



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2N0Y
BMRB ID : 25540
Title : NMR structure of the complex between the C-terminal domain of the Rift Valley fever virus protein NSs and the PH domain of the Tfb1 subunit of TFIID
Authors : Cyr, N.; de la Fuente, C.; Lecoq, L.; Guendel, I.; Chabot, P.R.; Kehn-Hall, K.; Omichinski, J.G.
Deposited on : 2015-03-18

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

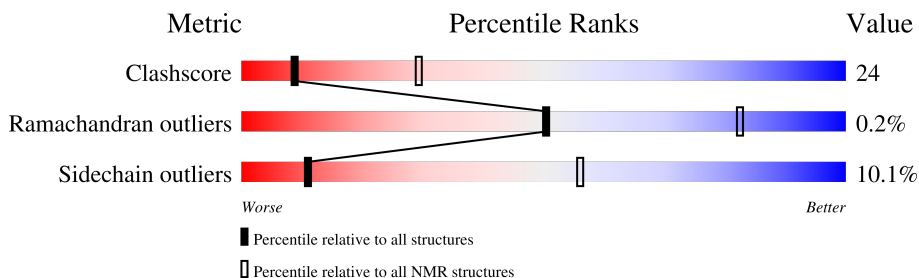
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 93%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	115	
2	B	24	

2 Ensemble composition and analysis i

This entry contains 20 models. Model 12 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:3-A:66, A:85-A:111, B:261-B:263 (94)	0.37	12

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 and 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2137 atoms, of which 1056 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RNA polymerase II transcription factor B subunit 1.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	115	1821	559	919	161	177	5	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	PRO	MET	engineered mutation	UNP P32776

- Molecule 2 is a protein called Non-structural protein NS-S.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
2	B	24	316	104	137	24	50	1	0

There are 5 discrepancies between the modelled and reference sequences:

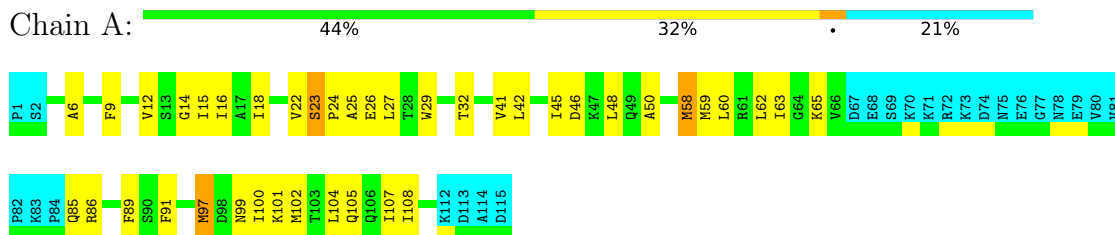
Chain	Residue	Modelled	Actual	Comment	Reference
B	242	GLY	-	expression tag	UNP P21698
B	243	GLY	-	expression tag	UNP P21698
B	244	GLY	-	expression tag	UNP P21698
B	245	GLY	-	expression tag	UNP P21698
B	246	TYR	-	expression tag	UNP P21698

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: RNA polymerase II transcription factor B subunit 1



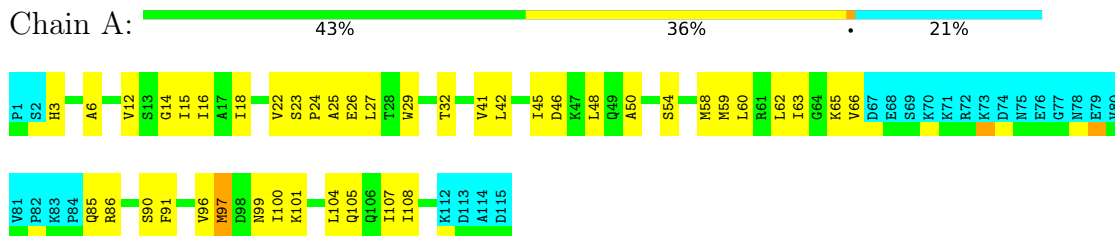
- Molecule 2: Non-structural protein NS-S



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

The representative model is number 12. Colouring as in section 4.1 above.

- Molecule 1: RNA polymerase II transcription factor B subunit 1



- Molecule 2: Non-structural protein NS-S



G242	G243	G244	G245	Y246	D247	Y248	E249	W250	E251	S252	E253	E254	E255	S256	D257	D258	D259	G260	F261	Y264	D265
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

5 Refinement protocol and experimental data overview

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

Of the 260 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
CNS	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	1693
Number of shifts mapped to atoms	1693
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	93%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.44±0.03	0±0/725 (0.0± 0.0%)	0.56±0.01	0±0/978 (0.0± 0.0%)
2	B	0.37±0.07	0±0/28 (0.0± 0.0%)	0.44±0.09	0±0/38 (0.0± 0.0%)
All	All	0.43	1/15060 (0.0%)	0.56	0/20320 (0.0%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.2±0.4
All	All	0	5

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	91	PHE	CE2-CZ	5.06	1.47	1.37	4	1

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	23	SER	Peptide	5

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	714	736	733	35±4
2	B	27	24	24	1±1
All	All	14820	15200	15140	705

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 24.

5 of 135 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:LEU:HD23	1:A:105:GLN:HG3	0.98	1.36	12	16
1:A:48:LEU:HD22	1:A:104:LEU:HB2	0.84	1.50	3	20
1:A:60:LEU:HB2	1:A:91:PHE:CE1	0.81	2.10	4	10
1:A:22:VAL:HG11	1:A:26:GLU:HB2	0.78	1.54	14	10
1:A:48:LEU:HD23	1:A:105:GLN:HG2	0.77	1.52	16	4

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	91/115 (79%)	84±1 (93±1%)	7±1 (7±1%)	0±0 (0±0%)	50	82
2	B	3/24 (12%)	3±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	1880/2780 (68%)	1745 (93%)	131 (7%)	4 (0%)	50	82

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	25	ALA	4

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	81/103 (79%)	73±1 (90±2%)	8±1 (10±2%)	11	56
2	B	3/19 (16%)	3±0 (90±15%)	0±0 (10±15%)	11	56
All	All	1680/2440 (69%)	1511 (90%)	169 (10%)	11	56

