wwPDB NMR Structure Validation Summary Report (i)

Jun 5, 2023 – 01:27 PM EDT

PDB ID	:	2M8G
BMRB ID	:	19251
Title	:	Structure, function, and tethering of DNA-binding domains in 54 transcriptional activators
Authors	:	Hong, E.; Wemmer, D.
Deposited on	:	2013-05-19

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 (i) 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 (1)) were used in the production of this report:

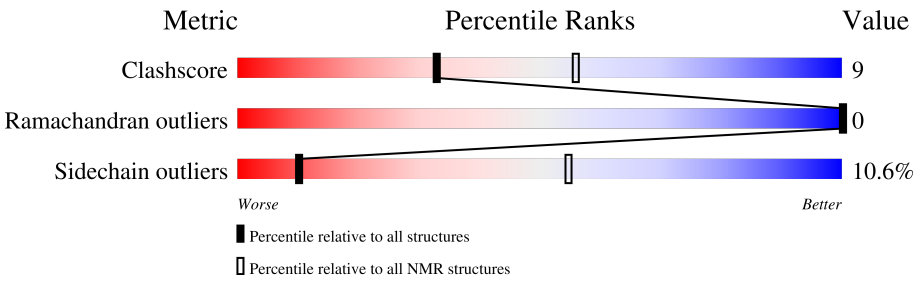
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 75%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	X	70	41% 16% 43%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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	X:454-X:493 (40)	0.11	11

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 2 clusters and 5 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1101 atoms, of which 515 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Transcriptional regulator.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	X	70	1101	377	515	104	105	0

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: Transcriptional regulator

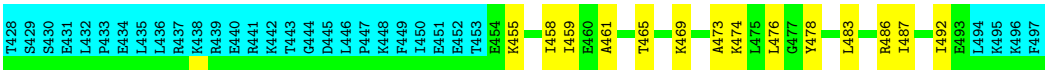
Chain X: 41% 16% 43%

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

The representative model is number 11. Colouring as in section 4.1 above.

- Molecule 1: Transcriptional regulator

Chain X: 37% 20% 43%



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	
MOLMOL	refinement	
CYANA	refinement	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	658
Number of shifts mapped to atoms	577
Number of unparsed shifts	0
Number of shifts with mapping errors	81
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	75%

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	X	334	301	366	6±1
All	All	6680	6020	7320	129

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 19 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:X:458:ILE:HD13	1:X:476:LEU:HD13	0.67	1.65	16	18
1:X:469:LYS:HG3	1:X:483:LEU:HD23	0.65	1.67	6	1
1:X:487:ILE:HD13	1:X:492:ILE:HD12	0.64	1.69	12	20
1:X:459:ILE:HD12	1:X:492:ILE:HG23	0.59	1.73	10	11
1:X:469:LYS:CE	1:X:480:LEU:HD13	0.58	2.28	15	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	X	40/70 (57%)	40±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	800/1400 (57%)	800 (100%)	0 (0%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	X	34/63 (54%)	30±1 (89±4%)	4±1 (11±4%)	10	55
All	All	680/1260 (54%)	608 (89%)	72 (11%)	10	55

5 of 12 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	X	455	LYS	20
1	X	486	ARG	15
1	X	474	LYS	8
1	X	489	LYS	8
1	X	488	LYS	6

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 (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 75% for the well-defined parts and 62% 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	658
Number of shifts mapped to atoms	577
Number of unparsed shifts	0
Number of shifts with mapping errors	81
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 81) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	X	430	SER	HB2	3.898	0.02	1
1	X	431	GLU	HB2	1.938	0.02	1
1	X	431	GLU	HG2	2.254	0.02	2
1	X	432	LEU	HB2	1.619	0.02	1
1	X	433	PRO	HB2	2.33	0.02	2
1	X	433	PRO	HG2	2.062	0.02	1
1	X	433	PRO	HD2	3.897	0.02	2
1	X	434	GLU	HB2	2.031	0.02	1
1	X	445	ASP	HB2	2.722	0.02	2
1	X	448	LYS	HB2	1.789	0.02	1
1	X	449	PHE	HB2	3.198	0.02	1
1	X	450	ILE	HG12	1.501	0.02	2
1	X	451	GLU	HB2	2.113	0.02	1
1	X	451	GLU	HG2	2.393	0.02	2

