



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 9QSB / pdb_00009qsb
BMRB ID : 34989
Title : The solution structure of the cyanobacterial calcium binding protein CSE at 293 K
Authors : Kleusberg, F.; Scholl, J.; Selim, K.A.; Coles, M.
Deposited on : 2025-04-04

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

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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) : 2.50

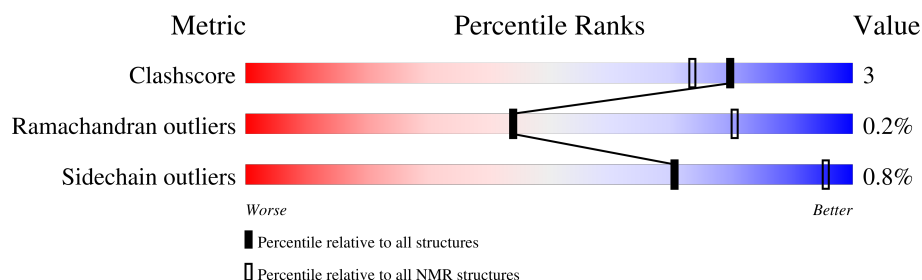
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 95%.

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	96	35% 39% 26%

2 Ensemble composition and analysis

This entry contains 12 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:3-A:73 (71)	0.93	1

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, 6, 11, 12
2	5, 7, 8, 9
Single-model clusters	10

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1451 atoms, of which 708 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Asr1131 protein.

Mol	Chain	Residues	Atoms						Trace
1	A	96	Total	C	H	N	O	S	0
			1449	452	708	132	156	1	

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	expression tag	UNP Q8YXT0
A	-17	SER	-	expression tag	UNP Q8YXT0
A	-16	SER	-	expression tag	UNP Q8YXT0
A	-15	HIS	-	expression tag	UNP Q8YXT0
A	-14	HIS	-	expression tag	UNP Q8YXT0
A	-13	HIS	-	expression tag	UNP Q8YXT0
A	-12	HIS	-	expression tag	UNP Q8YXT0
A	-11	HIS	-	expression tag	UNP Q8YXT0
A	-10	HIS	-	expression tag	UNP Q8YXT0
A	-9	SER	-	expression tag	UNP Q8YXT0
A	-8	SER	-	expression tag	UNP Q8YXT0
A	-7	GLY	-	expression tag	UNP Q8YXT0
A	-6	LEU	-	expression tag	UNP Q8YXT0
A	-5	VAL	-	expression tag	UNP Q8YXT0
A	-4	PRO	-	expression tag	UNP Q8YXT0
A	-3	ARG	-	expression tag	UNP Q8YXT0
A	-2	GLY	-	expression tag	UNP Q8YXT0
A	-1	SER	-	expression tag	UNP Q8YXT0
A	0	HIS	-	expression tag	UNP Q8YXT0

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

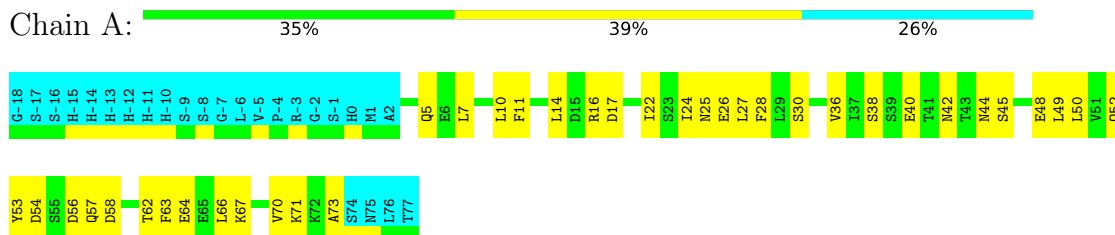
Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2

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.

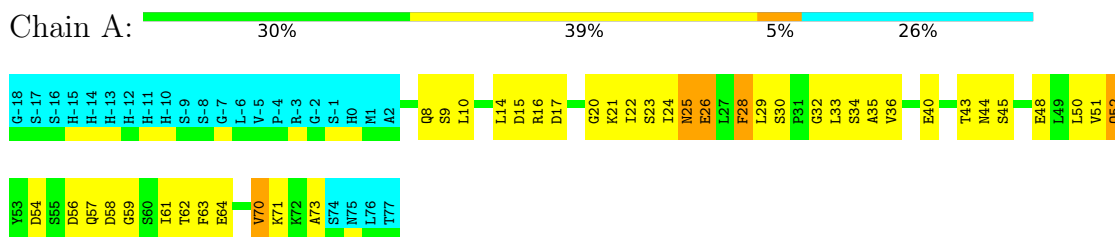
- Molecule 1: Asr1131 protein



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

The representative model is number 1. Colouring as in section 4.1 above.

- Molecule 1: Asr1131 protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *matrix relaxation*.

Of the 12200 calculated structures, 12 were deposited, based on the following criterion: *back calculated data agree with experimental NOESY spectrum*.

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

Software name	Classification	Version
CoMAND	refinement	
X-PLOR NIH	structure calculation	

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	1117
Number of shifts mapped to atoms	1117
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	95%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

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	1.97±0.34	13±6/559 (2.4± 1.1%)	2.47±0.29	41±14/756 (5.4± 1.9%)
All	All	2.00	158/6708 (2.4%)	2.49	487/9072 (5.4%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.9±0.8
All	All	0	11

5 of 126 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	30	SER	CA-CB	10.05	1.67	1.52	1	3
1	A	25	ASN	CA-C	9.54	1.65	1.52	5	1
1	A	22	ILE	CA-C	8.48	1.62	1.52	6	2
1	A	52	GLN	N-CA	-8.39	1.35	1.46	9	1
1	A	36	VAL	CA-C	-8.02	1.43	1.52	5	1

5 of 280 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	73	ALA	CA-C-N	13.90	138.90	120.28	8	5
1	A	73	ALA	C-N-CA	13.90	138.90	120.28	8	5
1	A	58	ASP	CA-CB-CG	10.32	122.92	112.60	5	7

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	8	GLN	N-CA-C	10.31	122.52	111.28	7	3
1	A	56	ASP	CA-CB-CG	9.90	122.50	112.60	8	5

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	53	TYR	Sidechain,Peptide	6
1	A	28	PHE	Sidechain	2
1	A	16	ARG	Sidechain	2
1	A	11	PHE	Sidechain	1

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	553	540	540	3±2
2	A	2	0	0	0±0
All	All	6660	6480	6480	36

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 3.