5 of 26 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	16	ILE	20
1	A	97	MET	20
1	A	12	VAL	19
1	A	58	MET	19
1	A	85	GLN	15

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 93% for the well-defined parts and 93% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping [i](#)

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

Total number of shifts	1693
Number of shifts mapped to atoms	1693
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	139	-0.13 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	129	-0.10 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}'$	133	0.12 ± 0.10	None needed (< 0.5 ppm)
^{15}N	132	-0.24 ± 0.24	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 93%, i.e. 1222 atoms were assigned a chemical shift out of a possible 1309. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	466/470 (99%)	189/190 (99%)	186/188 (99%)	91/92 (99%)
Sidechain	684/754 (91%)	467/493 (95%)	209/232 (90%)	8/29 (28%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	72/85 (85%)	36/42 (86%)	35/36 (97%)	1/7 (14%)
Overall	1222/1309 (93%)	692/725 (95%)	430/456 (94%)	100/128 (78%)

7.1.4 Statistically unusual chemical shifts [i](#)

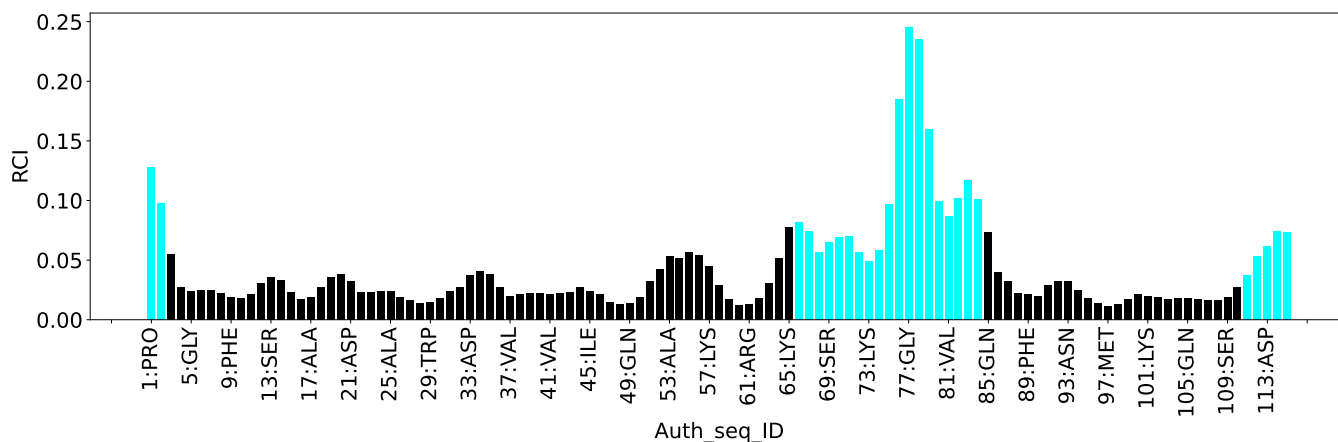
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	103	THR	HG1	4.44	0.08 – 2.19	15.7
1	A	10	GLU	HG2	0.62	1.24 – 3.30	-8.0
1	A	10	GLU	HG3	1.05	1.20 – 3.30	-5.7
1	A	9	PHE	HB2	1.12	1.20 – 4.80	-5.2

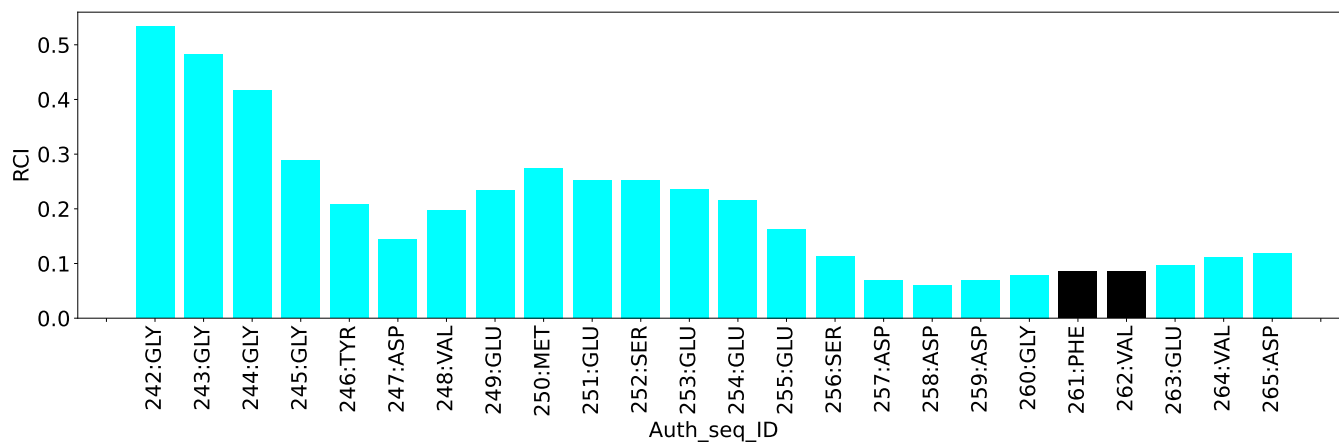
7.1.5 Random Coil Index (RCI) plots [i](#)

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:



Random coil index (RCI) for chain B:



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	3053
Intra-residue ($ i-j =0$)	1190
Sequential ($ i-j =1$)	622
Medium range ($ i-j >1$ and $ i-j <5$)	417
Long range ($ i-j \geq 5$)	794
Inter-chain	30
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	222
Number of unmapped restraints	0
Number of restraints per residue	23.6
Number of long range restraints per residue ¹	5.7

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)	112.5	0.2
0.2-0.5 (Medium)	89.7	0.5
>0.5 (Large)	112.0	11.38

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)	27.5	9.9
10.0-20.0 (Medium)	1.1	19.6
>20.0 (Large)	1.0	29.7

