



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 4, 2026 – 11:16 PM UTC

PDB ID : 2MZE / pdb_00002mze
BMRB ID : 25485
Title : NMR Solution Structure of the PRO Form of Human Matrilysin (proMMP-7)
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Deposited on : 2015-02-11

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) : 2.49

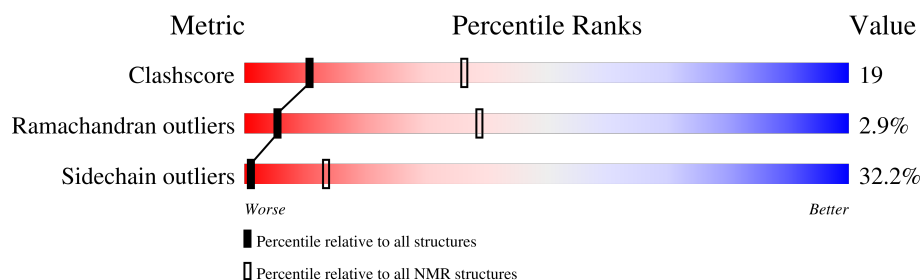
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 84%.

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	250	42% 32% 6% 20%

2 Ensemble composition and analysis

This entry contains 20 models. Model 18 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:23, A:35-A:72, A:82-A:216, A:224-A:239 (201)	0.64	18

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 3 clusters. No single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3883 atoms, of which 1913 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Matrilysin.

Mol	Chain	Residues	Atoms						Trace
1	A	250	Total	C	H	N	O	S	0
			3879	1251	1913	341	365	9	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	ALA	GLU	engineered mutation	UNP P09237

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

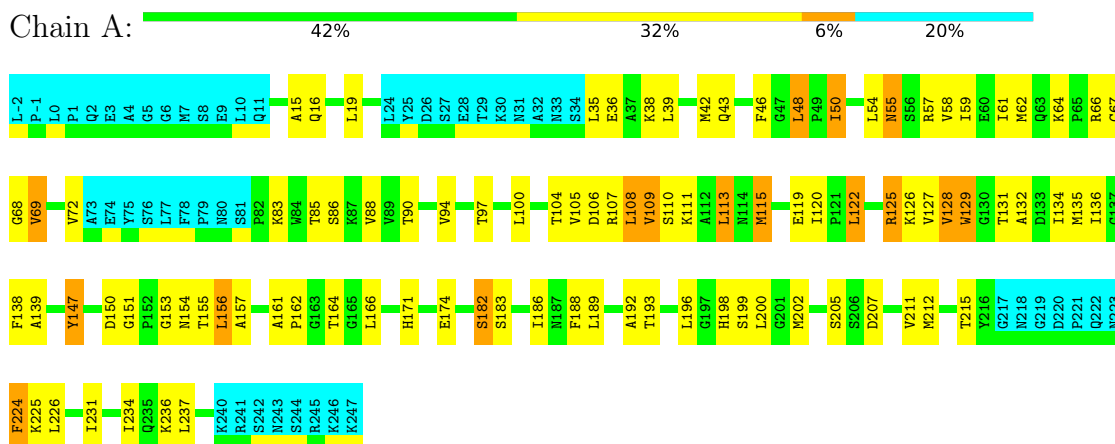
Mol	Chain	Residues	Atoms	
3	A	2	Total	Zn
			2	2

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.

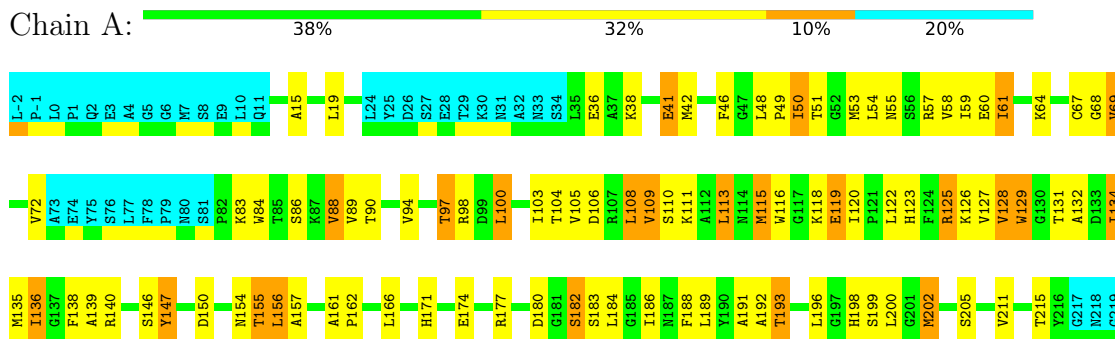
- Molecule 1: Matrilysin



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

The representative model is number 18. Colouring as in section 4.1 above.

- Molecule 1: Matrilysin



P220	P221	Q222	N223	F224	K225	L226	S227	Q228		I231		I234	Q235	K236	L237	Y238	G239	K240	R241	S242	N243	S244	R245	K246	K247

5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
TALOS	geometry optimization	
CYANA	structure solution	2.1
CYANA	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	2659
Number of shifts mapped to atoms	2658
Number of unparsed shifts	0
Number of shifts with mapping errors	1
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

6 Model quality

6.1 Standard geometry

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

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1590	1555	1556	58±6
All	All	31880	31100	31120	1169

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 19.

