Full wwPDB NMR Structure Validation Report (i)

Dec 25, 2024 – 01:32 AM EST

PDB ID	:	2N8E
BMRB ID	:	25847
Title	:	Three-dimensional structure of cyclic PVIIA
Authors	:	Kwon, S.; Schroeder, C.; Craik, D.
Deposited on	:	2015-10-13

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:

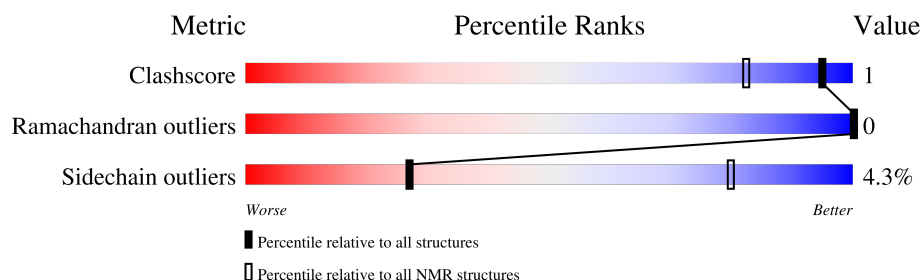|		
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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	Percentile Ranks	Value
Clashscore		1
Ramachandran outliers		0
Sidechain outliers		4.3%

Worse — Better

▮ Percentile relative to all structures
▯ Percentile relative to all NMR structures

Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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	34	97% ·

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 20 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:1-A:3, A:5-A:34 (33)	1.43	20

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

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

3 Entry composition ⓘ

There is only 1 type of molecule in this entry. The entry contains 518 atoms, of which 252 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Kappa-conotoxin PVIIA.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	34	518	159	252	53	48	6	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	LEU	-	linker	UNP P56633
A	29	PRO	-	linker	UNP P56633
A	30	GLU	-	linker	UNP P56633
A	31	THR	-	linker	UNP P56633
A	32	GLY	-	linker	UNP P56633
A	33	GLY	-	linker	UNP P56633
A	34	GLY	-	linker	UNP P56633

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.
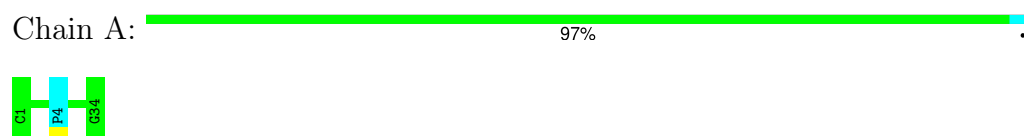
• Molecule 1: Kappa-conotoxin PVIIA

Chain A:
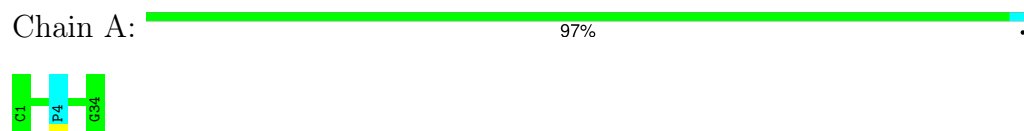
4.2 Scores per residue for each member of the ensemble
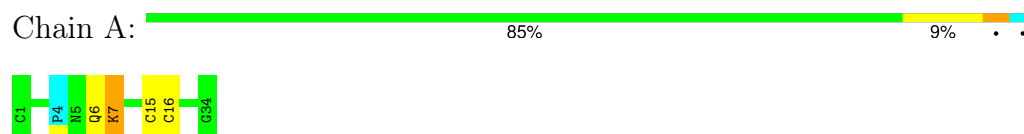
Colouring as in section 4.1 above.

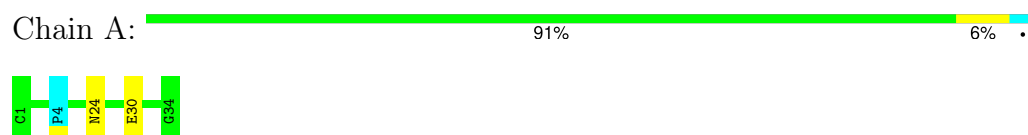### 4.2.1 Score per residue for model 1

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.2 Score per residue for model 2

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.3 Score per residue for model 3

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.4 Score per residue for model 4

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.5 Score per residue for model 5

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.6 Score per residue for model 6

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.7 Score per residue for model 7

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.8 Score per residue for model 8

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.9 Score per residue for model 9

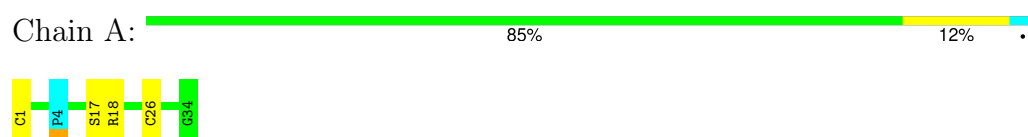• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.10 Score per residue for model 10

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.11 Score per residue for model 11

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.12 Score per residue for model 12

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.13 Score per residue for model 13
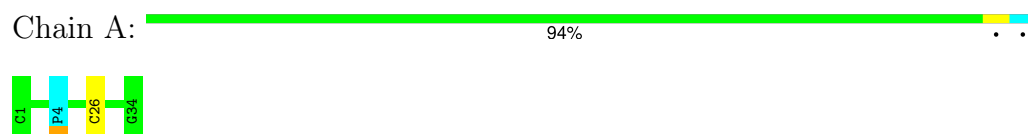
• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

4.2.14 Score per residue for model 14

• Molecule 1: Kappa-conotoxin PVIIA
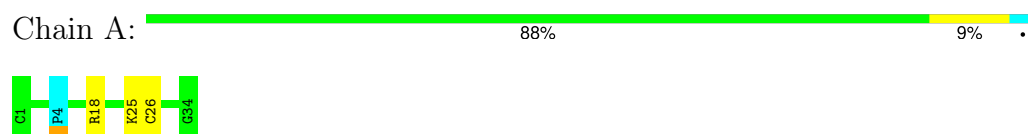
Chain A:
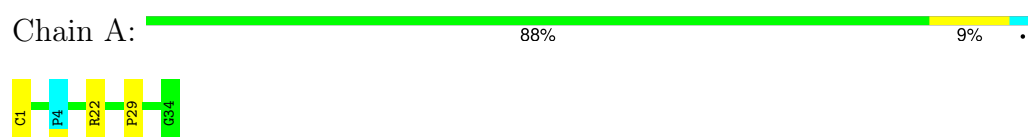
4.2.15 Score per residue for model 15