9 Distance violation analysis i

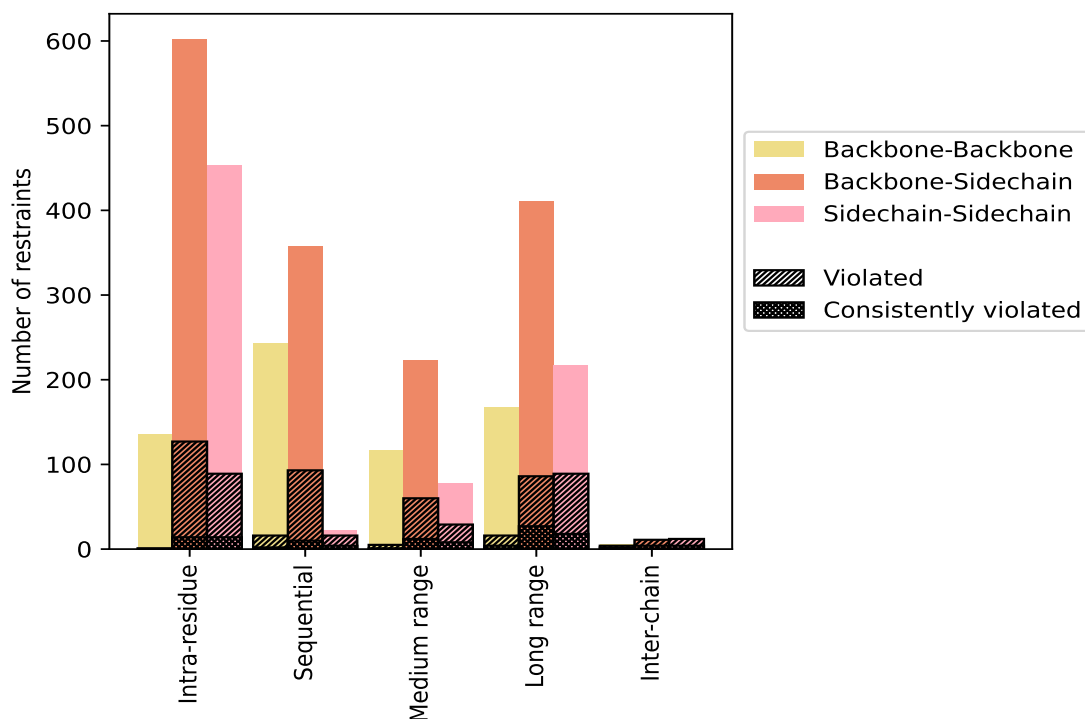
9.1 Summary of distance violations i

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	1190	39.0	217	18.2	7.1	28	2.4	0.9
Backbone-Backbone	135	4.4	1	0.7	0.0	0	0.0	0.0
Backbone-Sidechain	602	19.7	127	21.1	4.2	14	2.3	0.5
Sidechain-Sidechain	453	14.8	89	19.6	2.9	14	3.1	0.5
Sequential ($i-j =1$)	622	20.4	125	20.1	4.1	16	2.6	0.5
Backbone-Backbone	243	8.0	16	6.6	0.5	2	0.8	0.1
Backbone-Sidechain	357	11.7	93	26.1	3.0	10	2.8	0.3
Sidechain-Sidechain	22	0.7	16	72.7	0.5	4	18.2	0.1
Medium range ($i-j >1$ & $i-j <5$)	417	13.7	94	22.5	3.1	21	5.0	0.7
Backbone-Backbone	117	3.8	5	4.3	0.2	1	0.9	0.0
Backbone-Sidechain	223	7.3	60	26.9	2.0	12	5.4	0.4
Sidechain-Sidechain	77	2.5	29	37.7	0.9	8	10.4	0.3
Long range ($i-j \geq 5$)	794	26.0	191	24.1	6.3	49	6.2	1.6
Backbone-Backbone	167	5.5	16	9.6	0.5	4	2.4	0.1
Backbone-Sidechain	410	13.4	86	21.0	2.8	27	6.6	0.9
Sidechain-Sidechain	217	7.1	89	41.0	2.9	18	8.3	0.6
Inter-chain	30	1.0	27	90.0	0.9	10	33.3	0.3
Backbone-Backbone	5	0.2	4	80.0	0.1	2	40.0	0.1
Backbone-Sidechain	12	0.4	11	91.7	0.4	4	33.3	0.1
Sidechain-Sidechain	13	0.4	12	92.3	0.4	4	30.8	0.1
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	3053	100.0	654	21.4	21.4	124	4.1	4.1
Backbone-Backbone	667	21.8	42	6.3	1.4	9	1.3	0.3
Backbone-Sidechain	1604	52.5	377	23.5	12.3	67	4.2	2.2
Sidechain-Sidechain	782	25.6	235	30.1	7.7	48	6.1	1.6

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 disulfid 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	100	57	50	97	13	317	0.6	10.37	0.92	0.31
2	97	69	48	101	16	331	0.62	10.42	0.93	0.31
3	95	59	45	110	16	325	0.59	7.79	0.81	0.29
4	95	49	43	102	18	307	0.63	7.89	0.88	0.32
5	90	54	44	93	15	296	0.64	11.38	1.03	0.31
6	96	59	42	103	13	313	0.6	10.21	0.92	0.29
7	92	52	41	98	18	301	0.58	10.15	0.94	0.28
8	99	55	42	96	16	308	0.63	10.01	0.93	0.33
9	104	56	47	104	15	326	0.62	9.1	0.89	0.32
10	100	56	47	108	17	328	0.61	10.21	0.93	0.31
11	97	54	43	108	17	319	0.58	6.89	0.75	0.32