5 of 299 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:120:ILE:HD12	1:A:122:LEU:HD12	0.97	1.34	3	18
1:A:156:LEU:HD21	1:A:186:ILE:HG21	0.96	1.38	5	20
1:A:127:VAL:HG11	1:A:132:ALA:HB2	0.94	1.37	7	20
1:A:113:LEU:HD13	1:A:196:LEU:HD12	0.91	1.39	14	7
1:A:42:MET:HE2	1:A:61:ILE:HD11	0.83	1.49	11	2

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	201/250 (80%)	173±2 (86±1%)	22±2 (11±1%)	6±2 (3±1%)	5	39
All	All	4020/5000 (80%)	3462 (86%)	440 (11%)	118 (3%)	5	39

5 of 19 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	55	ASN	20
1	A	147	TYR	20
1	A	224	PHE	18
1	A	122	LEU	15
1	A	151	GLY	7

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	166/208 (80%)	113±3 (68±2%)	53±3 (32±2%)	1	13
All	All	3320/4160 (80%)	2252 (68%)	1068 (32%)	1	13

5 of 110 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	69	VAL	20
1	A	88	VAL	20
1	A	108	LEU	20
1	A	109	VAL	20
1	A	111	LYS	20

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 79% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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

Total number of shifts	2659
Number of shifts mapped to atoms	2658
Number of unparsed shifts	0
Number of shifts with mapping errors	1
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	12

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

- No matching atom found in the structure. All 1 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	195	ALA	HB1	1.306	.	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
$^{13}\text{C}_\alpha$	236	-0.28 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	212	0.26 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	231	0.04 ± 0.12	None needed (< 0.5 ppm)
^{15}N	218	-0.18 ± 0.38	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 84%, i.e. 2298 atoms were assigned a chemical shift out of a possible 2729. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	971/1004 (97%)	394/412 (96%)	392/402 (98%)	185/190 (97%)
Sidechain	1149/1428 (80%)	789/933 (85%)	352/444 (79%)	8/51 (16%)
Aromatic	178/297 (60%)	91/148 (61%)	82/136 (60%)	5/13 (38%)
Overall	2298/2729 (84%)	1274/1493 (85%)	826/982 (84%)	198/254 (78%)

7.1.4 Statistically unusual chemical shifts [i](#)

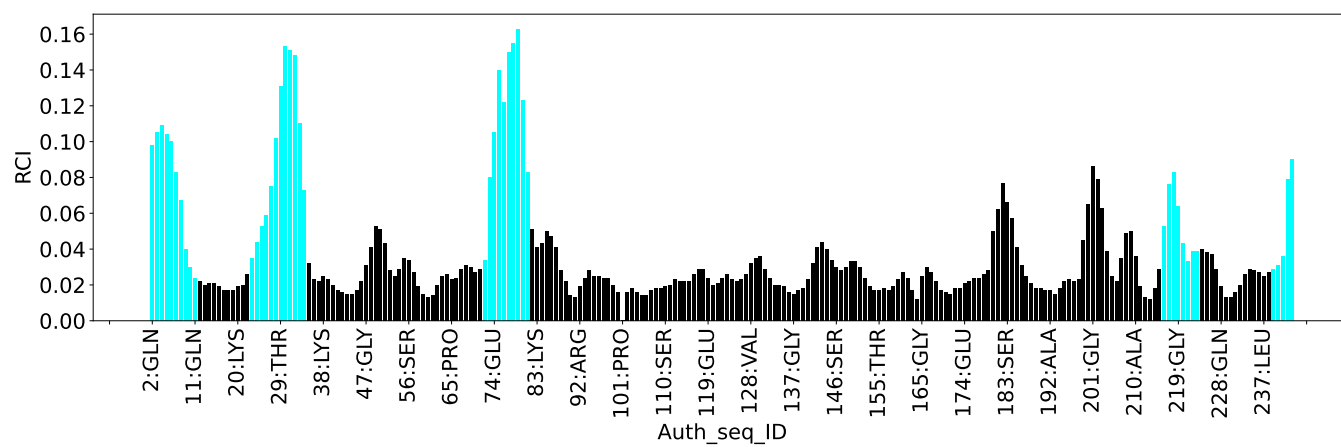
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	107	ARG	NE	119.85	76.53 – 92.65	21.9
1	A	92	ARG	NE	117.04	76.53 – 92.65	20.1
1	A	60	GLU	HB2	0.60	1.00 – 3.05	-6.9
1	A	162	PRO	HB3	-0.32	0.25 – 3.76	-6.6
1	A	22	PHE	CE2	122.89	124.80 – 136.72	-6.6
1	A	60	GLU	HB3	0.64	0.95 – 3.05	-6.5
1	A	65	PRO	HA	2.44	2.78 – 6.00	-6.1
1	A	22	PHE	CE1	122.89	124.17 – 137.29	-6.0
1	A	62	MET	HG3	0.38	0.54 – 4.26	-5.4
1	A	144	GLY	H	5.17	5.23 – 11.42	-5.1
1	A	211	VAL	H	11.59	4.98 – 11.56	5.0
1	A	153	GLY	H	11.43	5.23 – 11.42	5.0

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis [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	2528
Intra-residue ($ i-j =0$)	685
Sequential ($ i-j =1$)	684
Medium range ($ i-j >1$ and $ i-j <5$)	383
Long range ($ i-j \geq 5$)	728
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	357
Number of unmapped restraints	0
Number of restraints per residue	11.4
Number of long range restraints per residue ¹	2.9

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 [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)	118.5	0.2
0.2-0.5 (Medium)	355.0	0.5
>0.5 (Large)	1455.5	3.27

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)	31.1	6.87
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