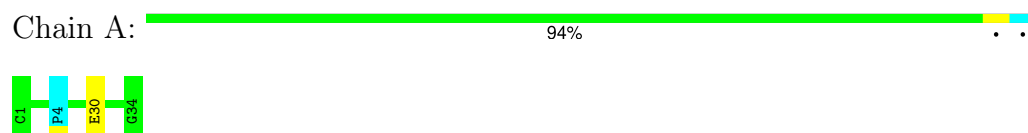• Molecule 1: Kappa-conotoxin PVIIA
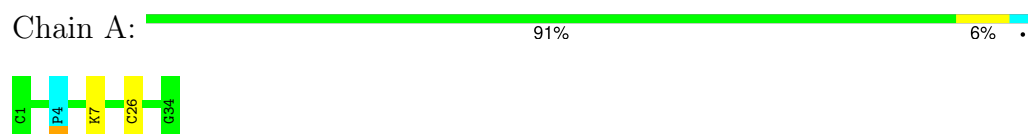
Chain A:

4.2.16 Score per residue for model 16

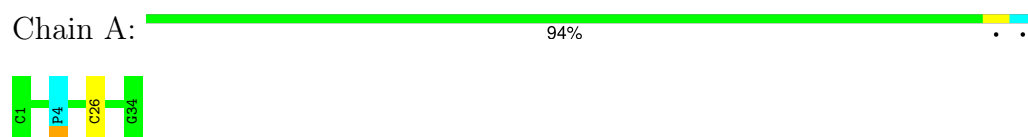• Molecule 1: Kappa-conotoxin PVIIA
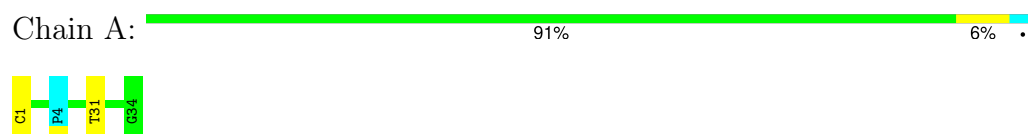
Chain A:

4.2.17 Score per residue for model 17

• Molecule 1: Kappa-conotoxin PVIIA
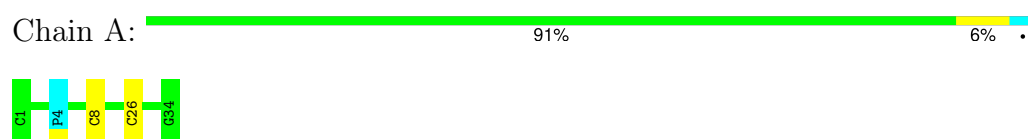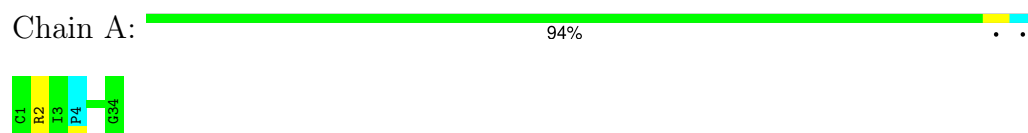
Chain A:

4.2.18   Score per residue for model 18
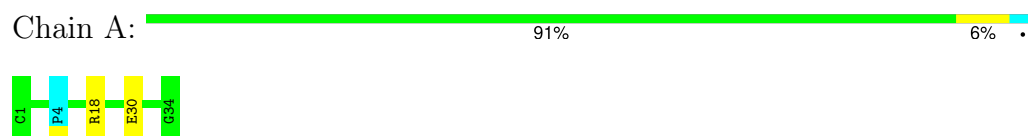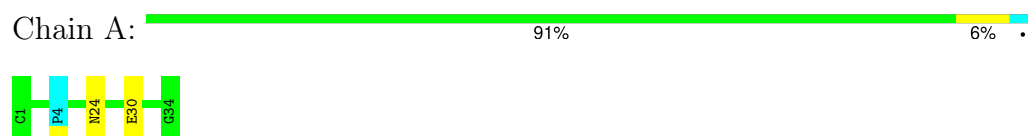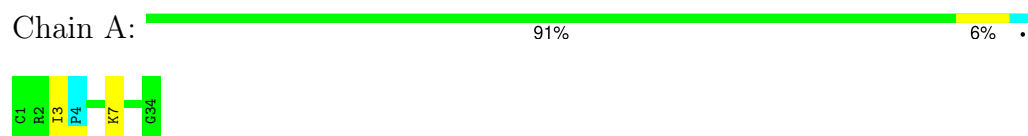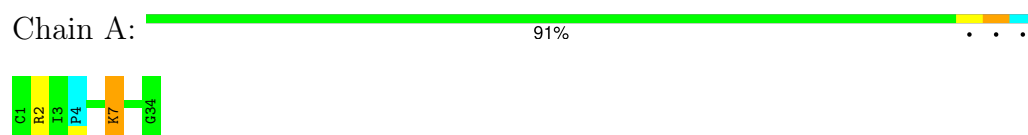
• Molecule 1: Kappa-conotoxin PVIIA
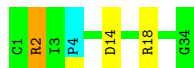
Chain A:

4.2.19   Score per residue for model 19

• Molecule 1: Kappa-conotoxin PVIIA
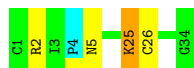
Chain A:

4.2.20   Score per residue for model 20 (medoid)

• Molecule 1: Kappa-conotoxin PVIIA

Chain A:

5 Refinement protocol and experimental data overview ⓘ

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

Of the 50 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	
TALOS	geometry optimization	
CYANA	structure solution	

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	359
Number of shifts mapped to atoms	359
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

6   Model quality ⓘ

6.1   Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HYP

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	258	245	245	0±1
All	All	5160	4900	4897	10

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	Models Total
1:A:8:CYS:HB3	1:A:26:CYS:SG	0.56	2.41	9	1
1:A:6:GLN:HB2	1:A:15:CYS:SG	0.56	2.40	2	1
1:A:5:ASN:HA	1:A:25:LYS:HD3	0.45	1.87	19	1
1:A:7:LYS:O	1:A:7:LYS:HE2	0.43	2.13	2	1
1:A:25:LYS:HD2	1:A:26:CYS:N	0.43	2.28	19	1
1:A:7:LYS:N	1:A:7:LYS:HE3	0.42	2.29	13	1
1:A:18:ARG:N	1:A:18:ARG:HD2	0.42	2.30	6	1
1:A:1:CYS:SG	1:A:31:THR:HA	0.41	2.55	16	1
1:A:1:CYS:HB2	1:A:29:PRO:HD3	0.41	1.92	14	1
1:A:2:ARG:HD2	1:A:14:ASP:O	0.41	2.15	18	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	31/34 (91%)	29±1 (95±4%)	2±1 (5±4%)	0±0 (0±0%)	100	100
All	All	620/680 (91%)	587 (95%)	33 (5%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 Protein sidechains ⓘ

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	30/30 (100%)	29±1 (96±3%)	1±1 (4±3%)	27	80
All	All	600/600 (100%)	574 (96%)	26 (4%)	27	80