5 of 32 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:ASN:O	1:A:29:LEU:HG	1.07	1.45	1	1
1:A:24:ILE:HG13	1:A:50:LEU:HD22	1.03	1.30	3	1
1:A:7:LEU:HD21	1:A:67:LYS:HA	0.99	1.28	8	1
1:A:7:LEU:CD2	1:A:67:LYS:HA	0.91	1.95	8	2
1:A:54:ASP:OD1	2:A:202:CA:CA	0.88	1.50	6	4

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	71/96 (74%)	69±2 (97±3%)	2±2 (3±3%)	0±0 (0±1%)	44 80
All	All	852/1152 (74%)	825 (97%)	25 (3%)	2 (0%)	44 80

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	57	GLN	2

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	65/86 (76%)	64±1 (99±1%)	0±1 (1±1%)	70 95
All	All	780/1032 (76%)	774 (99%)	6 (1%)	70 95

5 of 6 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	ILE	1
1	A	11	PHE	1
1	A	43	THR	1
1	A	62	THR	1
1	A	14	LEU	1

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 95% for the well-defined parts and 90% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_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	1117
Number of shifts mapped to atoms	1117
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 $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	93	0.12 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	88	0.54 ± 0.14	Should be checked
$^{13}\text{C}'$	85	-0.16 ± 0.14	None needed (< 0.5 ppm)
^{15}N	90	0.51 ± 0.28	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 95%, i.e. 889 atoms were assigned a chemical shift out of a possible 935. 12 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	348/354 (98%)	143/143 (100%)	136/142 (96%)	69/69 (100%)
Sidechain	503/542 (93%)	340/348 (98%)	152/176 (86%)	11/18 (61%)

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	Total	^1H	^{13}C	^{15}N
Aromatic	38/39 (97%)	19/19 (100%)	19/20 (95%)	0/0 (—%)
Overall	889/935 (95%)	502/510 (98%)	307/338 (91%)	80/87 (92%)

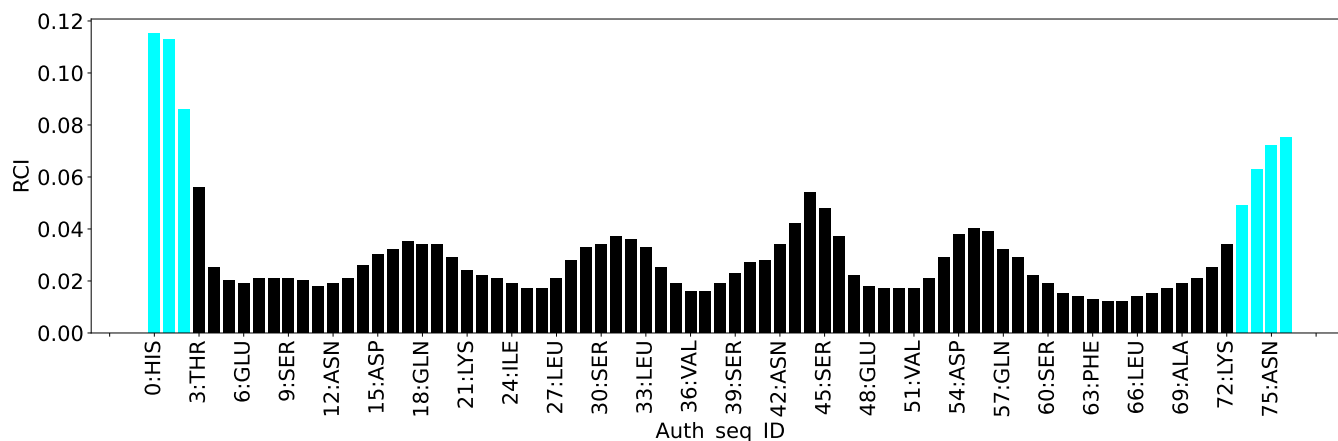
7.1.4 Statistically unusual chemical shifts [i](#)

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	927
Intra-residue ($ i-j =0$)	246
Sequential ($ i-j =1$)	300
Medium range ($ i-j >1$ and $ i-j <5$)	212
Long range ($ i-j \geq 5$)	61
Inter-chain	0
Hydrogen bond restraints	108
Disulfide bond restraints	0
Total dihedral-angle restraints	336
Number of unmapped restraints	0
Number of restraints per residue	12.9
Number of long range restraints per residue ¹	0.8

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)	98.3	0.2
0.2-0.5 (Medium)	118.8	0.5
>0.5 (Large)	64.4	5.39

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)	103.8	9.99
10.0-20.0 (Medium)	42.6	19.94
>20.0 (Large)	31.8	170.55

