



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:47 AM UTC

PDB ID : 9RXE / pdb_00009rx
BMRB ID : 50216
Title : Solution structure of the HR1c domain of human PKN1
Authors : Sophocleous, G.; Mott, H.R.
Deposited on : 2025-07-11

This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ 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

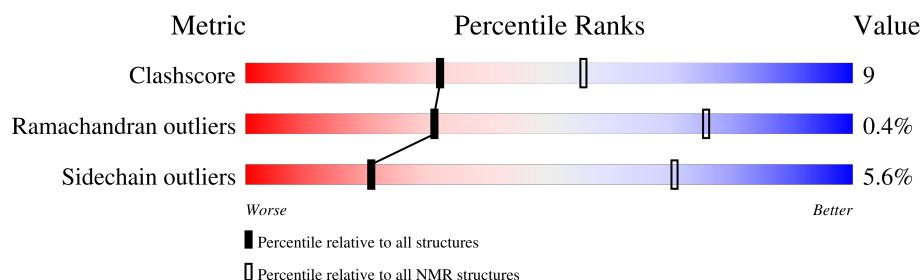
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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	104	

2 Ensemble composition and analysis

This entry contains 45 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:207-A:297 (91)	0.77	1

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 5 clusters and 1 single-model cluster was found.

Cluster number	Models
1	2, 3, 9, 12, 14, 23, 25, 27, 28, 30, 31, 35, 42, 45
2	8, 11, 13, 18, 19, 20, 22, 34, 39, 40, 41
3	1, 10, 15, 21, 26, 29, 32, 33, 37, 43
4	4, 7, 16, 24, 38
5	5, 6, 17, 36
Single-model clusters	44

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1617 atoms, of which 819 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Serine/threonine-protein kinase N1.

Mol	Chain	Residues	Atoms						Trace
1	A	104	Total	C	H	N	O	S	0
			1617	489	819	155	153	1	

There are 7 discrepancies between the modelled and reference sequences:

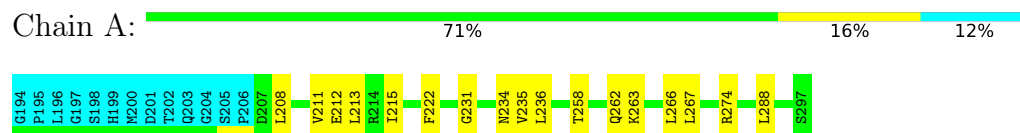
Chain	Residue	Modelled	Actual	Comment	Reference
A	194	GLY	-	expression tag	UNP Q16512
A	195	PRO	-	expression tag	UNP Q16512
A	196	LEU	-	expression tag	UNP Q16512
A	197	GLY	-	expression tag	UNP Q16512
A	198	SER	-	expression tag	UNP Q16512
A	199	HIS	-	expression tag	UNP Q16512
A	200	MET	-	expression tag	UNP Q16512

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.

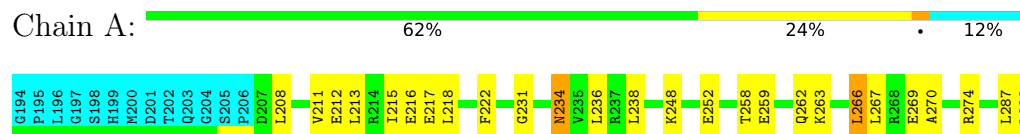
- Molecule 1: Serine/threonine-protein kinase N1



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

The representative model is number 1. Colouring as in section 4.1 above.

- Molecule 1: Serine/threonine-protein kinase N1



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 45 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	structure calculation	
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	1178
Number of shifts mapped to atoms	1178
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

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	0.39±0.01	0±0/717 (0.0± 0.0%)	0.73±0.01	0±0/960 (0.0± 0.0%)
All	All	0.40	0/32265 (0.0%)	0.73	1/43200 (0.0%)

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	221	HIS	CA-CB-CG	5.14	118.94	113.80	9	1

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	710	737	733	12±3
All	All	31950	33165	32985	559

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 9.