All 11 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	7	LYS	4
1	A	30	GLU	4
1	A	18	ARG	4
1	A	2	ARG	4
1	A	24	ASN	3
1	A	25	LYS	2
1	A	16	CYS	1
1	A	1	CYS	1
1	A	17	SER	1
1	A	3	ILE	1
1	A	22	ARG	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	HYP	A	4	1	7,8,9	1.28±0.13	1±1 (17±7%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	HYP	A	4	1	5,10,12	1.48±0.27	1±1 (16±10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	A	4	1	-	0±0,0,11,13	0±0,1,1,1

All unique bond 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(Å)	Ideal(Å)	Models Worst	Total
1	A	4	HYP	CD-CG	2.97	1.47	1.53	2	14
1	A	4	HYP	CB-CG	2.68	1.47	1.52	5	10
1	A	4	HYP	CA-N	2.27	1.44	1.48	3	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(^{o})	Ideal(^{o})	Models Worst	Total
1	A	4	HYP	CB-CG-CD	3.64	107.21	103.16	17	15
1	A	4	HYP	CG-CB-CA	2.18	106.28	103.75	17	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates ⓘ

There are no oligosaccharides 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 78% for the well-defined parts and 78% 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	359
Number of shifts mapped to atoms	359
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_\alpha$	30	0.36 ± 0.29	None needed (< 0.5 ppm)
$^{13}C_\beta$	30	0.82 ± 0.30	Should be applied
$^{13}C'$	0	—	None (insufficient data)
^{15}N	31	0.94 ± 0.69	None needed (imprecise)

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 78%, i.e. 338 atoms were assigned a chemical shift out of a possible 436. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	128/166 (77%)	67/68 (99%)	30/66 (45%)	31/32 (97%)
Sidechain	202/243 (83%)	133/153 (87%)	59/73 (81%)	10/17 (59%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	8/27 (30%)	8/14 (57%)	0/12 (0%)	0/1 (0%)
Overall	338/436 (78%)	208/235 (89%)	89/151 (59%)	41/50 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 338 atoms were assigned a chemical shift out of a possible 436. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	128/166 (77%)	67/68 (99%)	30/66 (45%)	31/32 (97%)
Sidechain	202/243 (83%)	133/153 (87%)	59/73 (81%)	10/17 (59%)
Aromatic	8/27 (30%)	8/14 (57%)	0/12 (0%)	0/1 (0%)
Overall	338/436 (78%)	208/235 (89%)	89/151 (59%)	41/50 (82%)

7.1.4   Statistically unusual chemical shifts   ⓘ

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	19	LYS	NZ	121.19	19.79 – 46.09	33.6
1	A	7	LYS	NZ	113.01	19.79 – 46.09	30.4
1	A	2	ARG	NE	121.19	76.53 – 92.65	22.7
1	A	18	ARG	NE	120.26	76.53 – 92.65	22.1
1	A	22	ARG	NE	119.73	76.53 – 92.65	21.8
1	A	19	LYS	HE3	1.73	1.92 – 3.89	-6.0

7.1.5   Random Coil Index (RCI) plots   ⓘ

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:
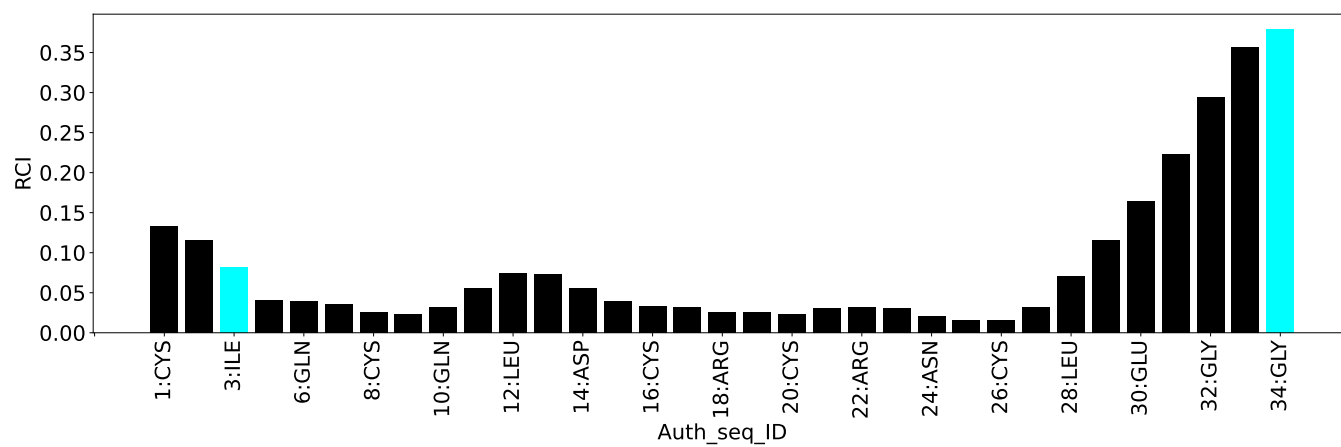
8 NMR restraints analysis ⓘ

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	385
Intra-residue ($|i\text{-}j|$=0)	139
Sequential ($|i\text{-}j|$=1)	146
Medium range ($|i\text{-}j|$>1 and $|i\text{-}j|$<5)	46
Long range ($|i\text{-}j|$≥5)	46
Inter-chain	0
Hydrogen bond restraints	8
Disulfide bond restraints	0
Total dihedral-angle restraints	37
Number of unmapped restraints	0
Number of restraints per residue	12.4
Number of long range restraints per residue[1]	1.5

[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)	1.5	0.19
0.2-0.5 (Medium)	0.3	0.4
>0.5 (Large)	0.3	1.49

8.2.2 Average number of dihedral-angle violations per model ⓘ

Dihedral-angle violations less than 1° are not included in the calculation.

| Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	0.2	1.46
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