9 Distance violation analysis ⓘ

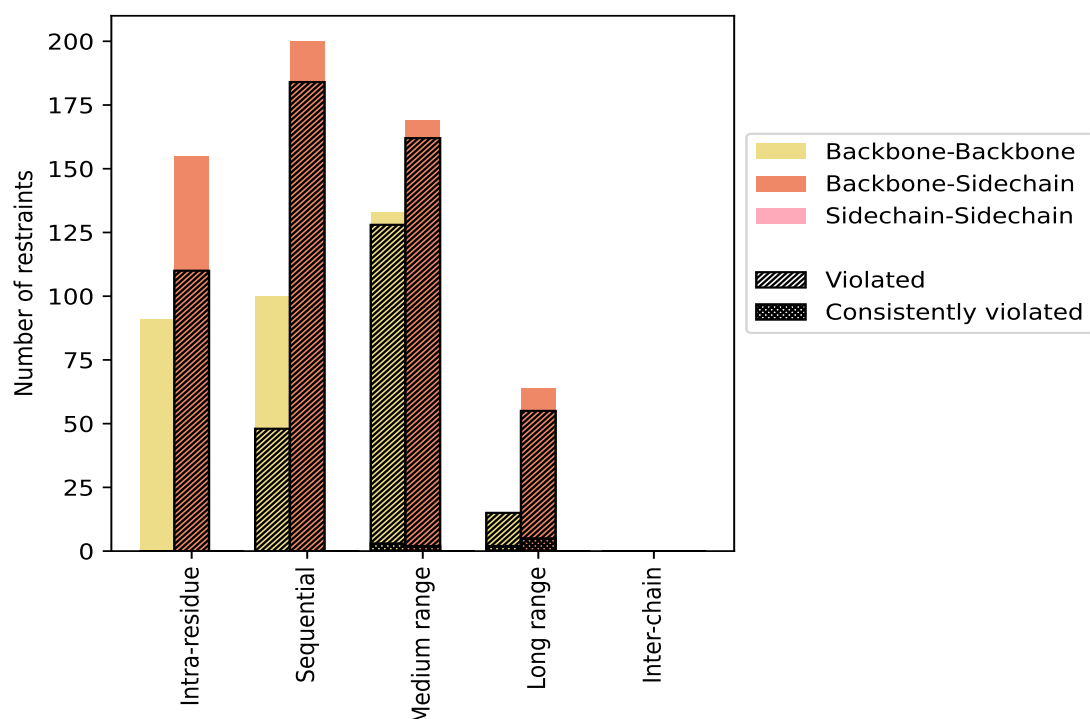
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	246	26.5	110	44.7	11.9	0	0.0	0.0
Backbone-Backbone	91	9.8	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	155	16.7	110	71.0	11.9	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	300	32.4	232	77.3	25.0	0	0.0	0.0
Backbone-Backbone	100	10.8	48	48.0	5.2	0	0.0	0.0
Backbone-Sidechain	200	21.6	184	92.0	19.8	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	212	22.9	203	95.8	21.9	3	1.4	0.3
Backbone-Backbone	133	14.3	128	96.2	13.8	3	2.3	0.3
Backbone-Sidechain	79	8.5	75	94.9	8.1	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range ($i-j \geq 5$)	61	6.6	52	85.2	5.6	5	8.2	0.5
Backbone-Backbone	15	1.6	15	100.0	1.6	2	13.3	0.2
Backbone-Sidechain	46	5.0	37	80.4	4.0	3	6.5	0.3
Sidechain-Sidechain	0	0.0	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	108	11.7	105	97.2	11.3	4	3.7	0.4
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	927	100.0	702	75.7	75.7	12	1.3	1.3
Backbone-Backbone	339	36.6	191	56.3	20.6	5	1.5	0.5
Backbone-Sidechain	588	63.4	511	86.9	55.1	7	1.2	0.8
Sidechain-Sidechain	0	0.0	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 [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	32	88	142	36	0	298	0.45	4.3	0.55	0.25
2	33	88	146	39	0	306	0.39	4.84	0.46	0.23
3	26	81	135	40	0	282	0.47	5.39	0.55	0.29
4	28	79	137	45	0	289	0.44	4.64	0.49	0.27
5	30	91	144	30	0	295	0.37	3.15	0.33	0.26
6	30	87	124	43	0	284	0.42	4.69	0.52	0.25
7	33	75	132	34	0	274	0.39	2.49	0.39	0.26
8	39	91	137	43	0	310	0.42	2.87	0.45	0.24
9	36	70	140	45	0	291	0.47	2.62	0.47	0.28
10	29	58	108	41	0	236	0.49	3.03	0.51	0.3

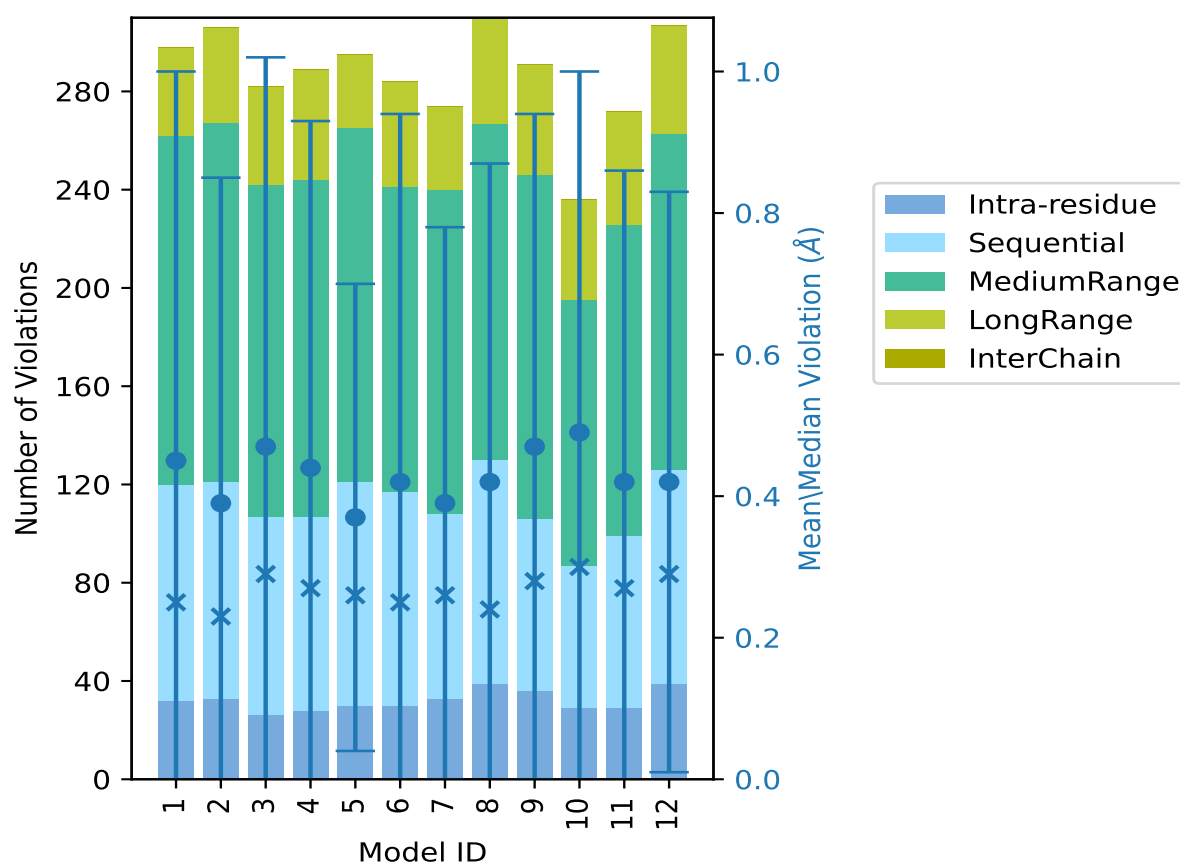
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	29	70	127	46	0	272	0.42	2.75	0.44	0.27
12	39	87	137	44	0	307	0.42	2.54	0.41	0.29