5 of 144 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:287:LEU:HA	1:A:290:GLU:HG2	0.82	1.49	13	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:208:LEU:HA	1:A:211:VAL:HG22	0.78	1.56	36	1
1:A:208:LEU:HA	1:A:211:VAL:CG2	0.72	2.14	36	1
1:A:237:ARG:HA	1:A:237:ARG:HE	0.71	1.43	35	2
1:A:272:GLU:HA	1:A:275:LEU:HD22	0.68	1.65	38	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	90/104 (87%)	88±1 (98±1%)	2±1 (2±1%)	0±0 (0±1%)	31	76
All	All	4050/4680 (87%)	3964 (98%)	70 (2%)	16 (0%)	31	76

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	296	SER	16

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	72/82 (88%)	68±1 (94±2%)	4±1 (6±2%)	21	70
All	All	3240/3690 (88%)	3058 (94%)	182 (6%)	21	70

5 of 30 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	213	LEU	38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	266	LEU	28
1	A	254	GLN	18
1	A	236	LEU	14
1	A	267	LEU	13

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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 83% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_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	1178
Number of shifts mapped to atoms	1178
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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
$^{13}\text{C}_\alpha$	104	-0.39 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	96	0.00 ± 0.02	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	97	-0.32 ± 0.20	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 83%, i.e. 1059 atoms were assigned a chemical shift out of a possible 1281. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	363/454 (80%)	184/184 (100%)	91/182 (50%)	88/88 (100%)
Sidechain	669/785 (85%)	459/508 (90%)	206/237 (87%)	4/40 (10%)

Continued on next page...

Continued from previous page...

	Total	^1H	^{13}C	^{15}N
Aromatic	27/42 (64%)	14/21 (67%)	13/13 (100%)	0/8 (0%)
Overall	1059/1281 (83%)	657/713 (92%)	310/432 (72%)	92/136 (68%)

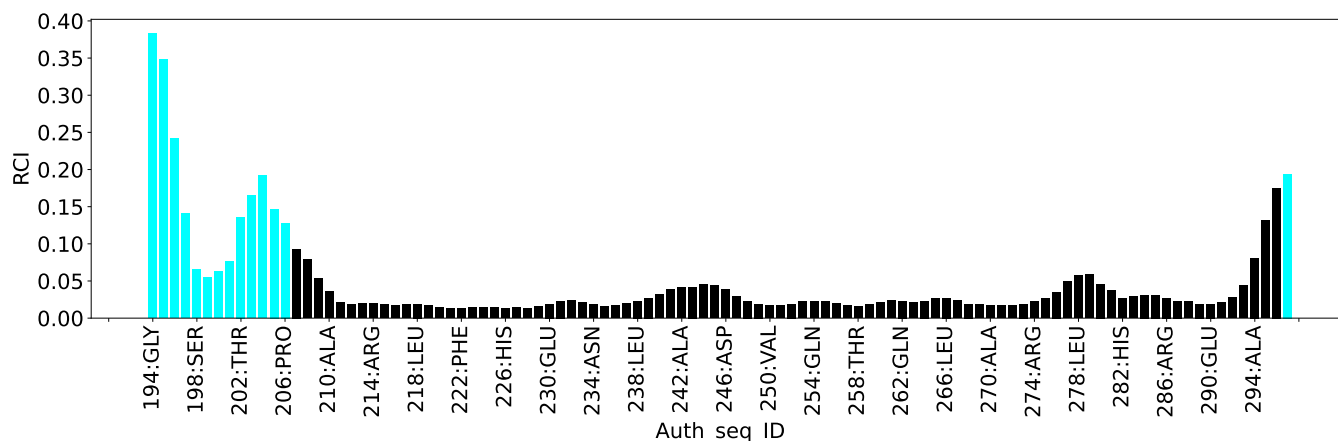
7.1.4 Statistically unusual chemical shifts [i](#)

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	5088
Intra-residue ($ i-j =0$)	1954
Sequential ($ i-j =1$)	1130
Medium range ($ i-j >1$ and $ i-j <5$)	1310
Long range ($ i-j \geq 5$)	694
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	48.9
Number of long range restraints per residue ¹	6.7

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)	64.4	0.2
0.2-0.5 (Medium)	119.6	0.5
>0.5 (Large)	158.0	4.4

