wwPDB NMR Structure Validation Summary Report (i)

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BMRB ID	:	27435
Title	:	NMR Solution Structure of the Monomeric Form of the Phage L Decoration Protein
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Deposited on	:	2018-07-13

This is a wwPDB NMR Structure Validation Summary 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 (1)) were used in the production of this report:

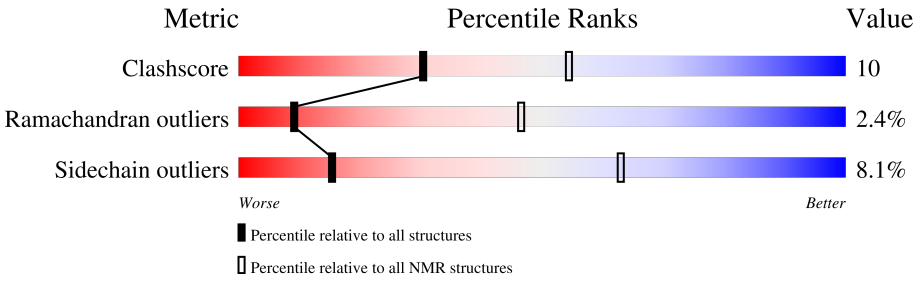
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal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

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment is 77%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	C	137	45% 9% • 42% •

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	C:12-C:87 (76)	1.73	2

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 4 clusters and 2 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1933 atoms, of which 940 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Dec protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	C	134	1933	625	940	157	208	3	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q5C838
C	-1	SER	-	expression tag	UNP Q5C838
C	0	HIS	-	expression tag	UNP Q5C838

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: Dec protein

Chain C: 45% 9% • 42% •

GLY SER HIS M1 A2 N3 P4 N5 F6 T7 P8 S9 W10 P11 L12 Y13 K14 D15 A16 V19 Y20 V21 K27 N38 D47 S51 K59 P60 F82 Y86 T87 S88 A89 S90 G91 S92 V93 A94 N95 A96 E97 T98 A99 D100 K101 L102 S103 T104 A105 R106 T107 I108

T109 L110 T111 G112 A113 V114 T115 G116 S117 A118 S119 F120 D121 G122 S123 A124 N125 V126 T127 I128 E129 T130 T131 S132 G133 S134

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

The representative model is number 2. Colouring as in section 4.1 above.

• Molecule 1: Dec protein

Chain C: 35% 15% 5% 42% •

GLY SER HIS M1 A2 N3 P4 N5 F6 T7 P8 S9 W10 P11 L12 Y13 K14 D15 A16 V19 Y20 V21 L24 P25 I26 K27 A37 E40 F41 A46 D47 Q48 S51 V55 P60 F67 R68 E73 L74 L75 N85 Y86 T87 S88 A89 S90 G91 S92 V93

A94 N95 A96 E97 T98 A99 D100 K101 L102 S103 T104 A105 R106 T107 I108 T109 L110 T111 G112 A113 V114 T115 G116 S117 A118 S119 F120 D121 G122 S123 A124 N125 V126 T127 I128 E129 T130 T131 S132 G133 S134

5 Refinement protocol and experimental data overview (i)

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

Of the 250 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations.*

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

Software name	**Classification**	**Version**
ARIA	refinement	2.3.1
ARIA	structure calculation	2.3.1.

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	1340
Number of shifts mapped to atoms	1321
Number of unparsed shifts	0
Number of shifts with mapping errors	19
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	77%

6 Model quality (i)

6.1 Standard geometry (i)

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 (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	C	593	561	561	11±5
All	All	11860	11220	11220	228

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 10.

5 of 126 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:83:GLU:HA	1:C:86:TYR:CE2	0.73	2.19	15	1
1:C:83:GLU:HA	1:C:86:TYR:CE1	0.72	2.20	3	2
1:C:83:GLU:HA	1:C:87:THR:OG1	0.68	1.88	8	3
1:C:27:LYS:HB3	1:C:40:GLU:O	0.67	1.89	13	3
1:C:15:ASP:HA	1:C:85:ASN:O	0.64	1.91	7	3

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	C	76/137 (55%)	67±2 (88±3%)	7±2 (9±3%)	2±1 (2±1%)	9 46
All	All	1520/2740 (55%)	1343 (88%)	140 (9%)	37 (2%)	9 46

5 of 10 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	C	60	PRO	20
1	C	87	THR	5
1	C	47	ASP	2
1	C	43	GLY	2
1	C	66	LEU	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	C	59/105 (56%)	54±2 (92±3%)	5±2 (8±3%)	15 63
All	All	1180/2100 (56%)	1085 (92%)	95 (8%)	15 63

5 of 27 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	C	51	SER	18
1	C	15	ASP	14
1	C	21	VAL	10
1	C	27	LYS	5
1	C	86	TYR	5

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 77% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1340
Number of shifts mapped to atoms	1321
Number of unparsed shifts	0
Number of shifts with mapping errors	19
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

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 19) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	C	-2	GLY	HA2	4.323	0.000	1
1	C	-2	GLY	C	174.2	0.000	1
1	C	-2	GLY	CA	45.127	0.000	1
1	C	-1	SER	H	8.161	0.005	1
1	C	-1	SER	HA	4.418	0.010	1
1	C	-1	SER	HB2	3.871	0.009	1
1	C	-1	SER	C	174.236	0.000	1
1	C	-1	SER	CA	58.057	0.000	1
1	C	-1	SER	CB	63.244	0.000	1
1	C	-1	SER	N	115.499	0.009	1
1	C	0	HIS	H	8.615	0.005	1
1	C	0	HIS	HA	4.684	0.004	1
1	C	0	HIS	HB2	3.116	0.004	2
1	C	0	HIS	HB3	3.21	0.001	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	C	0	HIS	HD2	7.31	0.000	1
1	C	0	HIS	C	174.24	0.000	1
1	C	0	HIS	CA	55.16	0.000	1
1	C	0	HIS	CB	28.529	0.000	1
1	C	0	HIS	N	120.244	0.059	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	137	0.32 ± 0.08	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	123	0.80 ± 0.11	Should be checked
$^{13}C'$	137	0.12 ± 0.11	None needed (< 0.5 ppm)
^{15}N	130	0.48 ± 0.30	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 77%, i.e. 760 atoms were assigned a chemical shift out of a possible 987. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	378/380 (99%)	153/155 (99%)	152/152 (100%)	73/73 (100%)
Sidechain	352/486 (72%)	246/318 (77%)	100/154 (65%)	6/14 (43%)
Aromatic	30/121 (25%)	30/56 (54%)	0/65 (0%)	0/0 (—%)
Overall	760/987 (77%)	429/529 (81%)	252/371 (68%)	79/87 (91%)

