



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 5NF8 / pdb_00005nf8
BMRB ID : 34115
Title : Solution structure of detergent-solubilized Rcf1, a yeast mitochondrial inner membrane protein involved in respiratory Complex III/IV supercomplex formation
Authors : Zhou, S.; Pettersson, P.; Sjöholm, J.; Sjöstrand, D.; Hogbom, M.; Brzezinski, P.; Maler, L.; Adelroth, P.
Deposited on : 2017-03-13

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with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

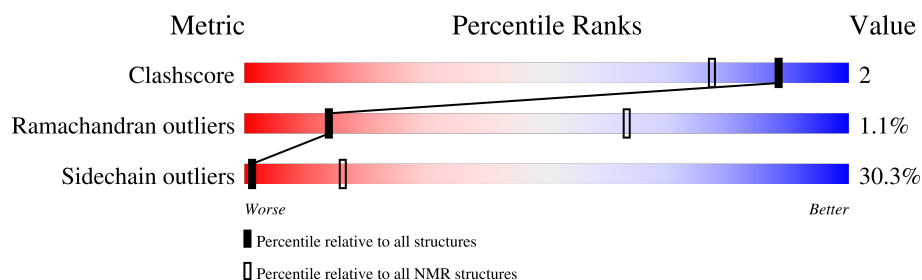
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 40%.

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	174	
1	B	174	

2 Ensemble composition and analysis

This entry contains 15 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:12-A:159, B:12-B:159 (296)	1.91	13

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 4 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5272 atoms, of which 2684 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Respiratory supercomplex factor 1, mitochondrial.

Mol	Chain	Residues	Atoms						Trace
1	A	159	Total	C	H	N	O	S	0
			2636	816	1342	232	239	7	
1	B	159	Total	C	H	N	O	S	0
			2636	816	1342	232	239	7	

There are 30 discrepancies between the modelled and reference sequences:

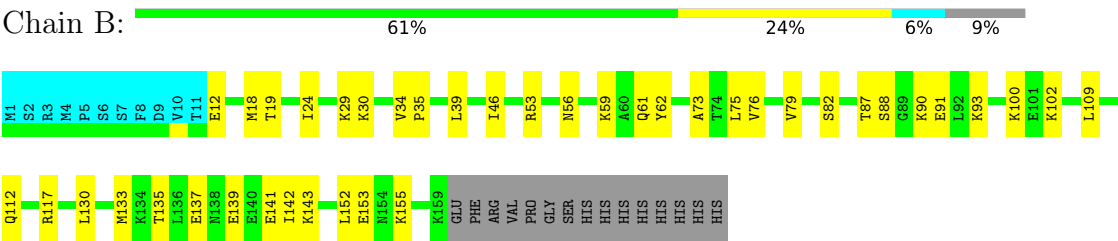
Chain	Residue	Modelled	Actual	Comment	Reference
A	160	GLU	-	expression tag	UNP B3LLM2
A	161	PHE	-	expression tag	UNP B3LLM2
A	162	ARG	-	expression tag	UNP B3LLM2
A	163	VAL	-	expression tag	UNP B3LLM2
A	164	PRO	-	expression tag	UNP B3LLM2
A	165	GLY	-	expression tag	UNP B3LLM2
A	166	SER	-	expression tag	UNP B3LLM2
A	167	HIS	-	expression tag	UNP B3LLM2
A	168	HIS	-	expression tag	UNP B3LLM2
A	169	HIS	-	expression tag	UNP B3LLM2
A	170	HIS	-	expression tag	UNP B3LLM2
A	171	HIS	-	expression tag	UNP B3LLM2
A	172	HIS	-	expression tag	UNP B3LLM2
A	173	HIS	-	expression tag	UNP B3LLM2
A	174	HIS	-	expression tag	UNP B3LLM2
B	160	GLU	-	expression tag	UNP B3LLM2
B	161	PHE	-	expression tag	UNP B3LLM2
B	162	ARG	-	expression tag	UNP B3LLM2
B	163	VAL	-	expression tag	UNP B3LLM2
B	164	PRO	-	expression tag	UNP B3LLM2
B	165	GLY	-	expression tag	UNP B3LLM2
B	166	SER	-	expression tag	UNP B3LLM2
B	167	HIS	-	expression tag	UNP B3LLM2
B	168	HIS	-	expression tag	UNP B3LLM2
B	169	HIS	-	expression tag	UNP B3LLM2
B	170	HIS	-	expression tag	UNP B3LLM2
B	171	HIS	-	expression tag	UNP B3LLM2
B	172	HIS	-	expression tag	UNP B3LLM2
B	173	HIS	-	expression tag	UNP B3LLM2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	174	HIS	-	expression tag	UNP B3LLM2

● Molecule 1: Respiratory supercomplex factor 1, mitochondrial



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 15 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	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	1779
Number of shifts mapped to atoms	1779
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	40%

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	A	1209	1258	1257	3±1
1	B	1209	1258	1257	6±3
All	All	36270	37740	37710	139

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 2.

5 of 72 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:78:LEU:HD11	1:B:95:LYS:HE2	0.81	1.53	4	1
1:B:127:ARG:HA	1:B:130:LEU:HD23	0.71	1.62	5	1
1:B:78:LEU:HD13	1:B:78:LEU:C	0.70	2.11	1	6
1:B:149:LEU:HA	1:B:152:LEU:HD12	0.67	1.66	7	2
1:B:78:LEU:C	1:B:78:LEU:HD13	0.65	2.16	11	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR

entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	147/174 (84%)	137±2 (93±1%)	8±2 (6±1%)	1±1 (1±1%)	15	65
1	B	147/174 (84%)	137±3 (94±2%)	8±3 (5±2%)	2±1 (1±1%)	13	61
All	All	4410/5220 (84%)	4122 (93%)	239 (5%)	49 (1%)	14	63

5 of 28 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	B	130	LEU	5
1	A	61	GLN	4
1	B	35	PRO	4
1	B	61	GLN	3
1	A	62	TYR	2

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	126/151 (83%)	91±5 (72±4%)	35±5 (28±4%)	1	20
1	B	126/151 (83%)	85±4 (67±3%)	41±4 (33±3%)	1	12
All	All	3780/4530 (83%)	2636 (70%)	1144 (30%)	1	16