9.1 Summary of distance violations ⓘ

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

Restraints type	Count	$\%^1$	Violated[3]			Consistently Violated[4]		
			Count	$\%^2$	$\%^1$	Count	$\%^2$	$\%^1$
Intra-residue (|i-j|=0)	139	36.1	5	3.6	1.3	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	117	30.4	4	3.4	1.0	0	0.0	0.0
Sidechain-Sidechain	22	5.7	1	4.5	0.3	0	0.0	0.0
Sequential (|i-j|=1)	146	37.9	9	6.2	2.3	0	0.0	0.0
Backbone-Backbone	40	10.4	1	2.5	0.3	0	0.0	0.0
Backbone-Sidechain	80	20.8	3	3.8	0.8	0	0.0	0.0
Sidechain-Sidechain	26	6.8	5	19.2	1.3	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	46	11.9	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	9	2.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	20	5.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	17	4.4	0	0.0	0.0	0	0.0	0.0
Long range (|i-j|≥5)	46	11.9	4	8.7	1.0	0	0.0	0.0
Backbone-Backbone	15	3.9	2	13.3	0.5	0	0.0	0.0
Backbone-Sidechain	21	5.5	2	9.5	0.5	0	0.0	0.0
Sidechain-Sidechain	10	2.6	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	8	2.1	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	385	100.0	18	4.7	4.7	0	0.0	0.0
Backbone-Backbone	64	16.6	3	4.7	0.8	0	0.0	0.0
Backbone-Sidechain	246	63.9	9	3.7	2.3	0	0.0	0.0
Sidechain-Sidechain	75	19.5	6	8.0	1.6	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 ⓘ
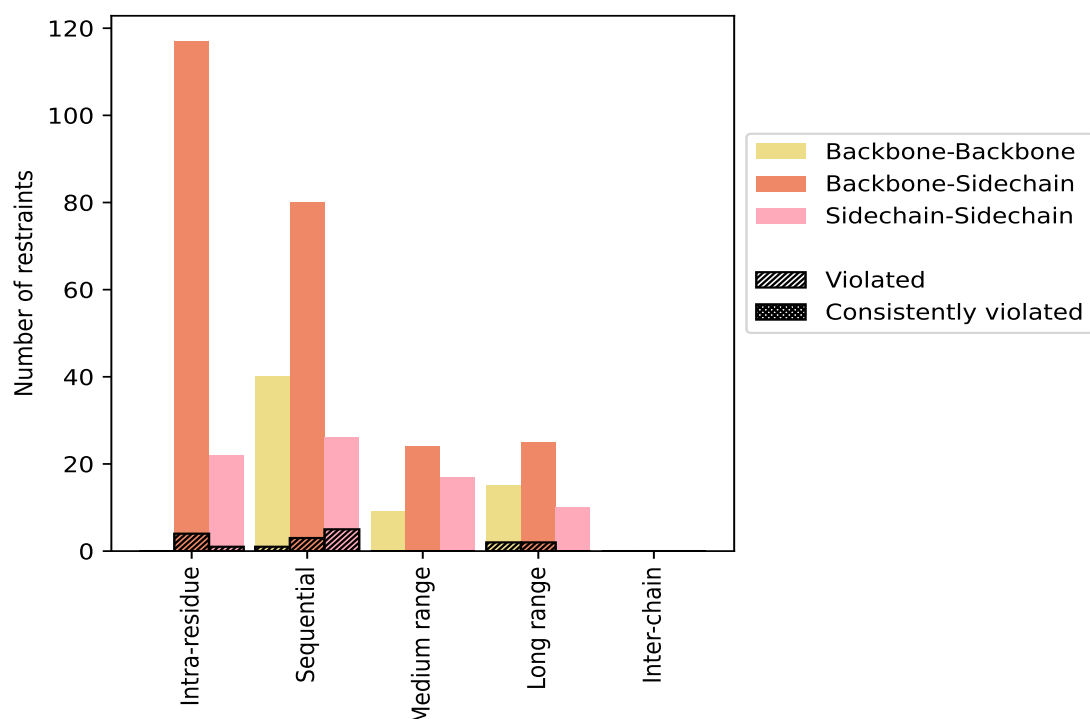
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

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	3	0	0	0	3	0.7	1.49	0.56	0.4
2	0	1	0	0	0	1	1.2	1.2	0.0	1.2
3	1	0	0	0	0	1	0.11	0.11	0.0	0.11
4	1	5	0	0	0	6	0.32	1.27	0.43	0.13
5	1	0	0	0	0	1	0.15	0.15	0.0	0.15
6	0	0	0	1	0	1	0.13	0.13	0.0	0.13
7	0	2	0	1	0	3	0.2	0.25	0.03	0.19
8	0	2	0	2	0	4	0.18	0.37	0.11	0.12
9	0	2	0	0	0	2	0.15	0.17	0.02	0.15
10	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				
11	0	1	0	0	0	1	0.16	0.16	0.0	0.16
12	1	1	0	0	0	2	0.41	0.69	0.28	0.41
13	0	2	0	0	0	2	0.57	0.95	0.38	0.57
14	1	2	0	0	0	3	0.42	0.95	0.38	0.19
15	1	1	0	0	0	2	0.12	0.12	0.0	0.12
16	0	2	0	1	0	3	0.2	0.34	0.1	0.13
17	1	1	0	0	0	2	0.44	0.77	0.32	0.44
18	0	0	0	1	0	1	0.13	0.13	0.0	0.13
19	0	2	0	1	0	3	0.16	0.23	0.05	0.14
20	1	0	0	1	0	2	0.11	0.11	0.0	0.11

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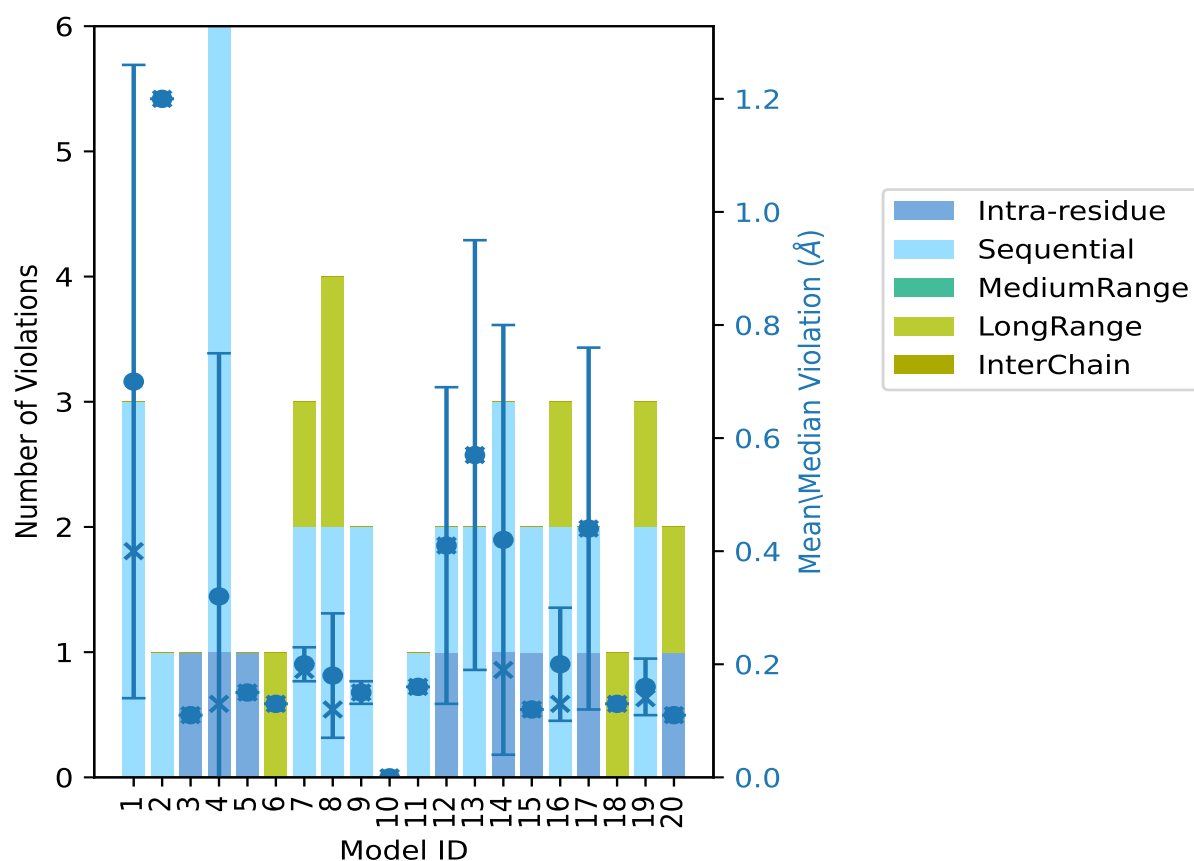
The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

