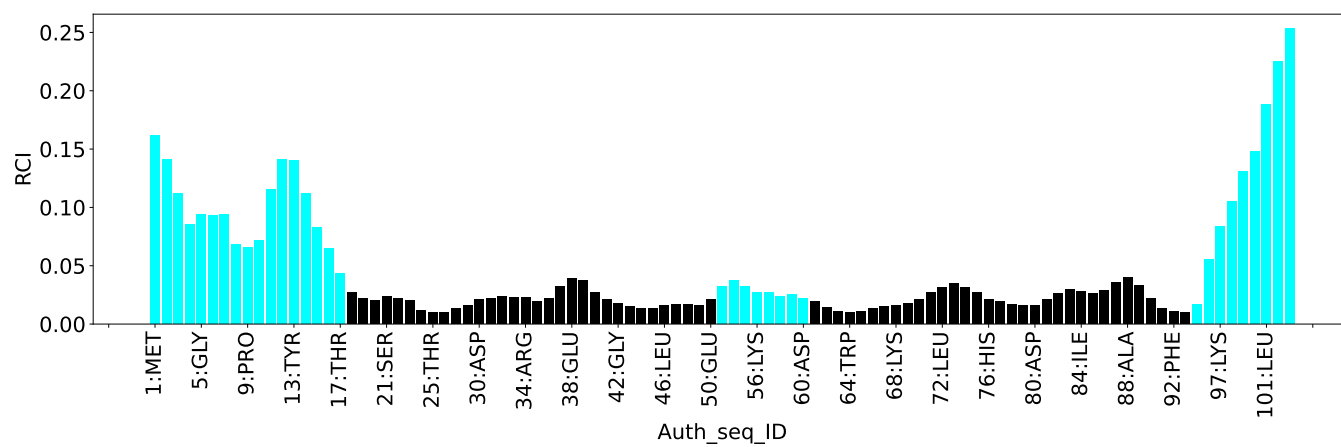
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	74	LYS	HD3	0.10	0.54 – 2.65	-7.1
1	A	41	ILE	CG2	9.20	10.93 – 24.12	-6.3
1	A	35	VAL	HG21	-0.87	-0.58 – 2.19	-6.0
1	A	35	VAL	HG22	-0.87	-0.58 – 2.19	-6.0
1	A	35	VAL	HG23	-0.87	-0.58 – 2.19	-6.0
1	A	68	LYS	HG2	-0.12	0.13 – 2.61	-6.0
1	A	68	LYS	HG3	-0.05	0.04 – 2.67	-5.3
1	A	74	LYS	HD2	0.57	0.58 – 2.64	-5.0

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	1459
Intra-residue ($ i-j =0$)	447
Sequential ($ i-j =1$)	436
Medium range ($ i-j >1$ and $ i-j <5$)	224
Long range ($ i-j \geq 5$)	327
Inter-chain	0
Hydrogen bond restraints	25
Disulfide bond restraints	0
Total dihedral-angle restraints	108
Number of unmapped restraints	0
Number of restraints per residue	14.0
Number of long range restraints per residue ¹	3.0

¹Long 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)	150.1	0.2
0.2-0.5 (Medium)	61.0	0.49
>0.5 (Large)	1.9	0.89

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)	14.8	9.19
10.0-20.0 (Medium)	0.1	11.3
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