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	X	452	GLU	HB2	2.093	0.02	2
1	X	454	GLU	HB2	2.123	0.02	1
1	X	454	GLU	HG2	2.478	0.02	1
1	X	455	LYS	HB2	1.68	0.02	2
1	X	455	LYS	HG2	1.204	0.02	2
1	X	455	LYS	HD2	1.683	0.02	1
1	X	455	LYS	HE2	2.957	0.02	2
1	X	456	LYS	HB2	1.897	0.02	1
1	X	456	LYS	HG2	1.573	0.02	2
1	X	457	ARG	HB2	1.978	0.02	2
1	X	457	ARG	HG2	1.77	0.02	2
1	X	457	ARG	HD2	3.234	0.02	2
1	X	458	ILE	HG12	2.144	0.02	2
1	X	459	ILE	HG12	1.847	0.02	2
1	X	460	GLU	HB2	2.122	0.02	2
1	X	460	GLU	HG2	2.465	0.02	2
1	X	462	LEU	HB2	1.693	0.02	2
1	X	463	GLU	HB2	2.235	0.02	2
1	X	463	GLU	HG2	2.542	0.02	2
1	X	464	LYS	HB2	1.957	0.02	2
1	X	464	LYS	HG2	1.616	0.02	2
1	X	464	LYS	HD2	1.668	0.02	1
1	X	467	TYR	HB2	3.343	0.02	2
1	X	471	ARG	HB2	1.993	0.02	2
1	X	471	ARG	HG2	1.833	0.02	2
1	X	471	ARG	HD2	3.281	0.02	1
1	X	474	LYS	HB2	1.984	0.02	1
1	X	474	LYS	HG2	1.623	0.02	2
1	X	474	LYS	HD2	1.755	0.02	1
1	X	475	LEU	HB2	1.814	0.02	2
1	X	476	LEU	HB2	1.378	0.02	2
1	X	478	TYR	HB2	3.7	0.02	2
1	X	480	LEU	HB2	1.721	0.02	1
1	X	481	ARG	HB2	1.874	0.02	2
1	X	481	ARG	HG2	1.735	0.02	2
1	X	481	ARG	HD2	3.214	0.02	1
1	X	482	GLN	HB2	2.326	0.02	2
1	X	482	GLN	HG2	2.364	0.02	2
1	X	483	LEU	HB2	2.26	0.02	2
1	X	484	ASP	HB2	2.767	0.02	2
1	X	485	TYR	HB2	3.245	0.02	2

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	X	486	ARG	HB2	1.764	0.02	1
1	X	486	ARG	HG2	1.904	0.02	2
1	X	486	ARG	HD2	3.04	0.02	2
1	X	487	ILE	HG12	1.891	0.02	2
1	X	488	LYS	HB2	1.852	0.02	2
1	X	488	LYS	HG2	1.468	0.02	2
1	X	488	LYS	HD2	1.674	0.02	1
1	X	488	LYS	HE2	2.968	0.02	1
1	X	489	LYS	HB2	1.259	0.02	2
1	X	489	LYS	HG2	1.086	0.02	2
1	X	489	LYS	HD2	1.393	0.02	2
1	X	489	LYS	HE2	2.843	0.02	1
1	X	490	TYR	HB2	3.265	0.02	2
1	X	492	ILE	HG12	1.703	0.02	2
1	X	493	GLU	HB2	1.942	0.02	1
1	X	493	GLU	HG2	2.267	0.02	2
1	X	494	LEU	HB2	1.739	0.02	2
1	X	495	LYS	HB2	1.258	0.02	2
1	X	495	LYS	HG2	0.9721	0.02	1
1	X	495	LYS	HD2	1.48	0.02	1
1	X	495	LYS	HE2	2.836	0.02	1
1	X	496	LYS	HB2	1.716	0.02	2
1	X	496	LYS	HG2	1.313	0.02	1
1	X	496	LYS	HD2	1.641	0.02	1
1	X	496	LYS	HE2	2.966	0.02	1
1	X	497	PHE	HB2	3.198	0.02	2

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	61	-1.64 ± 0.18	Should be checked
$^{13}C_{\beta}$	55	-0.83 ± 0.22	Should be checked
$^{13}C'$	0	—	None (insufficient data)
^{15}N	57	-0.81 ± 0.21	Should be applied