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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, 359(IR:134, SQ:137, MR:46, LR:42, 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]	%
3	4	0	3	0	10	1	5.0
1	2	0	0	0	3	2	10.0
1	2	0	0	0	3	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	1	0	1	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	1	0	0	0	1	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 ⓘ
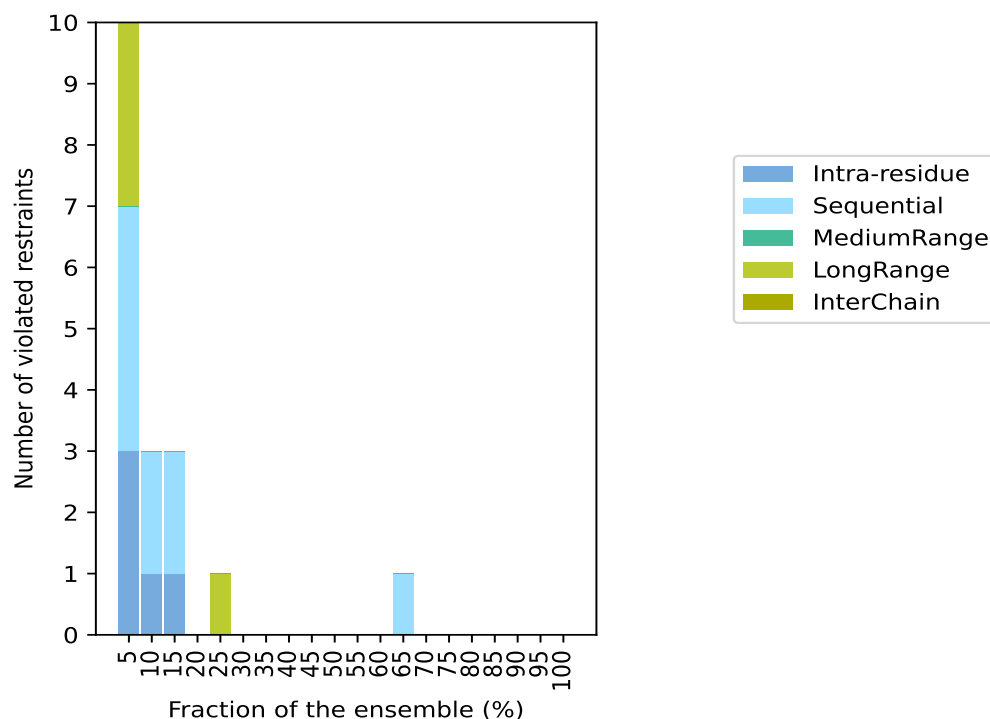
9.4 Most violated distance restraints in the ensemble ⓘ

9.4.1 Histogram : Distribution of mean distance violations ⓘ

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models in the ensemble
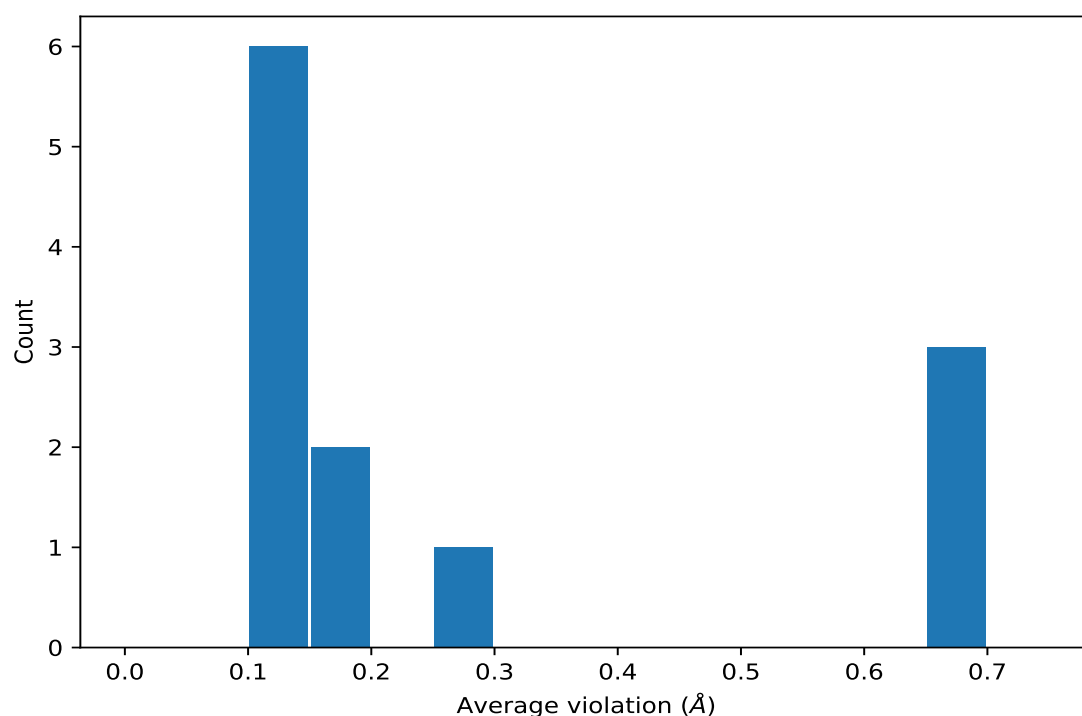
9.4.2 Table: Most violated distance restraints ⓘ

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	13	0.68	0.45	0.69
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	13	0.68	0.45	0.69
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	13	0.68	0.45	0.69
(1,160)	1:2:A:ARG:H	1:16:A:CYS:HA	5	0.13	0.02	0.13
(1,46)	1:1:A:CYS:HA	1:2:A:ARG:H	3	0.18	0.02	0.19
(1,291)	1:7:A:LYS:HD2	1:8:A:CYS:H	3	0.13	0.02	0.11
(1,291)	1:7:A:LYS:HD3	1:8:A:CYS:H	3	0.13	0.02	0.11
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD2	3	0.11	0.0	0.11
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD3	3	0.11	0.0	0.11
(1,239)	1:3:A:ILE:HB	1:4:A:HYP:HD22	2	0.28	0.12	0.28
(1,129)	1:3:A:ILE:HB	1:4:A:HYP:HD23	2	0.16	0.05	0.16
(1,42)	1:31:A:THR:HA	1:31:A:THR:HG1	2	0.13	0.02	0.13

[1]Number of violated models, [2]Standard deviation

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.