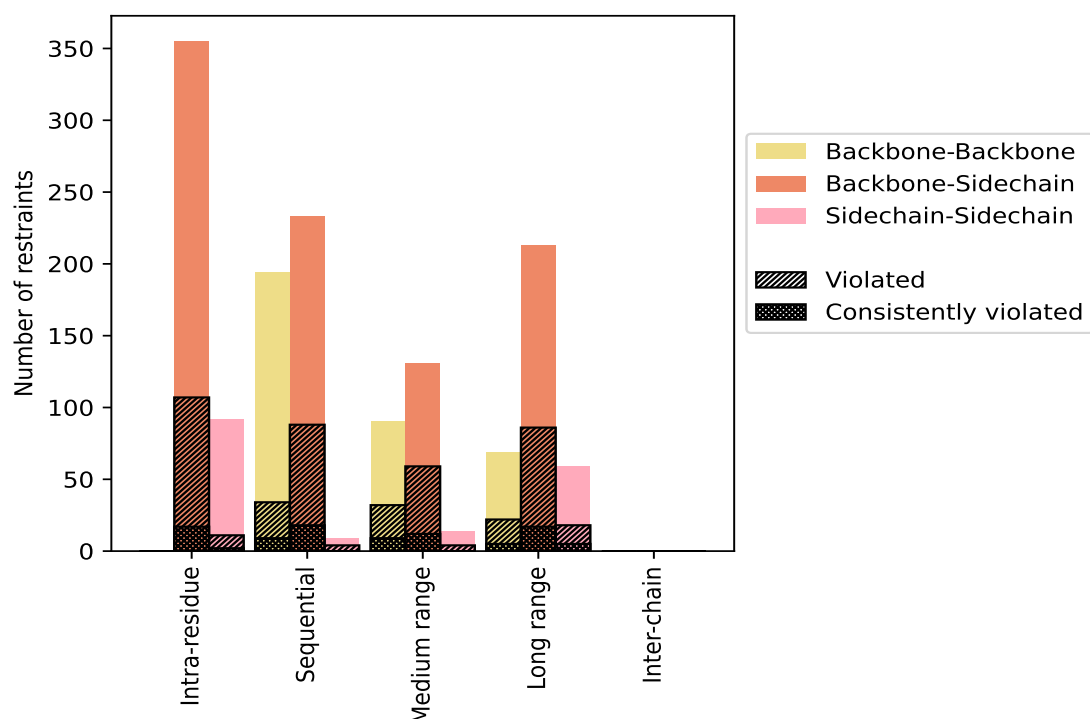
9.1 Summary of distance violations ⓘ

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	447	30.6	118	26.4	8.1	19	4.3	1.3
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	355	24.3	107	30.1	7.3	17	4.8	1.2
Sidechain-Sidechain	92	6.3	11	12.0	0.8	2	2.2	0.1
Sequential (i-j =1)	436	29.9	126	28.9	8.6	27	6.2	1.9
Backbone-Backbone	194	13.3	34	17.5	2.3	9	4.6	0.6
Backbone-Sidechain	233	16.0	88	37.8	6.0	18	7.7	1.2
Sidechain-Sidechain	9	0.6	4	44.4	0.3	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	224	15.4	92	41.1	6.3	20	8.9	1.4
Backbone-Backbone	90	6.2	32	35.6	2.2	9	10.0	0.6
Backbone-Sidechain	120	8.2	56	46.7	3.8	11	9.2	0.8
Sidechain-Sidechain	14	1.0	4	28.6	0.3	0	0.0	0.0
Long range (i-j ≥5)	327	22.4	121	37.0	8.3	27	8.3	1.9
Backbone-Backbone	69	4.7	22	31.9	1.5	5	7.2	0.3
Backbone-Sidechain	199	13.6	81	40.7	5.6	17	8.5	1.2
Sidechain-Sidechain	59	4.0	18	30.5	1.2	5	8.5	0.3
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	25	1.7	8	32.0	0.5	1	4.0	0.1
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1459	100.0	465	31.9	31.9	94	6.4	6.4
Backbone-Backbone	353	24.2	88	24.9	6.0	23	6.5	1.6
Backbone-Sidechain	932	63.9	340	36.5	23.3	64	6.9	4.4
Sidechain-Sidechain	174	11.9	37	21.3	2.5	7	4.0	0.5

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	43	60	44	62	0	209	0.18	0.61	0.06	0.17
2	49	61	43	65	0	218	0.18	0.58	0.06	0.17
3	47	56	40	68	0	211	0.18	0.61	0.07	0.17
4	48	54	49	59	0	210	0.18	0.78	0.07	0.18
5	46	63	43	67	0	219	0.18	0.48	0.06	0.18
6	46	64	44	71	0	225	0.18	0.56	0.07	0.17
7	41	63	49	72	0	225	0.18	0.82	0.07	0.16
8	48	60	45	72	0	225	0.18	0.57	0.06	0.17
9	44	64	45	64	0	217	0.18	0.77	0.07	0.17
10	45	59	51	70	0	225	0.18	0.57	0.07	0.17