7.1.4 Statistically unusual chemical shifts (i)

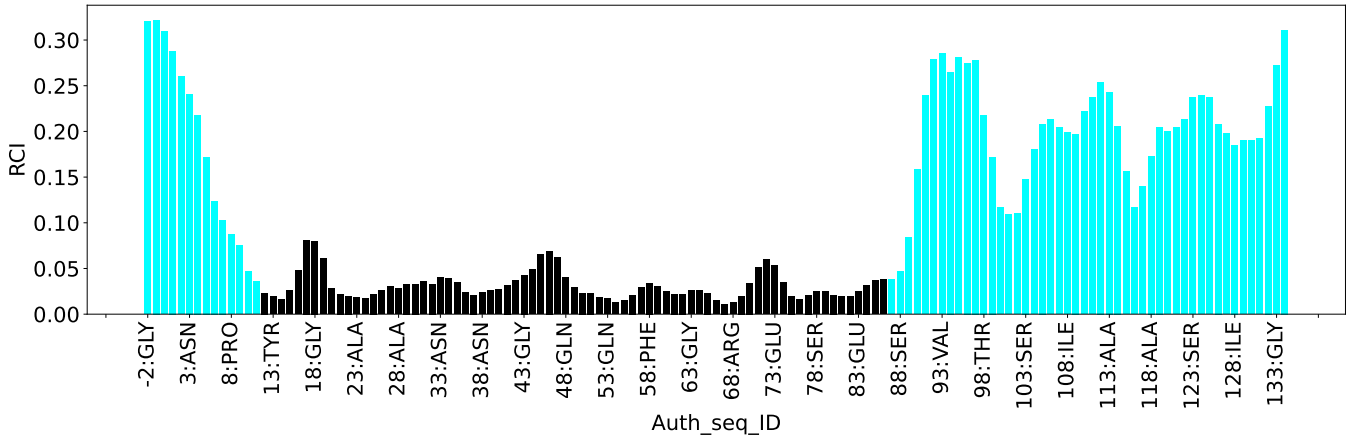
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	C	24	LEU	HD21	-1.92	-0.65 – 2.13	-9.6
1	C	24	LEU	HD22	-1.92	-0.65 – 2.13	-9.6
1	C	24	LEU	HD23	-1.92	-0.65 – 2.13	-9.6

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 C:



8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	891
Intra-residue (|i-j|=0)	276
Sequential (|i-j|=1)	344
Medium range (|i-j|>1 and |i-j|<5)	94
Long range (|i-j|≥5)	110
Inter-chain	0
Hydrogen bond restraints	67
Disulfide bond restraints	0
Total dihedral-angle restraints	174
Number of unmapped restraints	0
Number of restraints per residue	7.8
Number of long range restraints per residue[1]	1.0

[1]Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations (i)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model (i)

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	40.3	0.2
0.2-0.5 (Medium)	27.1	0.5
>0.5 (Large)	16.9	3.12

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)	5.5	4.9
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis (i)

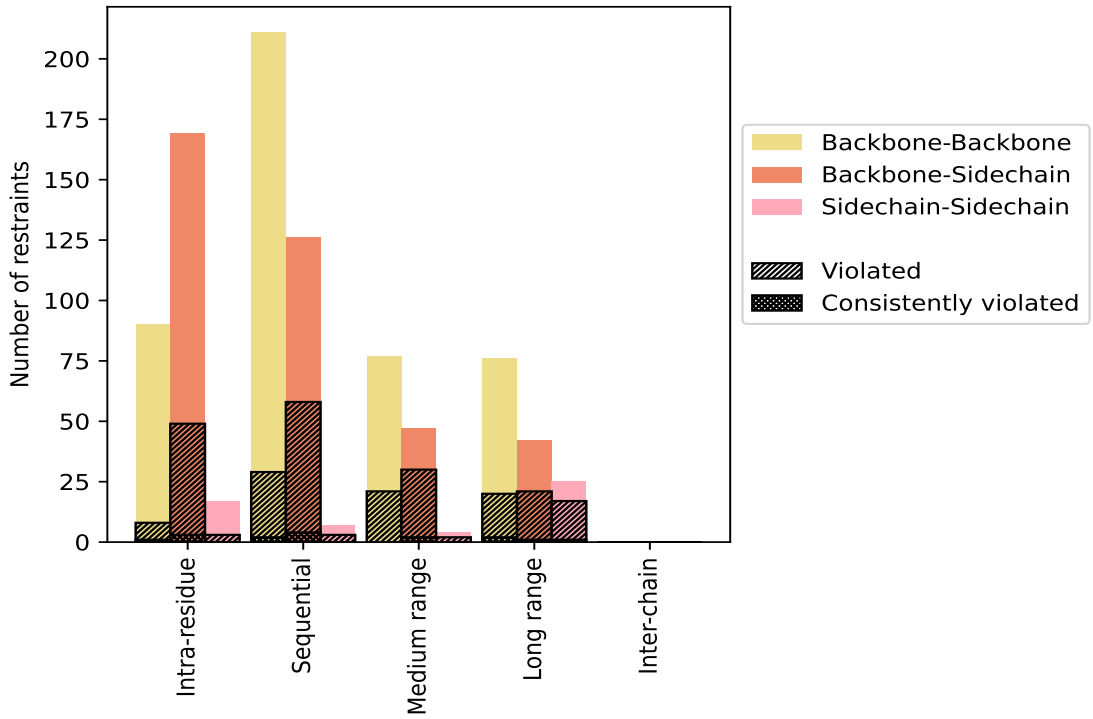
9.1 Summary of distance violations (i)