5 of 205 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	18	MET	15
1	B	46	ILE	15
1	B	75	LEU	15
1	B	135	THR	15
1	B	87	THR	14

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 40% for the well-defined parts and 39% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

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	1779
Number of shifts mapped to atoms	1779
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	154	-0.85 ± 0.17	Should be checked
$^{13}\text{C}_\beta$	145	1.26 ± 0.15	Should be checked
$^{13}\text{C}'$	146	-0.77 ± 0.13	Should be applied
^{15}N	149	0.63 ± 0.14	Should be applied

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 40%, i.e. 1735 atoms were assigned a chemical shift out of a possible 4302. 0 out of 50 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	721/1490 (48%)	289/606 (48%)	288/592 (49%)	144/292 (49%)
Sidechain	989/2592 (38%)	674/1664 (41%)	315/798 (39%)	0/130 (0%)

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	Total	^1H	^{13}C	^{15}N
Aromatic	25/220 (11%)	23/106 (22%)	2/104 (2%)	0/10 (0%)
Overall	1735/4302 (40%)	986/2376 (41%)	605/1494 (40%)	144/432 (33%)

7.1.4 Statistically unusual chemical shifts [i](#)

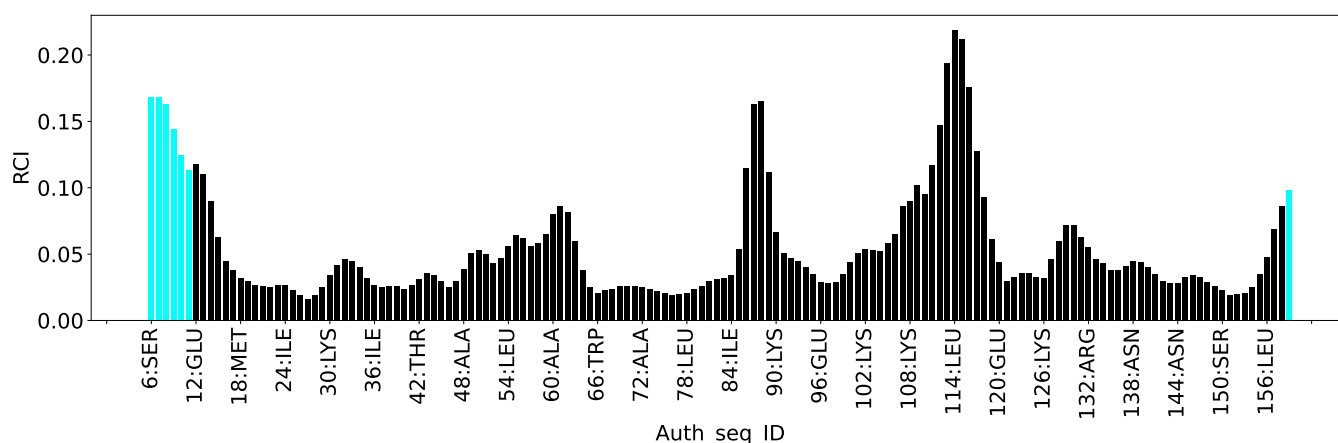
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	19	THR	HG1	4.41	0.08 – 2.19	15.5

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	2496
Intra-residue ($ i-j =0$)	932
Sequential ($ i-j =1$)	436
Medium range ($ i-j >1$ and $ i-j <5$)	608
Long range ($ i-j \geq 5$)	406
Inter-chain	114
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	506
Number of unmapped restraints	0
Number of restraints per residue	8.6
Number of long range restraints per residue ¹	1.2

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)	86.9	0.2
0.2-0.5 (Medium)	143.9	0.5
>0.5 (Large)	102.3	3.74

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)	3.8	9.7
10.0-20.0 (Medium)	0.1	13.95
>20.0 (Large)	0.4	151.32