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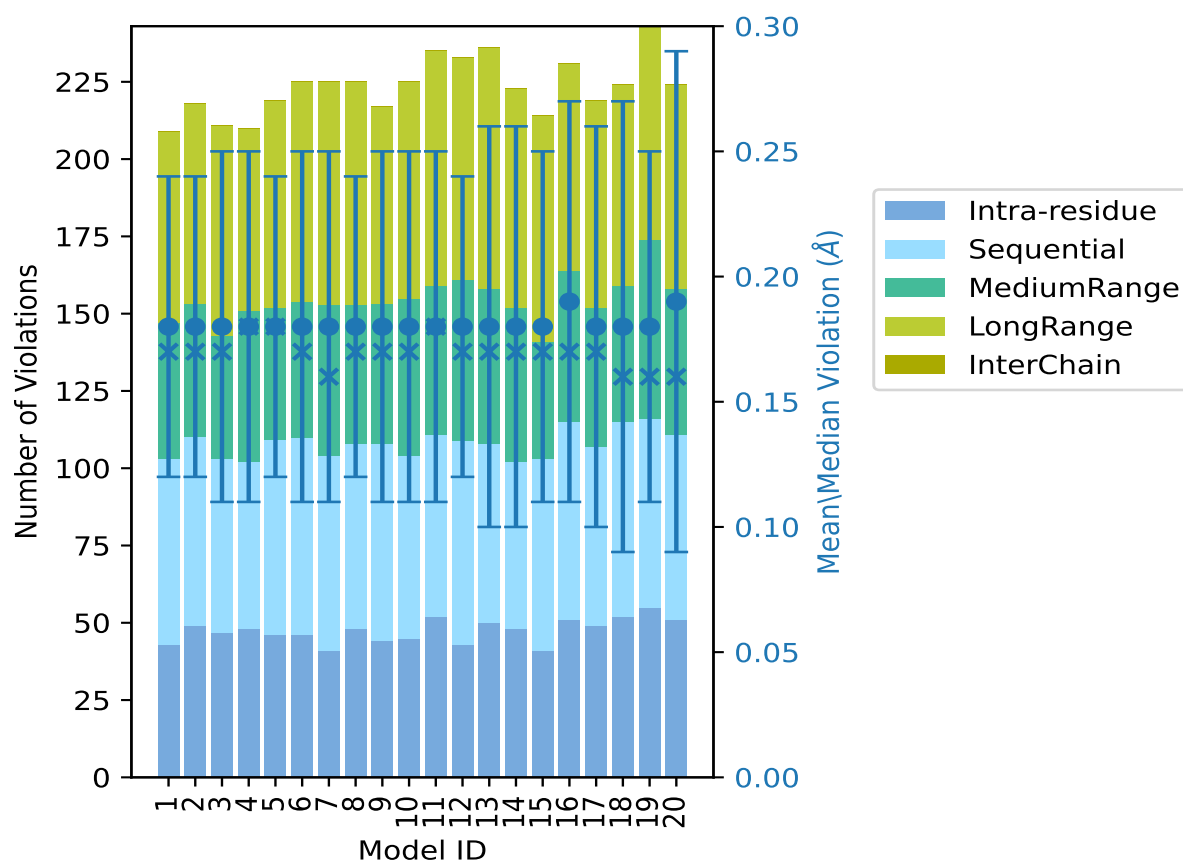
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	52	59	48	76	0	235	0.18	0.61	0.07	0.18
12	43	66	52	72	0	233	0.18	0.41	0.06	0.17
13	50	58	50	78	0	236	0.18	0.78	0.08	0.17
14	48	54	50	71	0	223	0.18	0.85	0.08	0.17
15	41	62	38	73	0	214	0.18	0.59	0.07	0.17
16	51	64	49	67	0	231	0.19	0.77	0.08	0.17
17	49	58	45	67	0	219	0.18	0.65	0.08	0.17
18	52	63	44	65	0	224	0.18	0.77	0.09	0.16
19	55	61	58	69	0	243	0.18	0.56	0.07	0.16
20	51	60	47	66	0	224	0.19	0.89	0.1	0.16

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

⁵Inter-chain restraints, ⁶Standard 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

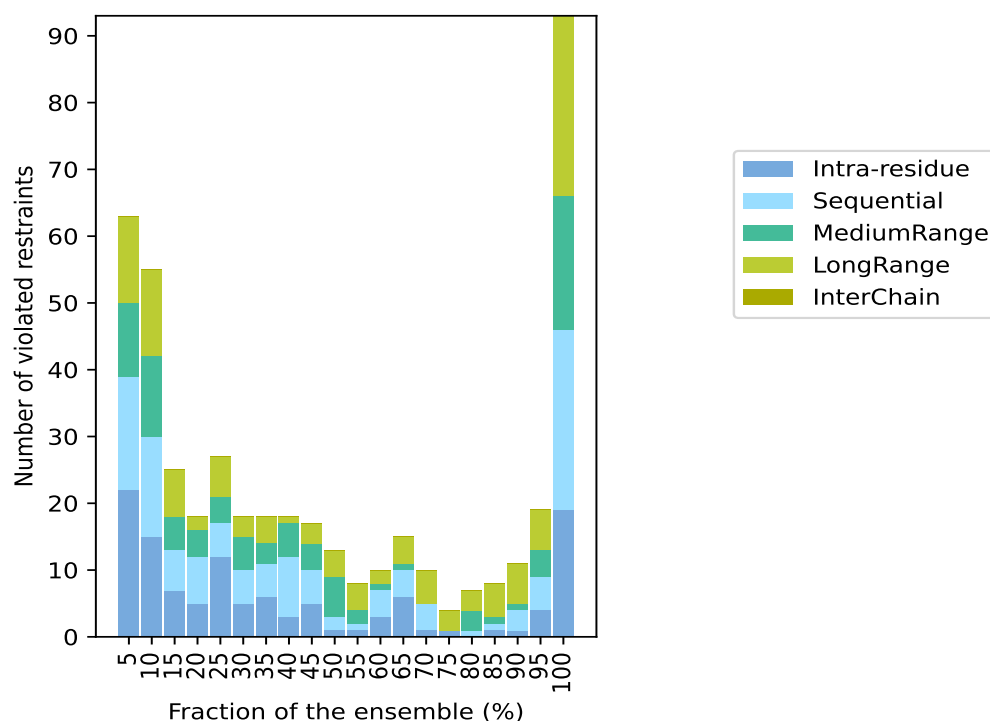
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 977(IR:329, SQ:310, MR:132, LR:206, IC:0) restraints are 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	%
22	17	11	13	0	63	1	5.0
15	15	12	13	0	55	2	10.0
7	6	5	7	0	25	3	15.0
5	7	4	2	0	18	4	20.0
12	5	4	6	0	27	5	25.0
5	5	5	3	0	18	6	30.0
6	5	3	4	0	18	7	35.0
3	9	5	1	0	18	8	40.0
5	5	4	3	0	17	9	45.0
1	2	6	4	0	13	10	50.0
1	1	2	4	0	8	11	55.0
3	4	1	2	0	10	12	60.0
6	4	1	4	0	15	13	65.0
1	4	0	5	0	10	14	70.0
1	0	0	3	0	4	15	75.0
0	1	3	3	0	7	16	80.0
1	1	1	5	0	8	17	85.0
1	3	1	6	0	11	18	90.0
4	5	4	6	0	19	19	95.0
19	27	20	27	0	93	20	100.0