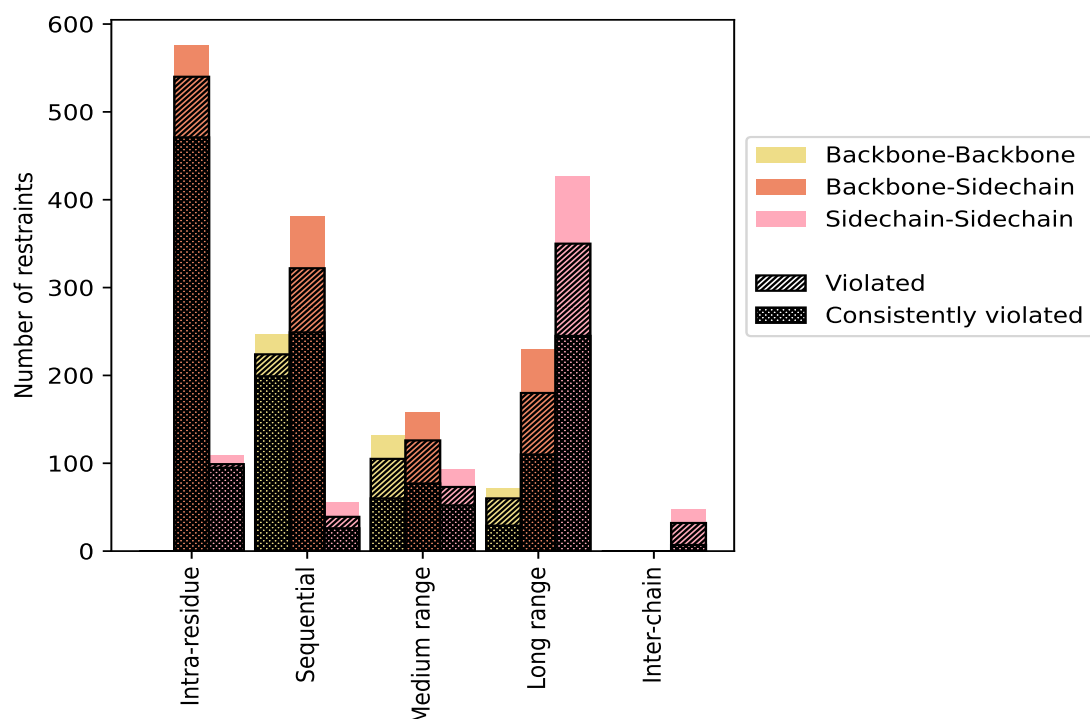
9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	685	27.1	639	93.3	25.3	566	82.6	22.4
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	576	22.8	540	93.8	21.4	471	81.8	18.6
Sidechain-Sidechain	109	4.3	99	90.8	3.9	95	87.2	3.8
Sequential (i-j =1)	684	27.1	585	85.5	23.1	474	69.3	18.8
Backbone-Backbone	247	9.8	224	90.7	8.9	199	80.6	7.9
Backbone-Sidechain	381	15.1	322	84.5	12.7	249	65.4	9.8
Sidechain-Sidechain	56	2.2	39	69.6	1.5	26	46.4	1.0
Medium range (i-j >1 & i-j <5)	383	15.2	304	79.4	12.0	189	49.3	7.5
Backbone-Backbone	132	5.2	105	79.5	4.2	60	45.5	2.4
Backbone-Sidechain	158	6.2	126	79.7	5.0	77	48.7	3.0
Sidechain-Sidechain	93	3.7	73	78.5	2.9	52	55.9	2.1
Long range (i-j ≥5)	728	28.8	590	81.0	23.3	384	52.7	15.2
Backbone-Backbone	71	2.8	60	84.5	2.4	29	40.8	1.1
Backbone-Sidechain	230	9.1	180	78.3	7.1	110	47.8	4.4
Sidechain-Sidechain	427	16.9	350	82.0	13.8	245	57.4	9.7
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	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	2528	100.0	2150	85.0	85.0	1620	64.1	64.1
Backbone-Backbone	450	17.8	389	86.4	15.4	288	64.0	11.4
Backbone-Sidechain	1345	53.2	1168	86.8	46.2	907	67.4	35.9
Sidechain-Sidechain	733	29.0	593	80.9	23.5	425	58.0	16.8

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	603	546	258	514	23	1944	1.07	3.27	0.65	1.02
2	615	535	252	505	23	1930	1.07	3.26	0.65	1.0
3	614	543	250	506	22	1935	1.06	3.27	0.65	1.0
4	611	539	260	502	21	1933	1.06	3.22	0.64	0.99
5	609	536	256	510	23	1934	1.07	3.27	0.65	1.01
6	614	544	258	503	23	1942	1.06	3.22	0.65	0.98
7	612	547	260	501	22	1942	1.06	3.25	0.65	1.0
8	608	546	258	504	23	1939	1.06	3.16	0.65	0.99
9	614	549	258	496	27	1944	1.05	3.22	0.66	0.97
10	613	543	259	499	21	1935	1.06	3.22	0.65	0.99

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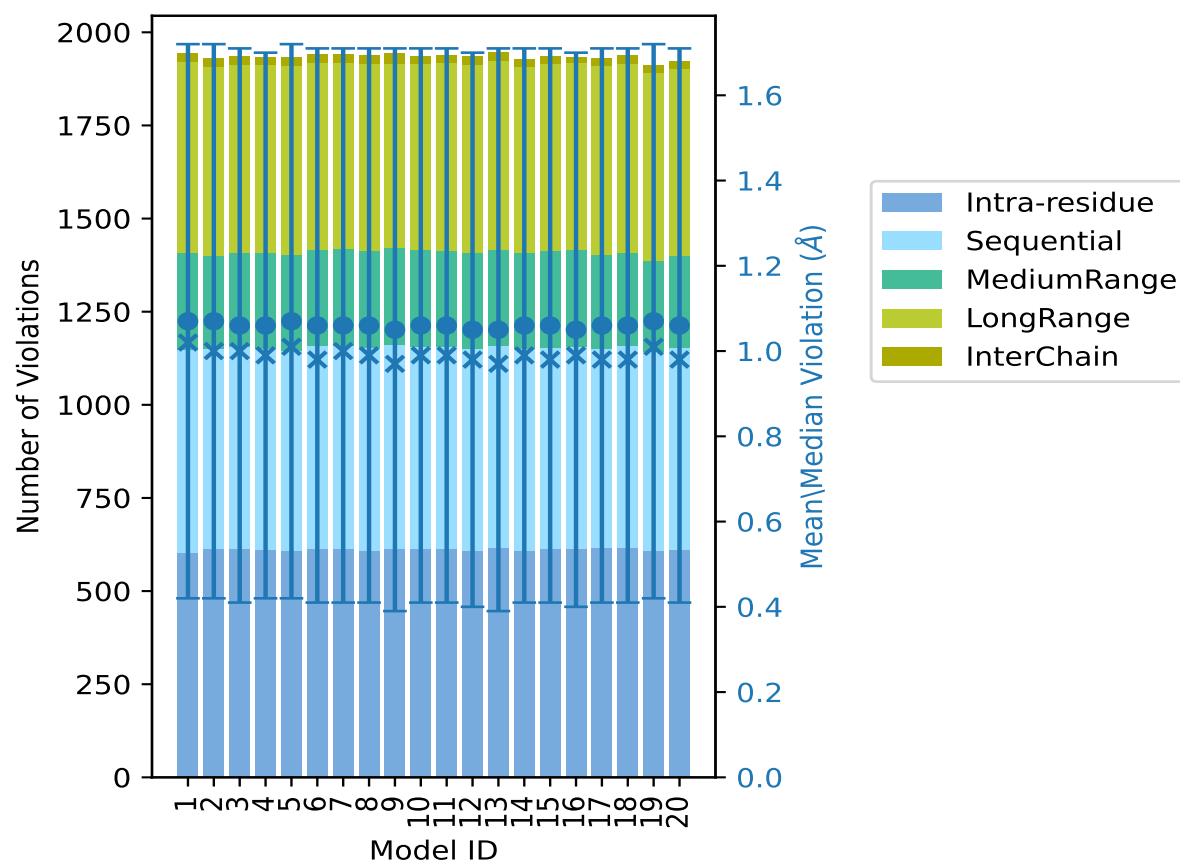
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	613	544	256	506	20	1939	1.06	3.27	0.65	0.99
12	608	543	259	502	23	1935	1.05	3.25	0.65	0.98
13	616	543	256	509	23	1947	1.05	3.25	0.66	0.97
14	609	543	256	499	21	1928	1.06	3.26	0.65	0.99
15	614	541	258	503	21	1937	1.06	3.2	0.65	0.98
16	613	543	260	503	14	1933	1.05	3.26	0.65	0.99
17	616	535	251	507	20	1929	1.06	3.21	0.65	0.98
18	617	542	250	506	23	1938	1.06	3.26	0.65	0.98
19	608	535	243	505	20	1911	1.07	3.27	0.65	1.01
20	612	541	248	501	19	1921	1.06	3.23	0.65	0.98

