



wwPDB NMR Structure Validation Summary Report ⓘ

Dec 25, 2024 – 04:40 PM EST

PDB ID : 6YP5
BMRB ID : 34513
Title : Solution NMR structure of the oligomerization domain of respiratory syncytial virus phosphoprotein
Authors : Cardone, C.; Bontems, F.; Bardiaux, B.; Sizun, C.
Deposited on : 2020-04-15

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

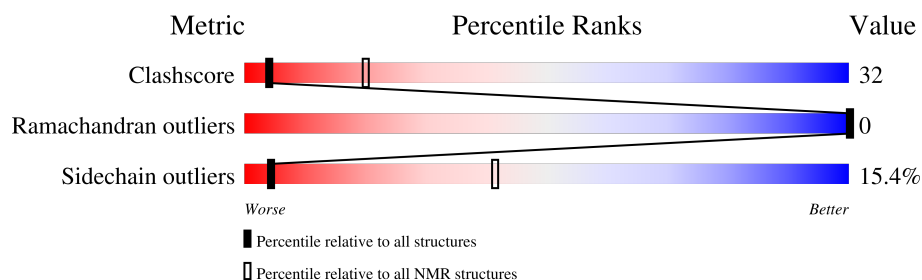
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 23%.

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	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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

Mol	Chain	Length	Quality of chain
1	A	45	20% 31% 7% 29% 13%
1	B	45	18% 33% 7% 29% 13%
1	C	45	20% 31% 7% 29% 13%
1	D	45	18% 33% 7% 29% 13%

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 9 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:131-A:156, B:131-B:156, C:131-C:156, D:131-D:156 (104)	0.40	9

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2332 atoms, of which 1180 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms						Trace
1	A	39	Total	C	H	N	O	S	0
			583	174	295	53	60	1	
1	B	39	Total	C	H	N	O	S	0
			583	174	295	53	60	1	
1	C	39	Total	C	H	N	O	S	0
			583	174	295	53	60	1	
1	D	39	Total	C	H	N	O	S	0
			583	174	295	53	60	1	

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	119	GLY	-	expression tag	UNP G8FRA5
A	120	SER	-	expression tag	UNP G8FRA5
A	121	GLY	-	expression tag	UNP G8FRA5
A	122	SER	-	expression tag	UNP G8FRA5
A	123	GLY	-	expression tag	UNP G8FRA5
A	124	SER	-	expression tag	UNP G8FRA5
A	125	GLY	-	expression tag	UNP G8FRA5
A	126	SER	-	expression tag	UNP G8FRA5
B	119	GLY	-	expression tag	UNP G8FRA5
B	120	SER	-	expression tag	UNP G8FRA5
B	121	GLY	-	expression tag	UNP G8FRA5
B	122	SER	-	expression tag	UNP G8FRA5
B	123	GLY	-	expression tag	UNP G8FRA5
B	124	SER	-	expression tag	UNP G8FRA5
B	125	GLY	-	expression tag	UNP G8FRA5
B	126	SER	-	expression tag	UNP G8FRA5
C	119	GLY	-	expression tag	UNP G8FRA5
C	120	SER	-	expression tag	UNP G8FRA5
C	121	GLY	-	expression tag	UNP G8FRA5
C	122	SER	-	expression tag	UNP G8FRA5
C	123	GLY	-	expression tag	UNP G8FRA5
C	124	SER	-	expression tag	UNP G8FRA5
C	125	GLY	-	expression tag	UNP G8FRA5
C	126	SER	-	expression tag	UNP G8FRA5
D	119	GLY	-	expression tag	UNP G8FRA5

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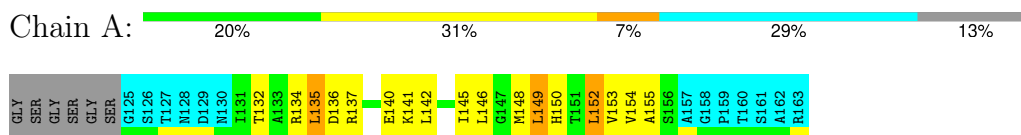
Chain	Residue	Modelled	Actual	Comment	Reference
D	120	SER	-	expression tag	UNP G8FRA5
D	121	GLY	-	expression tag	UNP G8FRA5
D	122	SER	-	expression tag	UNP G8FRA5
D	123	GLY	-	expression tag	UNP G8FRA5
D	124	SER	-	expression tag	UNP G8FRA5
D	125	GLY	-	expression tag	UNP G8FRA5
D	126	SER	-	expression tag	UNP G8FRA5

4 Residue-property plots [i](#)

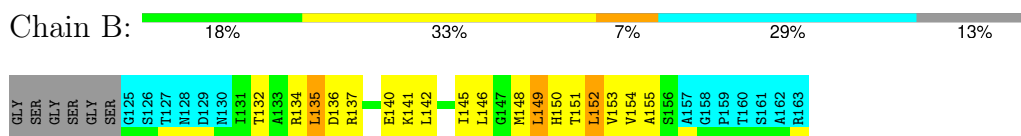
4.1 Average score per residue in the NMR ensemble

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.

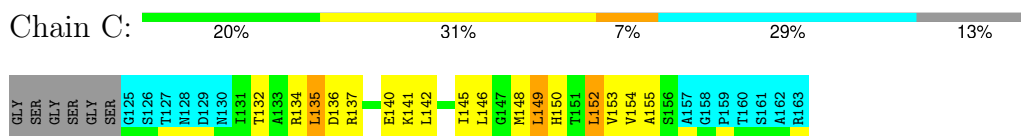
• Molecule 1: Phosphoprotein



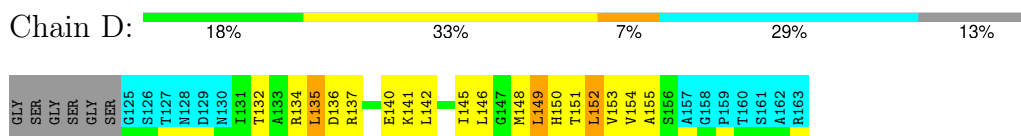
• Molecule 1: Phosphoprotein



• Molecule 1: Phosphoprotein



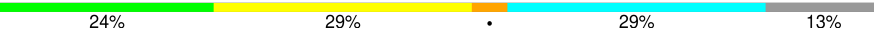
• Molecule 1: Phosphoprotein



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


The representative model is number 9. Colouring as in section 4.1 above.