9 Distance violation analysis ⓘ

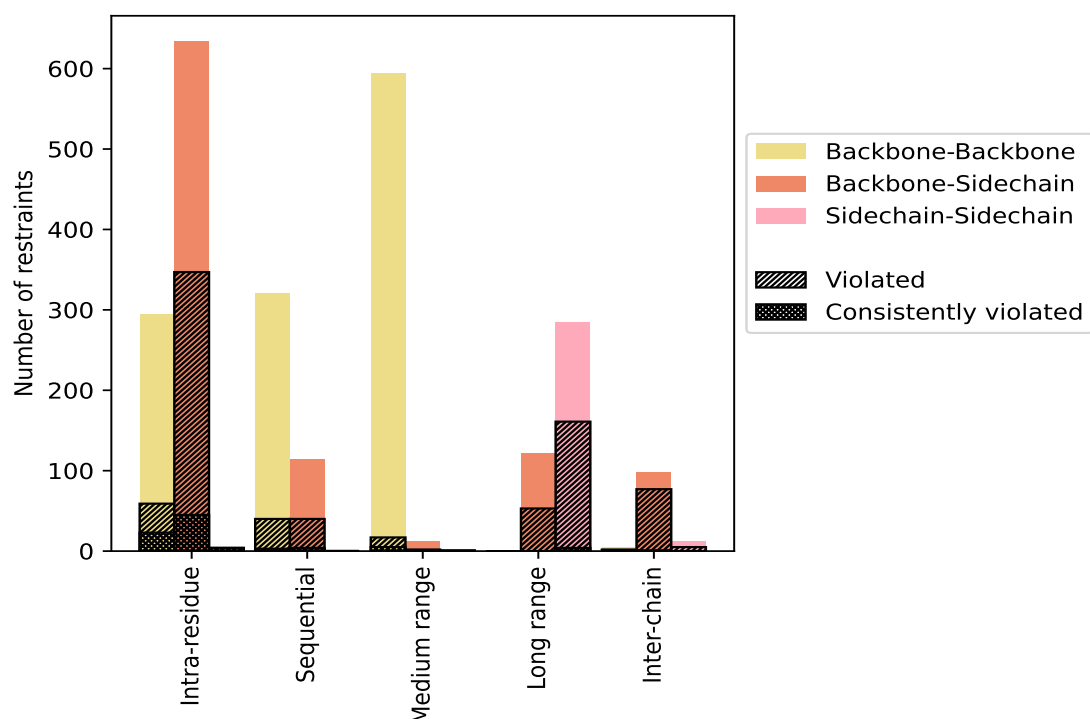
9.1 Summary of distance violations ⓘ

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)	932	37.3	410	44.0	16.4	72	7.7	2.9
Backbone-Backbone	294	11.8	59	20.1	2.4	23	7.8	0.9
Backbone-Sidechain	634	25.4	347	54.7	13.9	45	7.1	1.8
Sidechain-Sidechain	4	0.2	4	100.0	0.2	4	100.0	0.2
Sequential (i-j =1)	436	17.5	80	18.3	3.2	7	1.6	0.3
Backbone-Backbone	320	12.8	40	12.5	1.6	3	0.9	0.1
Backbone-Sidechain	114	4.6	40	35.1	1.6	4	3.5	0.2
Sidechain-Sidechain	2	0.1	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	608	24.4	20	3.3	0.8	5	0.8	0.2
Backbone-Backbone	594	23.8	17	2.9	0.7	5	0.8	0.2
Backbone-Sidechain	12	0.5	2	16.7	0.1	0	0.0	0.0
Sidechain-Sidechain	2	0.1	1	50.0	0.0	0	0.0	0.0
Long range (i-j ≥5)	406	16.3	214	52.7	8.6	4	1.0	0.2
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	122	4.9	53	43.4	2.1	0	0.0	0.0
Sidechain-Sidechain	284	11.4	161	56.7	6.5	4	1.4	0.2
Inter-chain	114	4.6	84	73.7	3.4	1	0.9	0.0
Backbone-Backbone	4	0.2	2	50.0	0.1	0	0.0	0.0
Backbone-Sidechain	98	3.9	77	78.6	3.1	1	1.0	0.0
Sidechain-Sidechain	12	0.5	5	41.7	0.2	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2496	100.0	808	32.4	32.4	89	3.6	3.6
Backbone-Backbone	1212	48.6	118	9.7	4.7	31	2.6	1.2
Backbone-Sidechain	980	39.3	519	53.0	20.8	50	5.1	2.0
Sidechain-Sidechain	304	12.2	171	56.2	6.9	8	2.6	0.3

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	198	30	8	46	32	314	0.5	2.76	0.45	0.31
2	194	30	7	56	24	311	0.43	2.99	0.37	0.32
3	188	33	7	46	20	294	0.39	1.61	0.3	0.3
4	226	33	9	96	42	406	0.54	2.9	0.49	0.36
5	201	36	9	62	23	331	0.44	2.08	0.39	0.32
6	204	34	7	78	35	358	0.5	3.04	0.43	0.34
7	187	30	10	63	42	332	0.5	2.97	0.48	0.33
8	220	31	7	68	39	365	0.53	3.06	0.48	0.34
9	210	30	8	58	34	340	0.5	3.18	0.46	0.32
10	203	29	9	69	40	350	0.54	3.6	0.56	0.32

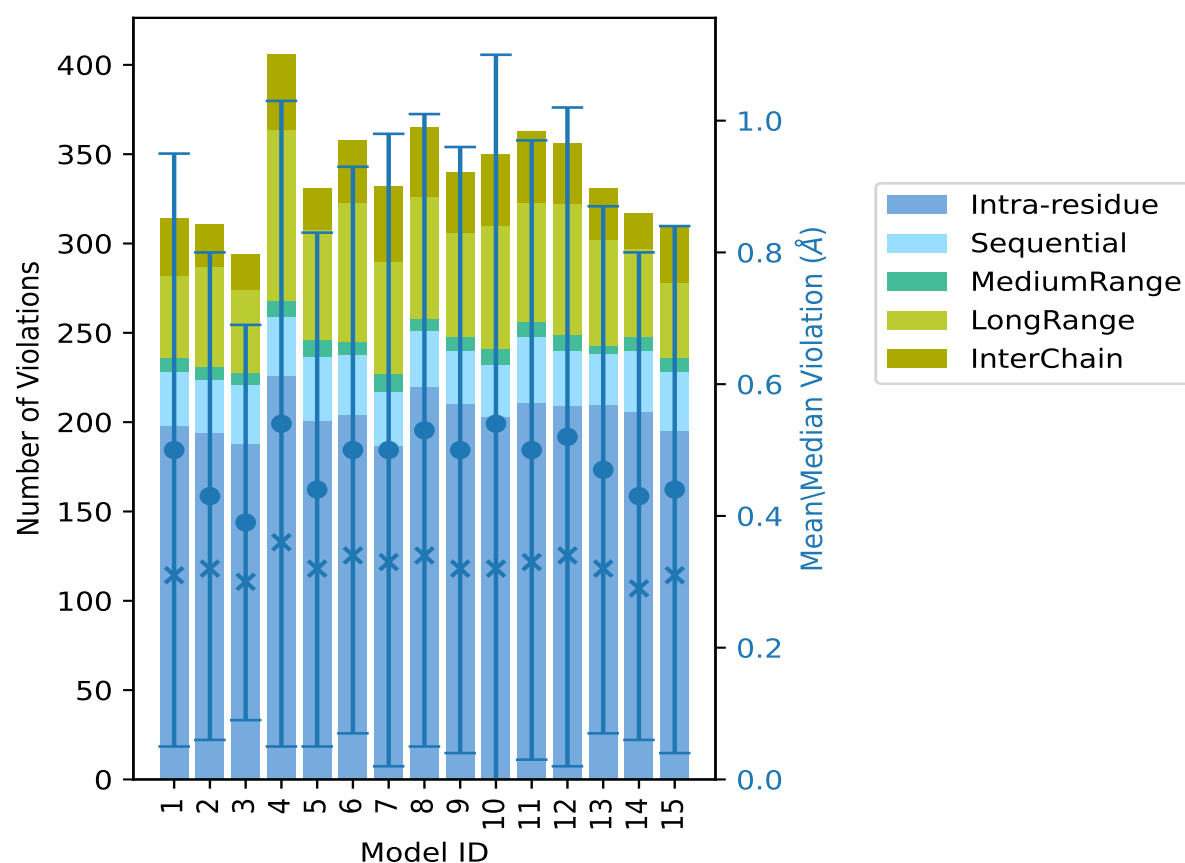
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	211	37	8	67	40	363	0.5	3.6	0.47	0.33
12	209	31	9	73	34	356	0.52	3.74	0.5	0.34
13	210	28	5	59	29	331	0.47	2.47	0.4	0.32
14	206	34	8	49	20	317	0.43	2.54	0.37	0.29
15	195	33	8	42	31	309	0.44	2.85	0.4	0.31