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

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	276	31.0	60	21.7	6.7	4	1.4	0.4
Backbone-Backbone	90	10.1	8	8.9	0.9	1	1.1	0.1
Backbone-Sidechain	169	19.0	49	29.0	5.5	3	1.8	0.3
Sidechain-Sidechain	17	1.9	3	17.6	0.3	0	0.0	0.0
Sequential (|i-j|=1)	344	38.6	90	26.2	10.1	6	1.7	0.7
Backbone-Backbone	211	23.7	29	13.7	3.3	2	0.9	0.2
Backbone-Sidechain	126	14.1	58	46.0	6.5	4	3.2	0.4
Sidechain-Sidechain	7	0.8	3	42.9	0.3	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	94	10.5	47	50.0	5.3	2	2.1	0.2
Backbone-Backbone	43	4.8	15	34.9	1.7	0	0.0	0.0
Backbone-Sidechain	47	5.3	30	63.8	3.4	2	4.3	0.2
Sidechain-Sidechain	4	0.4	2	50.0	0.2	0	0.0	0.0
Long range (|i-j|≥5)	110	12.3	51	46.4	5.7	4	3.6	0.4
Backbone-Backbone	43	4.8	13	30.2	1.5	2	4.7	0.2
Backbone-Sidechain	42	4.7	21	50.0	2.4	1	2.4	0.1
Sidechain-Sidechain	25	2.8	17	68.0	1.9	1	4.0	0.1
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	67	7.5	13	19.4	1.5	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	891	100.0	261	29.3	29.3	16	1.8	1.8
Backbone-Backbone	454	51.0	78	17.2	8.8	5	1.1	0.6
Backbone-Sidechain	384	43.1	158	41.1	17.7	10	2.6	1.1
Sidechain-Sidechain	53	5.9	25	47.2	2.8	1	1.9	0.1

[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	17	32	14	19	0	82	0.37	2.01	0.38	0.22
2	22	26	12	22	0	82	0.38	1.88	0.37	0.21
3	24	32	19	17	0	92	0.37	3.12	0.43	0.21
4	21	32	19	18	0	90	0.36	2.32	0.38	0.19
5	20	29	12	17	0	78	0.36	1.5	0.33	0.22
6	21	32	14	18	0	85	0.35	2.52	0.38	0.23
7	18	36	14	15	0	83	0.36	2.01	0.37	0.18
8	17	35	14	23	0	89	0.31	1.62	0.34	0.17
9	21	29	15	23	0	88	0.37	1.93	0.35	0.21
10	19	22	17	20	0	78	0.35	1.81	0.35	0.21
11	19	34	16	23	0	92	0.38	2.17	0.41	0.21

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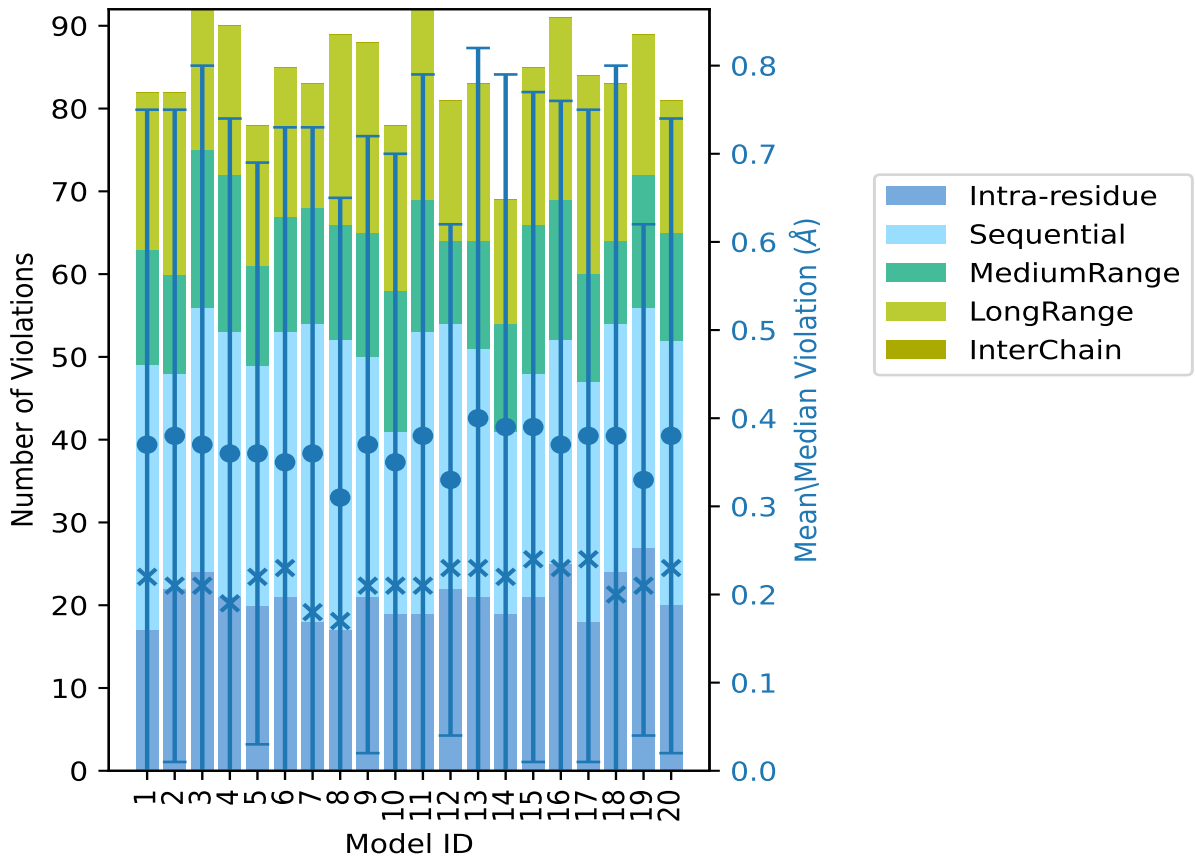
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	22	32	10	17	0	81	0.33	1.43	0.29	0.23
13	21	30	13	19	0	83	0.4	1.96	0.42	0.23
14	19	22	13	15	0	69	0.39	1.96	0.4	0.22
15	21	27	18	19	0	85	0.39	1.98	0.38	0.24
16	25	27	17	22	0	91	0.37	2.22	0.39	0.23
17	18	29	13	24	0	84	0.38	1.82	0.37	0.24
18	24	30	10	19	0	83	0.38	2.61	0.42	0.2
19	27	29	16	17	0	89	0.33	1.44	0.29	0.21
20	20	32	13	16	0	81	0.38	2.31	0.36	0.23

[1]Intra-residue restraints, [2]Sequential restraints, [3]Medium range restraints, [4]Long range restraints, [5]Inter-chain restraints, [6]Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model (i)