8.2.2 Average number of dihedral-angle violations per model [i](#)

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis ⓘ

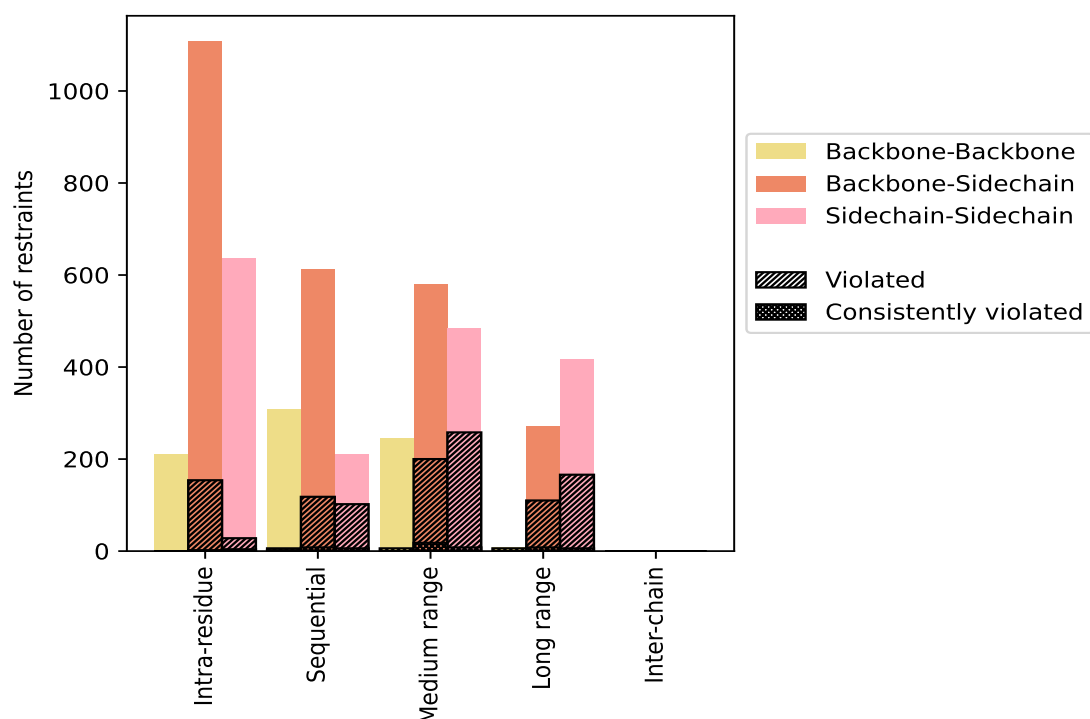
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	1954	38.4	182	9.3	3.6	6	0.3	0.1
Backbone-Backbone	210	4.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	1108	21.8	154	13.9	3.0	2	0.2	0.0
Sidechain-Sidechain	636	12.5	28	4.4	0.6	4	0.6	0.1
Sequential ($i-j =1$)	1130	22.2	226	20.0	4.4	16	1.4	0.3
Backbone-Backbone	308	6.1	6	1.9	0.1	2	0.6	0.0
Backbone-Sidechain	612	12.0	118	19.3	2.3	8	1.3	0.2
Sidechain-Sidechain	210	4.1	102	48.6	2.0	6	2.9	0.1
Medium range ($i-j >1$ & $i-j <5$)	1310	25.7	464	35.4	9.1	26	2.0	0.5
Backbone-Backbone	246	4.8	6	2.4	0.1	0	0.0	0.0
Backbone-Sidechain	580	11.4	200	34.5	3.9	18	3.1	0.4
Sidechain-Sidechain	484	9.5	258	53.3	5.1	8	1.7	0.2
Long range ($i-j \geq 5$)	694	13.6	282	40.6	5.5	14	2.0	0.3
Backbone-Backbone	8	0.2	6	75.0	0.1	0	0.0	0.0
Backbone-Sidechain	270	5.3	110	40.7	2.2	8	3.0	0.2
Sidechain-Sidechain	416	8.2	166	39.9	3.3	6	1.4	0.1
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	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	5088	100.0	1154	22.7	22.7	62	1.2	1.2
Backbone-Backbone	772	15.2	18	2.3	0.4	2	0.3	0.0
Backbone-Sidechain	2570	50.5	582	22.6	11.4	36	1.4	0.7
Sidechain-Sidechain	1746	34.3	554	31.7	10.9	24	1.4	0.5

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	44	74	136	80	0	334	0.57	3.11	0.44	0.45
2	32	72	156	74	0	334	0.53	1.91	0.4	0.42
3	38	66	162	104	0	370	0.56	2.07	0.41	0.44
4	44	66	164	84	0	358	0.58	2.63	0.45	0.43
5	40	72	166	66	0	344	0.58	3.5	0.49	0.43
6	36	68	168	98	0	370	0.57	2.63	0.46	0.43
7	32	80	160	106	0	378	0.56	2.43	0.44	0.41
8	40	58	152	90	0	340	0.54	2.31	0.4	0.44
9	48	70	164	134	0	416	0.61	2.54	0.47	0.5
10	36	78	166	72	0	352	0.54	2.38	0.41	0.42

Continued on next page...