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 [i](#)



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

9.3 Distance violation statistics for the ensemble [i](#)

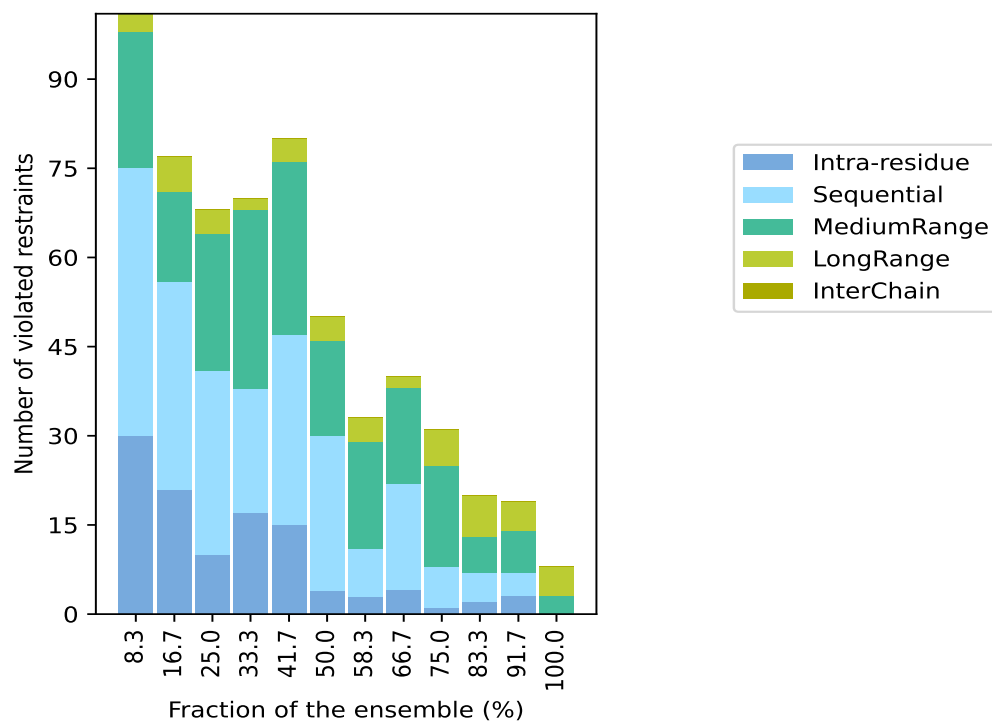
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 222(IR:136, SQ:68, MR:9, LR:9, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
30	45	23	3	0	101	1	8.3
21	35	15	6	0	77	2	16.7
10	31	23	4	0	68	3	25.0
17	21	30	2	0	70	4	33.3
15	32	29	4	0	80	5	41.7
4	26	16	4	0	50	6	50.0
3	8	18	4	0	33	7	58.3
4	18	16	2	0	40	8	66.7
1	7	17	6	0	31	9	75.0
2	5	6	7	0	20	10	83.3
3	4	7	5	0	19	11	91.7
0	0	3	5	0	8	12	100.0