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

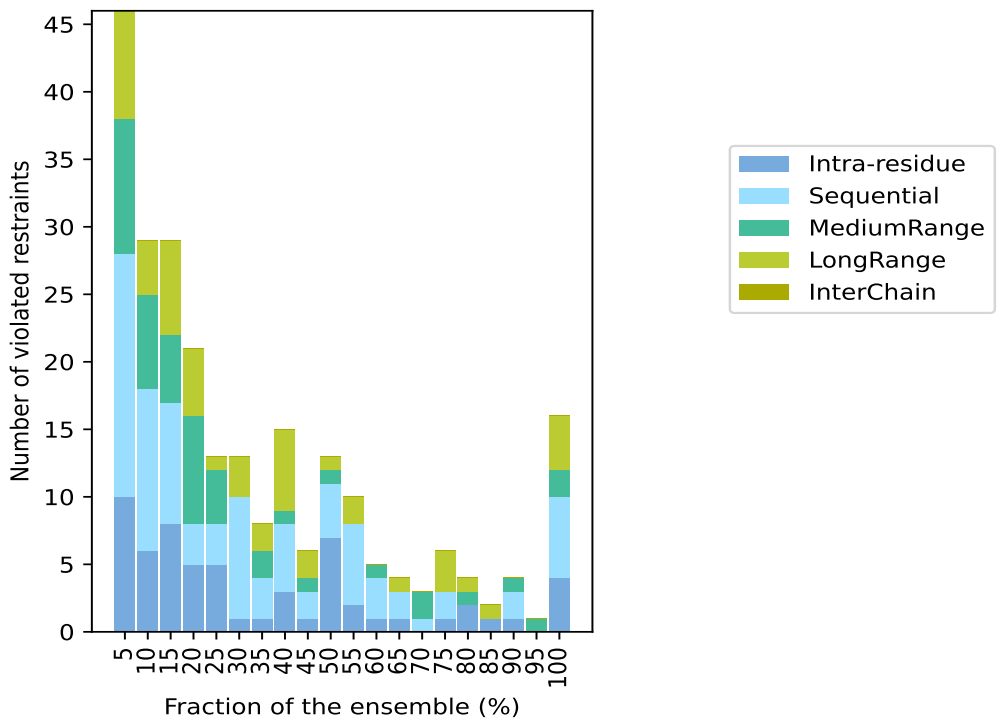
9.3 Distance violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 576(IR:216, SQ:254, MR:47, LR:59, 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]	%
10	18	10	8	0	46	1	5.0
6	12	7	4	0	29	2	10.0
8	9	5	7	0	29	3	15.0
5	3	8	5	0	21	4	20.0
5	3	4	1	0	13	5	25.0
1	9	0	3	0	13	6	30.0
1	3	2	2	0	8	7	35.0
3	5	1	6	0	15	8	40.0
1	2	1	2	0	6	9	45.0
7	4	1	1	0	13	10	50.0
2	6	0	2	0	10	11	55.0
1	3	1	0	0	5	12	60.0
1	2	0	1	0	4	13	65.0
0	1	2	0	0	3	14	70.0
1	2	0	3	0	6	15	75.0
2	0	1	1	0	4	16	80.0
1	0	0	1	0	2	17	85.0
1	2	1	0	0	4	18	90.0
0	0	1	0	0	1	19	95.0
4	6	2	4	0	16	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

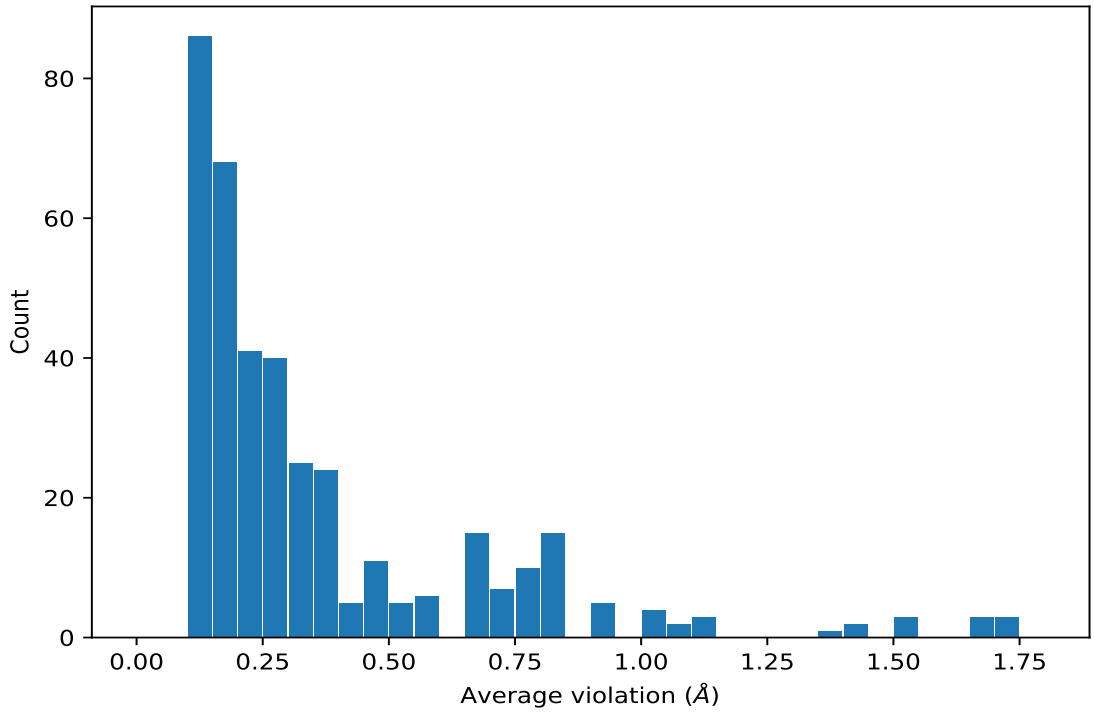
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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.