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

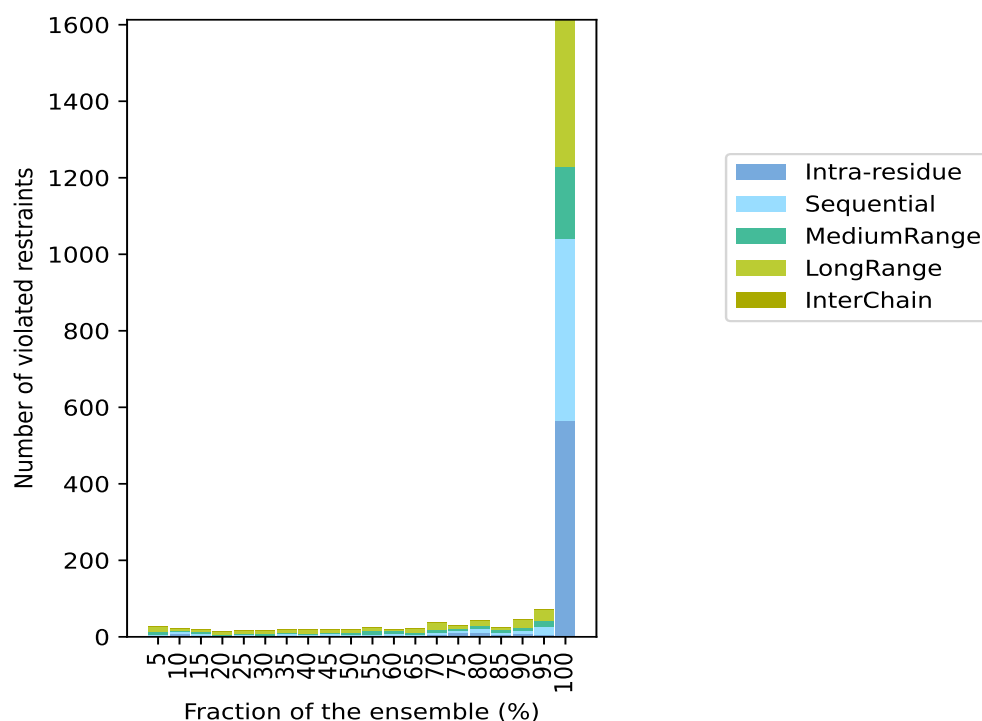
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 362(IR:46, SQ:99, MR:79, LR:138, IC:0) restraints are not 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	%
2	4	7	15	0	28	1	5.0
7	5	5	4	0	21	2	10.0
1	7	4	7	0	19	3	15.0
2	0	4	9	0	15	4	20.0
0	4	5	8	0	17	5	25.0
0	4	3	9	0	16	6	30.0
3	4	4	8	0	19	7	35.0
3	3	3	9	0	18	8	40.0
3	5	4	6	0	18	9	45.0
0	5	6	7	0	18	10	50.0
3	4	8	9	0	24	11	55.0
2	6	7	5	0	20	12	60.0
3	4	3	11	0	21	13	65.0
4	7	7	19	0	37	14	70.0
10	5	6	9	0	30	15	75.0
11	9	9	14	0	43	16	80.0
6	4	8	7	0	25	17	85.0
7	10	7	21	0	45	18	90.0
6	21	15	29	0	71	19	95.0
566	474	189	384	0	1613	20	100.0

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

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

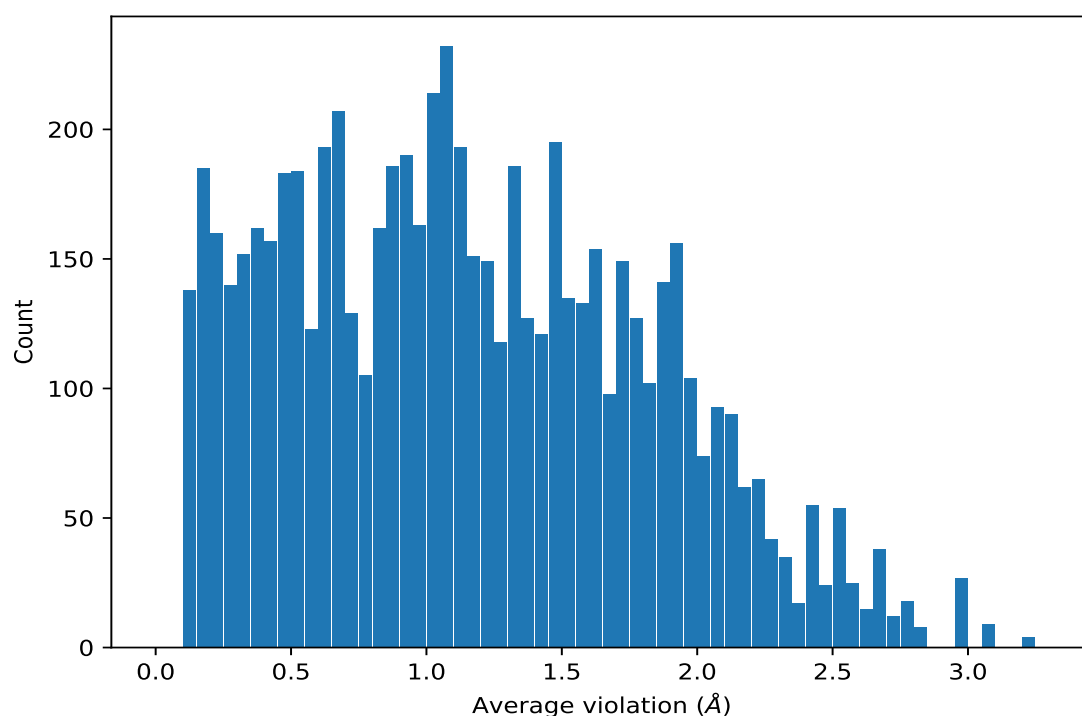
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