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

⁵Inter-chain restraints, ⁶ Number of models with violations

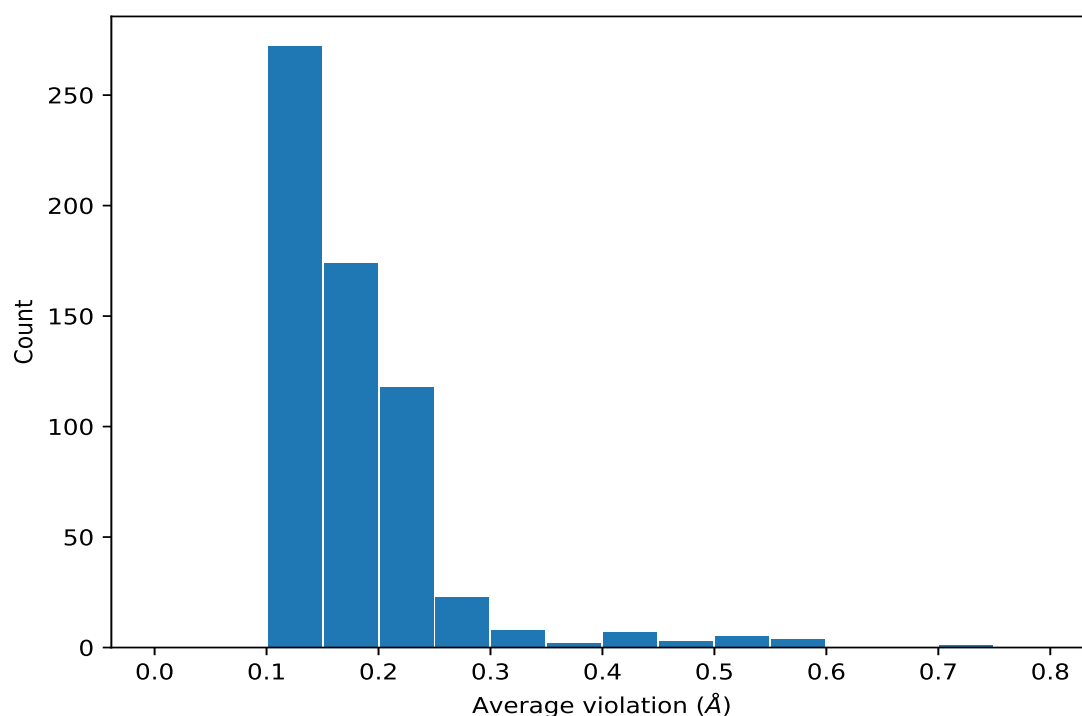
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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.

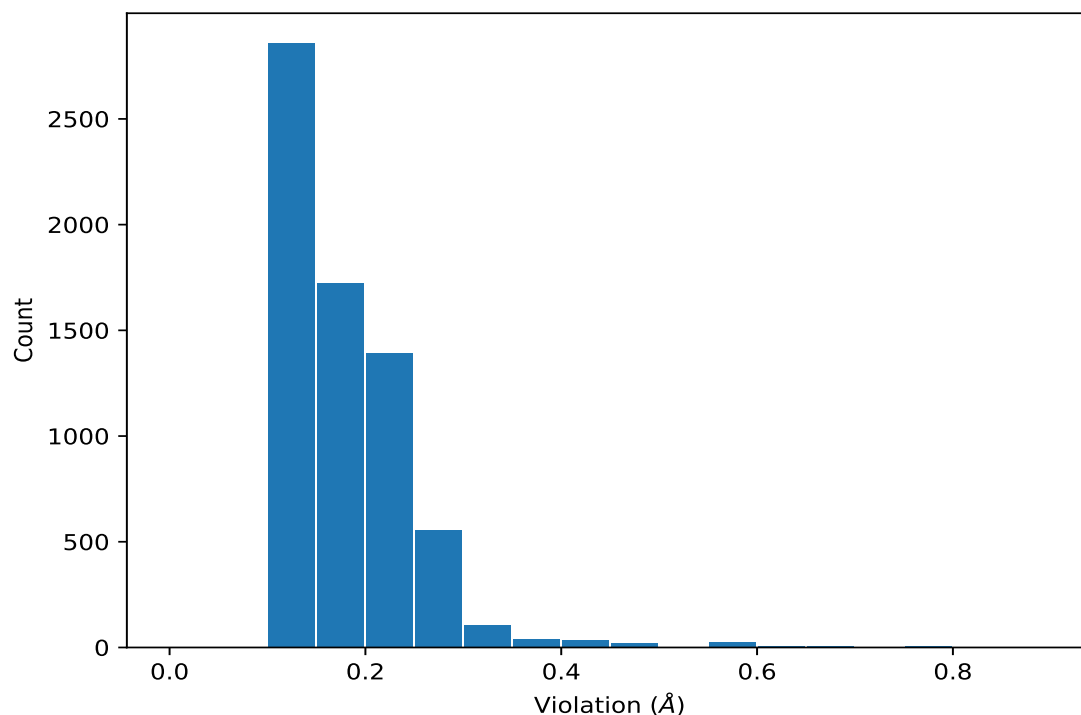
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,5)	1:31:A:VAL:O	1:22:A:VAL:N	20	0.29	0.01	0.28
(1,1033)	1:67:A:LYS:HA	1:67:A:LYS:HD3	20	0.27	0.05	0.26
(2,15)	1:64:A:TRP:O	1:92:A:PHE:H	20	0.26	0.03	0.26
(1,1159)	1:77:A:TRP:HB3	1:78:A:THR:H	20	0.26	0.03	0.26
(2,18)	1:23:A:HIS:O	1:93:A:THR:N	20	0.26	0.02	0.25
(1,1111)	1:74:A:LYS:HA	1:74:A:LYS:HD2	20	0.25	0.01	0.25
(1,340)	1:23:A:HIS:H	1:91:A:GLN:HA	20	0.25	0.02	0.25
(1,1328)	1:87:A:ASP:HA	1:88:A:ALA:H	20	0.25	0.01	0.25
(1,508)	1:33:A:LEU:HD21	1:48:A:LEU:H	20	0.25	0.02	0.25
(1,508)	1:33:A:LEU:HD22	1:48:A:LEU:H	20	0.25	0.02	0.25
(1,508)	1:33:A:LEU:HD23	1:48:A:LEU:H	20	0.25	0.02	0.25
(1,297)	1:22:A:VAL:H	1:31:A:VAL:H	20	0.24	0.02	0.24