• Molecule 1: Phosphoprotein

Chain A: 

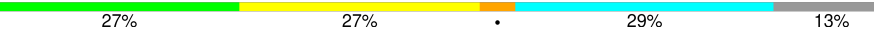
GLY	SER	GLY	SER	GLY	SER	G125	S126	T127	N128	D129	N130	T131	T132	A133	R134	L135	D136	R137	K141	L142	I145	L146	L149	H150	T151	L152	V153	V154	A155	S156	A157	G158	P159	T160	S161	A162	R163
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• Molecule 1: Phosphoprotein

Chain B: 


GLY	SER	GLY	SER	GLY	SER	G125	S126	T127	N128	D129	N130	T131	T132	A133	R134	L135	D136	R137	K141	L142	I145	L146	L149	H150	T151	L152	V153	V154	A155	S156	G158	P159	T160	S161	A162	R163
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• Molecule 1: Phosphoprotein

Chain C: 

GLY	SER	GLY	SER	GLY	SER	G125	S126	T127	N128	D129	N130	T131	T132	A133	R134	L135	D136	R137	K141	L142	I145	L146	L149	H150	T151	L152	V153	V154	A155	S156	A157	G158	P159	T160	S161	A162	R163
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• Molecule 1: Phosphoprotein

Chain D: 

GLY	SER	GLY	SER	GLY	SER	G125	S126	T127	N128	D129	N130	T131	T132	A133	R134	L135	D136	R137	K141	L142	I145	L146	L149	H150	T151	L152	V153	V154	A155	S156	A157	G158	P159	T160	S161	A162	R163
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5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
ARIA	refinement	2.3
ARIA	structure calculation	2.3

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	482
Number of shifts mapped to atoms	458
Number of unparsed shifts	0
Number of shifts with mapping errors	24
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	23%

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	201	219	218	16±5
1	B	201	219	218	16±5
1	C	201	219	218	16±5
1	D	201	219	218	16±5
All	All	16080	17520	17440	1079

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 32.

5 of 209 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:142:LEU:HA	1:A:145:ILE:HD12	0.88	1.45	3	20
1:C:142:LEU:HA	1:C:145:ILE:HD12	0.87	1.45	3	20
1:D:142:LEU:HA	1:D:145:ILE:HD12	0.87	1.45	3	20
1:B:142:LEU:HA	1:B:145:ILE:HD12	0.86	1.45	3	20
1:A:135:LEU:HD12	1:A:136:ASP:N	0.67	2.04	5	2

6.3 Torsion angles

6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	26/45 (58%)	26±0 (100±1%)	0±0 (0±1%)	0±0 (0±0%)	100	100
1	B	26/45 (58%)	26±0 (99±2%)	0±0 (1±2%)	0±0 (0±0%)	100	100
1	C	26/45 (58%)	26±0 (99±2%)	0±0 (1±2%)	0±0 (0±0%)	100	100
1	D	26/45 (58%)	26±0 (99±2%)	0±0 (1±2%)	0±0 (0±0%)	100	100
All	All	2080/3600 (58%)	2063 (99%)	17 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	23/35 (66%)	19±1 (85±4%)	4±1 (15±4%)	4	41
1	B	23/35 (66%)	19±1 (85±4%)	4±1 (15±4%)	4	41
1	C	23/35 (66%)	19±1 (85±4%)	4±1 (15±4%)	4	41
1	D	23/35 (66%)	19±1 (85±4%)	4±1 (15±4%)	4	41
All	All	1840/2800 (66%)	1556 (85%)	284 (15%)	4	41

5 of 32 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	149	LEU	20
1	A	152	LEU	20
1	B	149	LEU	20
1	B	152	LEU	20
1	C	149	LEU	20

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 23% for the well-defined parts and 22% 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	482
Number of shifts mapped to atoms	458
Number of unparsed shifts	0
Number of shifts with mapping errors	24
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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 24) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	119	GLY	CA	43.57	0.25	1
1	A	119	GLY	HA2	3.89	0.02	2
1	A	119	GLY	HA3	3.89	0.02	2
1	A	120	SER	CA	58.43	0.25	1
1	A	120	SER	CB	63.8	0.25	1
1	A	120	SER	HA	4.54	0.02	1
1	A	120	SER	HB2	3.88	0.02	2
1	A	120	SER	HB3	3.88	0.02	2
1	A	121	GLY	CA	45.16	0.25	1
1	A	121	GLY	HA2	4.04	0.02	2
1	A	121	GLY	HA3	4.05	0.02	2
1	A	122	SER	CA	58.46	0.25	1
1	A	122	SER	CB	63.7	0.25	1
1	A	122	SER	HA	4.5	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	122	SER	HB2	3.92	0.02	2
1	A	122	SER	HB3	3.92	0.02	2
1	A	123	GLY	CA	45.15	0.25	1
1	A	123	GLY	HA2	4.04	0.02	2
1	A	123	GLY	HA3	4.05	0.02	2
1	A	124	SER	CA	58.47	0.25	1
1	A	124	SER	CB	63.84	0.25	1
1	A	124	SER	HA	4.5	0.02	1
1	A	124	SER	HB2	3.93	0.02	1
1	A	124	SER	HB3	3.93	0.02	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
$^{13}\text{C}_\alpha$	45	-0.52 ± 0.13	Should be checked
$^{13}\text{C}_\beta$	39	0.21 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}'$	34	-0.54 ± 0.12	Should be applied
^{15}N	36	-0.36 ± 0.20	None needed (< 0.5 ppm)

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 23%, i.e. 343 atoms were assigned a chemical shift out of a possible 1492. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	131/524 (25%)	53/212 (25%)	52/208 (25%)	26/104 (25%)
Sidechain	210/936 (22%)	144/620 (23%)	66/288 (23%)	0/28 (0%)
Aromatic	2/32 (6%)	1/16 (6%)	1/8 (12%)	0/8 (0%)
Overall	343/1492 (23%)	198/848 (23%)	119/504 (24%)	26/140 (19%)

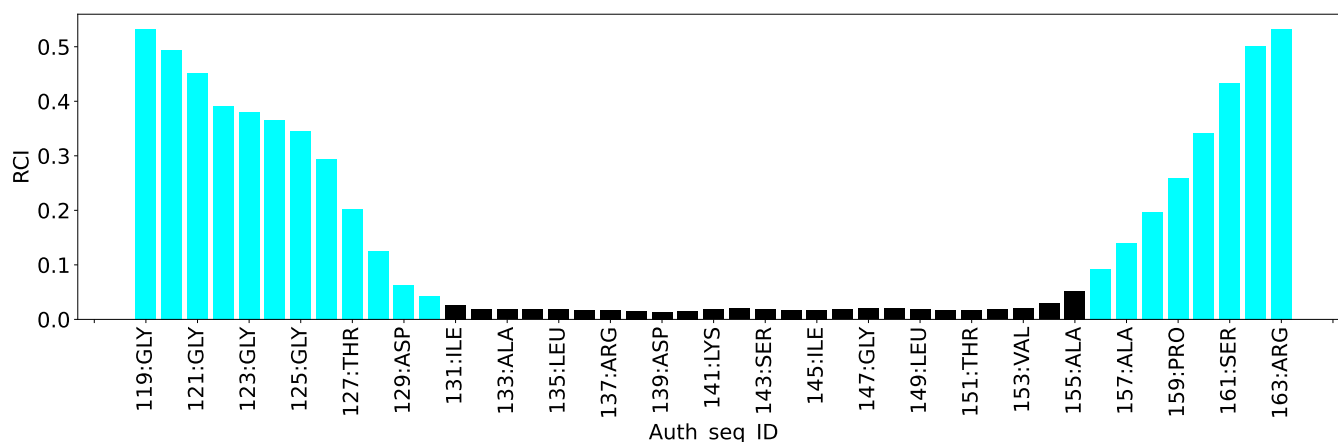
7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