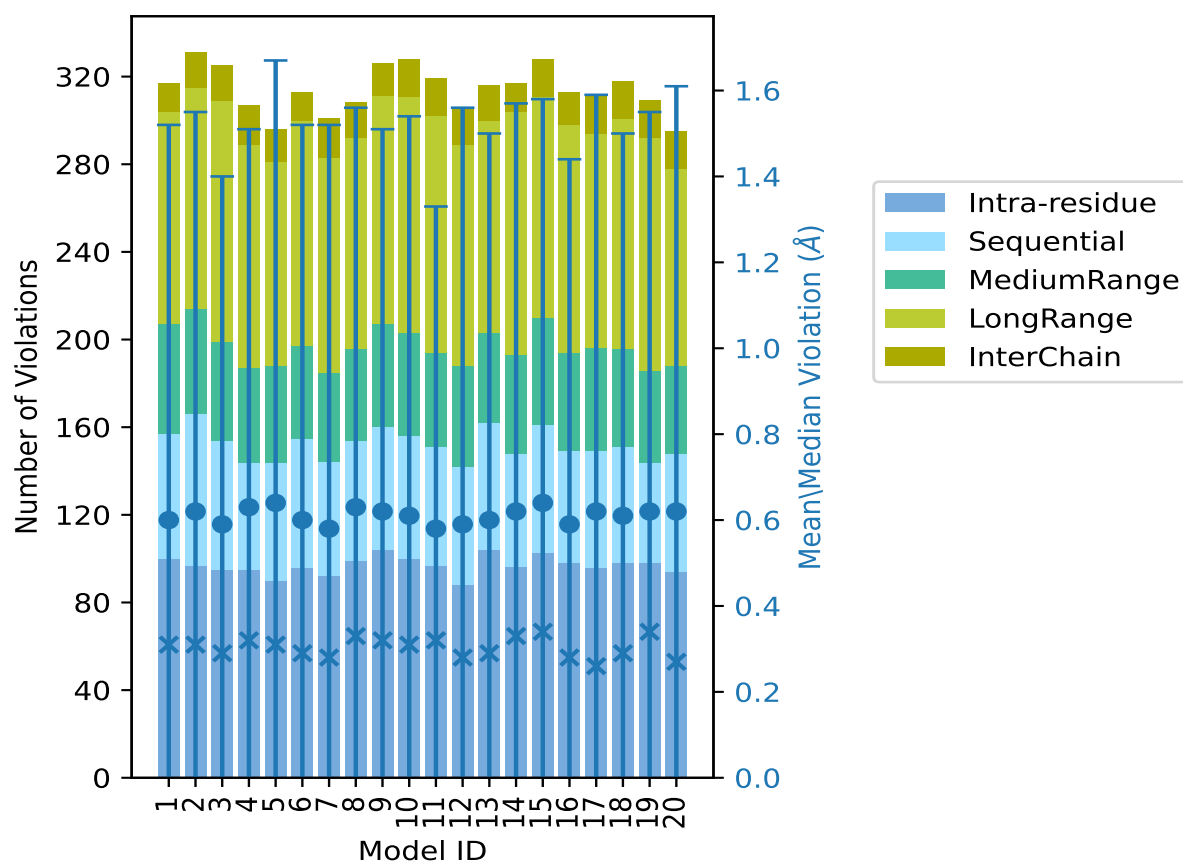
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
12	88	54	46	101	17	306	0.59	10.37	0.97	0.28
13	104	58	41	97	16	316	0.6	9.22	0.9	0.29
14	96	52	45	111	13	317	0.62	10.38	0.95	0.33
15	103	58	49	101	17	328	0.64	10.53	0.94	0.34
16	98	51	45	104	15	313	0.59	8.46	0.85	0.28
17	96	53	47	98	17	311	0.62	10.01	0.97	0.26
18	98	53	45	105	17	318	0.61	8.62	0.89	0.29
19	98	46	42	106	17	309	0.62	9.88	0.93	0.34
20	94	54	40	90	17	295	0.62	10.39	0.99	0.27

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

9.2.1 Bar graph : Distance Violation statistics for each model [\(i\)](#)



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

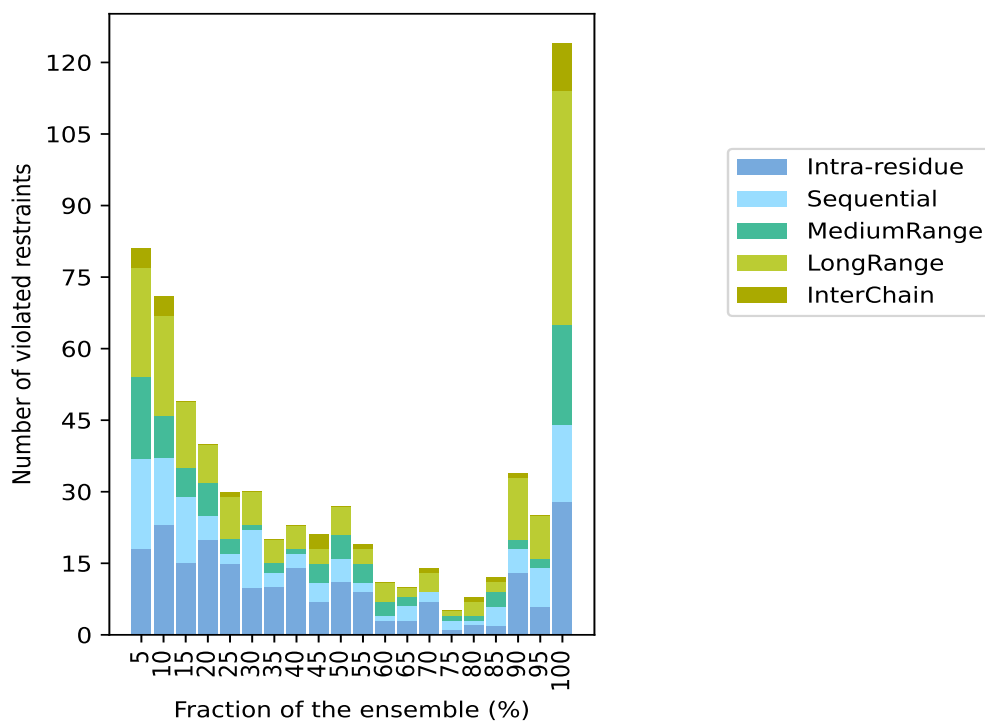
9.3 Distance violation statistics for the ensemble