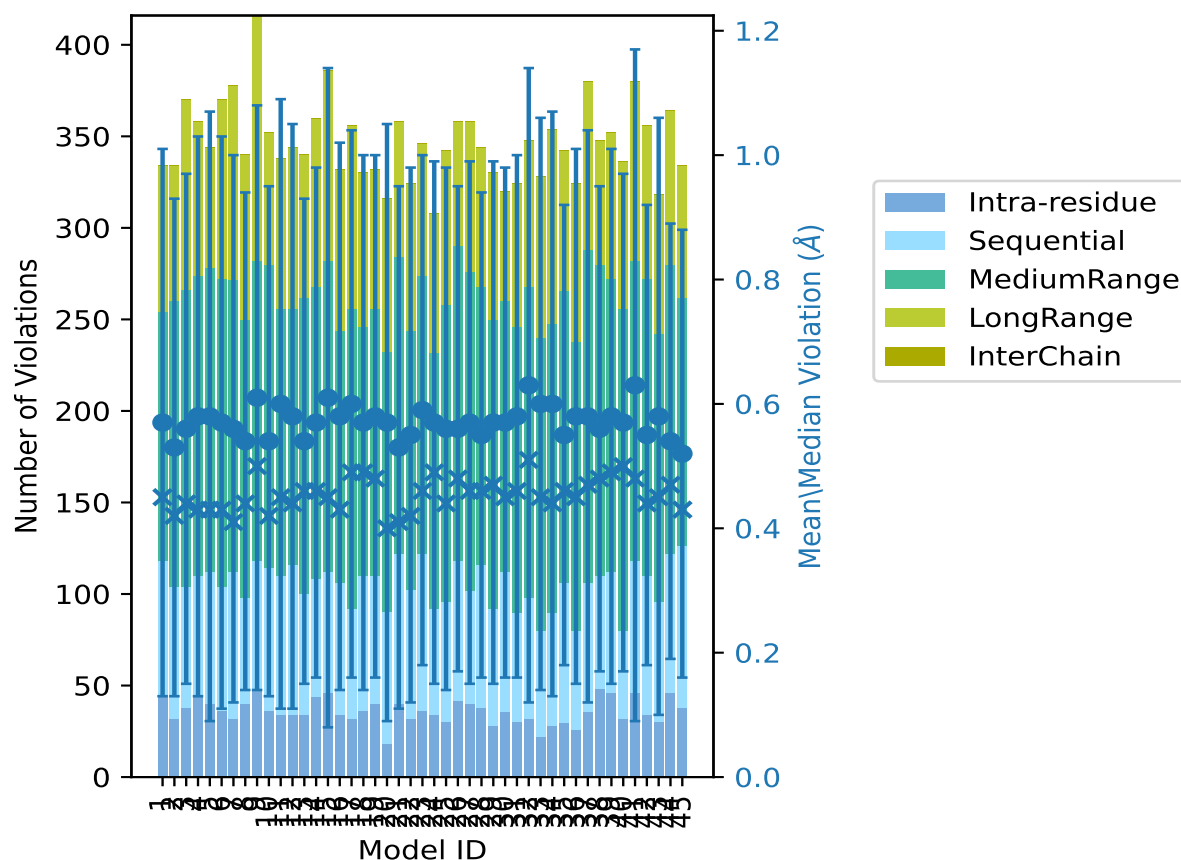
Continued from previous page...