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

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	3180
Intra-residue ($ i-j =0$)	1140
Sequential ($ i-j =1$)	532
Medium range ($ i-j >1$ and $ i-j <5$)	620
Long range ($ i-j \geq 5$)	0
Inter-chain	888
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	56
Number of unmapped restraints	0
Number of restraints per residue	18.0
Number of long range restraints per residue ¹	0.0

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)	120.2	0.2
0.2-0.5 (Medium)	252.4	0.5
>0.5 (Large)	304.8	3.47

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)	3.4	7.17
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

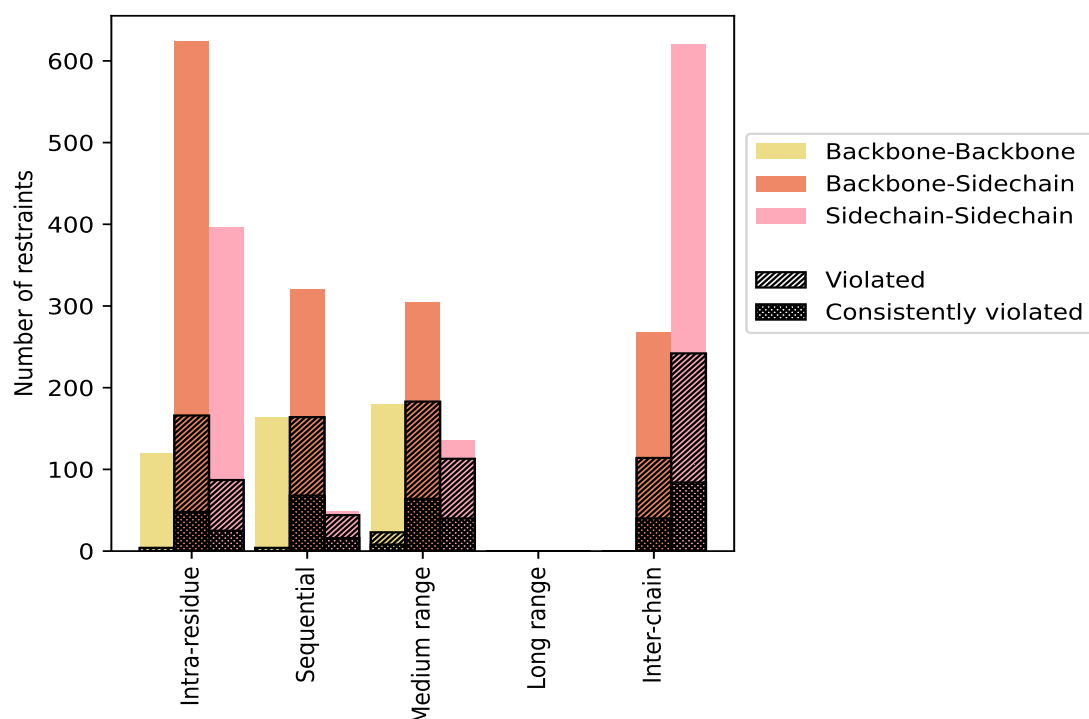
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	1140	35.8	257	22.5	8.1	73	6.4	2.3
Backbone-Backbone	120	3.8	4	3.3	0.1	0	0.0	0.0
Backbone-Sidechain	624	19.6	166	26.6	5.2	48	7.7	1.5
Sidechain-Sidechain	396	12.5	87	22.0	2.7	25	6.3	0.8
Sequential ($i-j =1$)	532	16.7	212	39.8	6.7	84	15.8	2.6
Backbone-Backbone	164	5.2	4	2.4	0.1	0	0.0	0.0
Backbone-Sidechain	320	10.1	164	51.2	5.2	68	21.2	2.1
Sidechain-Sidechain	48	1.5	44	91.7	1.4	16	33.3	0.5
Medium range ($i-j >1$ & $i-j <5$)	620	19.5	319	51.5	10.0	112	18.1	3.5
Backbone-Backbone	180	5.7	23	12.8	0.7	8	4.4	0.3
Backbone-Sidechain	304	9.6	183	60.2	5.8	64	21.1	2.0
Sidechain-Sidechain	136	4.3	113	83.1	3.6	40	29.4	1.3
Long range ($i-j \geq 5$)	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
Inter-chain	888	27.9	356	40.1	11.2	124	14.0	3.9
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	268	8.4	114	42.5	3.6	40	14.9	1.3
Sidechain-Sidechain	620	19.5	242	39.0	7.6	84	13.5	2.6
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	3180	100.0	1144	36.0	36.0	393	12.4	12.4
Backbone-Backbone	464	14.6	31	6.7	1.0	8	1.7	0.3
Backbone-Sidechain	1516	47.7	627	41.4	19.7	220	14.5	6.9
Sidechain-Sidechain	1200	37.7	486	40.5	15.3	165	13.8	5.2

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	148	136	186	0	223	693	0.57	2.97	0.46	0.44
2	145	152	204	0	196	697	0.61	2.93	0.49	0.46
3	129	152	191	0	223	695	0.55	3.0	0.44	0.42
4	180	140	177	0	206	703	0.54	3.31	0.46	0.42
5	136	128	189	0	198	651	0.61	2.83	0.48	0.47
6	142	132	172	0	218	664	0.62	2.93	0.51	0.46
7	155	132	211	0	216	714	0.65	3.13	0.52	0.48
8	145	131	200	0	224	700	0.66	3.05	0.51	0.5
9	124	132	181	0	211	648	0.64	2.74	0.51	0.48
10	165	131	200	0	225	721	0.58	3.02	0.48	0.43