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.
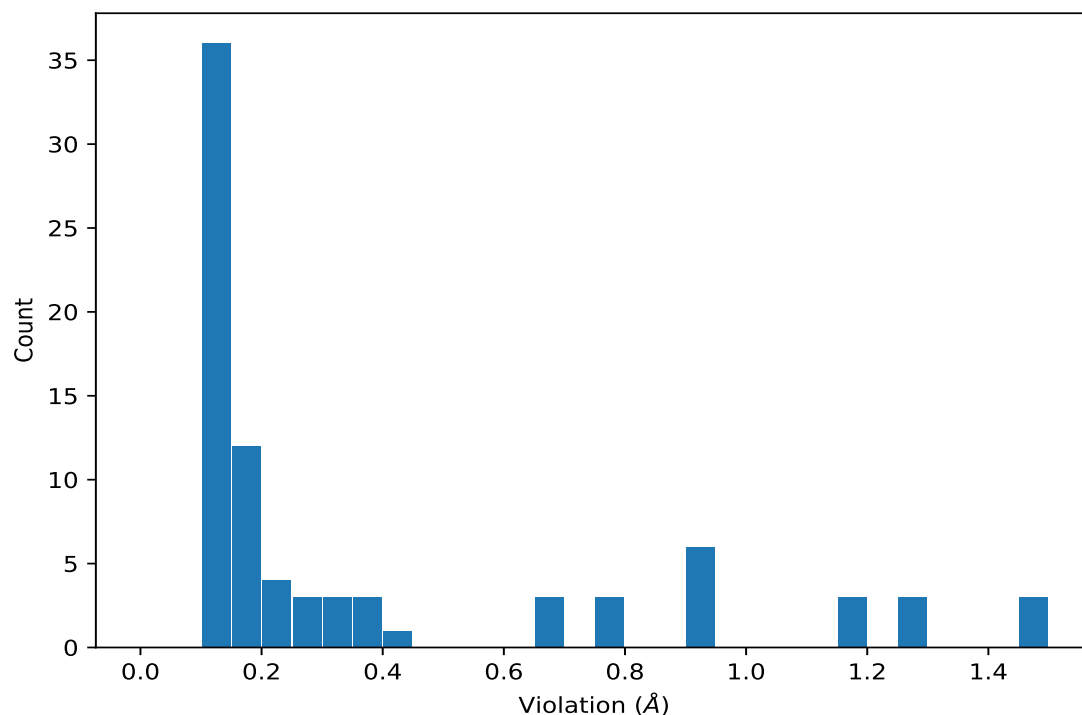
Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	1	1.49
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	1	1.49
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	1	1.49
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	4	1.27
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	4	1.27
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	4	1.27
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	2	1.2
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	2	1.2
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	2	1.2
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	13	0.95

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	13	0.95
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	13	0.95
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	14	0.95
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	14	0.95
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	14	0.95
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	17	0.77
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	17	0.77
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	17	0.77
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	12	0.69
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	12	0.69
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	12	0.69
(1,239)	1:3:A:ILE:HB	1:4:A:HYP:HD22	1	0.4
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	8	0.37
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	8	0.37
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	8	0.37
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	16	0.34
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	16	0.34
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	16	0.34
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	7	0.25
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	7	0.25
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	7	0.25
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	19	0.23
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	19	0.23
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	19	0.23
(1,129)	1:3:A:ILE:HB	1:4:A:HYP:HD23	1	0.21
(1,123)	1:3:A:ILE:HG21	1:4:A:HYP:HD22	14	0.19
(1,123)	1:3:A:ILE:HG22	1:4:A:HYP:HD22	14	0.19
(1,123)	1:3:A:ILE:HG23	1:4:A:HYP:HD22	14	0.19
(1,46)	1:1:A:CYS:HA	1:2:A:ARG:H	7	0.19
(1,46)	1:1:A:CYS:HA	1:2:A:ARG:H	13	0.19
(1,160)	1:2:A:ARG:H	1:16:A:CYS:HA	7	0.17
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	9	0.17
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	9	0.17
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	9	0.17
(1,291)	1:7:A:LYS:HD2	1:8:A:CYS:H	11	0.16
(1,291)	1:7:A:LYS:HD3	1:8:A:CYS:H	11	0.16
(1,239)	1:3:A:ILE:HB	1:4:A:HYP:HD22	4	0.16
(1,46)	1:1:A:CYS:HA	1:2:A:ARG:H	4	0.15
(1,42)	1:31:A:THR:HA	1:31:A:THR:HG1	5	0.15
(1,273)	1:5:A:ASN:HA	1:25:A:LYS:HB2	19	0.14
(1,273)	1:5:A:ASN:HA	1:25:A:LYS:HB3	19	0.14
(1,338)	1:19:A:LYS:HG2	1:20:A:CYS:H	9	0.13

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| Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,338)	1:19:A:LYS:HG3	1:20:A:CYS:H	9	0.13
(1,188)	1:19:A:LYS:HG2	1:20:A:CYS:H	16	0.13
(1,160)	1:2:A:ARG:H	1:16:A:CYS:HA	6	0.13
(1,160)	1:2:A:ARG:H	1:16:A:CYS:HA	8	0.13
(1,160)	1:2:A:ARG:H	1:16:A:CYS:HA	18	0.13
(1,52)	1:3:A:ILE:HB	1:3:A:ILE:HD11	12	0.13
(1,52)	1:3:A:ILE:HB	1:3:A:ILE:HD12	12	0.13
(1,52)	1:3:A:ILE:HB	1:3:A:ILE:HD13	12	0.13
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD2	17	0.12
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD3	17	0.12
(1,180)	1:19:A:LYS:HB3	1:27:A:VAL:H	16	0.12
(1,124)	1:3:A:ILE:HD11	1:4:A:HYP:HD22	15	0.12
(1,124)	1:3:A:ILE:HD12	1:4:A:HYP:HD22	15	0.12
(1,124)	1:3:A:ILE:HD13	1:4:A:HYP:HD22	15	0.12
(1,332)	1:18:A:ARG:HA	1:18:A:ARG:HD2	15	0.11
(1,332)	1:18:A:ARG:HA	1:18:A:ARG:HD3	15	0.11
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD2	3	0.11
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD3	3	0.11
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD2	14	0.11
(1,331)	1:18:A:ARG:H	1:18:A:ARG:HD3	14	0.11
(1,291)	1:7:A:LYS:HD2	1:8:A:CYS:H	8	0.11
(1,291)	1:7:A:LYS:HD3	1:8:A:CYS:H	8	0.11
(1,291)	1:7:A:LYS:HD2	1:8:A:CYS:H	19	0.11
(1,291)	1:7:A:LYS:HD3	1:8:A:CYS:H	19	0.11
(1,286)	1:7:A:LYS:HA	1:7:A:LYS:HE2	20	0.11
(1,286)	1:7:A:LYS:HA	1:7:A:LYS:HE3	20	0.11
(1,160)	1:2:A:ARG:H	1:16:A:CYS:HA	20	0.11
(1,139)	1:5:A:ASN:HA	1:26:A:CYS:H	8	0.11
(1,131)	1:28:A:LEU:HG	1:29:A:PRO:HD2	4	0.11
(1,129)	1:3:A:ILE:HB	1:4:A:HYP:HD23	4	0.11
(1,42)	1:31:A:THR:HA	1:31:A:THR:HG1	4	0.11