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	34	76	146	82	0	338	0.6	2.88	0.49	0.45
12	34	82	140	88	0	344	0.58	2.56	0.47	0.44
13	34	66	162	78	0	340	0.54	2.0	0.39	0.46
14	44	64	160	92	0	360	0.57	2.0	0.41	0.46
15	46	66	170	104	0	386	0.61	4.4	0.53	0.45
16	34	72	138	88	0	332	0.58	2.11	0.44	0.43
17	32	60	164	100	0	356	0.6	2.52	0.44	0.49
18	36	74	136	84	0	330	0.57	2.51	0.43	0.49
19	40	70	146	76	0	332	0.58	1.91	0.42	0.48
20	18	72	142	84	0	316	0.57	2.85	0.48	0.4
21	40	82	162	74	0	358	0.53	2.19	0.42	0.41
22	32	70	142	80	0	324	0.55	2.59	0.43	0.42
23	36	86	152	72	0	346	0.59	2.04	0.41	0.46
24	34	58	140	76	0	308	0.57	2.03	0.42	0.49
25	30	66	162	84	0	342	0.56	1.85	0.42	0.44
26	42	76	172	68	0	358	0.56	1.87	0.39	0.48
27	40	62	174	82	0	358	0.57	1.97	0.42	0.46
28	38	78	152	76	0	344	0.55	1.78	0.39	0.46
29	28	64	158	80	0	330	0.57	2.05	0.42	0.47
30	36	76	148	60	0	320	0.57	2.11	0.41	0.45
31	30	60	156	78	0	324	0.58	1.75	0.42	0.46
32	32	66	170	80	0	348	0.63	3.16	0.51	0.51
33	22	58	160	88	0	328	0.6	2.28	0.46	0.45
34	28	62	158	106	0	354	0.6	2.56	0.47	0.44
35	30	76	160	76	0	342	0.55	1.64	0.37	0.46
36	26	54	158	86	0	324	0.58	1.99	0.43	0.45
37	36	70	182	92	0	380	0.58	2.45	0.46	0.47
38	48	62	170	68	0	348	0.56	1.85	0.39	0.48
39	46	66	160	80	0	352	0.58	1.9	0.43	0.49
40	32	48	176	80	0	336	0.57	1.95	0.4	0.5
41	46	72	164	98	0	380	0.63	4.04	0.54	0.48
42	34	76	162	84	0	356	0.55	2.05	0.37	0.44
43	30	66	146	76	0	318	0.58	3.05	0.48	0.45
44	46	76	158	84	0	364	0.54	1.77	0.35	0.47
45	38	88	136	72	0	334	0.52	1.68	0.36	0.43

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 [i](#)

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 3934(IR:1772, SQ:904, MR:846, LR:412, 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	%
46	42	108	76	0	272	1	2.2
26	22	32	24	0	104	2	4.4
20	6	18	26	0	70	3	6.7
10	6	26	18	0	60	4	8.9
6	14	16	8	0	44	5	11.1
10	6	16	14	0	46	6	13.3

Continued on next page...

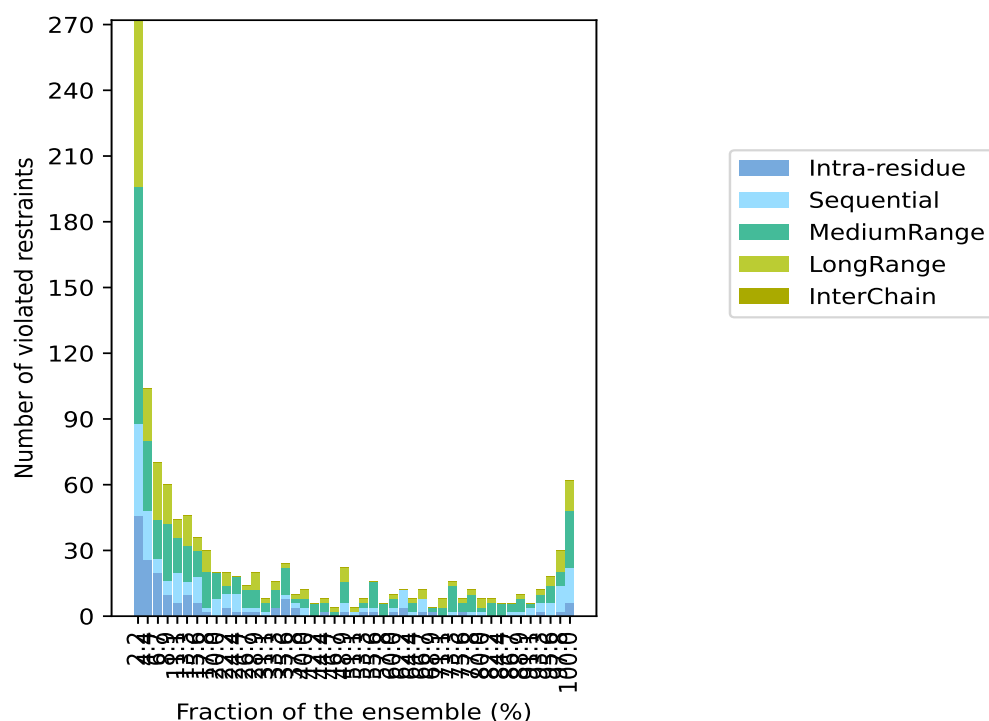
Continued from previous page...