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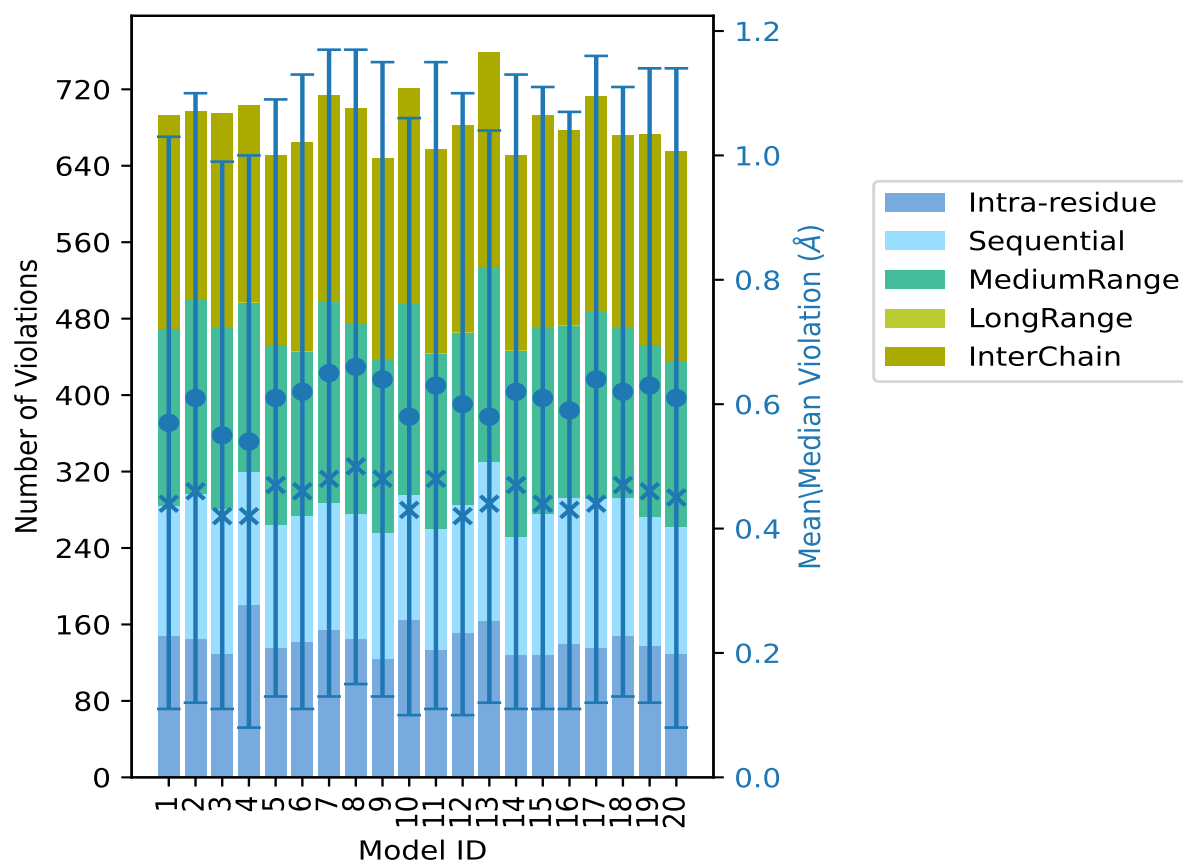
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	134	126	184	0	213	657	0.63	3.02	0.52	0.48
12	152	134	180	0	216	682	0.6	3.39	0.5	0.42
13	164	166	205	0	224	759	0.58	2.8	0.46	0.44
14	128	124	195	0	204	651	0.62	3.01	0.51	0.47
15	128	148	195	0	222	693	0.61	3.07	0.5	0.44
16	140	153	180	0	204	677	0.59	2.95	0.48	0.43
17	136	156	195	0	226	713	0.64	3.41	0.52	0.44
18	148	145	178	0	201	672	0.62	3.03	0.49	0.47
19	137	136	180	0	220	673	0.63	3.22	0.51	0.46
20	130	132	174	0	219	655	0.61	3.47	0.53	0.45

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

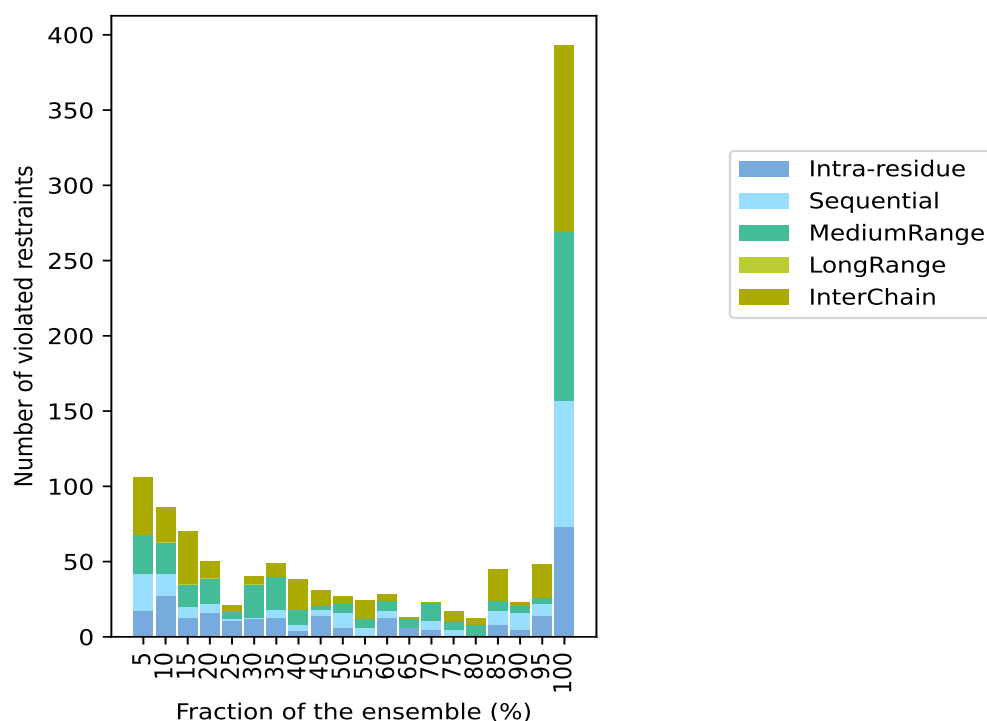
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 2036(IR:883, SQ:320, MR:301, LR:0, IC:532) restraints are 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	%
17	25	26	0	38	106	1	5.0
27	15	21	0	23	86	2	10.0
13	7	15	0	35	70	3	15.0
16	6	17	0	11	50	4	20.0
11	1	5	0	4	21	5	25.0
12	1	22	0	5	40	6	30.0
13	5	22	0	9	49	7	35.0
4	4	10	0	20	38	8	40.0
14	4	3	0	10	31	9	45.0
6	10	7	0	4	27	10	50.0
0	6	6	0	12	24	11	55.0
13	4	7	0	4	28	12	60.0
6	0	6	0	1	13	13	65.0
5	6	12	0	0	23	14	70.0
0	5	5	0	7	17	15	75.0
0	1	7	0	4	12	16	80.0
8	9	7	0	21	45	17	85.0
5	11	5	0	2	23	18	90.0
14	8	4	0	22	48	19	95.0
73	84	112	0	124	393	20	100.0