9.4 Most violated distance restraints in the ensemble [i](#)

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

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



9.4.2 Table: Most violated distance restraints [i](#)

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	20	3.24	0.03	3.25
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	20	3.24	0.03	3.25
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	20	3.24	0.03	3.25
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	20	3.24	0.03	3.25
(1,2125)	1:156:A:LEU:HD21	1:186:A:ILE:HG21	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD21	1:186:A:ILE:HG22	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD21	1:186:A:ILE:HG23	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD22	1:186:A:ILE:HG21	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD22	1:186:A:ILE:HG22	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD22	1:186:A:ILE:HG23	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD23	1:186:A:ILE:HG21	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD23	1:186:A:ILE:HG22	20	3.05	0.03	3.06
(1,2125)	1:156:A:LEU:HD23	1:186:A:ILE:HG23	20	3.05	0.03	3.06
(1,1968)	1:88:A:VAL:HG11	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG12	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG13	1:125:A:ARG:HB2	20	2.98	0.08	2.98

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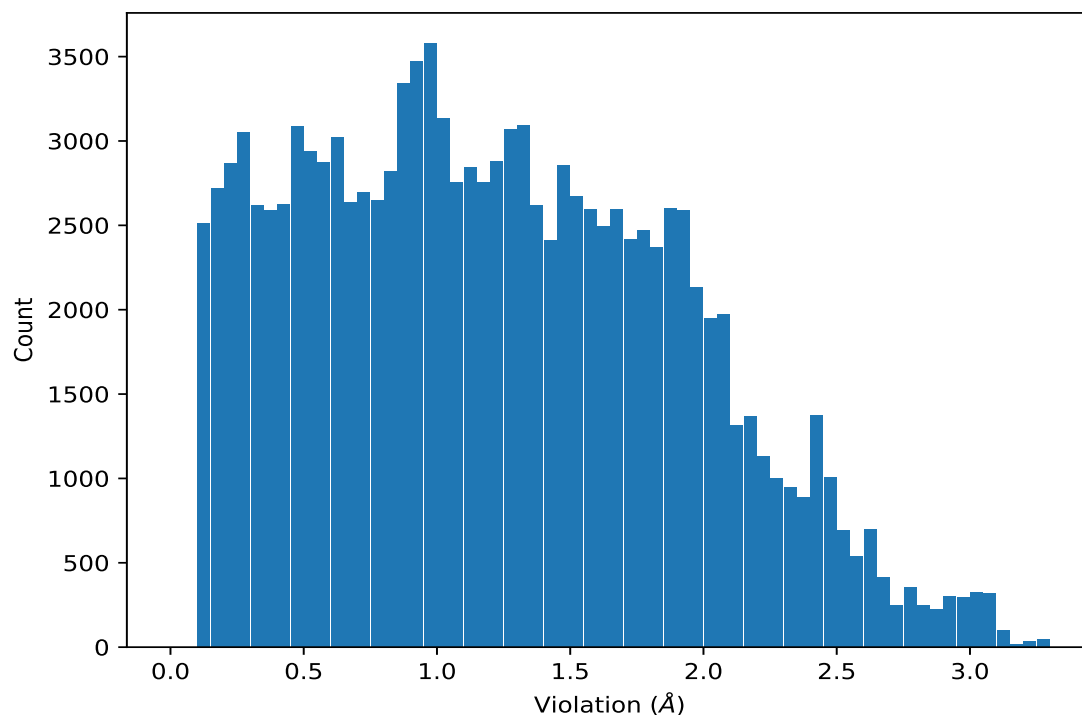
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1968)	1:88:A:VAL:HG11	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG12	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG13	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG11	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG11	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG12	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG12	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG13	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG13	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG21	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG21	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG22	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG22	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG23	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG23	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG21	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG22	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG23	1:125:A:ARG:HB2	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG21	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG22	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,1968)	1:88:A:VAL:HG23	1:125:A:ARG:HB3	20	2.98	0.08	2.98
(1,169)	1:157:A:ALA:HB1	1:172:A:PHE:HA	20	2.98	0.03	2.98
(1,169)	1:157:A:ALA:HB2	1:172:A:PHE:HA	20	2.98	0.03	2.98
(1,169)	1:157:A:ALA:HB3	1:172:A:PHE:HA	20	2.98	0.03	2.98
(1,1975)	1:156:A:LEU:HD21	1:186:A:ILE:HG13	20	2.83	0.07	2.85
(1,1975)	1:156:A:LEU:HD22	1:186:A:ILE:HG13	20	2.83	0.07	2.85
(1,1975)	1:156:A:LEU:HD23	1:186:A:ILE:HG13	20	2.83	0.07	2.85
(1,457)	1:122:A:LEU:HB3	1:123:A:HIS:H	20	2.83	0.03	2.82
(1,131)	1:205:A:SER:HB2	1:210:A:ALA:HB1	20	2.82	0.31	2.96
(1,131)	1:205:A:SER:HB2	1:210:A:ALA:HB2	20	2.82	0.31	2.96
(1,131)	1:205:A:SER:HB2	1:210:A:ALA:HB3	20	2.82	0.31	2.96
(1,152)	1:94:A:VAL:HB	1:137:A:GLY:HA3	20	2.81	0.04	2.81
(1,2087)	1:104:A:THR:HG21	1:108:A:LEU:HD21	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG21	1:108:A:LEU:HD22	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG21	1:108:A:LEU:HD23	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG22	1:108:A:LEU:HD21	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG22	1:108:A:LEU:HD22	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG22	1:108:A:LEU:HD23	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG23	1:108:A:LEU:HD21	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG23	1:108:A:LEU:HD22	20	2.77	0.01	2.77
(1,2087)	1:104:A:THR:HG23	1:108:A:LEU:HD23	20	2.77	0.01	2.77
(1,219)	1:15:A:ALA:HB1	1:59:A:ILE:HD11	20	2.77	0.31	2.9