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

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

9.3 Distance violation statistics for the ensemble ⓘ

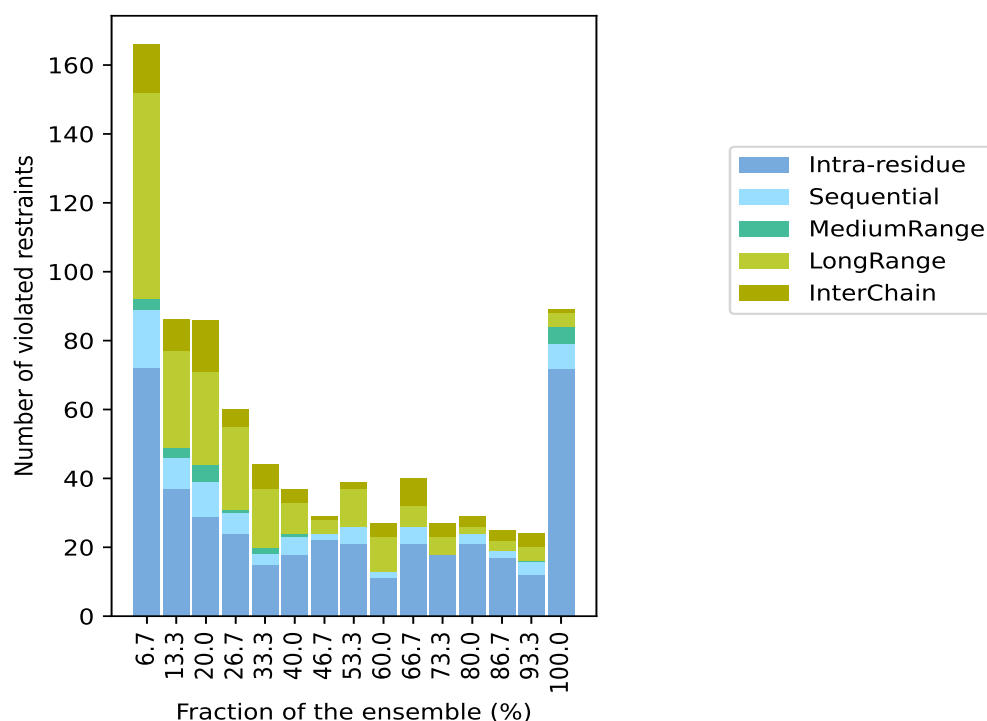
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1688(IR:522, SQ:356, MR:588, LR:192, IC:30) restraints are 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	%
72	17	3	60	14	166	1	6.7
37	9	3	28	9	86	2	13.3
29	10	5	27	15	86	3	20.0
24	6	1	24	5	60	4	26.7
15	3	2	17	7	44	5	33.3
18	5	1	9	4	37	6	40.0
22	2	0	4	1	29	7	46.7
21	5	0	11	2	39	8	53.3
11	2	0	10	4	27	9	60.0
21	5	0	6	8	40	10	66.7
18	0	0	5	4	27	11	73.3
21	3	0	2	3	29	12	80.0
17	2	0	3	3	25	13	86.7
12	4	0	4	4	24	14	93.3
72	7	5	4	1	89	15	100.0

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

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

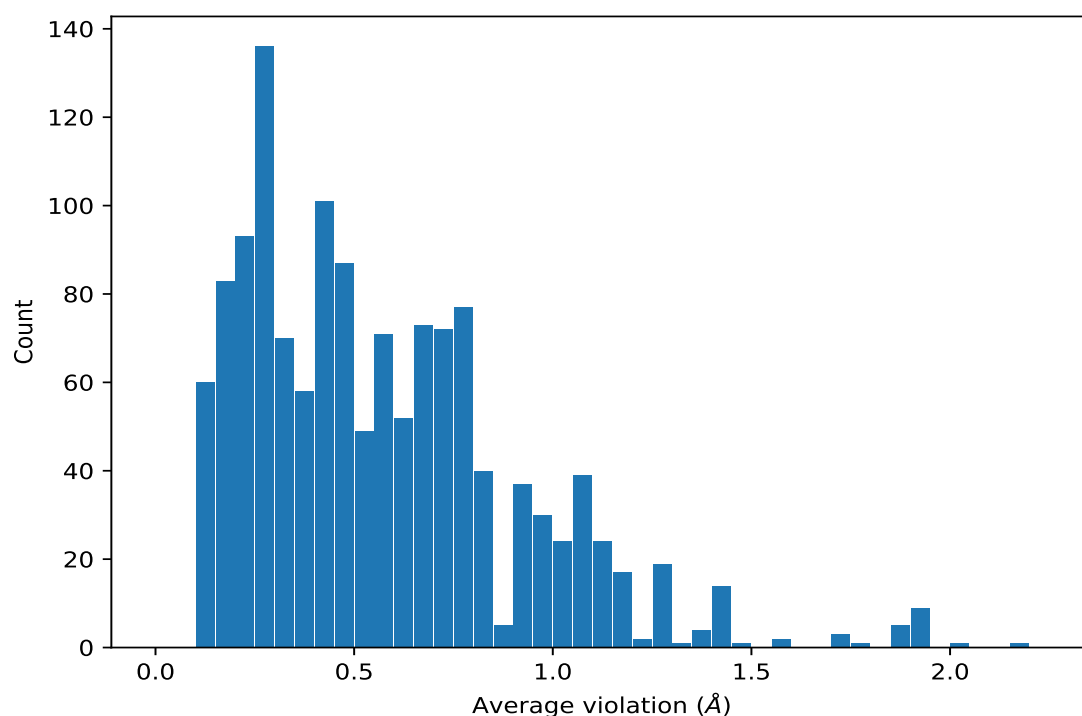
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,253)	1:40:A:LEU:HD11	1:145:A:LEU:HD21	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD11	1:145:A:LEU:HD22	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD11	1:145:A:LEU:HD23	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD12	1:145:A:LEU:HD21	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD12	1:145:A:LEU:HD22	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD12	1:145:A:LEU:HD23	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD13	1:145:A:LEU:HD21	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD13	1:145:A:LEU:HD22	15	1.93	0.19	1.99
(1,253)	1:40:A:LEU:HD13	1:145:A:LEU:HD23	15	1.93	0.19	1.99
(1,595)	1:79:A:VAL:HG21	1:92:A:LEU:HD11	15	1.43	0.48	1.42
(1,595)	1:79:A:VAL:HG21	1:92:A:LEU:HD12	15	1.43	0.48	1.42
(1,595)	1:79:A:VAL:HG21	1:92:A:LEU:HD13	15	1.43	0.48	1.42
(1,595)	1:79:A:VAL:HG22	1:92:A:LEU:HD11	15	1.43	0.48	1.42
(1,595)	1:79:A:VAL:HG22	1:92:A:LEU:HD12	15	1.43	0.48	1.42
(1,595)	1:79:A:VAL:HG22	1:92:A:LEU:HD13	15	1.43	0.48	1.42
(1,595)	1:79:A:VAL:HG23	1:92:A:LEU:HD11	15	1.43	0.48	1.42