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
6	12	12	6	0	36	7	15.6
2	2	16	10	0	30	8	17.8
0	8	12	0	0	20	9	20.0
4	6	4	6	0	20	10	22.2
2	8	8	0	0	18	11	24.4
2	2	8	2	0	14	12	26.7
2	2	8	8	0	20	13	28.9
0	2	4	2	0	8	14	31.1
4	0	8	4	0	16	15	33.3
8	2	12	2	0	24	16	35.6
4	2	2	2	0	10	17	37.8
0	4	4	4	0	12	18	40.0
0	0	6	0	0	6	19	42.2
2	0	4	2	0	8	20	44.4
0	0	2	2	0	4	21	46.7
2	4	10	6	0	22	22	48.9
0	2	0	2	0	4	23	51.1
2	2	2	2	0	8	24	53.3
2	2	12	0	0	16	25	55.6
0	0	6	0	0	6	26	57.8
2	2	4	2	0	10	27	60.0
4	8	0	0	0	12	28	62.2
0	2	4	2	0	8	29	64.4
2	6	0	4	0	12	30	66.7
2	0	2	0	0	4	31	68.9
0	0	4	4	0	8	32	71.1
0	2	12	2	0	16	33	73.3
2	0	4	2	0	8	34	75.6
0	2	8	2	0	12	35	77.8
0	2	2	4	0	8	36	80.0
0	0	6	2	0	8	37	82.2
0	0	6	0	0	6	38	84.4
0	2	4	0	0	6	39	86.7
0	2	6	2	0	10	40	88.9
0	4	2	0	0	6	41	91.1
2	4	4	2	0	12	42	93.3
0	6	8	4	0	18	43	95.6
2	12	6	10	0	30	44	97.8
6	16	26	14	0	62	45	100.0