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)
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	1	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	1	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	1	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	1	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	3	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	3	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	3	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	3	3.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	5	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	5	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	5	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	5	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	11	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	11	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	11	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	11	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	19	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	19	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	19	3.27
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	19	3.27
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	2	3.26
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	2	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	2	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	2	3.26
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	14	3.26
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	14	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	14	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	14	3.26
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	16	3.26
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	16	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	16	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	16	3.26
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD1	18	3.26
(1,419)	1:108:A:LEU:HB2	1:188:A:PHE:HD2	18	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD1	18	3.26
(1,419)	1:108:A:LEU:HB3	1:188:A:PHE:HD2	18	3.26
(1,1198)	1:78:A:PHE:H	1:79:A:PRO:HD2	7	3.25

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

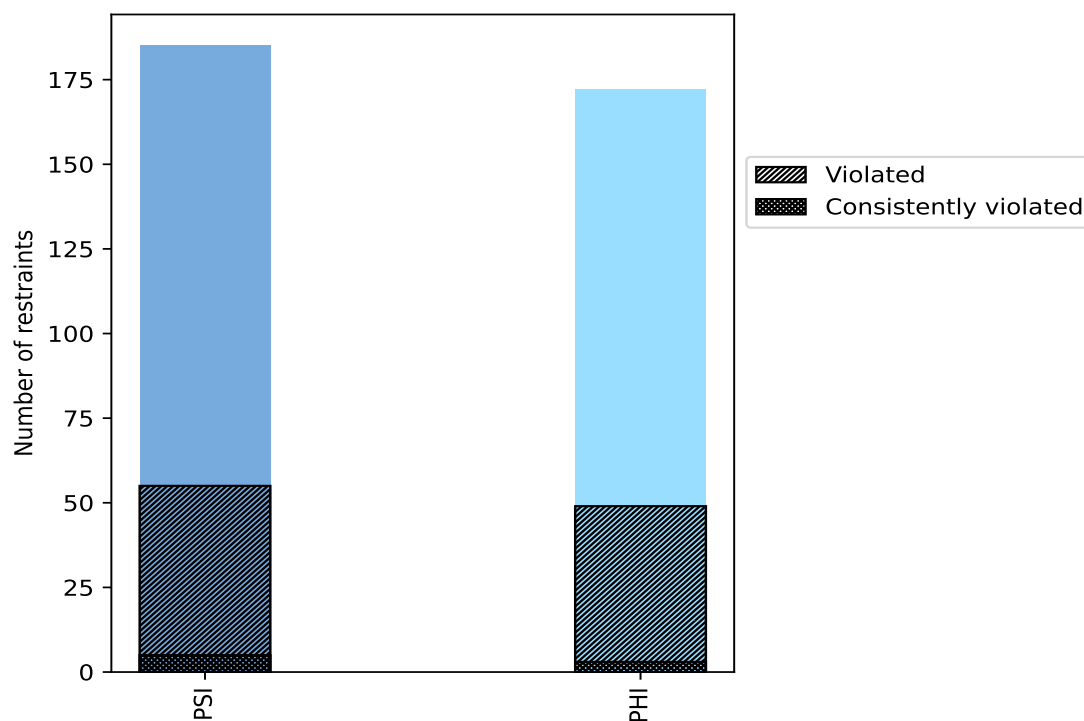
10.1 Summary of dihedral-angle violations [i](#)

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	185	51.8	55	29.7	15.4	5	2.7	1.4
PHI	172	48.2	49	28.5	13.7	3	1.7	0.8
Total	357	100.0	104	29.1	29.1	8	2.2	2.2

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](#)