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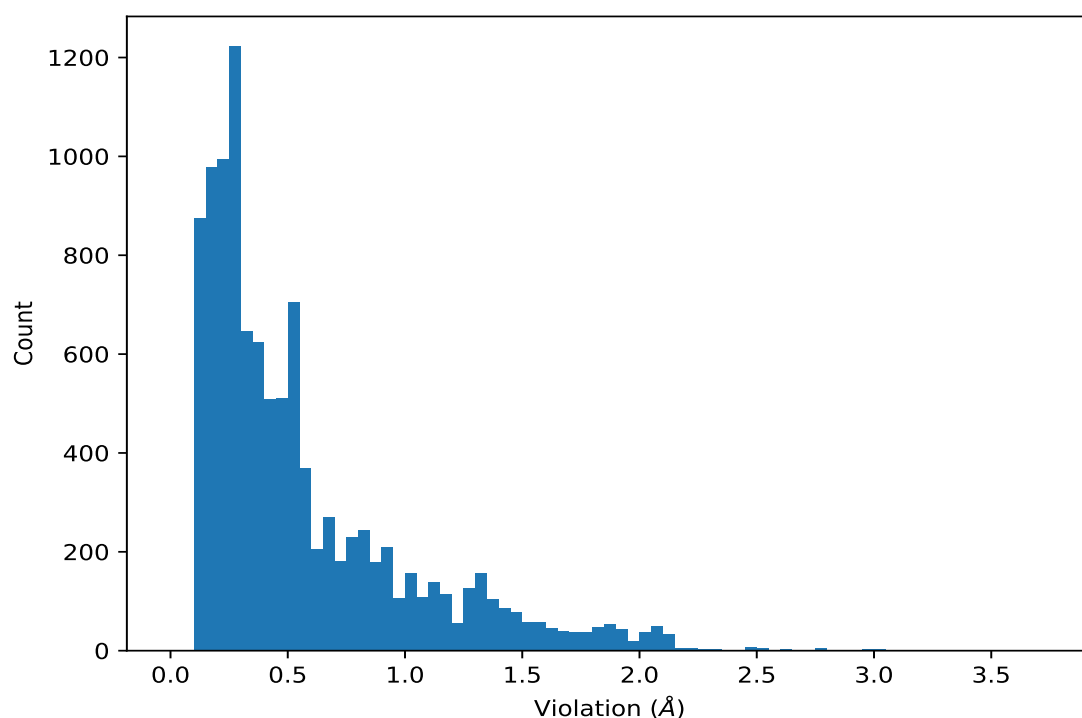
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,595)	1:79:A:VAL:HG23	1:92:A:LEU:HD12	15	1.43	0.48	1.42
(1,595)	1:79:A:VAL:HG23	1:92:A:LEU:HD13	15	1.43	0.48	1.42
(1,544)	1:75:A:LEU:HD11	1:99:A:LEU:HD11	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD11	1:99:A:LEU:HD12	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD11	1:99:A:LEU:HD13	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD12	1:99:A:LEU:HD11	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD12	1:99:A:LEU:HD12	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD12	1:99:A:LEU:HD13	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD13	1:99:A:LEU:HD11	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD13	1:99:A:LEU:HD12	15	1.25	0.64	1.34
(1,544)	1:75:A:LEU:HD13	1:99:A:LEU:HD13	15	1.25	0.64	1.34
(1,2429)	1:97:A:GLU:HG3	1:143:B:LYS:H	15	1.06	0.65	0.95
(1,937)	1:132:A:ARG:H	1:133:A:MET:H	15	0.87	0.18	0.9
(1,289)	1:45:A:VAL:H	1:45:A:VAL:HG11	15	0.79	0.02	0.79
(1,289)	1:45:A:VAL:H	1:45:A:VAL:HG12	15	0.79	0.02	0.79
(1,289)	1:45:A:VAL:H	1:45:A:VAL:HG13	15	0.79	0.02	0.79
(1,303)	1:46:A:ILE:H	1:46:A:ILE:HG21	15	0.74	0.05	0.75
(1,303)	1:46:A:ILE:H	1:46:A:ILE:HG22	15	0.74	0.05	0.75
(1,303)	1:46:A:ILE:H	1:46:A:ILE:HG23	15	0.74	0.05	0.75
(1,365)	1:52:A:VAL:HA	1:52:A:VAL:HG11	15	0.68	0.03	0.67
(1,365)	1:52:A:VAL:HA	1:52:A:VAL:HG12	15	0.68	0.03	0.67
(1,365)	1:52:A:VAL:HA	1:52:A:VAL:HG13	15	0.68	0.03	0.67
(1,1480)	1:45:B:VAL:H	1:45:B:VAL:HG21	15	0.53	0.01	0.53
(1,1480)	1:45:B:VAL:H	1:45:B:VAL:HG22	15	0.53	0.01	0.53
(1,1480)	1:45:B:VAL:H	1:45:B:VAL:HG23	15	0.53	0.01	0.53
(1,636)	1:84:A:ILE:HG21	1:85:A:TYR:H	15	0.53	0.05	0.56