¹Number of violated models, ²Standard 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)
(1,519)	1:34:A:ARG:HD3	1:34:A:ARG:HA	20	0.89
(1,100)	1:8:A:MET:H	1:12:A:CYS:HA	14	0.85
(1,100)	1:8:A:MET:H	1:12:A:CYS:HA	7	0.82
(1,520)	1:34:A:ARG:HG3	1:34:A:ARG:HA	13	0.78
(1,100)	1:8:A:MET:H	1:12:A:CYS:HA	4	0.78
(1,520)	1:34:A:ARG:HG3	1:34:A:ARG:HA	9	0.77
(1,520)	1:34:A:ARG:HG3	1:34:A:ARG:HA	16	0.77
(1,520)	1:34:A:ARG:HG3	1:34:A:ARG:HA	18	0.77
(1,994)	1:65:A:TRP:H	1:65:A:TRP:HB2	18	0.68
(1,994)	1:65:A:TRP:H	1:65:A:TRP:HB2	13	0.65

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

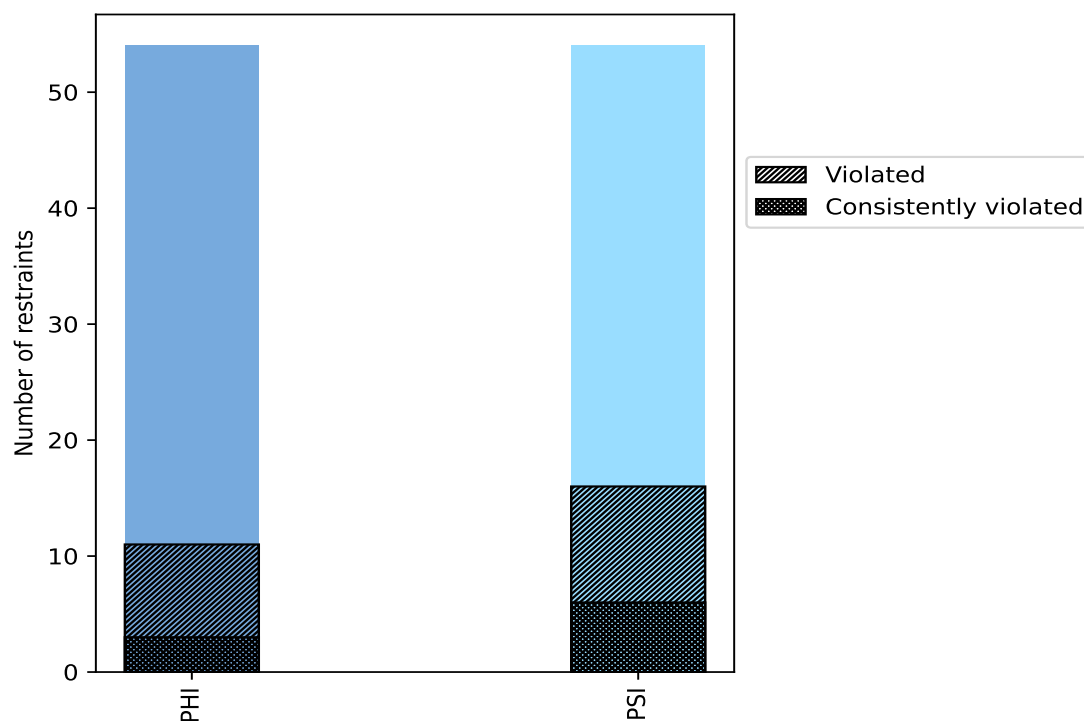
10.1 Summary of dihedral-angle violations [i](#)