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 75%, i.e. 460 atoms were assigned a chemical

shift out of a possible 610. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	157/203 (77%)	79/83 (95%)	39/80 (49%)	39/40 (98%)
Sidechain	287/371 (77%)	200/239 (84%)	86/112 (77%)	1/20 (5%)
Aromatic	16/36 (44%)	16/16 (100%)	0/20 (0%)	0/0 (—%)
Overall	460/610 (75%)	295/338 (87%)	125/212 (59%)	40/60 (67%)

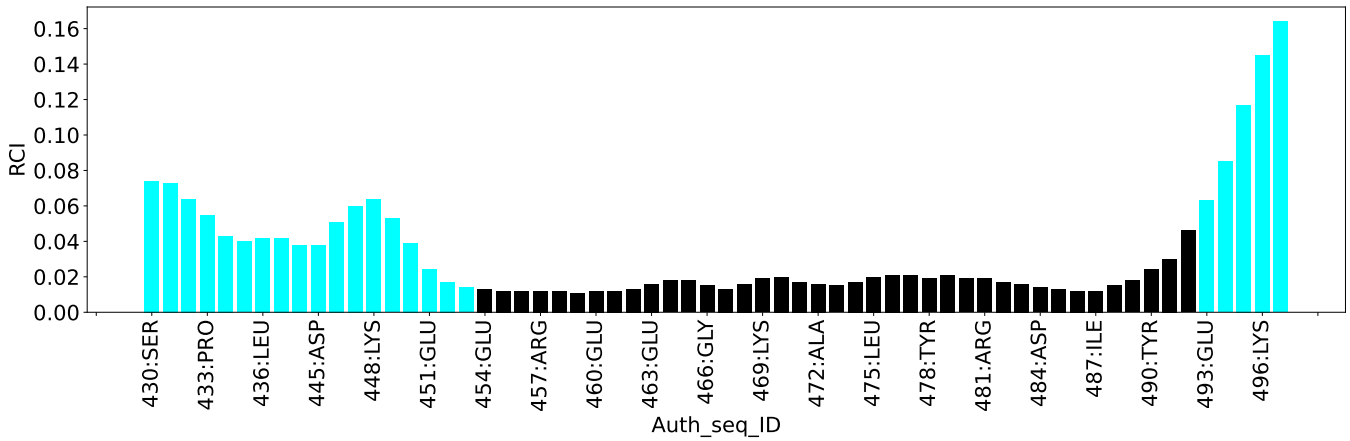
7.1.4 Statistically unusual chemical shifts (i)

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 X:



8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

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

Description	Value
Total distance restraints	1168
Intra-residue (|i-j|=0)	286
Sequential (|i-j|=1)	274
Medium range (|i-j|>1 and |i-j|<5)	284
Long range (|i-j|≥5)	252
Inter-chain	0
Hydrogen bond restraints	72
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	476
Number of restraints per residue	16.7
Number of long range restraints per residue[1]	3.6

[1]Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations (i)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model (i)

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	18.9	0.2
0.2-0.5 (Medium)	43.5	0.5
>0.5 (Large)	38.8	2.41

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 (i)