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	17	45.9	2	11.8	5.4	0	0.0	0.0
CHI1	3	8.1	0	0.0	0.0	0	0.0	0.0
PHI	17	45.9	1	5.9	2.7	0	0.0	0.0
Total	37	100.0	3	8.1	8.1	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 ⓘ
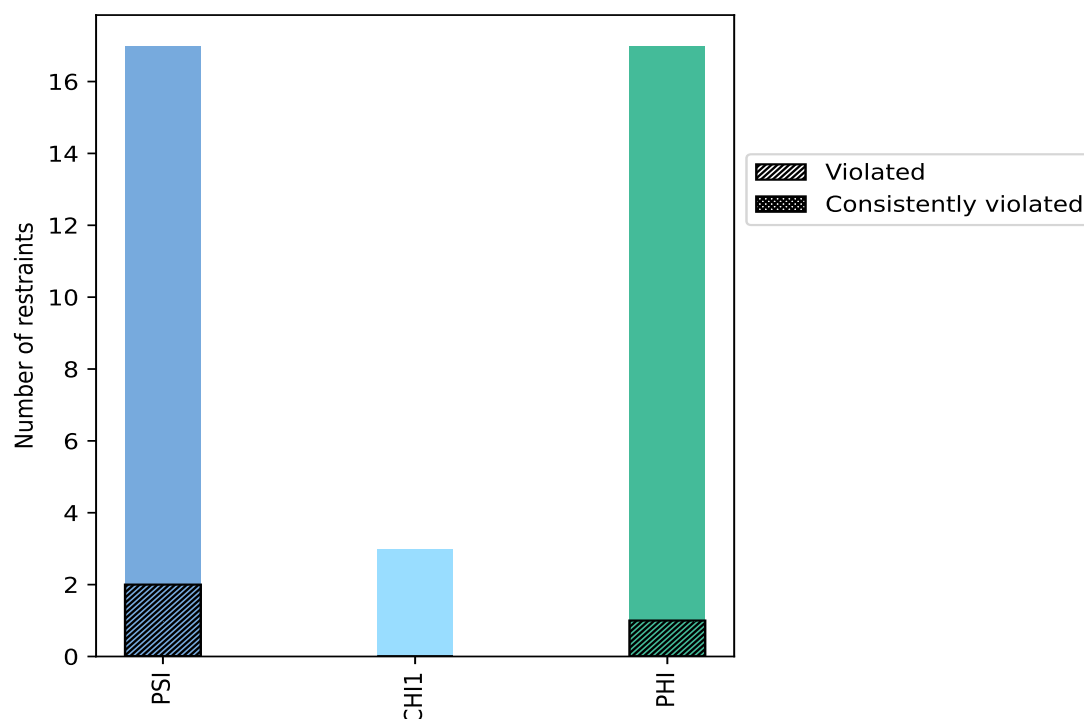
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model ⓘ

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	CHI1	PHI	Total				
1	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
3	0	0	0	0	0.0	0.0	0.0	0.0
4	0	0	1	1	1.46	1.46	0.0	1.46
5	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
7	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
9	0	0	0	0	0.0	0.0	0.0	0.0
10	1	0	0	1	1.07	1.07	0.0	1.07
11	0	0	0	0	0.0	0.0	0.0	0.0
12	0	0	0	0	0.0	0.0	0.0	0.0
13	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
15	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
17	0	0	0	0	0.0	0.0	0.0	0.0
18	1	0	0	1	1.21	1.21	0.0	1.21
19	0	0	0	0	0.0	0.0	0.0	0.0
20	0	0	1	1	1.19	1.19	0.0	1.19

10.2.1 Bar graph : Dihedral violation statistics for each model ⓘ
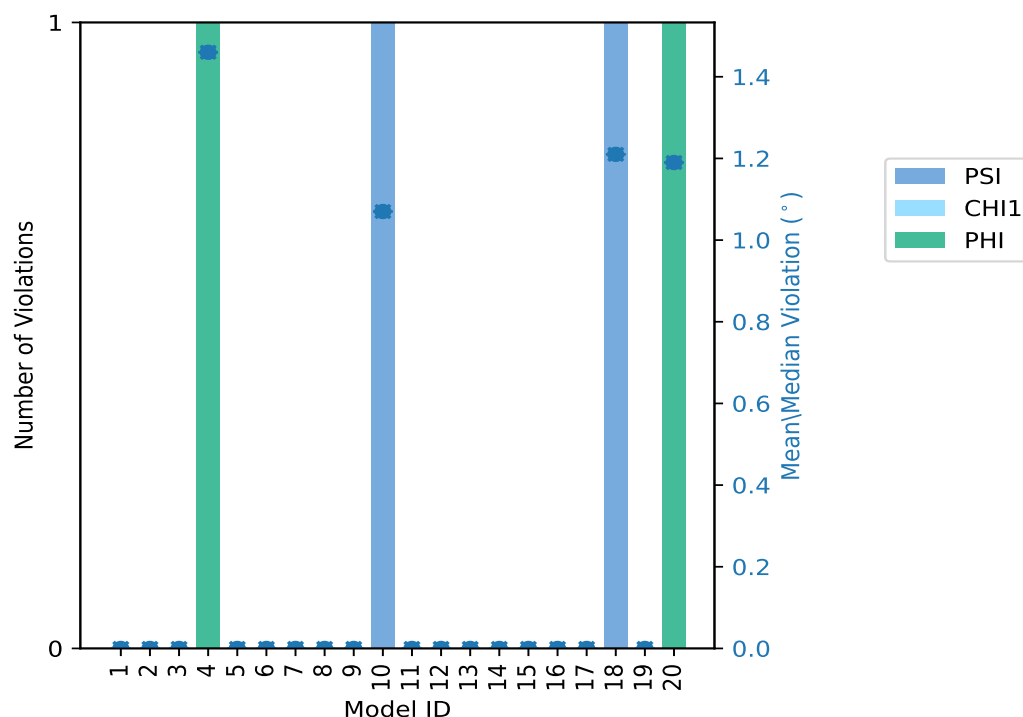
The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