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

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

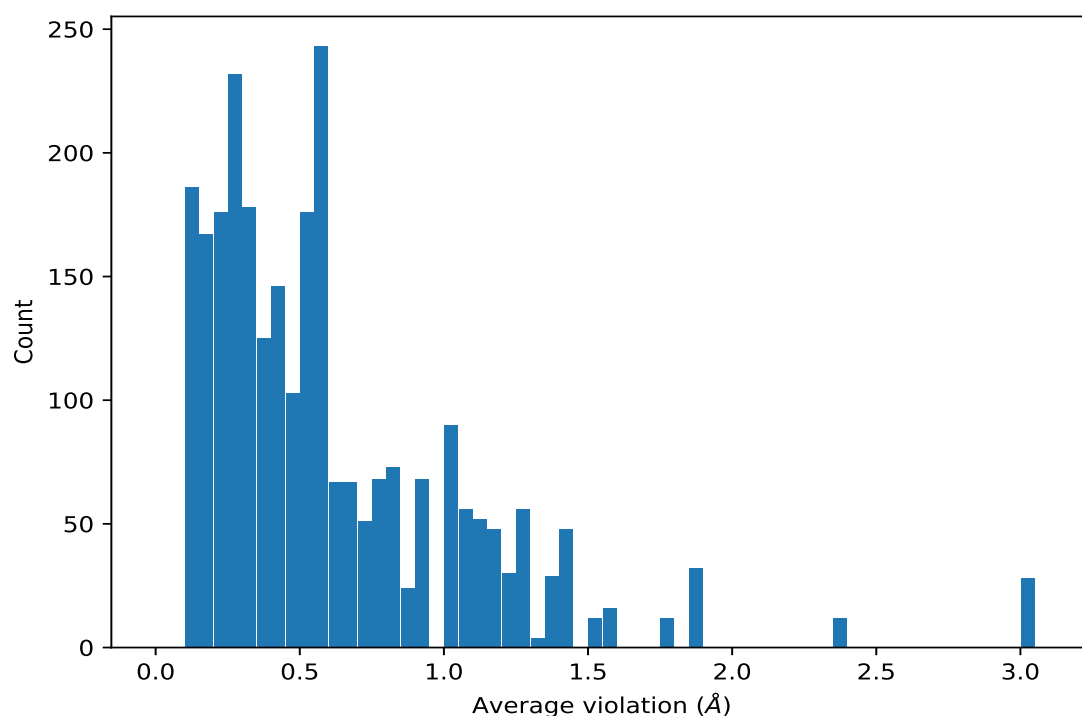
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,398)	1:142:B:LEU:HD21	1:148:A:MET:HE2	20	3.03	0.18	3.0
(1,398)	1:142:B:LEU:HD22	1:148:A:MET:HE1	20	3.03	0.18	3.0
(1,398)	1:142:B:LEU:HD23	1:148:A:MET:HE1	20	3.03	0.18	3.0
(1,398)	1:142:B:LEU:HD22	1:148:A:MET:HE3	20	3.03	0.18	3.0
(1,398)	1:142:B:LEU:HD23	1:148:A:MET:HE3	20	3.03	0.18	3.0
(1,398)	1:142:B:LEU:HD22	1:148:A:MET:HE2	20	3.03	0.18	3.0
(1,398)	1:142:B:LEU:HD23	1:148:A:MET:HE2	20	3.03	0.18	3.0
(1,397)	1:142:A:LEU:HD21	1:148:D:MET:HE2	20	3.03	0.18	3.01
(1,397)	1:142:A:LEU:HD22	1:148:D:MET:HE1	20	3.03	0.18	3.01
(1,397)	1:142:A:LEU:HD23	1:148:D:MET:HE1	20	3.03	0.18	3.01
(1,397)	1:142:A:LEU:HD22	1:148:D:MET:HE3	20	3.03	0.18	3.01
(1,397)	1:142:A:LEU:HD23	1:148:D:MET:HE3	20	3.03	0.18	3.01
(1,397)	1:142:A:LEU:HD22	1:148:D:MET:HE2	20	3.03	0.18	3.01
(1,397)	1:142:A:LEU:HD23	1:148:D:MET:HE2	20	3.03	0.18	3.01
(1,399)	1:142:C:LEU:HD21	1:148:B:MET:HE2	20	3.03	0.18	3.0
(1,399)	1:142:C:LEU:HD22	1:148:B:MET:HE1	20	3.03	0.18	3.0