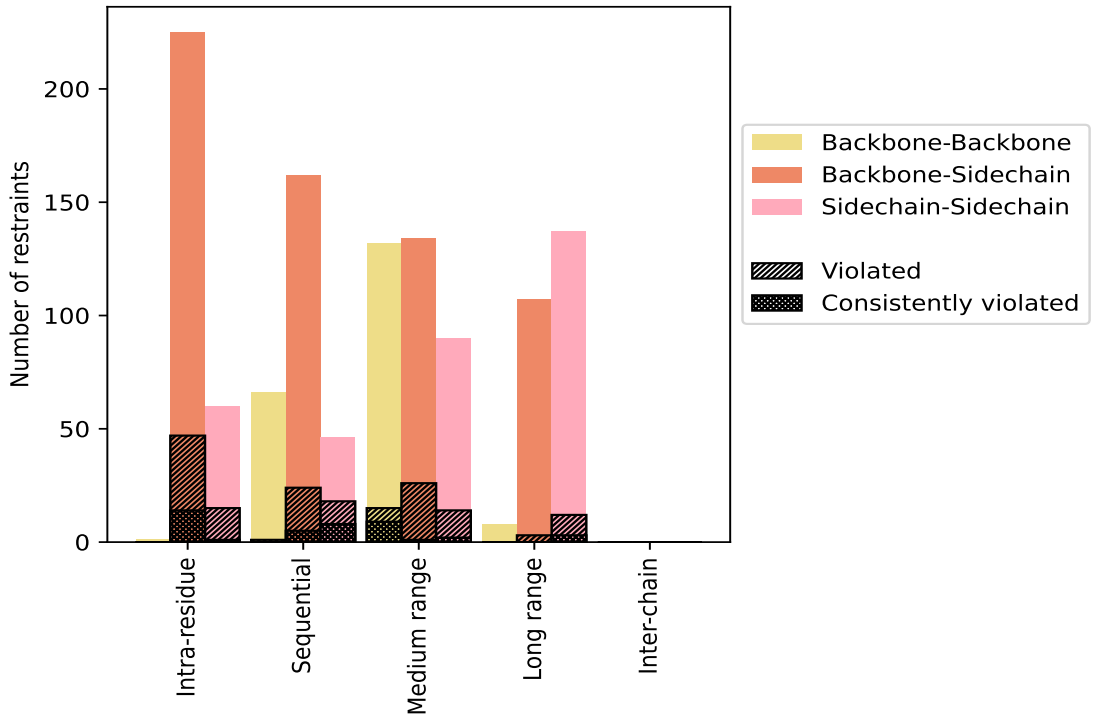
9.1 Summary of distance violations (i)

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.

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	286	24.5	62	21.7	5.3	15	5.2	1.3
Backbone-Backbone	1	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	225	19.3	47	20.9	4.0	14	6.2	1.2
Sidechain-Sidechain	60	5.1	15	25.0	1.3	1	1.7	0.1
Sequential (|i-j|=1)	274	23.5	43	15.7	3.7	13	4.7	1.1
Backbone-Backbone	66	5.7	1	1.5	0.1	0	0.0	0.0
Backbone-Sidechain	162	13.9	24	14.8	2.1	5	3.1	0.4
Sidechain-Sidechain	46	3.9	18	39.1	1.5	8	17.4	0.7
Medium range (|i-j|>1 & |i-j|<5)	284	24.3	40	14.1	3.4	3	1.1	0.3
Backbone-Backbone	60	5.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	134	11.5	26	19.4	2.2	1	0.7	0.1
Sidechain-Sidechain	90	7.7	14	15.6	1.2	2	2.2	0.2
Long range (|i-j|≥5)	252	21.6	15	6.0	1.3	3	1.2	0.3
Backbone-Backbone	8	0.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	107	9.2	3	2.8	0.3	0	0.0	0.0
Sidechain-Sidechain	137	11.7	12	8.8	1.0	3	2.2	0.3
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	72	6.2	15	20.8	1.3	9	12.5	0.8
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1168	100.0	175	15.0	15.0	43	3.7	3.7
Backbone-Backbone	207	17.7	16	7.7	1.4	9	4.3	0.8
Backbone-Sidechain	628	53.8	100	15.9	8.6	20	3.2	1.7
Sidechain-Sidechain	333	28.5	59	17.7	5.1	14	4.2	1.2

[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	37	24	28	7	0	96	0.45	1.51	0.31	0.34
2	36	24	30	7	0	97	0.48	1.41	0.29	0.4
3	33	23	29	7	0	92	0.51	1.63	0.33	0.42
4	37	25	29	11	0	102	0.49	1.9	0.34	0.36
5	42	28	35	7	0	112	0.5	1.94	0.37	0.38
6	44	23	30	9	0	106	0.5	1.82	0.37	0.4
7	35	23	30	6	0	94	0.46	1.57	0.3	0.4
8	37	25	33	11	0	106	0.5	1.98	0.36	0.38
9	37	28	32	8	0	105	0.49	1.94	0.36	0.4
10	41	24	34	11	0	110	0.48	2.41	0.36	0.37
11	36	24	32	6	0	98	0.49	2.19	0.35	0.39