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, 2399(IR:973, SQ:497, MR:323, LR:603, IC:3) 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	%
18	19	17	23	4	81	1	5.0
23	14	9	21	4	71	2	10.0
15	14	6	14	0	49	3	15.0
20	5	7	8	0	40	4	20.0
15	2	3	9	1	30	5	25.0
10	12	1	7	0	30	6	30.0
10	3	2	5	0	20	7	35.0
14	3	1	5	0	23	8	40.0
7	4	4	3	3	21	9	45.0
11	5	5	6	0	27	10	50.0
9	2	4	3	1	19	11	55.0
3	1	3	4	0	11	12	60.0
3	3	2	2	0	10	13	65.0
7	2	0	4	1	14	14	70.0
1	2	1	1	0	5	15	75.0
2	1	1	3	1	8	16	80.0
2	4	3	2	1	12	17	85.0
13	5	2	13	1	34	18	90.0
6	8	2	9	0	25	19	95.0
28	16	21	49	10	124	20	100.0

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints, ⁵Inter-chain restraints, ⁶ Number of models with violations

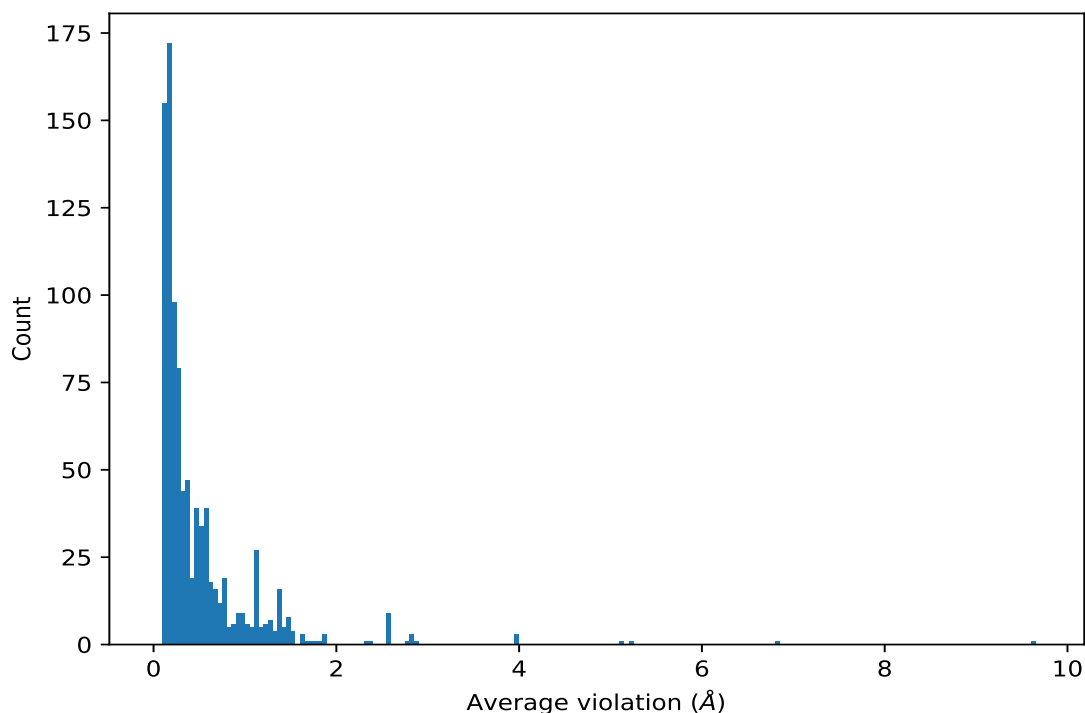
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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.

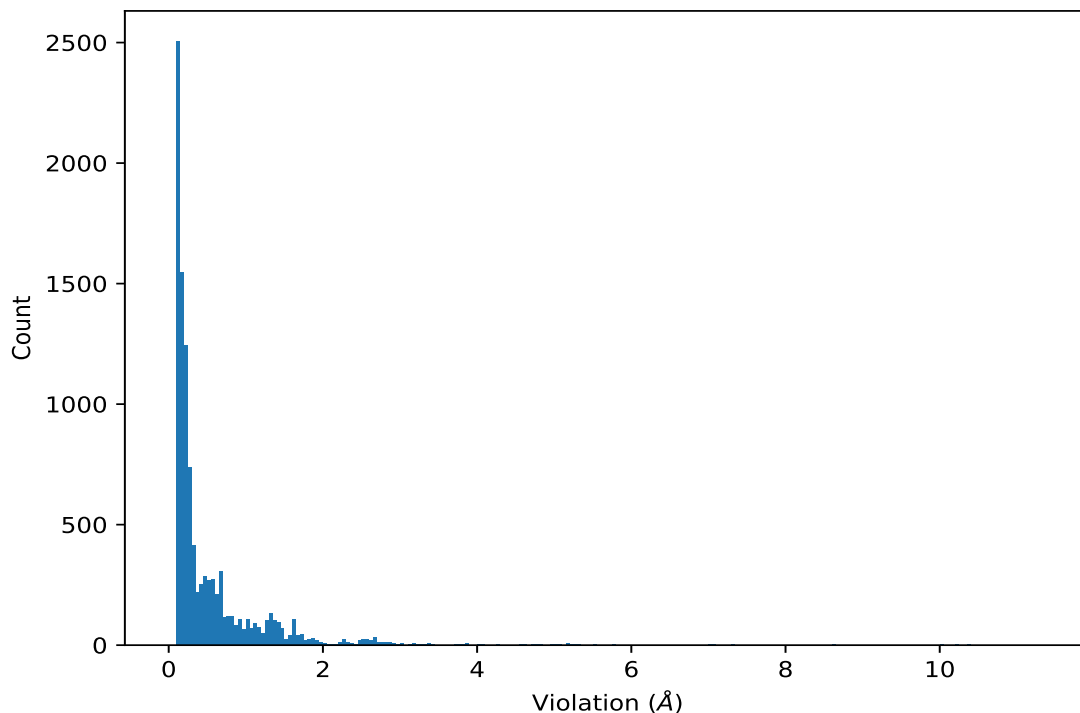
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	20	9.61	1.11	10.08
(1,3012)	2:B:259:ASP:H	1:A:59:MET:H	20	6.8	0.94	7.06
(1,3033)	2:B:263:GLU:HA	1:A:102:MET:HB3	20	5.2	0.44	5.08
(1,3038)	2:B:264:VAL:H	1:A:49:GLN:HG3	20	5.1	0.35	5.22
(1,3027)	2:B:262:VAL:HG21	1:A:101:LYS:HE3	20	3.97	0.8	3.88
(1,3027)	2:B:262:VAL:HG22	1:A:101:LYS:HE3	20	3.97	0.8	3.88
(1,3027)	2:B:262:VAL:HG23	1:A:101:LYS:HE3	20	3.97	0.8	3.88
(1,3028)	2:B:263:GLU:H	1:A:49:GLN:HG3	20	2.85	0.52	2.84
(1,127)	1:A:111:TYR:HE1	1:A:25:ALA:HB2	20	2.81	0.33	2.86
(1,127)	1:A:111:TYR:HE1	1:A:25:ALA:HB1	20	2.81	0.33	2.86
(1,127)	1:A:111:TYR:HE1	1:A:25:ALA:HB3	20	2.81	0.33	2.86
(1,3017)	2:B:261:PHE:H	1:A:61:ARG:HD3	20	2.78	0.9	2.78
(1,89)	1:A:111:TYR:HE1	1:A:107:ILE:HG22	20	2.59	0.1	2.58
(1,89)	1:A:111:TYR:HE1	1:A:107:ILE:HG21	20	2.59	0.1	2.58
(1,89)	1:A:111:TYR:HE1	1:A:107:ILE:HG23	20	2.59	0.1	2.58
(1,1236)	1:A:105:GLN:HE22	1:A:104:LEU:HB3	20	2.38	0.5	2.54