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	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
PHI	54	50.0	11	20.4	10.2	3	5.6	2.8
PSI	54	50.0	16	29.6	14.8	6	11.1	5.6
Total	108	100.0	27	25.0	25.0	9	8.3	8.3

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 [i](#)



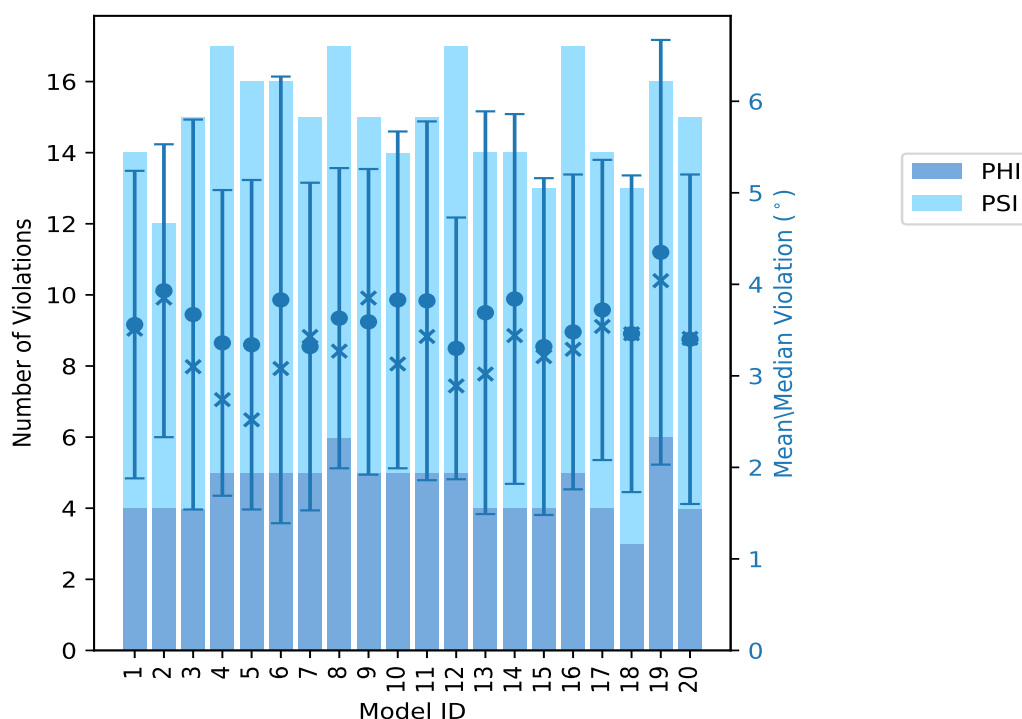
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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	4	10	14	3.56	6.41	1.68	3.51
2	4	8	12	3.93	6.8	1.6	3.85
3	4	11	15	3.67	9.19	2.13	3.1
4	5	12	17	3.36	6.97	1.67	2.74
5	5	11	16	3.34	7.35	1.8	2.52
6	5	11	16	3.83	10.58	2.44	3.08
7	5	10	15	3.32	6.89	1.79	3.43
8	6	11	17	3.63	7.15	1.64	3.27
9	5	10	15	3.59	7.13	1.67	3.85
10	5	9	14	3.83	7.59	1.84	3.13
11	5	10	15	3.82	8.28	1.96	3.43
12	5	12	17	3.3	6.36	1.43	2.89
13	4	10	14	3.69	8.35	2.2	3.02
14	4	10	14	3.84	7.26	2.02	3.44
15	4	9	13	3.32	7.63	1.84	3.21
16	5	12	17	3.48	7.02	1.72	3.29
17	4	10	14	3.72	6.62	1.64	3.54
18	3	10	13	3.46	7.41	1.73	3.46
19	6	10	16	4.35	11.3	2.32	4.04
20	4	11	15	3.4	7.39	1.8	3.41

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



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

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

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

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
3	1	4	1	5.0
3	1	4	2	10.0
0	1	1	3	15.0
0	1	1	4	20.0
1	0	1	5	25.0
0	1	1	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