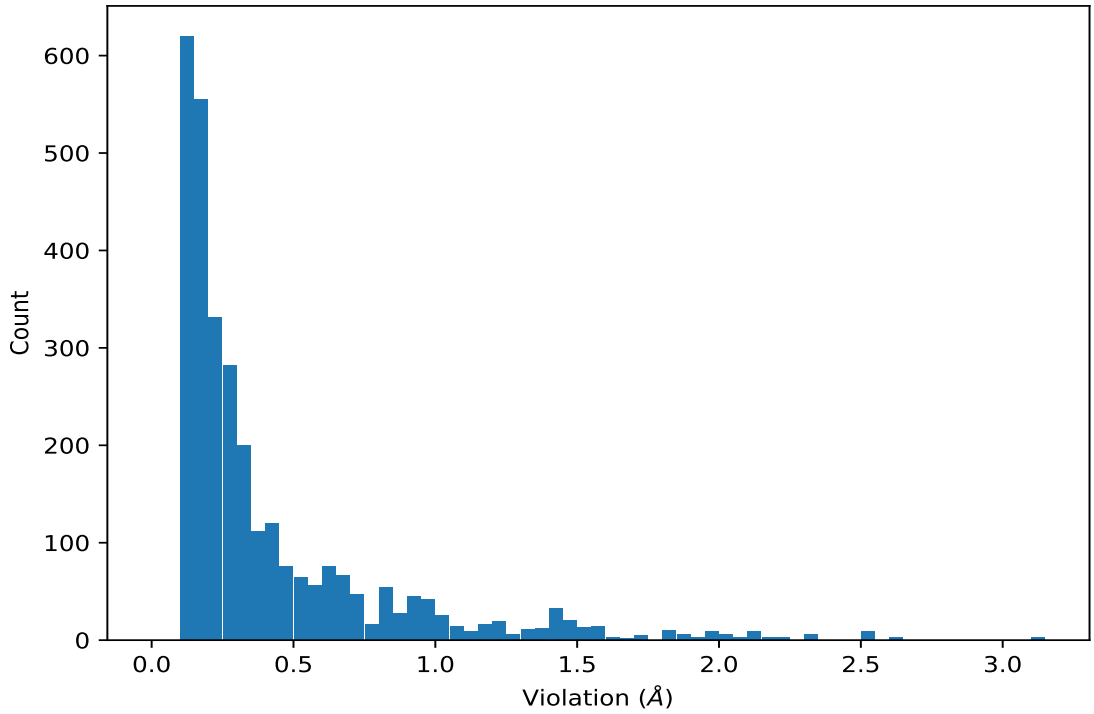
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	20	1.72	0.6	1.49
(4,638)	1:C:21:VAL:HG22	1:C:69:SER:HB2	20	1.72	0.6	1.49
(4,638)	1:C:21:VAL:HG23	1:C:69:SER:HB2	20	1.72	0.6	1.49
(4,335)	1:C:51:SER:HB3	1:C:55:VAL:H	20	1.35	0.24	1.41
(4,632)	1:C:18:GLY:HA2	1:C:17:ASP:HB2	20	0.95	0.04	0.96
(4,729)	1:C:30:LYS:H	1:C:29:ILE:HG13	20	0.82	0.03	0.83
(4,708)	1:C:61:GLU:HB2	1:C:62:VAL:H	20	0.65	0.27	0.73
(4,617)	1:C:16:ALA:HB1	1:C:16:ALA:HA	20	0.42	0.0	0.42
(4,617)	1:C:16:ALA:HB2	1:C:16:ALA:HA	20	0.42	0.0	0.42
(4,617)	1:C:16:ALA:HB3	1:C:16:ALA:HA	20	0.42	0.0	0.42
(4,705)	1:C:55:VAL:HA	1:C:55:VAL:HG11	20	0.31	0.02	0.3
(4,705)	1:C:55:VAL:HA	1:C:55:VAL:HG12	20	0.31	0.02	0.3
(4,705)	1:C:55:VAL:HA	1:C:55:VAL:HG13	20	0.31	0.02	0.3
(4,34)	1:C:32:ALA:H	1:C:33:ASN:H	20	0.31	0.05	0.32
(4,700)	1:C:88:SER:HB3	1:C:88:SER:HA	20	0.28	0.2	0.18
(4,751)	1:C:14:LYS:H	1:C:87:THR:H	20	0.25	0.05	0.26

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

9.5 All violated distance restraints (i)

9.5.1 Histogram : Distribution of distance violations (i)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.



9.5.2 Table : All distance violations (i)

The following table provides the 10 worst performing restraints, sorted by the violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	3	3.12
(4,638)	1:C:21:VAL:HG22	1:C:69:SER:HB2	3	3.12
(4,638)	1:C:21:VAL:HG23	1:C:69:SER:HB2	3	3.12
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	18	2.61
(4,638)	1:C:21:VAL:HG22	1:C:69:SER:HB2	18	2.61
(4,638)	1:C:21:VAL:HG23	1:C:69:SER:HB2	18	2.61
(4,734)	1:C:24:LEU:HD11	1:C:12:LEU:HD11	6	2.52
(4,734)	1:C:24:LEU:HD11	1:C:12:LEU:HD12	6	2.52

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,734)	1:C:24:LEU:HD11	1:C:12:LEU:HD13	6	2.52
(4,734)	1:C:24:LEU:HD12	1:C:12:LEU:HD11	6	2.52
(4,734)	1:C:24:LEU:HD12	1:C:12:LEU:HD12	6	2.52
(4,734)	1:C:24:LEU:HD12	1:C:12:LEU:HD13	6	2.52
(4,734)	1:C:24:LEU:HD13	1:C:12:LEU:HD11	6	2.52
(4,734)	1:C:24:LEU:HD13	1:C:12:LEU:HD12	6	2.52
(4,734)	1:C:24:LEU:HD13	1:C:12:LEU:HD13	6	2.52
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	4	2.32
(4,638)	1:C:21:VAL:HG22	1:C:69:SER:HB2	4	2.32
(4,638)	1:C:21:VAL:HG23	1:C:69:SER:HB2	4	2.32
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	20	2.31
(4,638)	1:C:21:VAL:HG22	1:C:69:SER:HB2	20	2.31
(4,638)	1:C:21:VAL:HG23	1:C:69:SER:HB2	20	2.31
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	16	2.22
(4,638)	1:C:21:VAL:HG22	1:C:69:SER:HB2	16	2.22
(4,638)	1:C:21:VAL:HG23	1:C:69:SER:HB2	16	2.22
(4,692)	1:C:68:ARG:HG2	1:C:74:LEU:HD21	11	2.17
(4,692)	1:C:68:ARG:HG2	1:C:74:LEU:HD22	11	2.17
(4,692)	1:C:68:ARG:HG2	1:C:74:LEU:HD23	11	2.17
(4,734)	1:C:24:LEU:HD11	1:C:12:LEU:HD11	11	2.1
(4,734)	1:C:24:LEU:HD11	1:C:12:LEU:HD12	11	2.1
(4,734)	1:C:24:LEU:HD11	1:C:12:LEU:HD13	11	2.1
(4,734)	1:C:24:LEU:HD12	1:C:12:LEU:HD11	11	2.1
(4,734)	1:C:24:LEU:HD12	1:C:12:LEU:HD12	11	2.1
(4,734)	1:C:24:LEU:HD12	1:C:12:LEU:HD13	11	2.1
(4,734)	1:C:24:LEU:HD13	1:C:12:LEU:HD11	11	2.1
(4,734)	1:C:24:LEU:HD13	1:C:12:LEU:HD12	11	2.1
(4,734)	1:C:24:LEU:HD13	1:C:12:LEU:HD13	11	2.1
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	6	2.07
(4,638)	1:C:21:VAL:HG22	1:C:69:SER:HB2	6	2.07
(4,638)	1:C:21:VAL:HG23	1:C:69:SER:HB2	6	2.07
(4,638)	1:C:21:VAL:HG21	1:C:69:SER:HB2	1	2.01