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)
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	5	11.38
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	15	10.53
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	2	10.42
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	20	10.39
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	14	10.38
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	1	10.37
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	12	10.37
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	6	10.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	10	10.21
(1,3010)	2:B:258:ASP:H	1:A:59:MET:H	7	10.15

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

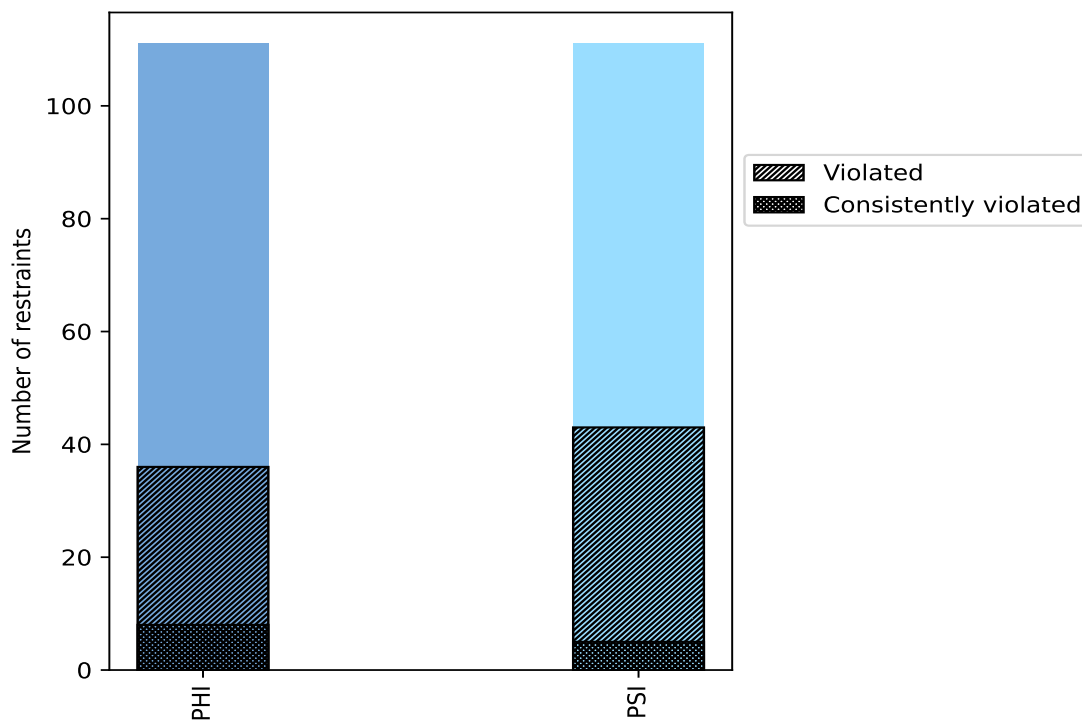
10.1 Summary of dihedral-angle violations [i](#)

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	111	50.0	36	32.4	16.2	8	7.2	3.6
PSI	111	50.0	43	38.7	19.4	5	4.5	2.3
Total	222	100.0	79	35.6	35.6	13	5.9	5.9

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

10.1.1 Bar chart : Distribution of dihedral-angles and violations [i](#)



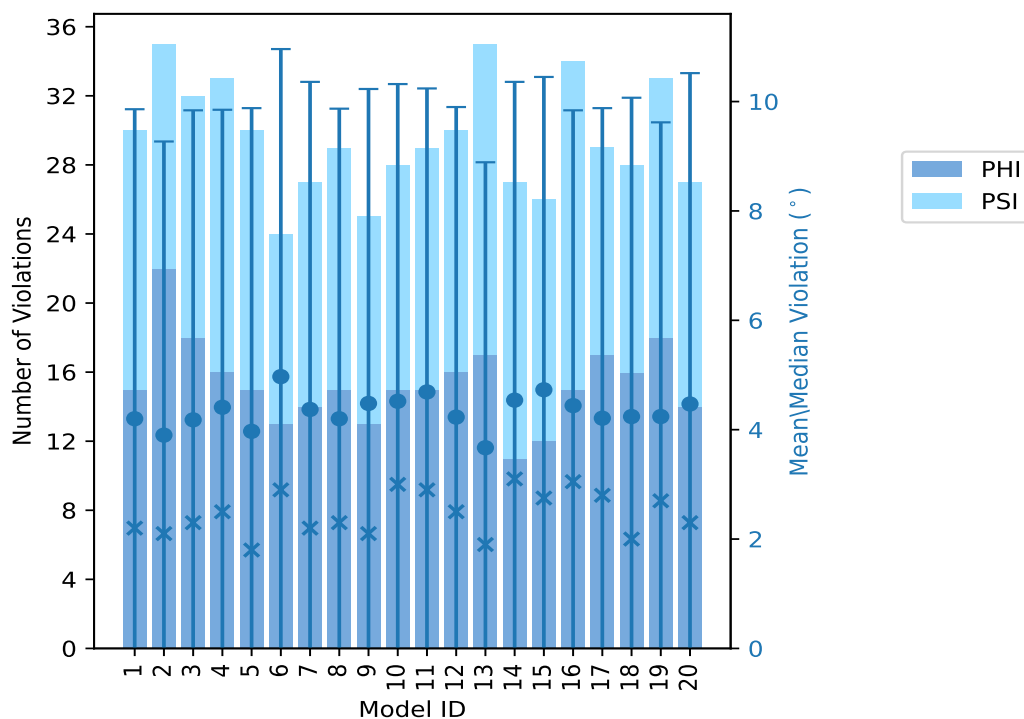
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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