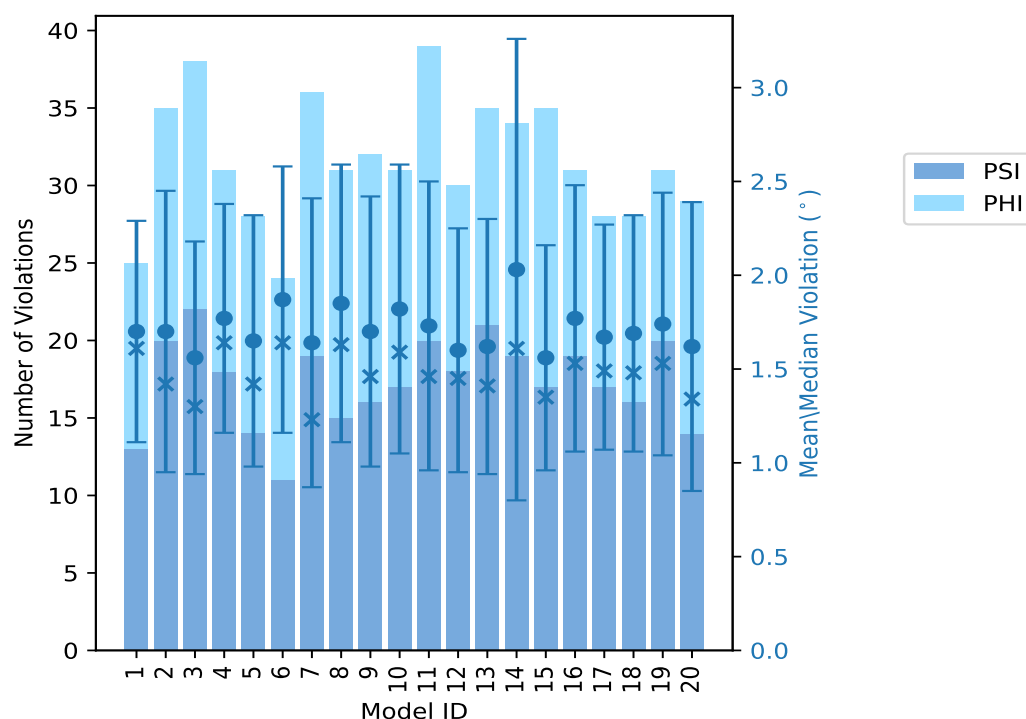
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	13	12	25	1.7	3.72	0.59	1.61
2	20	15	35	1.7	3.47	0.75	1.42
3	22	16	38	1.56	3.48	0.62	1.3
4	18	13	31	1.77	3.23	0.61	1.64
5	14	14	28	1.65	4.19	0.67	1.42
6	11	13	24	1.87	3.93	0.71	1.64
7	19	17	36	1.64	4.18	0.77	1.23
8	15	16	31	1.85	4.03	0.74	1.63
9	16	16	32	1.7	3.26	0.72	1.46
10	17	14	31	1.82	3.93	0.77	1.59
11	20	19	39	1.73	4.17	0.77	1.46
12	18	12	30	1.6	4.16	0.65	1.45
13	21	14	35	1.62	3.9	0.68	1.41
14	19	15	34	2.03	6.87	1.23	1.61
15	17	18	35	1.56	3.41	0.6	1.35
16	19	12	31	1.77	3.56	0.71	1.53
17	17	11	28	1.67	3.83	0.6	1.49
18	16	12	28	1.69	3.84	0.63	1.48
19	20	11	31	1.74	4.3	0.7	1.53
20	14	15	29	1.62	4.06	0.77	1.34

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	
PSI	PHI	Total	Count ¹	%
18	12	30	1	5.0
8	9	17	2	10.0
5	6	11	3	15.0
1	5	6	4	20.0
1	1	2	5	25.0
3	4	7	6	30.0
2	1	3	7	35.0
1	1	2	8	40.0
1	0	1	9	45.0
2	0	2	10	50.0
1	0	1	11	55.0

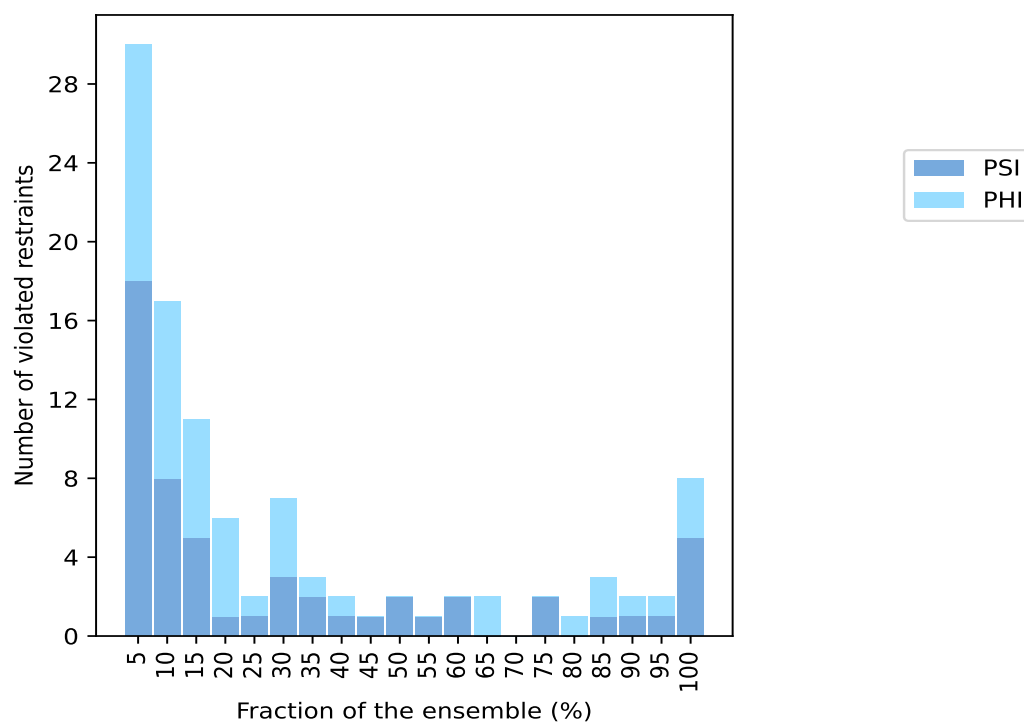
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Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
2	0	2	12	60.0
0	2	2	13	65.0
0	0	0	14	70.0
2	0	2	15	75.0
0	1	1	16	80.0
1	2	3	17	85.0
1	1	2	18	90.0
1	1	2	19	95.0
5	3	8	20	100.0