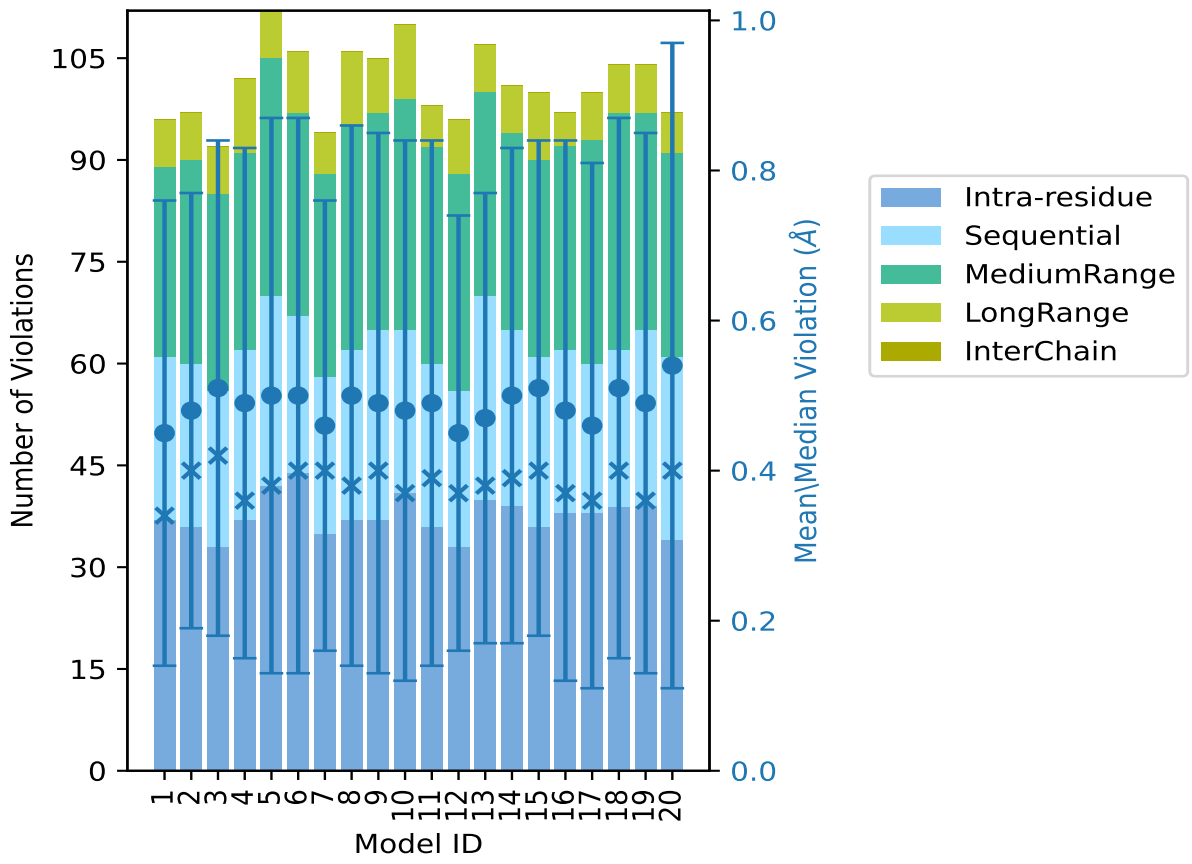
Continued on next page...

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				
12	33	23	32	8	0	96	0.45	1.42	0.29	0.37
13	40	30	30	7	0	107	0.47	1.64	0.3	0.38
14	39	26	29	7	0	101	0.5	1.49	0.33	0.39
15	36	25	29	10	0	100	0.51	1.78	0.33	0.4
16	38	24	30	5	0	97	0.48	2.14	0.36	0.37
17	38	22	33	7	0	100	0.46	2.23	0.35	0.36
18	39	23	35	7	0	104	0.51	1.54	0.36	0.4
19	39	26	32	7	0	104	0.49	1.68	0.36	0.36
20	34	27	30	6	0	97	0.54	2.12	0.43	0.4