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

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	15	15	30	4.2	28.8	5.66	2.2
2	22	13	35	3.9	29.5	5.37	2.1
3	18	14	32	4.18	29.5	5.66	2.3
4	16	17	33	4.41	29.4	5.44	2.5
5	15	15	30	3.97	29.7	5.91	1.8
6	13	11	24	4.97	28.4	5.99	2.9
7	14	13	27	4.37	29.4	5.99	2.2
8	15	14	29	4.2	28.7	5.67	2.3
9	13	12	25	4.48	27.3	5.75	2.1
10	15	13	28	4.52	29.2	5.8	3.0
11	15	14	29	4.69	28.1	5.55	2.9
12	16	14	30	4.23	29.5	5.67	2.5
13	17	18	35	3.67	28.3	5.22	1.9
14	11	16	27	4.54	28.9	5.82	3.1
15	12	14	26	4.73	28.0	5.72	2.75
16	15	19	34	4.44	28.9	5.4	3.05
17	17	12	29	4.21	28.3	5.67	2.8
18	16	12	28	4.24	28.6	5.83	2.0
19	18	15	33	4.24	29.2	5.38	2.7
20	14	13	27	4.47	29.3	6.05	2.3

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	%
11	11	22	1	5.0
3	6	9	2	10.0
0	6	6	3	15.0
3	4	7	4	20.0
3	1	4	5	25.0
1	1	2	6	30.0
0	3	3	7	35.0
0	0	0	8	40.0
1	0	1	9	45.0
2	0	2	10	50.0
1	1	2	11	55.0

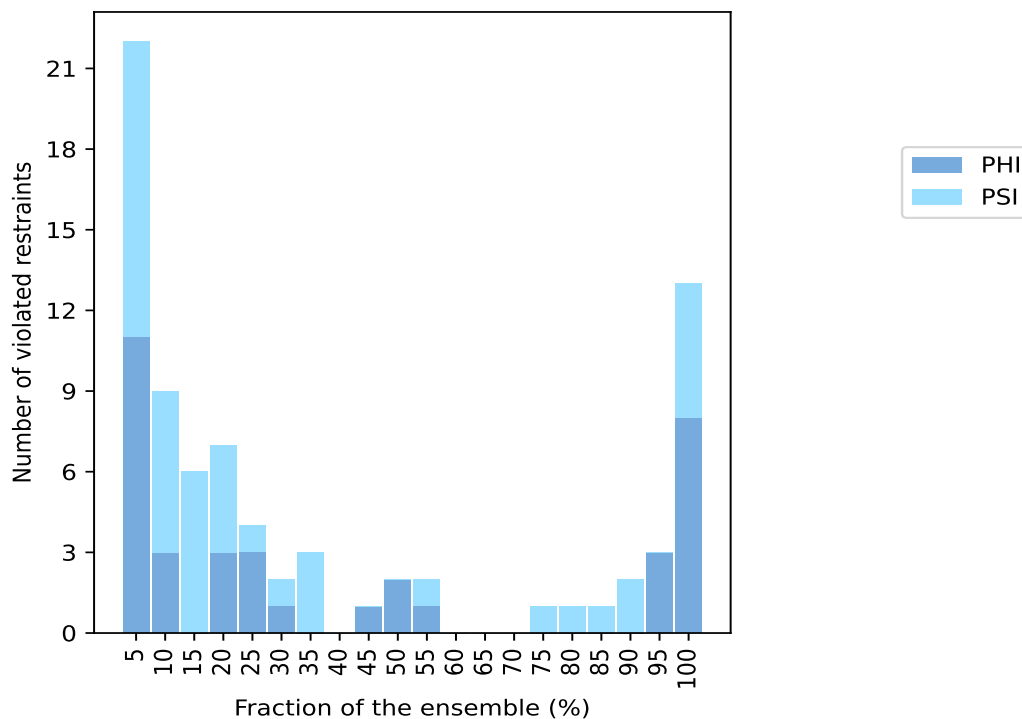
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	1	1	15	75.0
0	1	1	16	80.0
0	1	1	17	85.0
0	2	2	18	90.0
3	0	3	19	95.0
8	5	13	20	100.0