10 Dihedral-angle violation analysis (i)

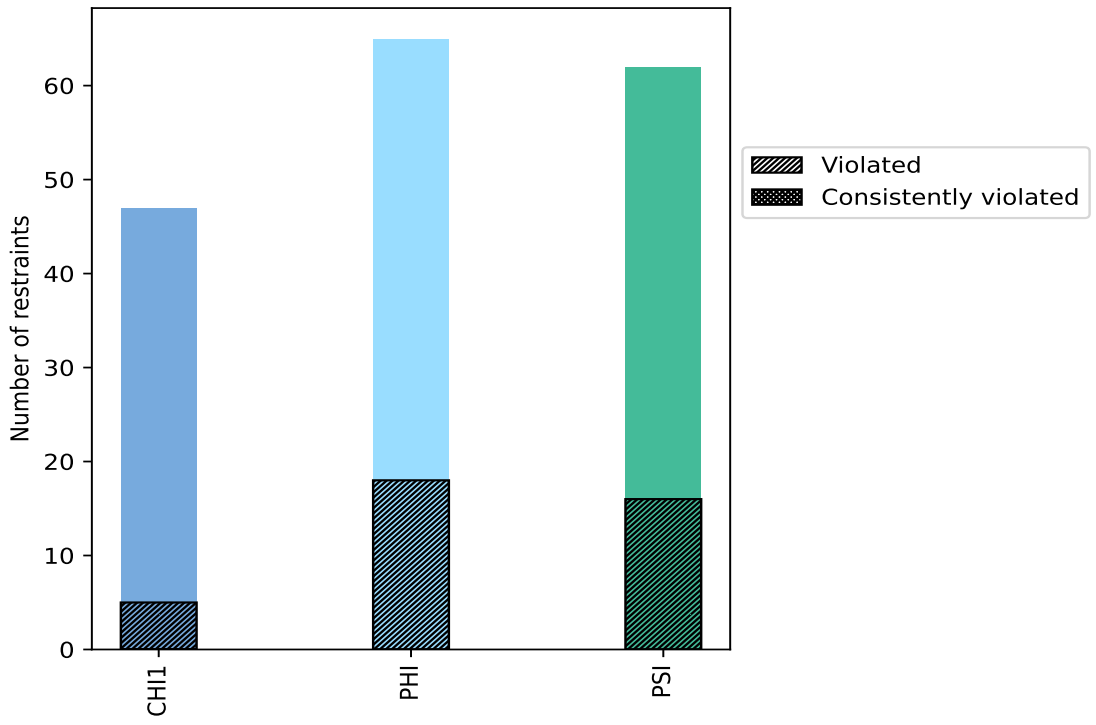
10.1 Summary of dihedral-angle violations (i)

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]
CHI1	47	27.0	5	10.6	2.9	0	0.0	0.0
PHI	65	37.4	18	27.7	10.3	0	0.0	0.0
PSI	62	35.6	16	25.8	9.2	0	0.0	0.0
Total	174	100.0	39	22.4	22.4	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 (i)



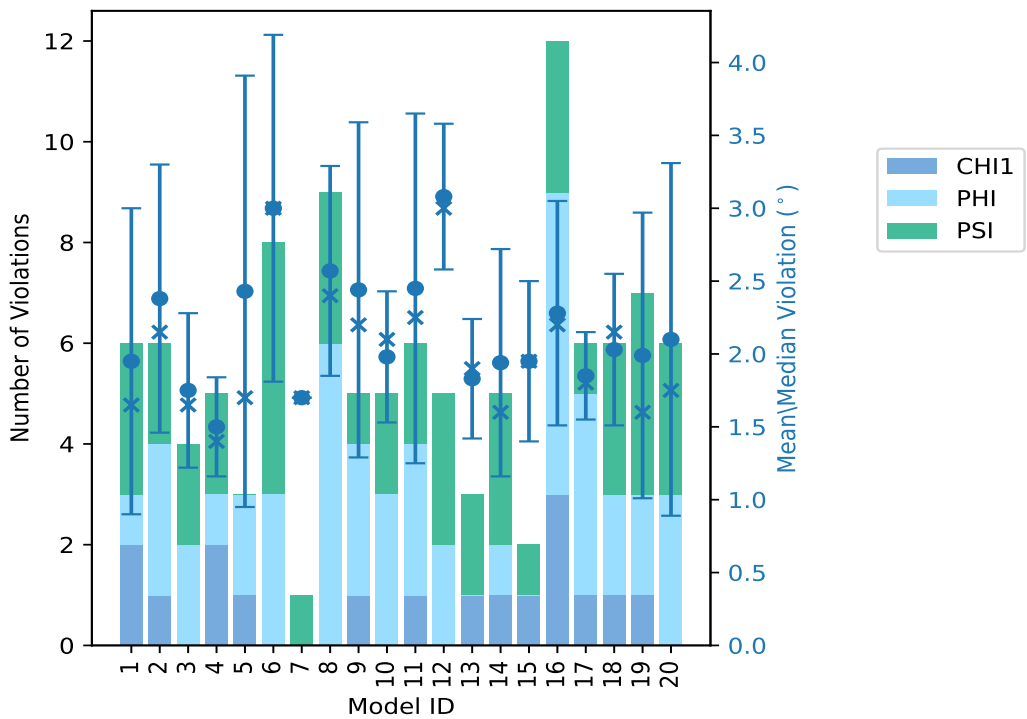
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model (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 (°)
	CHI1	PHI	PSI	Total				
1	2	1	3	6	1.95	4.2	1.05	1.65
2	1	3	2	6	2.38	4.3	0.92	2.15
3	0	2	2	4	1.75	2.5	0.53	1.65
4	2	1	2	5	1.5	2.1	0.34	1.4
5	1	2	0	3	2.43	4.5	1.48	1.7
6	0	3	5	8	3.0	4.9	1.19	3.0
7	0	0	1	1	1.7	1.7	0.0	1.7
8	0	6	3	9	2.57	4.0	0.72	2.4
9	1	3	1	5	2.44	4.6	1.15	2.2
10	0	3	2	5	1.98	2.7	0.45	2.1
11	1	3	2	6	2.45	4.0	1.2	2.25
12	0	2	3	5	3.08	4.0	0.5	3.0
13	1	0	2	3	1.83	2.3	0.41	1.9
14	1	1	3	5	1.94	3.3	0.78	1.6
15	1	0	1	2	1.95	2.5	0.55	1.95
16	3	6	3	12	2.28	3.9	0.77	2.2
17	1	4	1	6	1.85	2.4	0.3	1.8
18	1	2	3	6	2.03	2.6	0.52	2.15
19	1	2	4	7	1.99	4.2	0.98	1.6
20	0	3	3	6	2.1	4.6	1.21	1.75