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

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

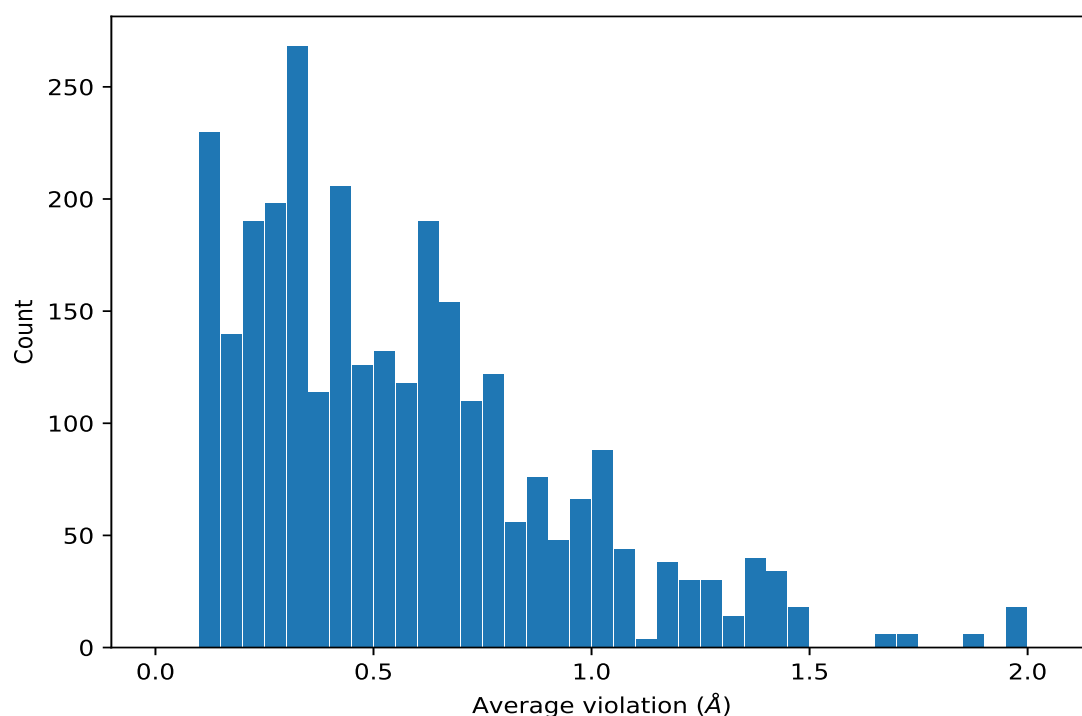
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,2139)	1:224:A:VAL:HG11	1:217:A:GLU:HA	45	1.71	0.29	1.64
(1,2139)	1:224:A:VAL:HG12	1:217:A:GLU:HA	45	1.71	0.29	1.64
(1,2139)	1:224:A:VAL:HG13	1:217:A:GLU:HA	45	1.71	0.29	1.64
(5,155)	1:224:A:VAL:HG11	1:217:A:GLU:HA	45	1.71	0.29	1.64
(5,155)	1:224:A:VAL:HG12	1:217:A:GLU:HA	45	1.71	0.29	1.64
(5,155)	1:224:A:VAL:HG13	1:217:A:GLU:HA	45	1.71	0.29	1.64
(1,2203)	1:230:A:GLU:HG3	1:229:A:ALA:HB1	45	1.41	0.18	1.43
(1,2203)	1:230:A:GLU:HG3	1:229:A:ALA:HB2	45	1.41	0.18	1.43
(1,2203)	1:230:A:GLU:HG2	1:229:A:ALA:HB2	45	1.41	0.18	1.43
(1,2203)	1:230:A:GLU:HG3	1:229:A:ALA:HB3	45	1.41	0.18	1.43
(1,2203)	1:230:A:GLU:HG2	1:229:A:ALA:HB3	45	1.41	0.18	1.43
(1,2203)	1:230:A:GLU:HG2	1:229:A:ALA:HB1	45	1.41	0.18	1.43
(5,219)	1:230:A:GLU:HG3	1:229:A:ALA:HB1	45	1.41	0.18	1.43
(5,219)	1:230:A:GLU:HG3	1:229:A:ALA:HB2	45	1.41	0.18	1.43
(5,219)	1:230:A:GLU:HG2	1:229:A:ALA:HB2	45	1.41	0.18	1.43
(5,219)	1:230:A:GLU:HG3	1:229:A:ALA:HB3	45	1.41	0.18	1.43

Continued on next page...

Continued from previous page...