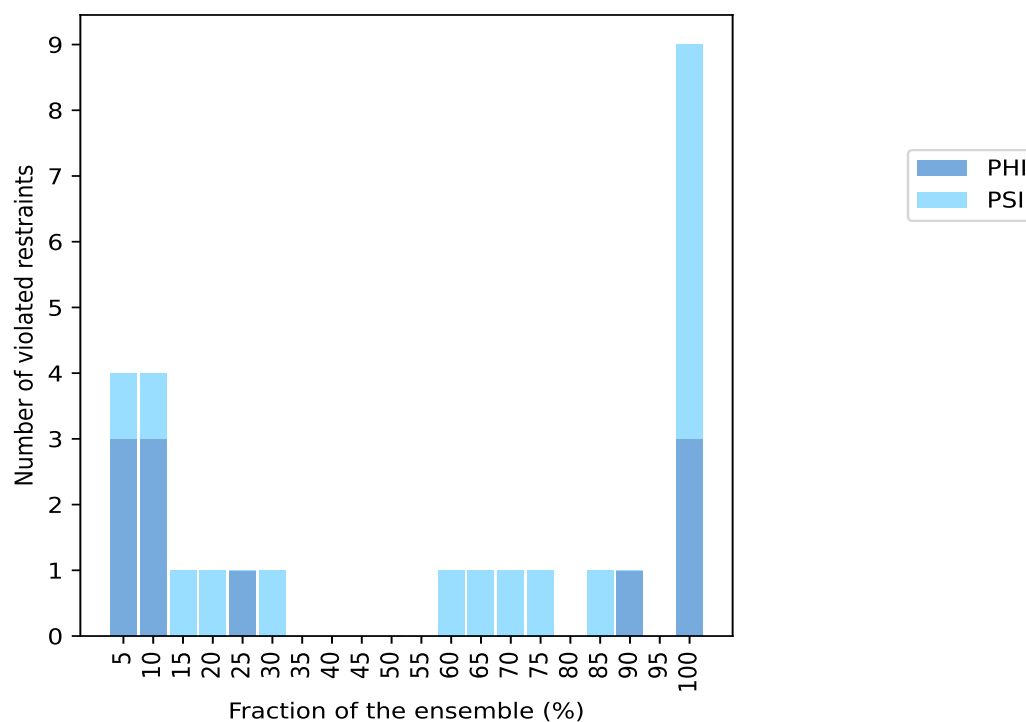
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	1	1	12	60.0
0	1	1	13	65.0
0	1	1	14	70.0
0	1	1	15	75.0
0	0	0	16	80.0
0	1	1	17	85.0
1	0	1	18	90.0
0	0	0	19	95.0
3	6	9	20	100.0

¹ Number of models with violations

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

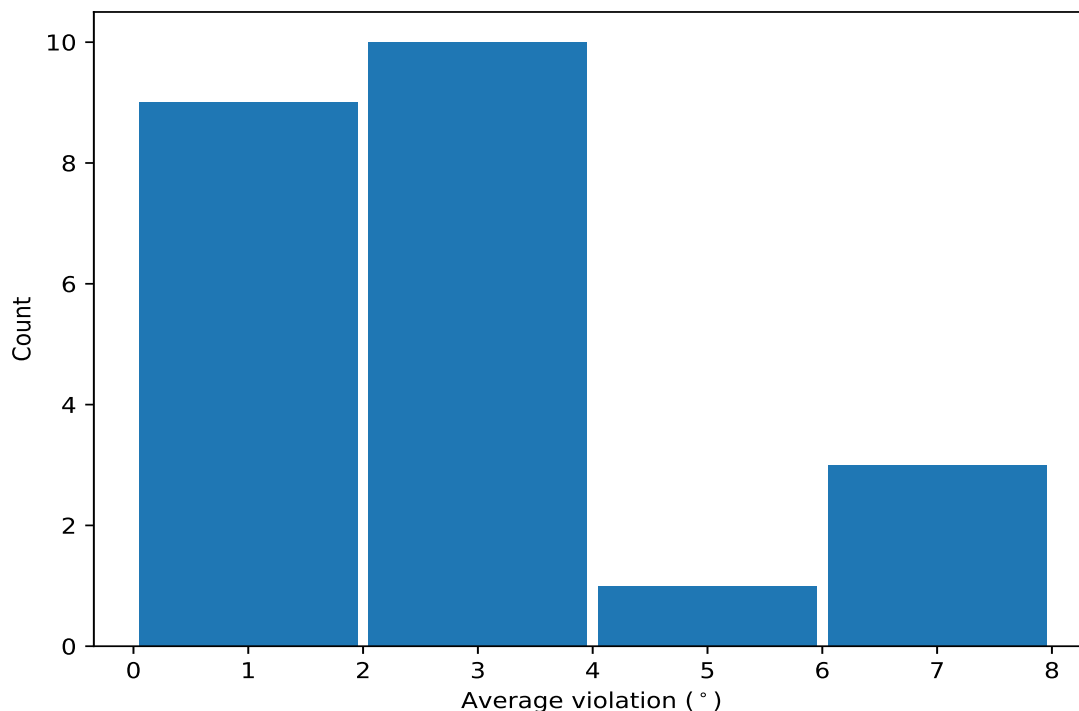


10.4 Most violated dihedral-angle restraints in the ensemble ⓘ

10.4.1 Histogram : Distribution of mean dihedral-angle violations ⓘ

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

in the ensemble



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.