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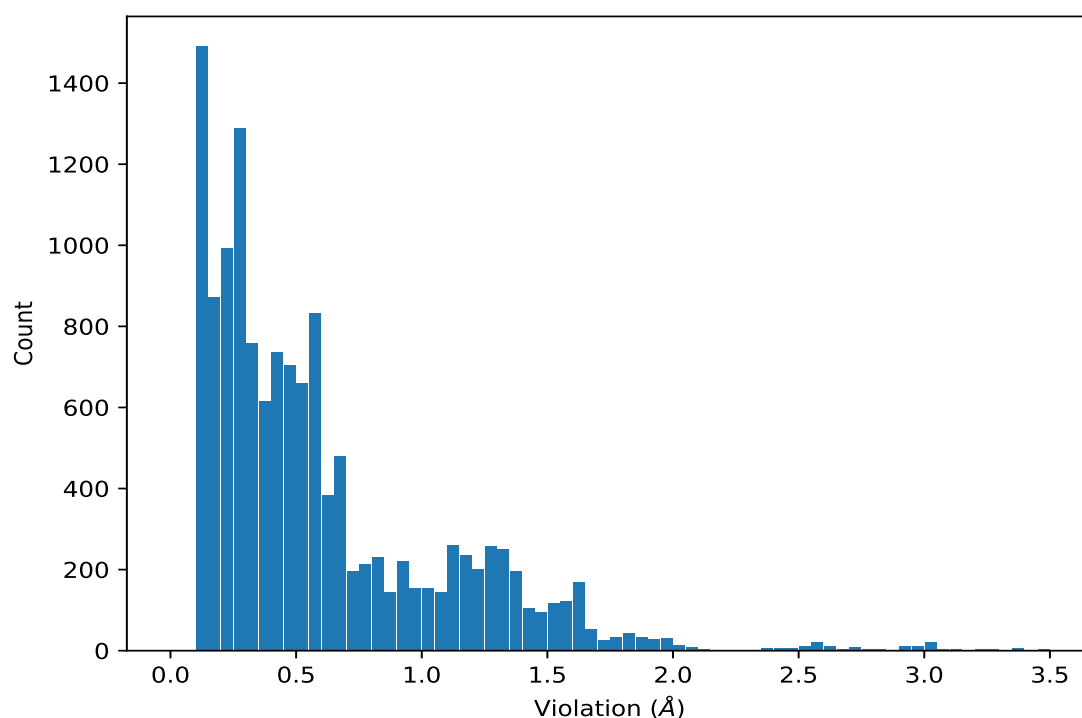
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,399)	1:142:C:LEU:HD23	1:148:B:MET:HE1	20	3.03	0.18	3.0
(1,399)	1:142:C:LEU:HD22	1:148:B:MET:HE3	20	3.03	0.18	3.0
(1,399)	1:142:C:LEU:HD23	1:148:B:MET:HE3	20	3.03	0.18	3.0
(1,399)	1:142:C:LEU:HD22	1:148:B:MET:HE2	20	3.03	0.18	3.0
(1,399)	1:142:C:LEU:HD23	1:148:B:MET:HE2	20	3.03	0.18	3.0
(1,400)	1:142:D:LEU:HD21	1:148:C:MET:HE2	20	3.03	0.18	3.0
(1,400)	1:142:D:LEU:HD22	1:148:C:MET:HE1	20	3.03	0.18	3.0
(1,400)	1:142:D:LEU:HD23	1:148:C:MET:HE1	20	3.03	0.18	3.0
(1,400)	1:142:D:LEU:HD22	1:148:C:MET:HE3	20	3.03	0.18	3.0
(1,400)	1:142:D:LEU:HD23	1:148:C:MET:HE3	20	3.03	0.18	3.0
(1,400)	1:142:D:LEU:HD22	1:148:C:MET:HE2	20	3.03	0.18	3.0
(1,400)	1:142:D:LEU:HD23	1:148:C:MET:HE2	20	3.03	0.18	3.0
(1,356)	1:145:D:ILE:HD11	1:141:C:LYS:HD3	20	2.39	0.46	2.55
(1,356)	1:145:D:ILE:HD13	1:141:C:LYS:HD3	20	2.39	0.46	2.55
(1,356)	1:145:D:ILE:HD12	1:141:C:LYS:HD3	20	2.39	0.46	2.55
(1,353)	1:145:A:ILE:HD11	1:141:D:LYS:HD3	20	2.39	0.46	2.55
(1,353)	1:145:A:ILE:HD13	1:141:D:LYS:HD3	20	2.39	0.46	2.55
(1,353)	1:145:A:ILE:HD12	1:141:D:LYS:HD3	20	2.39	0.46	2.55
(1,355)	1:145:C:ILE:HD11	1:141:B:LYS:HD3	20	2.39	0.46	2.55
(1,355)	1:145:C:ILE:HD13	1:141:B:LYS:HD3	20	2.39	0.46	2.55
(1,355)	1:145:C:ILE:HD12	1:141:B:LYS:HD3	20	2.39	0.46	2.55
(1,354)	1:145:B:ILE:HD11	1:141:A:LYS:HD3	20	2.39	0.46	2.55
(1,354)	1:145:B:ILE:HD13	1:141:A:LYS:HD3	20	2.39	0.46	2.55
(1,354)	1:145:B:ILE:HD12	1:141:A:LYS:HD3	20	2.39	0.46	2.55
(1,197)	1:151:A:THR:HG23	1:154:B:VAL:HG23	20	1.9	0.1	1.93
(1,197)	1:151:A:THR:HG23	1:154:B:VAL:HG22	20	1.9	0.1	1.93
(1,197)	1:151:A:THR:HG21	1:154:B:VAL:HG23	20	1.9	0.1	1.93
(1,197)	1:151:A:THR:HG21	1:154:B:VAL:HG22	20	1.9	0.1	1.93
(1,197)	1:151:A:THR:HG23	1:154:B:VAL:HG21	20	1.9	0.1	1.93
(1,197)	1:151:A:THR:HG22	1:154:B:VAL:HG21	20	1.9	0.1	1.93
(1,197)	1:151:A:THR:HG22	1:154:B:VAL:HG23	20	1.9	0.1	1.93
(1,197)	1:151:A:THR:HG22	1:154:B:VAL:HG22	20	1.9	0.1	1.93
(1,198)	1:151:B:THR:HG23	1:154:C:VAL:HG23	20	1.9	0.1	1.95

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)
(1,646)	1:161:B:SER:HB3	1:160:C:THR:HG22	20	3.47
(1,647)	1:161:C:SER:HB3	1:160:D:THR:HG22	20	3.46
(1,645)	1:161:A:SER:HB3	1:160:B:THR:HG22	20	3.46
(1,648)	1:161:D:SER:HB3	1:160:A:THR:HG22	20	3.45
(1,400)	1:142:D:LEU:HD22	1:148:C:MET:HE2	17	3.41
(1,398)	1:142:B:LEU:HD22	1:148:A:MET:HE2	17	3.41
(1,397)	1:142:A:LEU:HD22	1:148:D:MET:HE2	17	3.4
(1,398)	1:142:B:LEU:HD22	1:148:A:MET:HE3	12	3.39
(1,400)	1:142:D:LEU:HD22	1:148:C:MET:HE3	12	3.38
(1,399)	1:142:C:LEU:HD22	1:148:B:MET:HE2	17	3.38

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

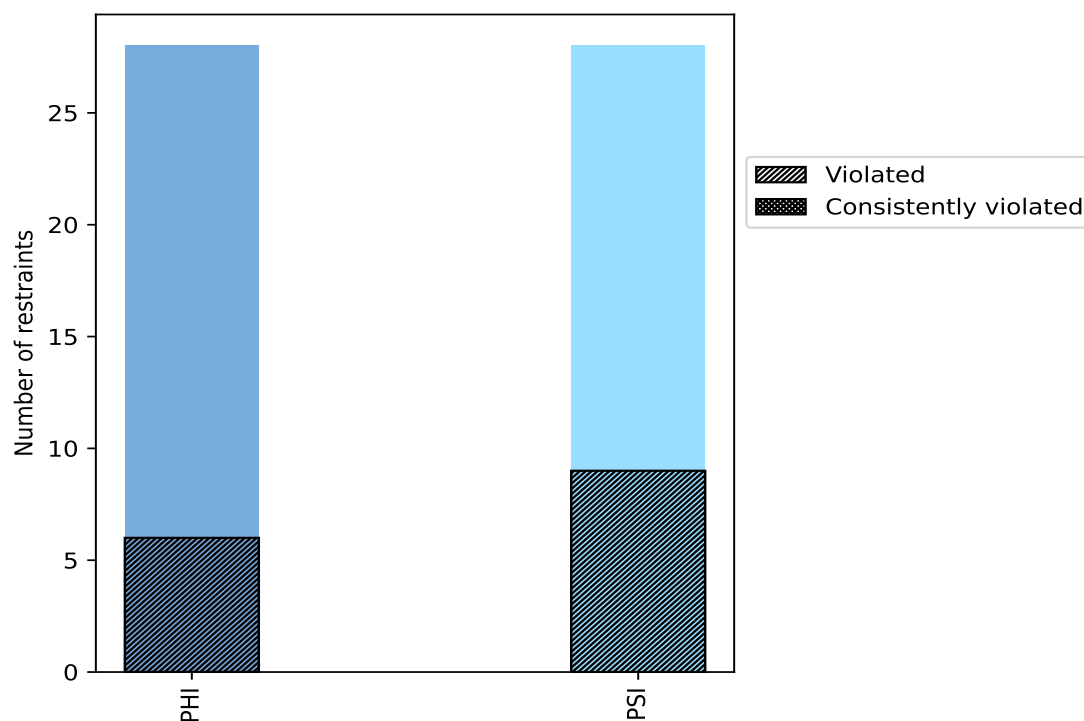
10.1 Summary of dihedral-angle violations [i](#)