10.3 Dihedral-angle violation statistics for the ensemble ⓘ

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

Number of violated restraints				Fraction of the ensemble	
PSI	CHI1	PHI	Total	Count[1]	%
2	0	0	2	1	5.0
0	0	1	1	2	10.0
0	0	0	0	3	15.0
0	0	0	0	4	20.0
0	0	0	0	5	25.0
0	0	0	0	6	30.0
0	0	0	0	7	35.0
0	0	0	0	8	40.0
0	0	0	0	9	45.0
0	0	0	0	10	50.0
0	0	0	0	11	55.0

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Number of violated restraints				Fraction of the ensemble	
PSI	CHI1	PHI	Total	Count[1]	%
0	0	0	0	12	60.0
0	0	0	0	13	65.0
0	0	0	0	14	70.0
0	0	0	0	15	75.0
0	0	0	0	16	80.0
0	0	0	0	17	85.0
0	0	0	0	18	90.0
0	0	0	0	19	95.0
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 ⓘ
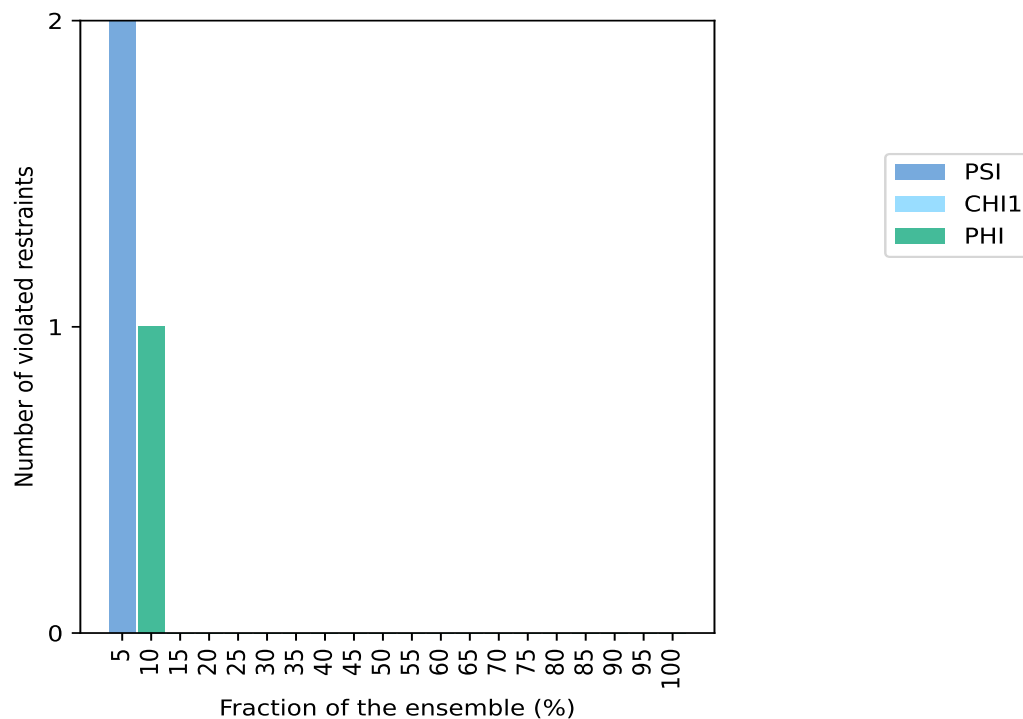
10.4   Most violated dihedral-angle restraints in the ensemble ⓘ

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
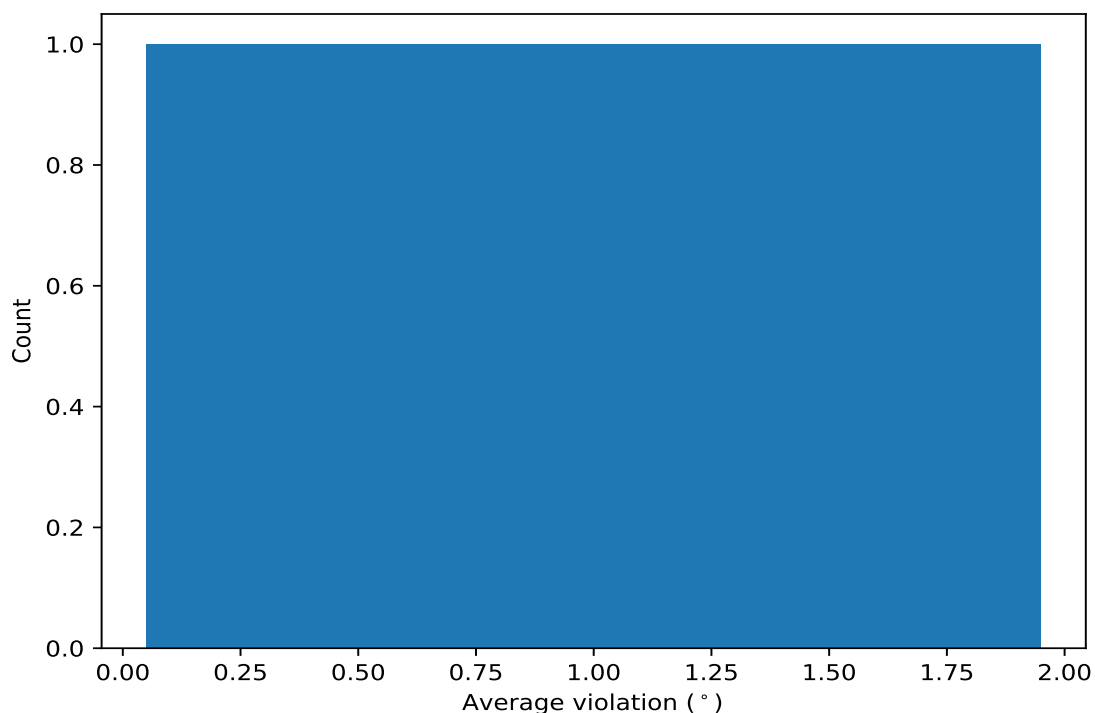
10.4.2   Table: Most violated dihedral-angle restraints ⓘ

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,10)	1:13:A:ASP:C	1:14:A:ASP:N	1:14:A:ASP:CA	1:14:A:ASP:C	2	1.32	0.14	1.32

[1] Number of violated models, [2]Standard deviation, All angle values are in degree (°)

10.5   All violated dihedral-angle restraints ⓘ

10.5.1   Histogram : Distribution of 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

10.5.2   Table: All violated dihedral-angle restraints ⓘ

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 (°)
(1,10)	1:13:A:ASP:C	1:14:A:ASP:N	1:14:A:ASP:CA	1:14:A:ASP:C	4	1.46
(1,14)	1:16:A:CYS:N	1:16:A:CYS:CA	1:16:A:CYS:C	1:17:A:SER:N	18	1.21
(1,10)	1:13:A:ASP:C	1:14:A:ASP:N	1:14:A:ASP:CA	1:14:A:ASP:C	20	1.19
(1,37)	1:28:A:LEU:N	1:28:A:LEU:CA	1:28:A:LEU:C	1:29:A:PRO:N	10	1.07