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

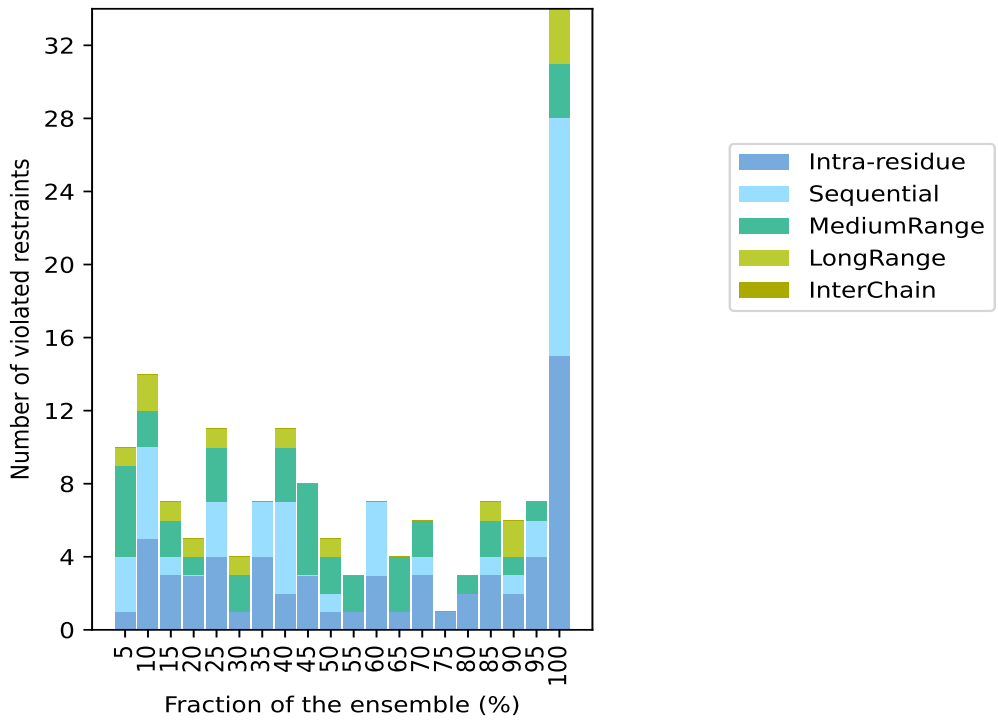
9.3 Distance violation statistics for the ensemble (i)

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, 936(IR:224, SQ:231, MR:244, LR:237, 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]	%
1	3	5	1	0	10	1	5.0
5	5	2	2	0	14	2	10.0
3	1	2	1	0	7	3	15.0
3	0	1	1	0	5	4	20.0
4	3	3	1	0	11	5	25.0
1	0	2	1	0	4	6	30.0
4	3	0	0	0	7	7	35.0
2	5	3	1	0	11	8	40.0
3	0	5	0	0	8	9	45.0
1	1	2	1	0	5	10	50.0
1	0	2	0	0	3	11	55.0
3	4	0	0	0	7	12	60.0
1	0	3	0	0	4	13	65.0
3	1	2	0	0	6	14	70.0
1	0	0	0	0	1	15	75.0
2	0	1	0	0	3	16	80.0
3	1	2	1	0	7	17	85.0
2	1	1	2	0	6	18	90.0
4	2	1	0	0	7	19	95.0
15	13	3	3	0	34	20	100.0

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

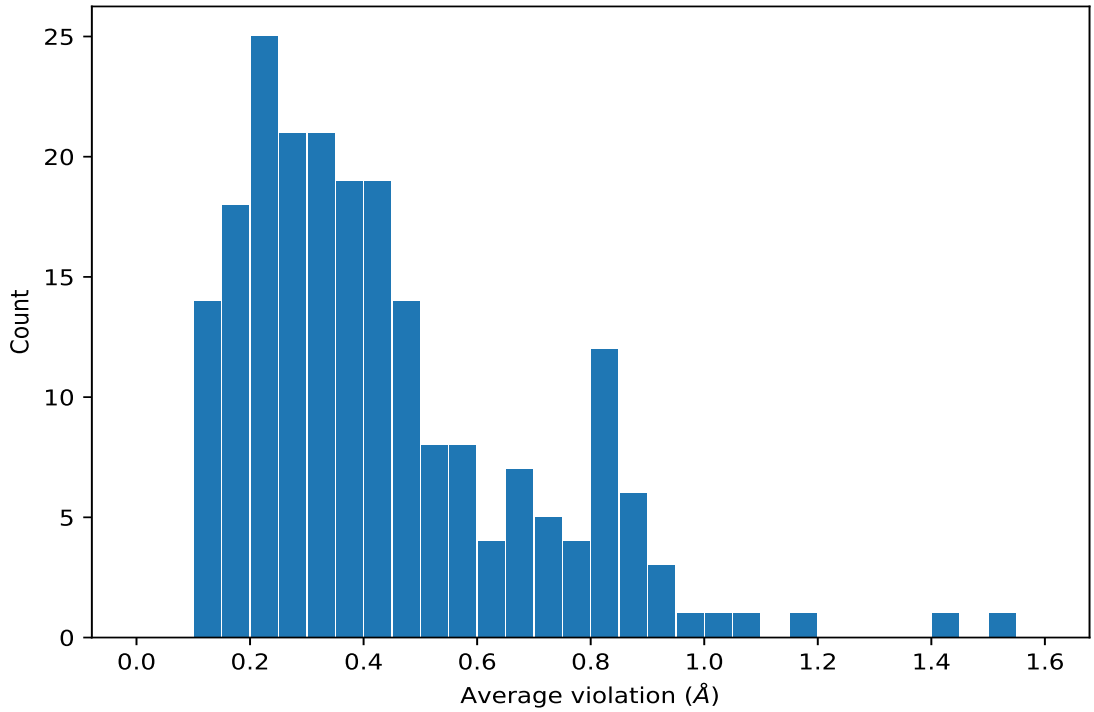
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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.