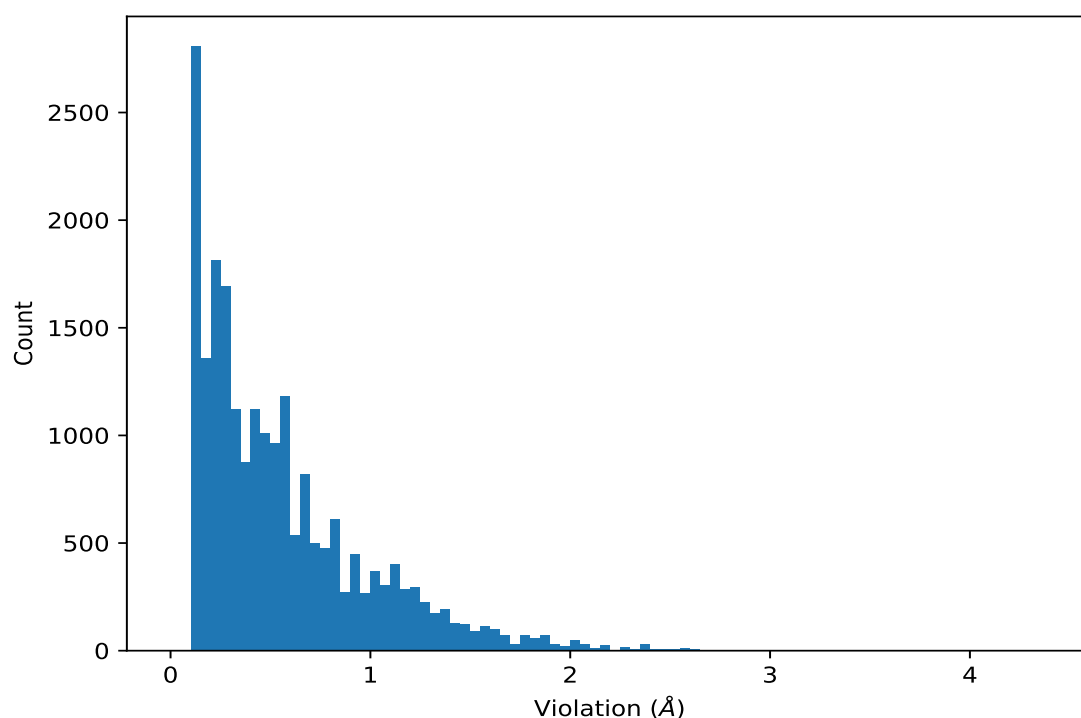
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(5,219)	1:230:A:GLU:HG2	1:229:A:ALA:HB3	45	1.41	0.18	1.43
(5,219)	1:230:A:GLU:HG2	1:229:A:ALA:HB1	45	1.41	0.18	1.43
(1,2395)	1:275:A:LEU:HD11	1:278:A:LEU:HA	45	1.38	0.44	1.59
(1,2395)	1:275:A:LEU:HD12	1:278:A:LEU:HA	45	1.38	0.44	1.59
(1,2395)	1:275:A:LEU:HD22	1:278:A:LEU:HA	45	1.38	0.44	1.59
(1,2395)	1:275:A:LEU:HD21	1:278:A:LEU:HA	45	1.38	0.44	1.59
(1,2395)	1:275:A:LEU:HD23	1:278:A:LEU:HA	45	1.38	0.44	1.59
(1,2395)	1:275:A:LEU:HD13	1:278:A:LEU:HA	45	1.38	0.44	1.59
(5,411)	1:275:A:LEU:HD11	1:278:A:LEU:HA	45	1.38	0.44	1.59
(5,411)	1:275:A:LEU:HD12	1:278:A:LEU:HA	45	1.38	0.44	1.59
(5,411)	1:275:A:LEU:HD22	1:278:A:LEU:HA	45	1.38	0.44	1.59
(5,411)	1:275:A:LEU:HD21	1:278:A:LEU:HA	45	1.38	0.44	1.59
(5,411)	1:275:A:LEU:HD23	1:278:A:LEU:HA	45	1.38	0.44	1.59
(5,411)	1:275:A:LEU:HD13	1:278:A:LEU:HA	45	1.38	0.44	1.59
(1,2059)	1:234:A:ASN:HD22	1:232:A:ALA:HA	45	1.37	0.49	1.64
(1,2059)	1:234:A:ASN:HD22	1:227:A:ALA:HA	45	1.37	0.49	1.64
(5,75)	1:234:A:ASN:HD22	1:232:A:ALA:HA	45	1.37	0.49	1.64
(5,75)	1:234:A:ASN:HD22	1:227:A:ALA:HA	45	1.37	0.49	1.64
(1,2321)	1:235:A:VAL:HG22	1:228:A:VAL:HB	45	1.24	0.18	1.24
(1,2321)	1:235:A:VAL:HG21	1:228:A:VAL:HB	45	1.24	0.18	1.24
(1,2321)	1:235:A:VAL:HG23	1:228:A:VAL:HB	45	1.24	0.18	1.24
(1,2321)	1:235:A:VAL:HG23	1:254:A:GLN:HG2	45	1.24	0.18	1.24
(5,337)	1:235:A:VAL:HG22	1:228:A:VAL:HB	45	1.24	0.18	1.24

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)
(5,376)	1:204:A:GLY:HA3	1:211:A:VAL:HG23	15	4.4
(1,2360)	1:204:A:GLY:HA3	1:211:A:VAL:HG23	15	4.4
(5,376)	1:204:A:GLY:HA3	1:208:A:LEU:HD13	41	4.04
(1,2360)	1:204:A:GLY:HA3	1:208:A:LEU:HD13	41	4.04
(5,376)	1:204:A:GLY:HA3	1:208:A:LEU:HD11	5	3.5
(1,2360)	1:204:A:GLY:HA3	1:208:A:LEU:HD11	5	3.5
(5,378)	1:206:A:PRO:HD3	1:208:A:LEU:HD12	32	3.16
(1,2362)	1:206:A:PRO:HD3	1:208:A:LEU:HD12	32	3.16
(5,376)	1:204:A:GLY:HA3	1:208:A:LEU:HD11	1	3.11
(1,2360)	1:204:A:GLY:HA3	1:208:A:LEU:HD11	1	3.11

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found