¹ Number of models with violations

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

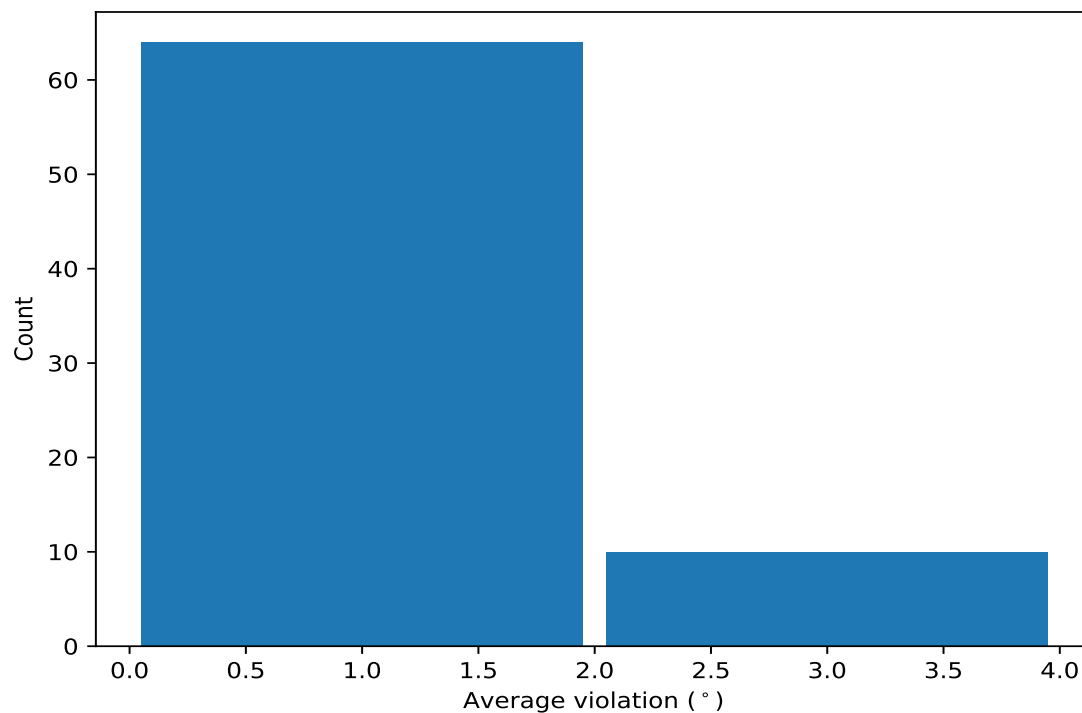


10.4 Most violated dihedral-angle restraints in the ensemble ⓘ

10.4.1 Histogram : Distribution of mean dihedral-angle violations ⓘ

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

in the ensemble



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

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

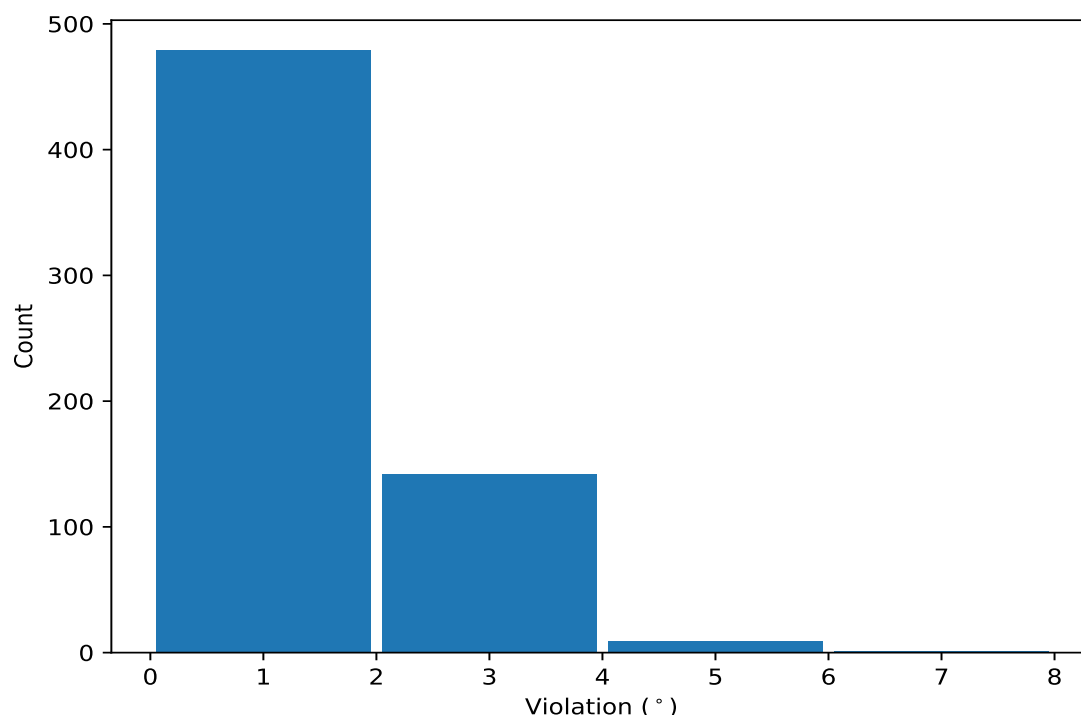
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	20	3.73	0.48	3.84
(1,165)	1:107:A:ARG:N	1:107:A:ARG:CA	1:107:A:ARG:C	1:108:A:LEU:N	20	2.82	0.32	2.94
(1,168)	1:108:A:LEU:C	1:109:A:VAL:N	1:109:A:VAL:CA	1:109:A:VAL:C	20	2.7	0.26	2.72
(1,333)	1:229:A:ASP:C	1:230:A:ASP:N	1:230:A:ASP:CA	1:230:A:ASP:C	20	2.14	0.51	2.05
(1,328)	1:226:A:LEU:N	1:226:A:LEU:CA	1:226:A:LEU:C	1:227:A:SER:N	20	2.11	0.59	2.12
(1,246)	1:170:A:ALA:N	1:170:A:ALA:CA	1:170:A:ALA:C	1:171:A:HIS:N	20	1.88	0.44	1.92
(1,191)	1:106:A:ASP:C	1:107:A:ARG:N	1:107:A:ARG:CA	1:107:A:ARG:C	20	1.69	0.24	1.65
(1,142)	1:94:A:VAL:N	1:94:A:VAL:CA	1:94:A:VAL:C	1:95:A:SER:N	20	1.41	0.17	1.4
(1,171)	1:110:A:SER:N	1:110:A:SER:CA	1:110:A:SER:C	1:111:A:LYS:N	19	1.81	0.38	1.9
(1,170)	1:109:A:VAL:C	1:110:A:SER:N	1:110:A:SER:CA	1:110:A:SER:C	19	1.22	0.22	1.13

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 (°)
(1,2)	1:21:A:ARG:N	1:21:A:ARG:CA	1:21:A:ARG:C	1:22:A:PHE:N	14	6.87
(1,36)	1:21:A:ARG:C	1:22:A:PHE:N	1:22:A:PHE:CA	1:22:A:PHE:C	14	5.09
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	14	4.59
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	19	4.3
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	5	4.19
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	7	4.18
(1,229)	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	1:153:A:GLY:N	11	4.17
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	12	4.16
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	20	4.06
(1,234)	1:157:A:ALA:N	1:157:A:ALA:CA	1:157:A:ALA:C	1:158:A:HIS:N	8	4.03