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

9.5.1 Histogram : Distribution of distance violations [i](#)

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



9.5.2 Table : All distance violations [i](#)

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2482)	1:93:A:LYS:H	1:147:B:LYS:HE2	12	3.74
(1,2482)	1:93:A:LYS:H	1:147:B:LYS:HE2	11	3.6
(1,2446)	1:139:A:GLU:H	1:100:B:LYS:HE3	10	3.6
(1,2448)	1:139:A:GLU:H	1:100:B:LYS:HE2	10	3.55
(1,2474)	1:93:A:LYS:H	1:147:B:LYS:HG2	10	3.2
(1,2474)	1:93:A:LYS:H	1:147:B:LYS:HG2	9	3.18
(1,1167)	1:155:A:LYS:H	1:155:A:LYS:HE2	8	3.06
(1,2440)	1:140:A:GLU:H	1:100:B:LYS:HE2	10	3.05
(1,1167)	1:155:A:LYS:H	1:155:A:LYS:HE2	6	3.04
(1,2468)	1:93:A:LYS:H	1:147:B:LYS:HB3	9	3.02

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

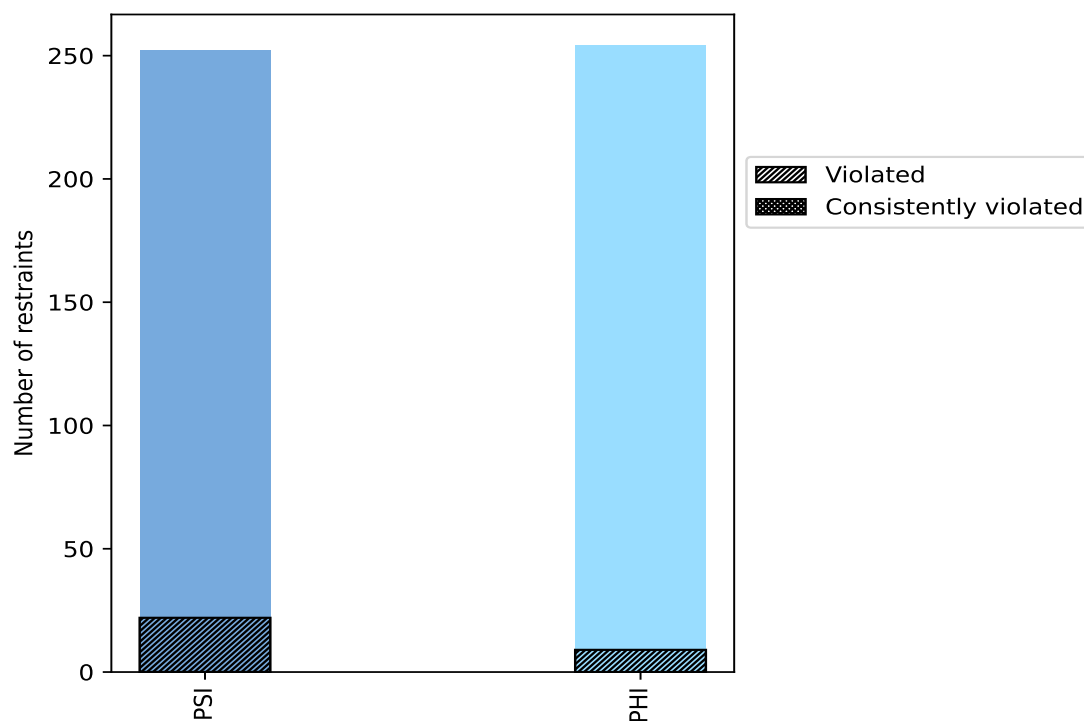
10.1 Summary of dihedral-angle violations [i](#)

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
PSI	252	49.8	22	8.7	4.3	0	0.0	0.0
PHI	254	50.2	9	3.5	1.8	0	0.0	0.0
Total	506	100.0	31	6.1	6.1	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 [i](#)



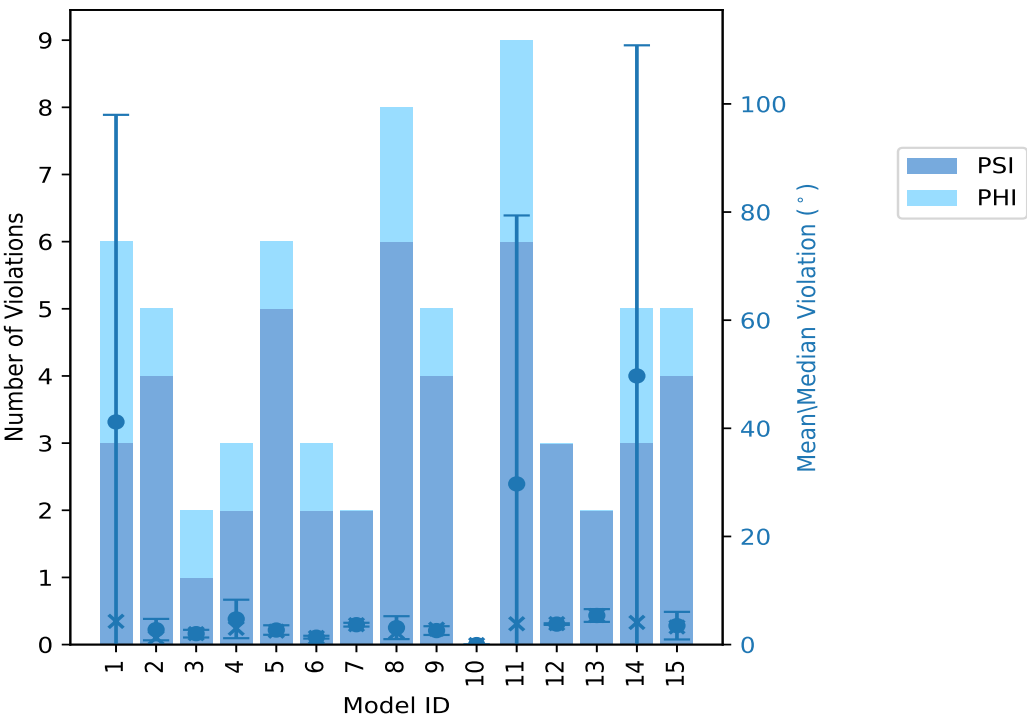
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model ⓘ