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

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

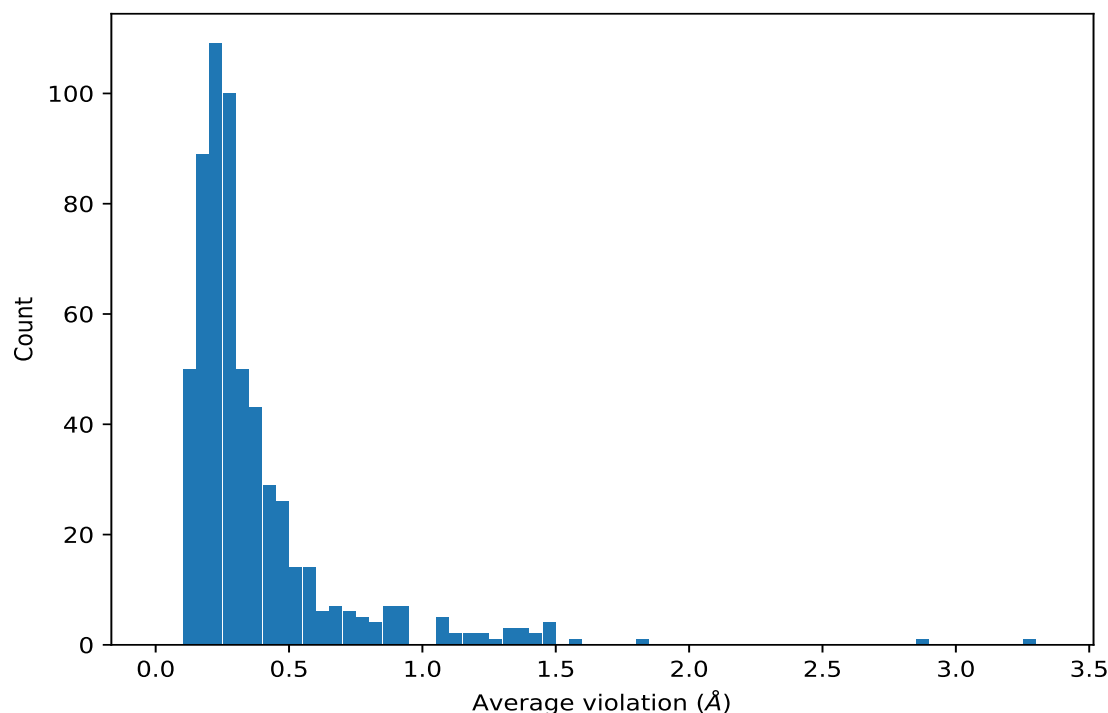
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(4,1)	1:37:A:ILE:H	1:49:A:LEU:CD1	12	1.81	0.92	1.9
(1,5)	1:-16:A:SER:H	1:-18:A:GLY:CA	12	1.41	0.53	1.51
(3,23)	1:18:A:GLN:H	1:15:A:ASP:O	12	1.35	0.72	1.5
(1,302)	1:24:A:ILE:H	1:60:A:SER:CB	12	1.33	0.73	1.25
(1,597)	1:54:A:ASP:H	1:57:A:GLN:CA	12	1.29	0.52	1.29
(3,89)	1:63:A:PHE:H	1:20:A:GLY:O	12	1.21	0.66	1.3
(1,674)	1:63:A:PHE:H	1:21:A:LYS:CB	12	1.18	0.58	1.36
(1,683)	1:63:A:PHE:H	1:20:A:GLY:C	12	1.14	0.64	1.16
(1,301)	1:24:A:ILE:H	1:60:A:SER:CA	12	1.08	0.41	1.15

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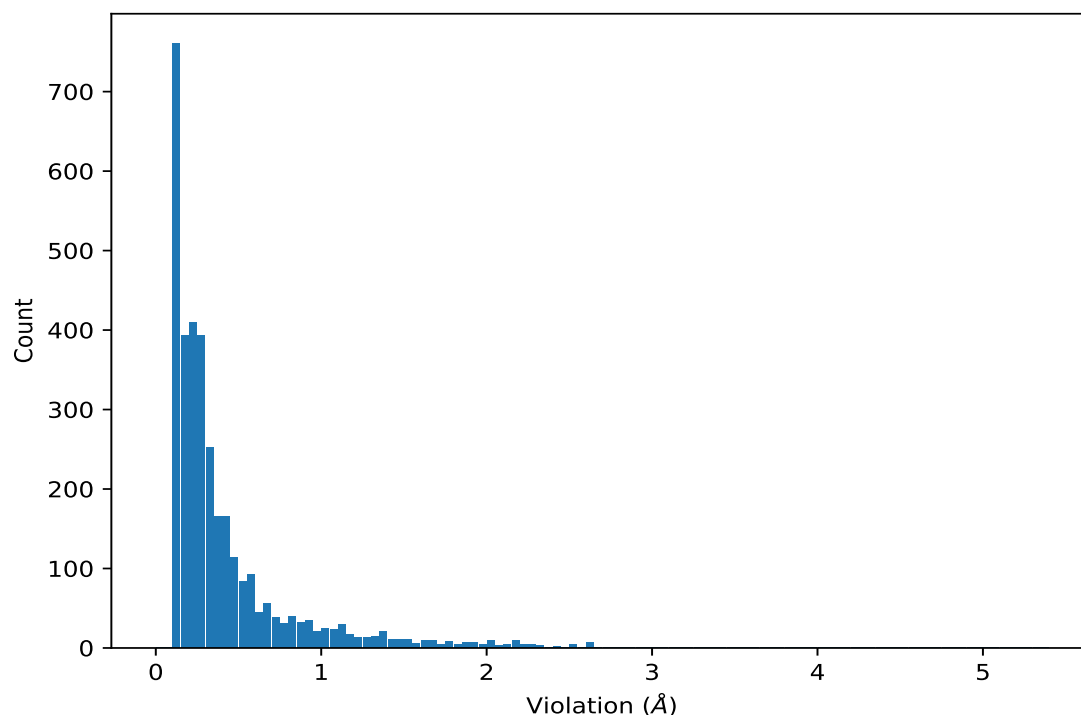
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,90)	1:63:A:PHE:N	1:20:A:GLY:O	12	1.07	0.65	1.14

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)
(2,1)	1:-8:A:SER:H	1:-18:A:GLY:CA	3	5.39
(1,810)	1:76:A:LEU:H	1:1:A:MET:CB	2	4.84
(1,810)	1:76:A:LEU:H	1:1:A:MET:CB	6	4.69
(1,810)	1:76:A:LEU:H	1:1:A:MET:CB	4	4.64

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,810)	1:76:A:LEU:H	1:1:A:MET:CB	1	4.3
(2,1)	1:-8:A:SER:H	1:-18:A:GLY:CA	6	3.93
(4,1)	1:37:A:ILE:H	1:49:A:LEU:CD1	3	3.37
(1,84)	1:2:A:ALA:H	1:40:A:GLU:CB	1	3.16
(1,810)	1:76:A:LEU:H	1:1:A:MET:CB	5	3.15
(1,810)	1:76:A:LEU:H	1:1:A:MET:CB	3	3.09