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
PHI	28	50.0	6	21.4	10.7	0	0.0	0.0
PSI	28	50.0	9	32.1	16.1	0	0.0	0.0
Total	56	100.0	15	26.8	26.8	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](#)



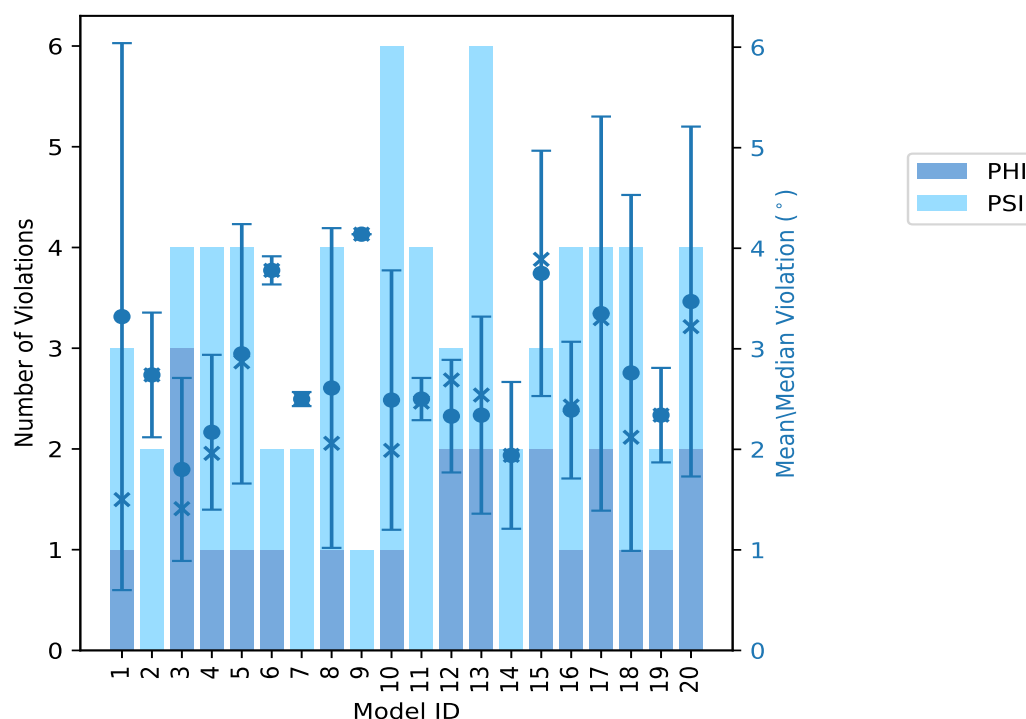
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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 (°)
	PHI	PSI	Total				
1	1	2	3	3.32	7.17	2.72	1.5
2	0	2	2	2.74	3.37	0.62	2.74
3	3	1	4	1.8	3.35	0.91	1.41
4	1	3	4	2.17	3.32	0.77	1.96
5	1	3	4	2.95	4.71	1.29	2.87
6	1	1	2	3.78	3.92	0.14	3.78
7	0	2	2	2.5	2.57	0.07	2.5
8	1	3	4	2.61	5.17	1.59	2.06
9	0	1	1	4.14	4.14	0.0	4.14
10	1	5	6	2.49	4.32	1.29	1.99
11	0	4	4	2.5	2.78	0.21	2.47
12	2	1	3	2.33	2.76	0.56	2.69
13	2	4	6	2.34	3.71	0.98	2.54
14	0	2	2	1.94	2.66	0.73	1.94
15	2	1	3	3.75	5.16	1.22	3.89
16	1	3	4	2.39	3.29	0.68	2.43
17	2	2	4	3.35	5.66	1.96	3.3
18	1	3	4	2.76	5.61	1.77	2.12
19	1	1	2	2.34	2.82	0.47	2.34
20	2	2	4	3.47	6.1	1.74	3.22

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

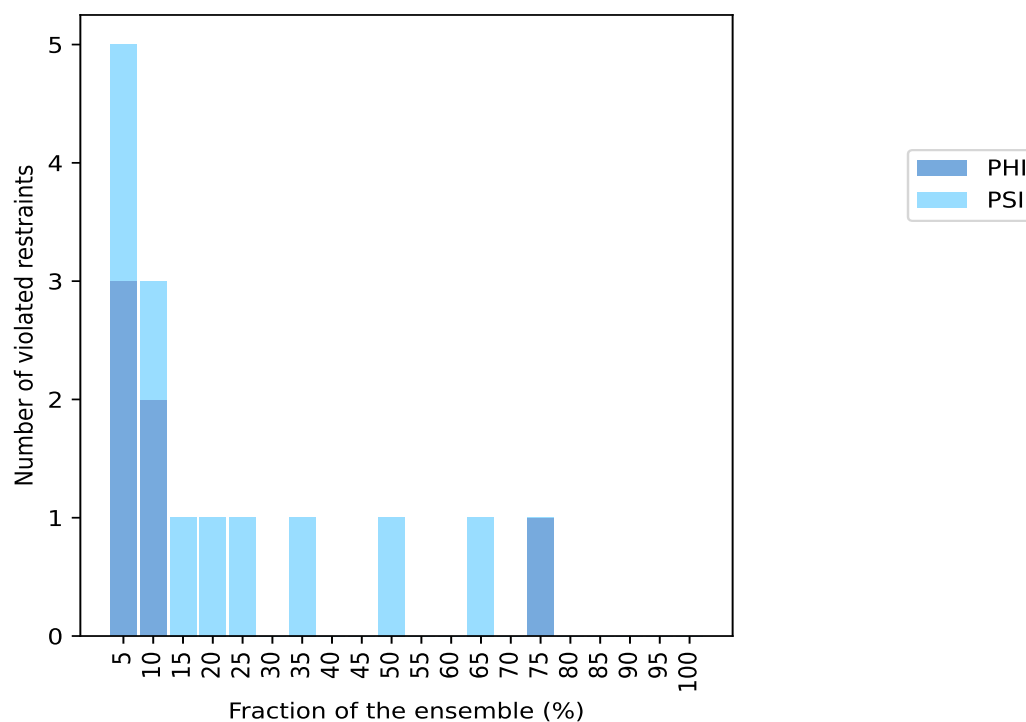
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	12	60.0
0	1	1	13	65.0
0	0	0	14	70.0
1	0	1	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