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

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PSI	PHI	Total				
1	3	3	6	41.18	151.02	56.8	4.3
2	4	1	5	2.77	6.07	1.98	1.28
3	1	1	2	2.02	2.73	0.71	2.02
4	2	1	3	4.74	9.7	3.56	3.01
5	5	1	6	2.69	3.85	0.88	2.49
6	2	1	3	1.37	1.71	0.26	1.32
7	2	0	2	3.68	4.03	0.35	3.68
8	6	2	8	3.13	8.22	2.12	2.29
9	4	1	5	2.59	3.56	0.81	2.86
10	0	0	0	0.0	0.0	0.0	0.0
11	6	3	9	29.72	151.32	49.65	3.85
12	3	0	3	3.79	3.92	0.15	3.88
13	2	0	2	5.38	6.56	1.18	5.38
14	3	2	5	49.69	151.28	61.15	4.1
15	4	1	5	3.5	8.2	2.55	3.26

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

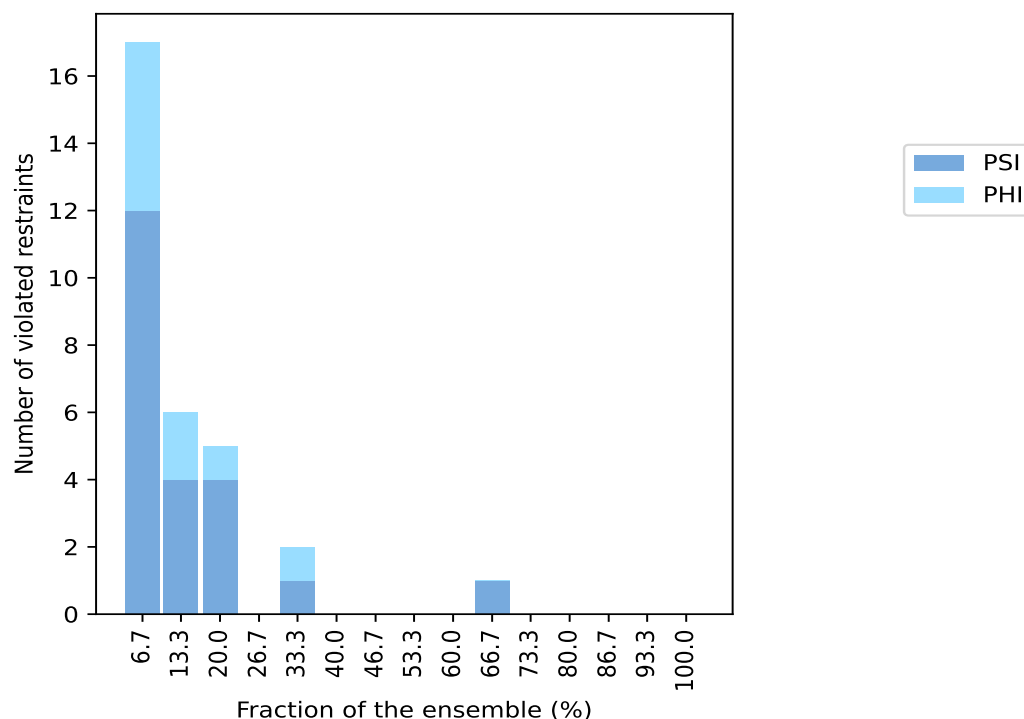
10.3 Dihedral-angle violation statistics for the ensemble [i](#)

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

Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
12	5	17	1	6.7
4	2	6	2	13.3
4	1	5	3	20.0
0	0	0	4	26.7
1	1	2	5	33.3
0	0	0	6	40.0
0	0	0	7	46.7
0	0	0	8	53.3
0	0	0	9	60.0
1	0	1	10	66.7
0	0	0	11	73.3
0	0	0	12	80.0
0	0	0	13	86.7
0	0	0	14	93.3
0	0	0	15	100.0

¹ Number of models with violations

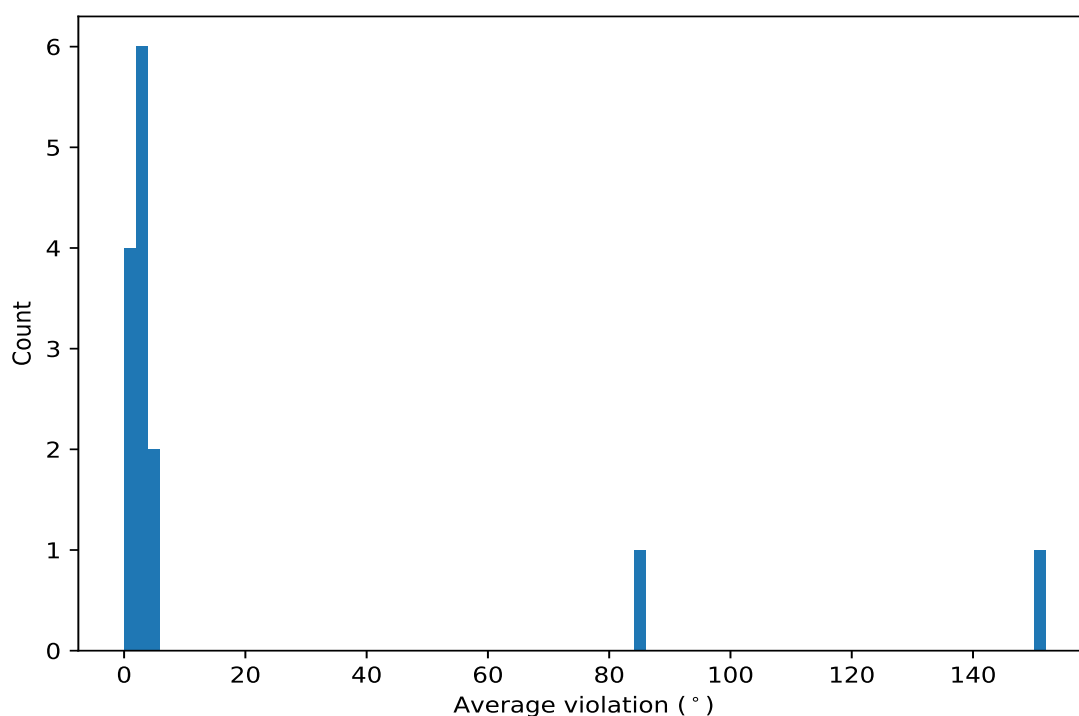
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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.