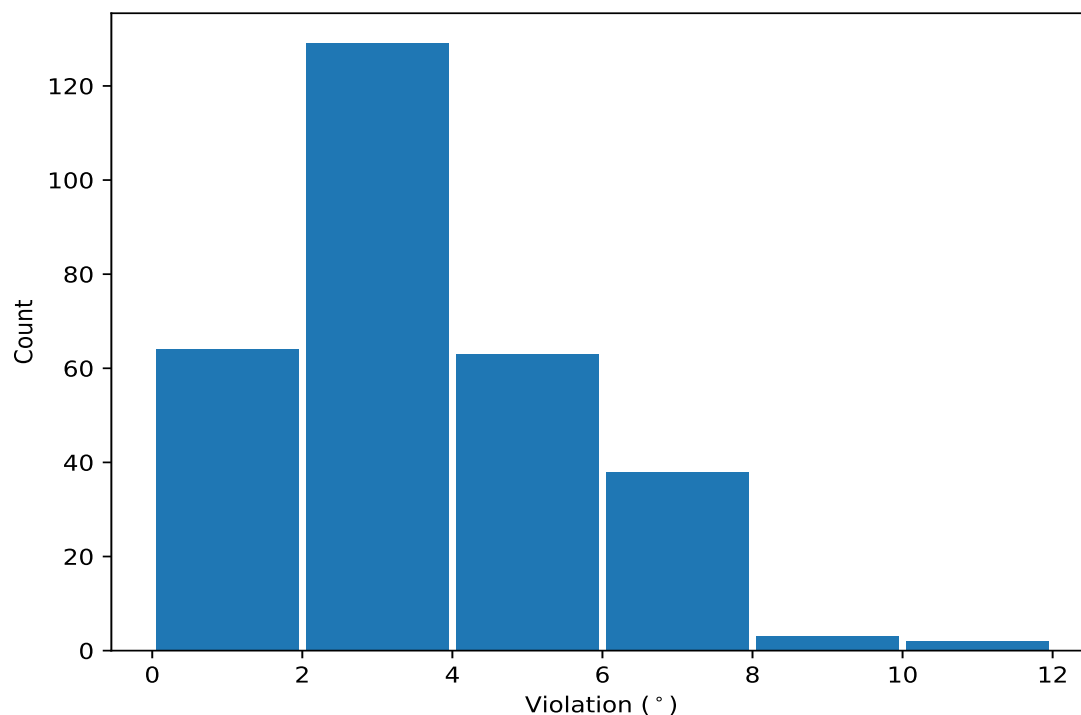
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,6)	1:20:A:LEU:N	1:20:A:LEU:CA	1:20:A:LEU:C	1:21:A:SER:N	20	7.17	1.32	6.79
(1,81)	1:74:A:LYS:C	1:75:A:THR:N	1:75:A:THR:CA	1:75:A:THR:C	20	6.22	1.01	6.47
(1,107)	1:92:A:PHE:C	1:93:A:THR:N	1:93:A:THR:CA	1:93:A:THR:C	20	6.15	1.4	5.84
(1,26)	1:34:A:ARG:N	1:34:A:ARG:CA	1:34:A:ARG:C	1:35:A:VAL:N	20	4.52	0.62	4.36
(1,104)	1:91:A:GLN:N	1:91:A:GLN:CA	1:91:A:GLN:C	1:92:A:PHE:N	20	3.91	0.99	3.83
(1,20)	1:31:A:VAL:N	1:31:A:VAL:CA	1:31:A:VAL:C	1:32:A:THR:N	20	3.75	0.55	3.74
(1,67)	1:63:A:LEU:C	1:64:A:TRP:N	1:64:A:TRP:CA	1:64:A:TRP:C	20	3.68	0.71	3.69
(1,16)	1:29:A:ARG:N	1:29:A:ARG:CA	1:29:A:ARG:C	1:30:A:ASP:N	20	3.37	0.92	3.67
(1,10)	1:22:A:VAL:N	1:22:A:VAL:CA	1:22:A:VAL:C	1:23:A:HIS:N	20	2.43	0.31	2.45
(1,83)	1:77:A:TRP:C	1:78:A:THR:N	1:78:A:THR:CA	1:78:A:THR:C	18	3.0	0.45	3.09

¹ Number of violated models, ²Standard 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 (°)
(1,6)	1:20:A:LEU:N	1:20:A:LEU:CA	1:20:A:LEU:C	1:21:A:SER:N	19	11.3
(1,6)	1:20:A:LEU:N	1:20:A:LEU:CA	1:20:A:LEU:C	1:21:A:SER:N	6	10.58
(1,107)	1:92:A:PHE:C	1:93:A:THR:N	1:93:A:THR:CA	1:93:A:THR:C	3	9.19
(1,81)	1:74:A:LYS:C	1:75:A:THR:N	1:75:A:THR:CA	1:75:A:THR:C	13	8.35
(1,107)	1:92:A:PHE:C	1:93:A:THR:N	1:93:A:THR:CA	1:93:A:THR:C	11	8.28
(1,107)	1:92:A:PHE:C	1:93:A:THR:N	1:93:A:THR:CA	1:93:A:THR:C	13	7.7
(1,6)	1:20:A:LEU:N	1:20:A:LEU:CA	1:20:A:LEU:C	1:21:A:SER:N	15	7.63
(1,107)	1:92:A:PHE:C	1:93:A:THR:N	1:93:A:THR:CA	1:93:A:THR:C	10	7.59
(1,81)	1:74:A:LYS:C	1:75:A:THR:N	1:75:A:THR:CA	1:75:A:THR:C	19	7.43
(1,6)	1:20:A:LEU:N	1:20:A:LEU:CA	1:20:A:LEU:C	1:21:A:SER:N	18	7.41