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	
CHI1	PHI	PSI	Total	Count[1]	%
3	7	4	14	1	5.0
0	4	7	11	2	10.0
0	2	1	3	3	15.0
1	2	0	3	4	20.0
0	2	2	4	5	25.0
0	0	1	1	6	30.0
0	0	0	0	7	35.0
0	1	0	1	8	40.0
0	0	1	1	9	45.0
1	0	0	1	10	50.0
0	0	0	0	11	55.0

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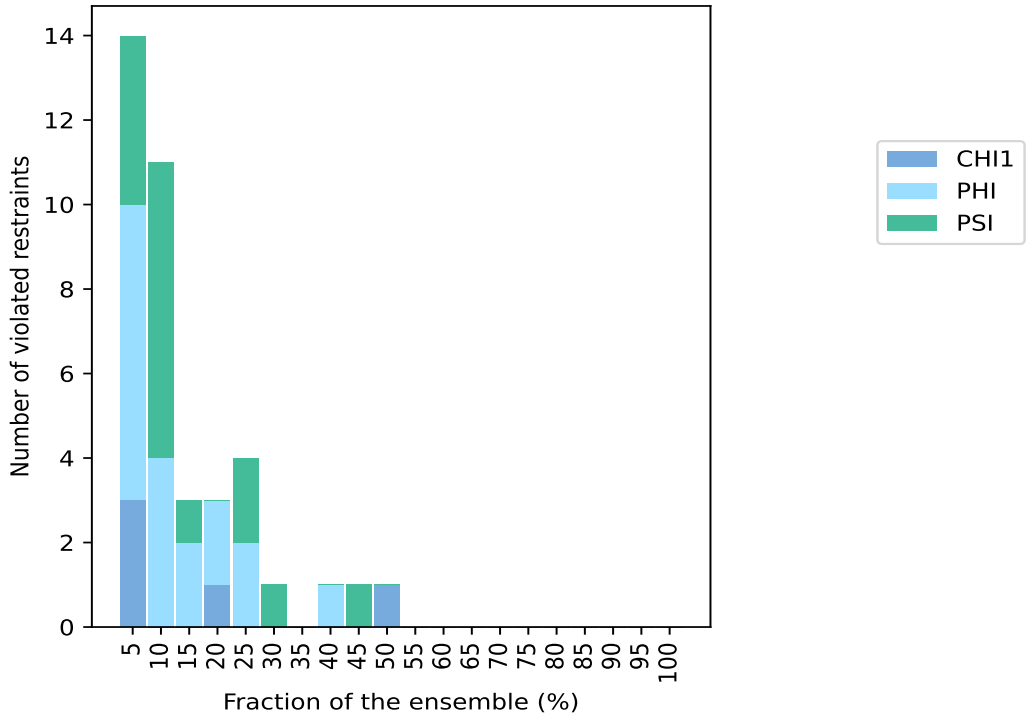
Number of violated restraints				Fraction of the ensemble	
CHI1	PHI	PSI	Total	Count[1]	%
0	0	0	0	12	60.0
0	0	0	0	13	65.0
0	0	0	0	14	70.0
0	0	0	0	15	75.0
0	0	0	0	16	80.0
0	0	0	0	17	85.0
0	0	0	0	18	90.0
0	0	0	0	19	95.0
0	0	0	0	20	100.0

[1] Number of models with violations

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

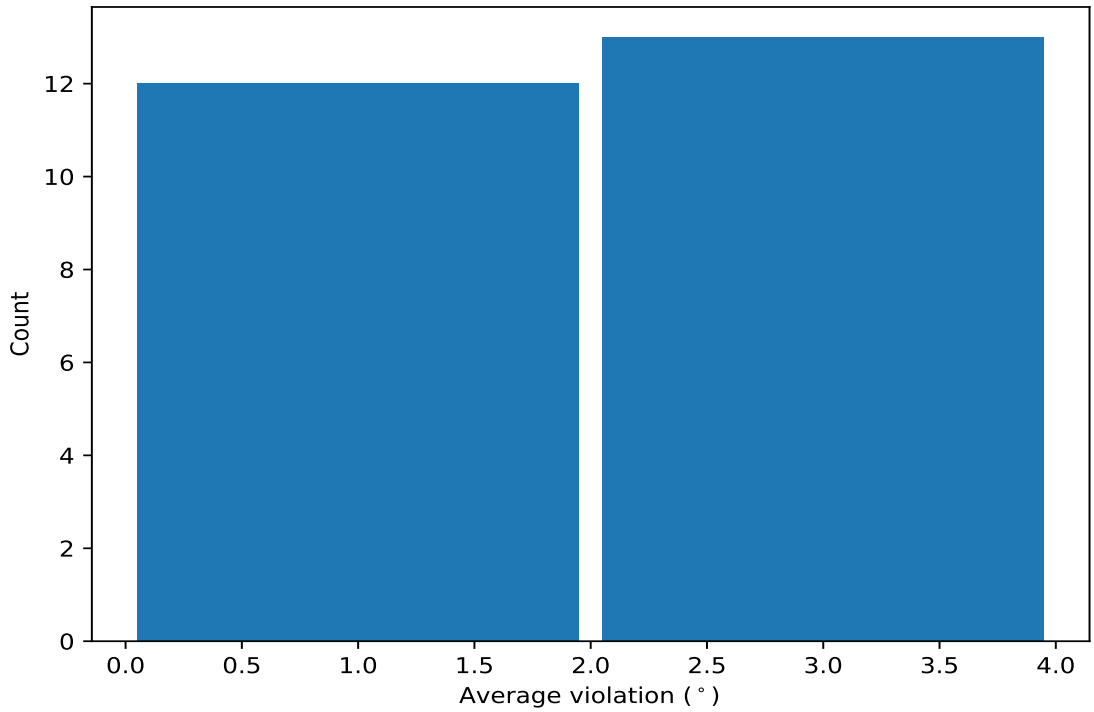


10.4 Most violated dihedral-angle restraints in the ensemble (i)

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.