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

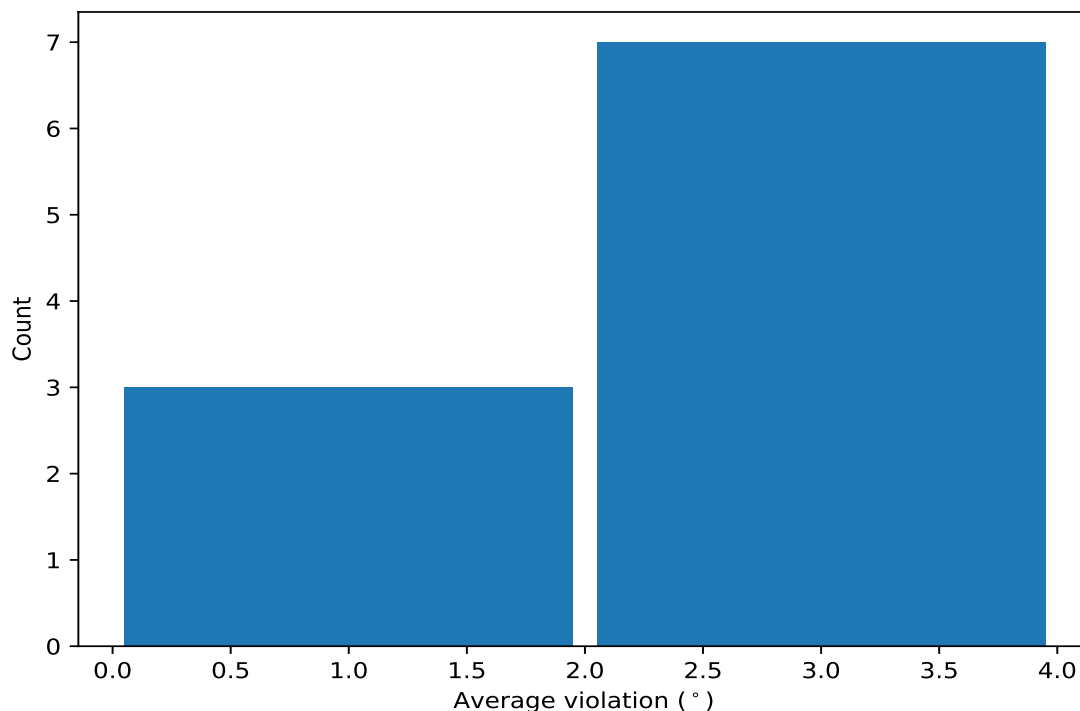


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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 ⓘ

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.

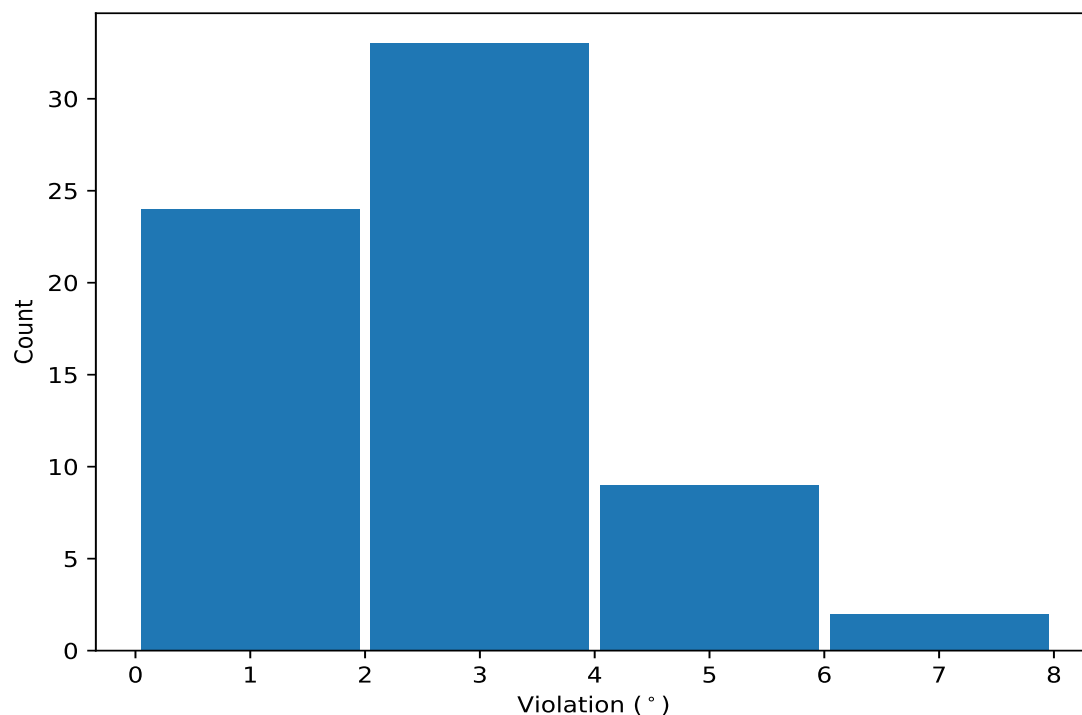
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	15	3.88	1.79	3.92
(1,8)	1:132:A:THR:N	1:132:A:THR:CA	1:132:A:THR:C	1:133:A:ALA:N	13	2.58	1.14	2.42
(1,54)	1:155:A:ALA:N	1:155:A:ALA:CA	1:155:A:ALA:C	1:156:A:SER:N	10	1.64	0.49	1.42
(1,14)	1:135:A:LEU:N	1:135:A:LEU:CA	1:135:A:LEU:C	1:136:A:ASP:N	7	2.9	0.66	2.88
(1,50)	1:153:A:VAL:N	1:153:A:VAL:CA	1:153:A:VAL:C	1:154:A:VAL:N	5	2.33	0.64	2.41
(1,56)	1:156:A:SER:N	1:156:A:SER:CA	1:156:A:SER:C	1:157:A:ALA:N	4	3.9	0.92	3.9
(1,16)	1:136:A:ASP:N	1:136:A:ASP:CA	1:136:A:ASP:C	1:137:A:ARG:N	3	1.99	0.55	1.72
(1,13)	1:134:A:ARG:C	1:135:A:LEU:N	1:135:A:LEU:CA	1:135:A:LEU:C	2	3.02	0.33	3.02
(1,5)	1:130:A:ASN:C	1:131:A:ILE:N	1:131:A:ILE:CA	1:131:A:ILE:C	2	2.42	0.23	2.42
(1,30)	1:143:A:SER:N	1:143:A:SER:CA	1:143:A:SER:C	1:144:A:GLU:N	2	1.02	0.01	1.02

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 (°)
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	1	7.17
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	20	6.1
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	17	5.66
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	18	5.61
(1,56)	1:156:A:SER:N	1:156:A:SER:CA	1:156:A:SER:C	1:157:A:ALA:N	8	5.17
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	15	5.16
(1,8)	1:132:A:THR:N	1:132:A:THR:CA	1:132:A:THR:C	1:133:A:ALA:N	17	4.89
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	5	4.71
(1,11)	1:133:A:ALA:C	1:134:A:ARG:N	1:134:A:ARG:CA	1:134:A:ARG:C	10	4.32
(1,8)	1:132:A:THR:N	1:132:A:THR:CA	1:132:A:THR:C	1:133:A:ALA:N	9	4.14