¹ Number of models with violations

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

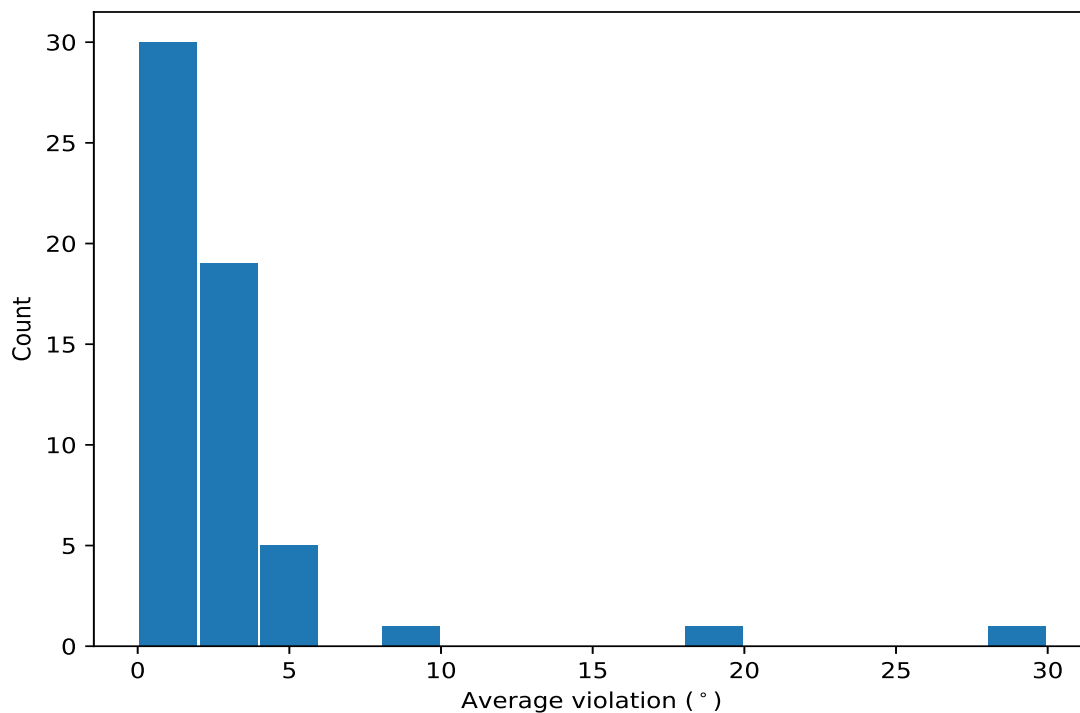


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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

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

in the ensemble



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

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

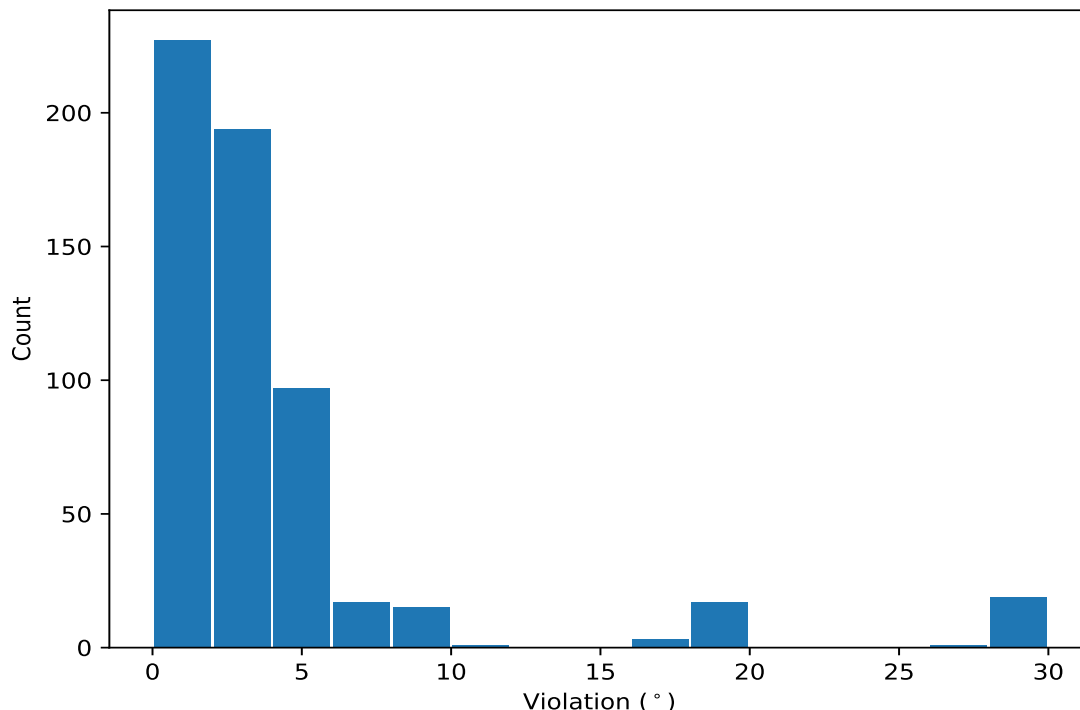
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	20	28.85	0.62	28.9
(1,221)	1:A:20:GLU:C	1:A:21:ASP:N	1:A:21:ASP:CA	1:A:21:ASP:C	20	18.62	0.57	18.55
(1,59)	1:A:23:SER:C	1:A:24:PRO:N	1:A:24:PRO:CA	1:A:24:PRO:C	20	8.41	1.29	8.55
(1,55)	1:A:21:ASP:C	1:A:22:VAL:N	1:A:22:VAL:CA	1:A:22:VAL:C	20	5.24	0.55	5.25
(1,58)	1:A:23:SER:N	1:A:23:SER:CA	1:A:23:SER:C	1:A:24:PRO:N	20	5.18	1.05	5.05
(1,63)	1:A:26:GLU:C	1:A:27:LEU:N	1:A:27:LEU:CA	1:A:27:LEU:C	20	4.54	0.53	4.55
(1,60)	1:A:24:PRO:N	1:A:24:PRO:CA	1:A:24:PRO:C	1:A:25:ALA:N	20	4.49	1.07	4.2
(1,120)	1:A:58:MET:N	1:A:58:MET:CA	1:A:58:MET:C	1:A:59:MET:N	20	3.91	1.37	3.95
(1,129)	1:A:62:LEU:C	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	20	3.0	0.97	2.9
(1,49)	1:A:16:ILE:C	1:A:17:ALA:N	1:A:17:ALA:CA	1:A:17:ALA:C	20	2.92	0.56	2.85

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 (°)
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	5	29.7
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	2	29.5
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	3	29.5
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	12	29.5
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	4	29.4
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	7	29.4
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	20	29.3
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	10	29.2
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	19	29.2
(1,220)	1:A:20:GLU:N	1:A:20:GLU:CA	1:A:20:GLU:C	1:A:21:ASP:N	14	28.9