10 Dihedral-angle violation analysis ⓘ

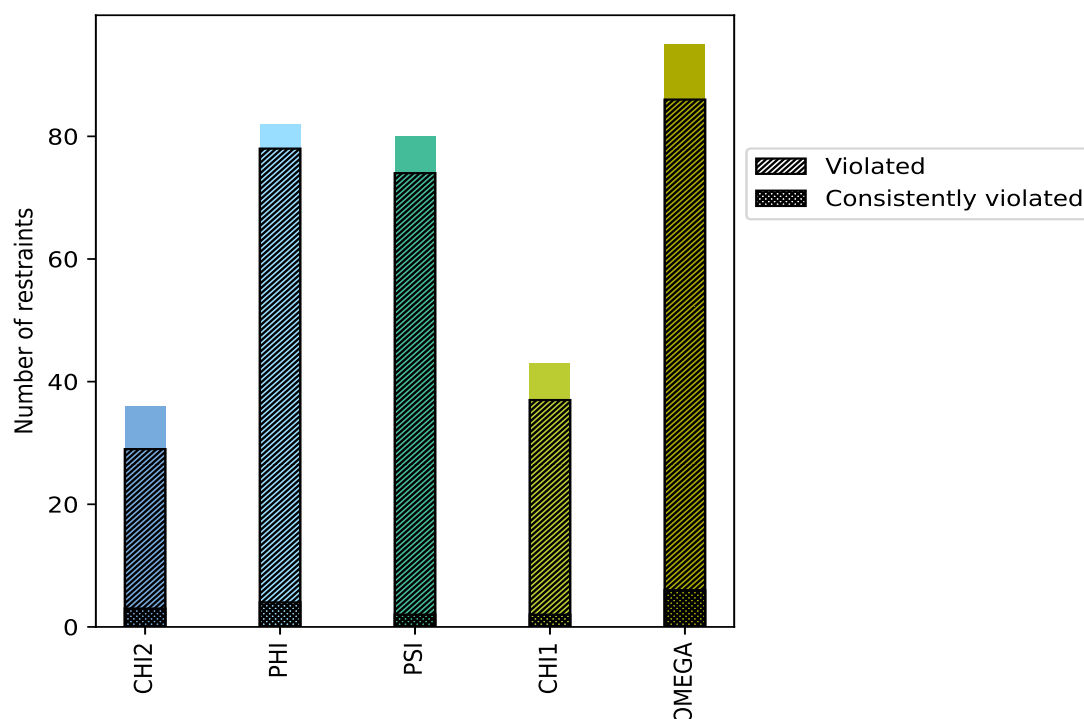
10.1 Summary of dihedral-angle violations ⓘ

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
CHI2	36	10.7	29	80.6	8.6	3	8.3	0.9
PHI	82	24.4	78	95.1	23.2	4	4.9	1.2
PSI	80	23.8	74	92.5	22.0	2	2.5	0.6
CHI1	43	12.8	37	86.0	11.0	2	4.7	0.6
OMEGA	95	28.3	86	90.5	25.6	6	6.3	1.8
Total	336	100.0	304	90.5	90.5	17	5.1	5.1

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

10.1.1 Bar chart : Distribution of dihedral-angles and violations ⓘ



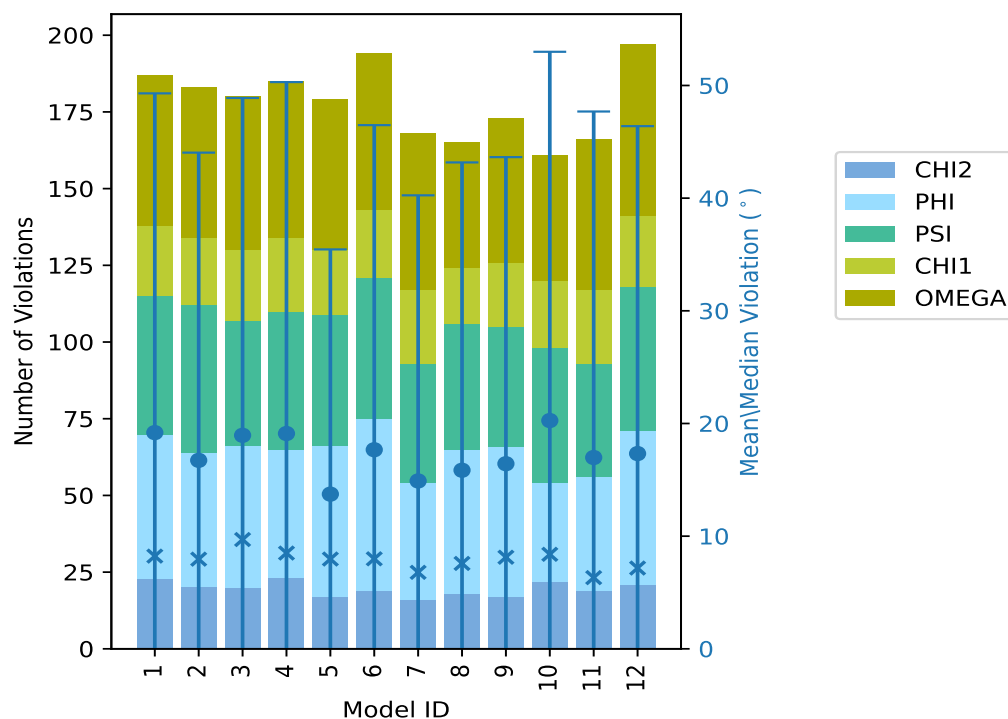
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model [i](#)

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations						Mean (°)	Max (°)	SD (°)	Median (°)
	CHI2	PHI	PSI	CHI1	OMEGA	Total				
1	23	47	45	23	49	187	19.19	155.69	30.11	8.23
2	20	44	48	22	49	183	16.73	170.55	27.31	7.96
3	20	46	41	23	50	180	18.95	168.85	29.94	9.7
4	23	42	45	24	51	185	19.11	162.82	31.19	8.5
5	17	49	43	21	49	179	13.73	158.15	21.72	7.97
6	19	56	46	22	51	194	17.67	161.1	28.81	7.99
7	16	38	39	24	51	168	14.9	155.65	25.35	6.79
8	18	47	41	18	41	165	15.85	169.65	27.32	7.58
9	17	49	39	21	47	173	16.43	157.32	27.21	8.13
10	22	32	44	22	41	161	20.26	162.42	32.73	8.39
11	19	37	37	24	49	166	16.98	154.65	30.71	6.32
12	21	50	47	23	56	197	17.33	168.67	29.06	7.17