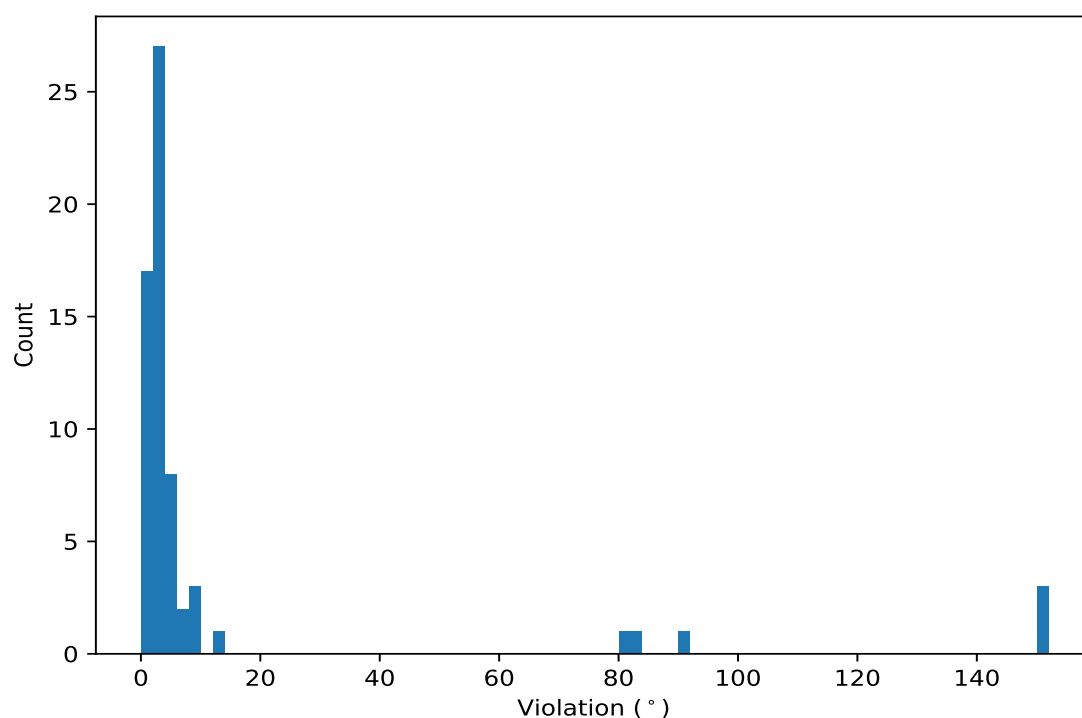
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,317)	1:45:B:VAL:N	1:45:B:VAL:CA	1:45:B:VAL:C	1:46:B:ILE:N	10	3.6	0.48	3.59
(1,371)	1:78:B:LEU:N	1:78:B:LEU:CA	1:78:B:LEU:C	1:79:B:VAL:N	5	4.86	2.17	4.06
(1,430)	1:116:B:ARG:C	1:117:B:ARG:N	1:117:B:ARG:CA	1:117:B:ARG:C	5	1.31	0.17	1.31
(1,35)	1:30:A:LYS:C	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	3	151.21	0.13	151.28
(1,34)	1:30:A:LYS:N	1:30:A:LYS:CA	1:30:A:LYS:C	1:31:A:GLN:N	3	85.14	3.65	83.55
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:PRO:N	3	4.78	3.51	2.94
(1,313)	1:43:B:GLY:N	1:43:B:GLY:CA	1:43:B:GLY:C	1:44:B:ALA:N	3	3.79	0.19	3.77
(1,455)	1:129:B:GLU:N	1:129:B:GLU:CA	1:129:B:GLU:C	1:130:B:LEU:N	3	2.51	0.28	2.44
(1,12)	1:19:A:THR:N	1:19:A:THR:CA	1:19:A:THR:C	1:20:A:PHE:N	2	3.37	0.21	3.37
(1,265)	1:19:B:THR:N	1:19:B:THR:CA	1:19:B:THR:C	1:20:B:PHE:N	2	2.52	1.4	2.52

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 (°)
(1,35)	1:30:A:LYS:C	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	11	151.32
(1,35)	1:30:A:LYS:C	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	14	151.28
(1,35)	1:30:A:LYS:C	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1	151.02
(1,34)	1:30:A:LYS:N	1:30:A:LYS:CA	1:30:A:LYS:C	1:31:A:GLN:N	14	90.18
(1,34)	1:30:A:LYS:N	1:30:A:LYS:CA	1:30:A:LYS:C	1:31:A:GLN:N	11	83.55
(1,34)	1:30:A:LYS:N	1:30:A:LYS:CA	1:30:A:LYS:C	1:31:A:GLN:N	1	81.68
(1,199)	1:127:A:ARG:C	1:128:A:ALA:N	1:128:A:ALA:CA	1:128:A:ALA:C	11	13.95
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:PRO:N	4	9.7
(1,273)	1:23:B:ARG:N	1:23:B:ARG:CA	1:23:B:ARG:C	1:24:B:ILE:N	8	8.22
(1,371)	1:78:B:LEU:N	1:78:B:LEU:CA	1:78:B:LEU:C	1:79:B:VAL:N	15	8.2