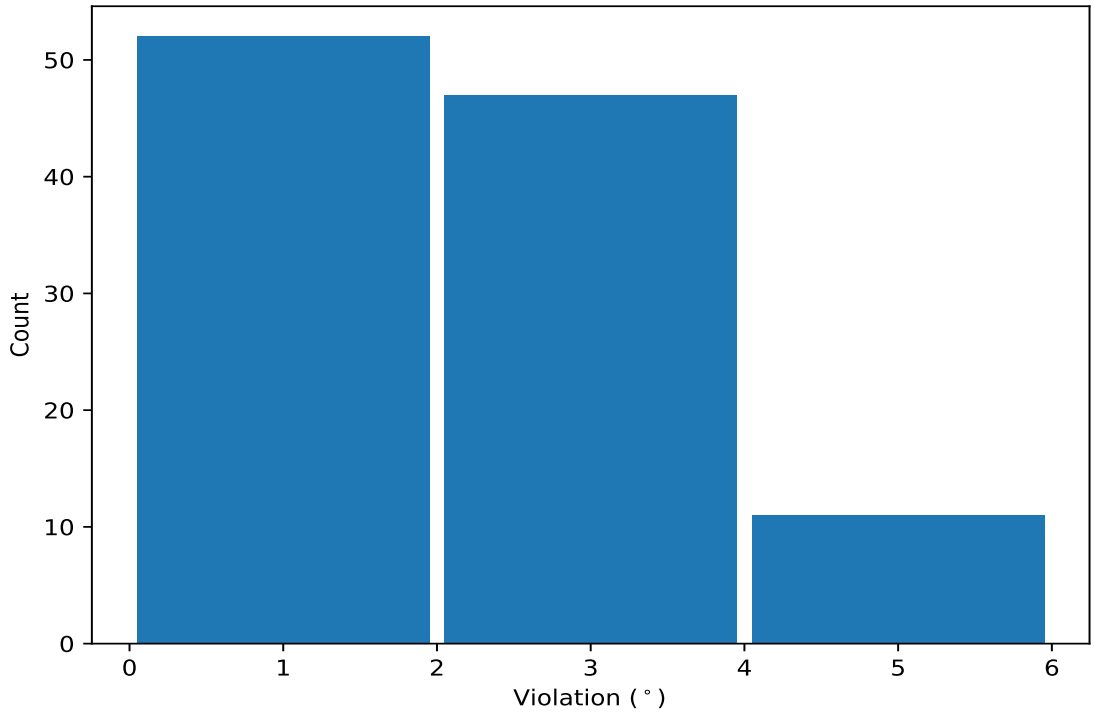
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,131)	1:C:15:ASP:N	1:C:15:ASP:CA	1:C:15:ASP:CB	1:C:15:ASP:CG	10	1.88	0.53	1.8
(1,4)	1:C:11:PRO:N	1:C:11:PRO:CA	1:C:11:PRO:C	1:C:12:LEU:N	9	2.28	1.07	2.1
(1,122)	1:C:86:TYR:C	1:C:87:THR:N	1:C:87:THR:CA	1:C:87:THR:C	8	3.6	1.26	4.25
(1,60)	1:C:45:TYR:N	1:C:45:TYR:CA	1:C:45:TYR:C	1:C:46:ALA:N	6	2.57	0.56	2.6
(1,62)	1:C:46:ALA:N	1:C:46:ALA:CA	1:C:46:ALA:C	1:C:47:ASP:N	5	3.4	0.96	4.0
(1,23)	1:C:20:TYR:C	1:C:21:VAL:N	1:C:21:VAL:CA	1:C:21:VAL:C	5	2.48	0.42	2.7
(1,28)	1:C:24:LEU:N	1:C:24:LEU:CA	1:C:24:LEU:C	1:C:25:PRO:N	5	1.74	0.41	1.7
(1,17)	1:C:17:ASP:C	1:C:18:GLY:N	1:C:18:GLY:CA	1:C:18:GLY:C	5	1.64	0.25	1.7
(1,103)	1:C:75:LEU:C	1:C:76:TYR:N	1:C:76:TYR:CA	1:C:76:TYR:C	4	1.93	0.36	2.1
(1,25)	1:C:22:SER:C	1:C:23:ALA:N	1:C:23:ALA:CA	1:C:23:ALA:C	4	1.72	0.5	1.65

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

10.5 All violated dihedral-angle restraints (i)

10.5.1 Histogram : Distribution of violations (i)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.



10.5.2 Table: All violated dihedral-angle restraints (i)

The following table provides the list of violationsfor the 10 worst performing restraints, sorted by the violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,122)	1:C:86:TYR:C	1:C:87:THR:N	1:C:87:THR:CA	1:C:87:THR:C	6	4.9
(1,122)	1:C:86:TYR:C	1:C:87:THR:N	1:C:87:THR:CA	1:C:87:THR:C	9	4.6
(1,122)	1:C:86:TYR:C	1:C:87:THR:N	1:C:87:THR:CA	1:C:87:THR:C	20	4.6
(1,122)	1:C:86:TYR:C	1:C:87:THR:N	1:C:87:THR:CA	1:C:87:THR:C	5	4.5
(1,62)	1:C:46:ALA:N	1:C:46:ALA:CA	1:C:46:ALA:C	1:C:47:ASP:N	2	4.3
(1,4)	1:C:11:PRO:N	1:C:11:PRO:CA	1:C:11:PRO:C	1:C:12:LEU:N	6	4.3
(1,62)	1:C:46:ALA:N	1:C:46:ALA:CA	1:C:46:ALA:C	1:C:47:ASP:N	1	4.2
(1,54)	1:C:39:ALA:N	1:C:39:ALA:CA	1:C:39:ALA:C	1:C:40:GLU:N	19	4.2
(1,62)	1:C:46:ALA:N	1:C:46:ALA:CA	1:C:46:ALA:C	1:C:47:ASP:N	11	4.0
(1,125)	1:C:100:ASP:C	1:C:101:LYS:N	1:C:101:LYS:CA	1:C:101:LYS:C	8	4.0