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

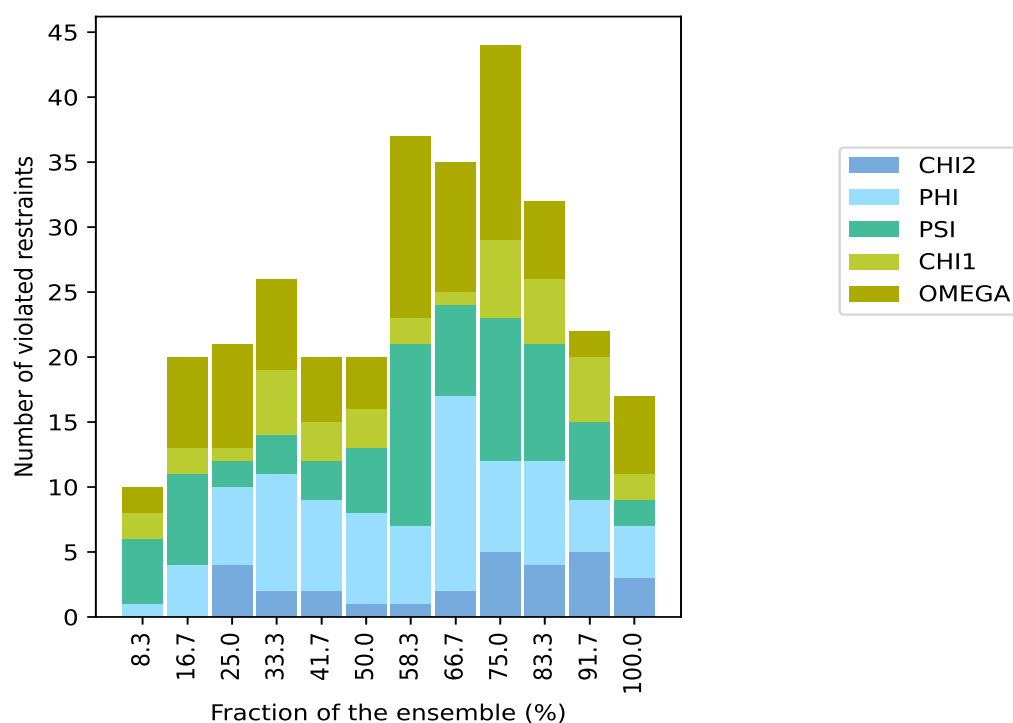
10.3 Dihedral-angle violation statistics for the ensemble [i](#)

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	
CHI2	PHI	PSI	CHI1	OMEGA	Total	Count ¹	%
0	1	5	2	2	10	1	8.3
0	4	7	2	7	20	2	16.7
4	6	2	1	8	21	3	25.0
2	9	3	5	7	26	4	33.3
2	7	3	3	5	20	5	41.7
1	7	5	3	4	20	6	50.0
1	6	14	2	14	37	7	58.3
2	15	7	1	10	35	8	66.7
5	7	11	6	15	44	9	75.0
4	8	9	5	6	32	10	83.3
5	4	6	5	2	22	11	91.7
3	4	2	2	6	17	12	100.0

¹ Number of models with violations

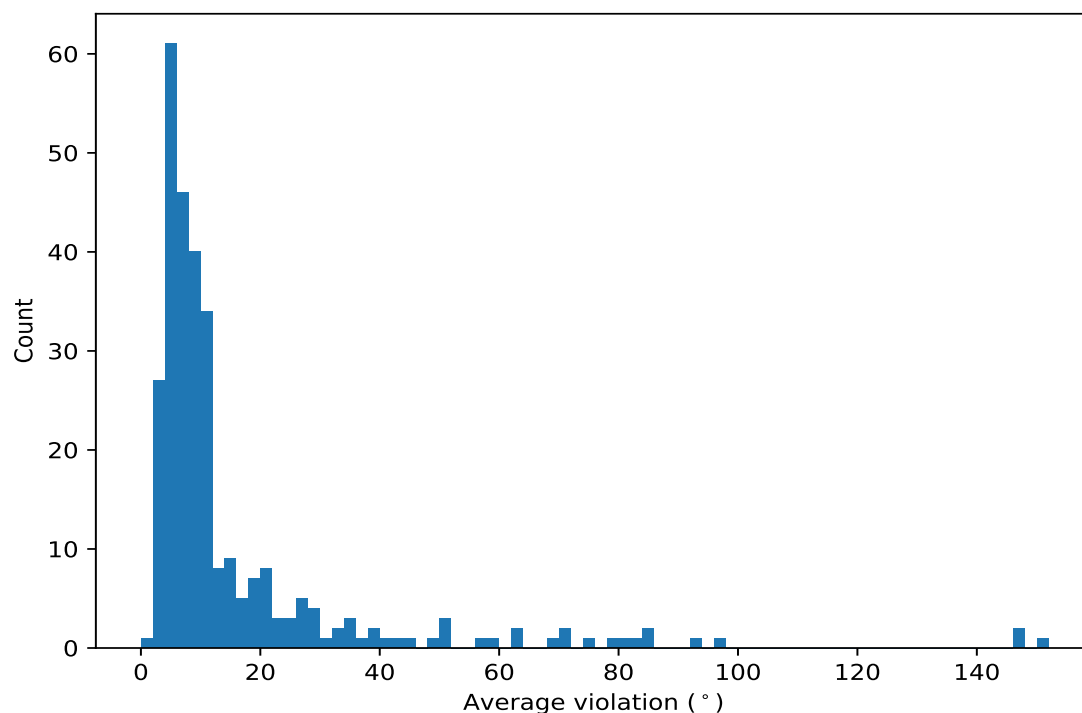
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

10.4.1 Histogram : Distribution of mean dihedral-angle violations [i](#)

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



10.4.2 Table: Most violated dihedral-angle restraints [i](#)

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

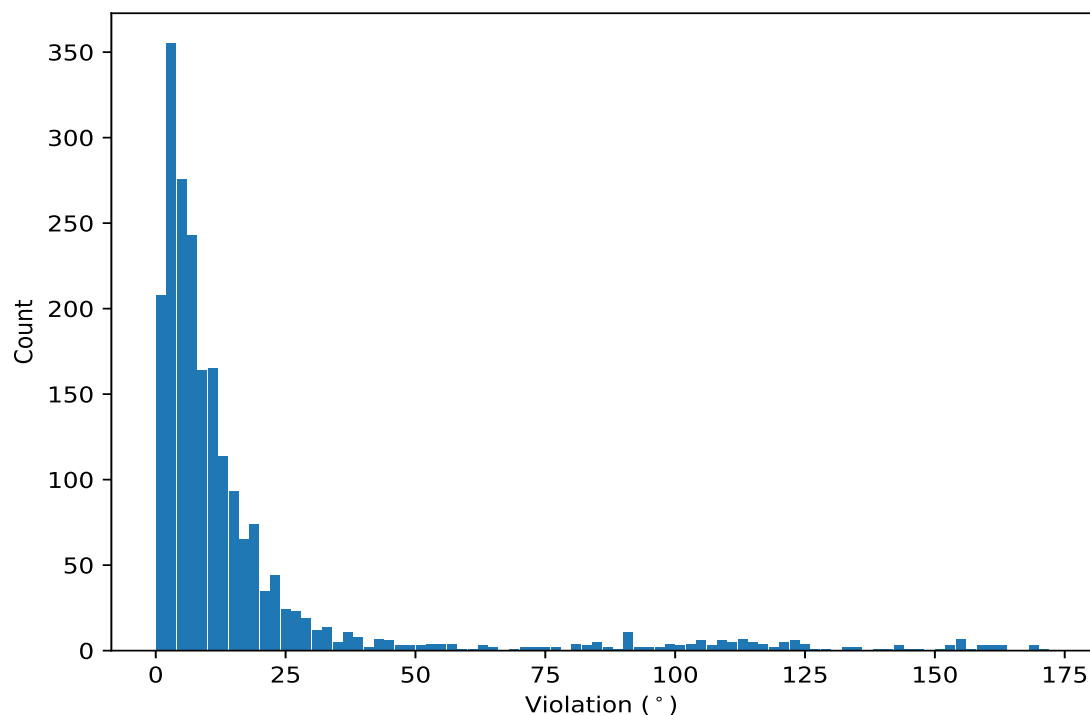
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,46)	1:-3:A:ARG:C	1:-2:A:GLY:N	1:-2:A:GLY:CA	1:-2:A:GLY:C	12	150.17	13.78	152.85
(1,4)	1:-17:A:SER:C	1:-16:A:SER:N	1:-16:A:SER:CA	1:-16:A:SER:C	12	147.68	17.89	155.65
(1,2)	1:-17:A:SER:N	1:-17:A:SER:CA	1:-17:A:SER:C	1:-16:A:SER:N	12	146.41	22.69	154.43
(1,29)	1:-10:A:HIS:C	1:-9:A:SER:N	1:-9:A:SER:CA	1:-9:A:SER:C	12	85.31	24.91	91.06
(1,24)	1:-11:A:HIS:C	1:-10:A:HIS:N	1:-10:A:HIS:CA	1:-10:A:HIS:C	12	74.97	26.97	88.44
(1,192)	1:37:A:ILE:CA	1:37:A:ILE:CB	1:37:A:ILE:CG1	1:37:A:ILE:CD1	12	68.82	51.91	105.82
(1,134)	1:21:A:LYS:N	1:21:A:LYS:CA	1:21:A:LYS:CB	1:21:A:LYS:CG	12	36.2	47.93	9.25
(1,64)	1:4:A:GLU:N	1:4:A:GLU:CA	1:4:A:GLU:CB	1:4:A:GLU:CG	12	29.18	34.43	16.91
(1,123)	1:18:A:GLN:N	1:18:A:GLN:CA	1:18:A:GLN:C	1:19:A:ASP:N	12	20.48	7.63	22.66
(1,127)	1:19:A:ASP:CA	1:19:A:ASP:CB	1:19:A:ASP:CG	1:19:A:ASP:OD1	12	18.9	12.96	17.5

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 (°)
(1,46)	1:-3:A:ARG:C	1:-2:A:GLY:N	1:-2:A:GLY:CA	1:-2:A:GLY:C	2	170.55
(1,4)	1:-17:A:SER:C	1:-16:A:SER:N	1:-16:A:SER:CA	1:-16:A:SER:C	8	169.65
(1,2)	1:-17:A:SER:N	1:-17:A:SER:CA	1:-17:A:SER:C	1:-16:A:SER:N	3	168.85
(1,119)	1:17:A:ASP:CA	1:17:A:ASP:CB	1:17:A:ASP:CG	1:17:A:ASP:OD1	12	168.67
(1,2)	1:-17:A:SER:N	1:-17:A:SER:CA	1:-17:A:SER:C	1:-16:A:SER:N	4	162.82
(1,46)	1:-3:A:ARG:C	1:-2:A:GLY:N	1:-2:A:GLY:CA	1:-2:A:GLY:C	10	162.42
(1,4)	1:-17:A:SER:C	1:-16:A:SER:N	1:-16:A:SER:CA	1:-16:A:SER:C	3	162.03
(1,2)	1:-17:A:SER:N	1:-17:A:SER:CA	1:-17:A:SER:C	1:-16:A:SER:N	6	161.1
(1,2)	1:-17:A:SER:N	1:-17:A:SER:CA	1:-17:A:SER:C	1:-16:A:SER:N	12	160.46
(1,46)	1:-3:A:ARG:C	1:-2:A:GLY:N	1:-2:A:GLY:CA	1:-2:A:GLY:C	8	160.4