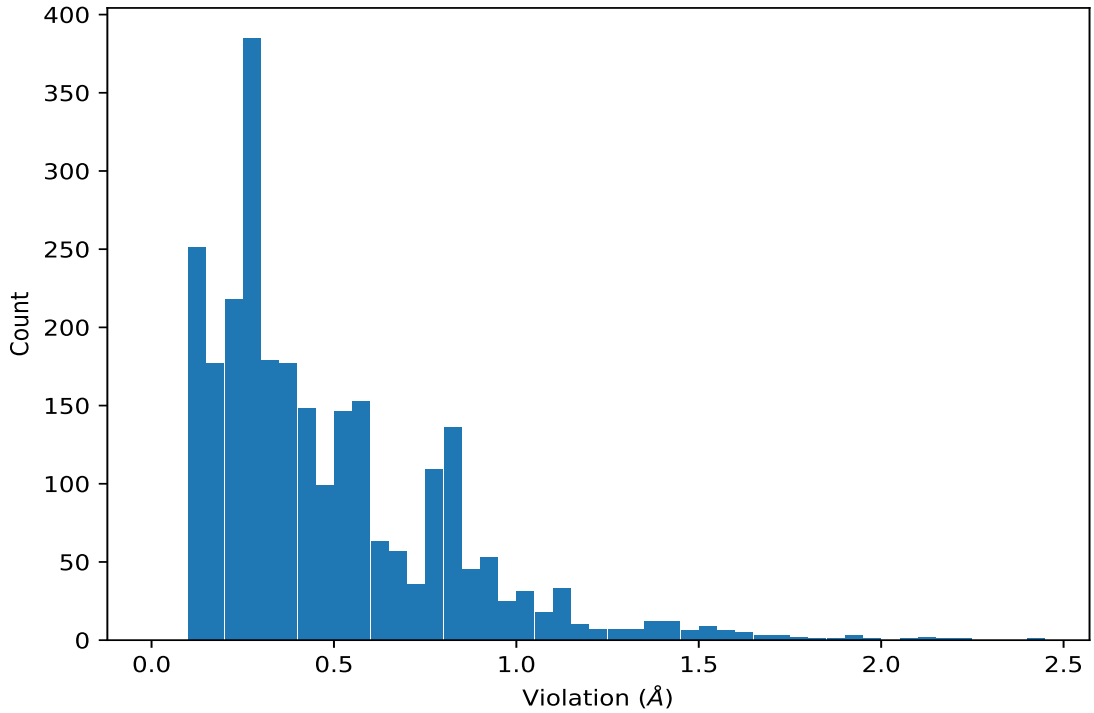
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,953)	1:X:455:LYS:HE3	1:X:456:LYS:HB3	20	1.53	0.36	1.42
(1,943)	1:X:451:GLU:HG3	1:X:452:GLU:HB3	20	1.16	0.28	1.24
(1,1092)	1:X:495:LYS:HB3	1:X:496:LYS:HB3	20	1.08	0.53	1.1
(1,300)	1:X:492:ILE:HB	1:X:493:GLU:HB3	20	1.03	0.24	1.13
(1,954)	1:X:455:LYS:HE3	1:X:456:LYS:HG3	20	0.95	0.29	0.85
(1,986)	1:X:461:ALA:HB1	1:X:464:LYS:HB3	20	0.88	0.12	0.86
(1,986)	1:X:461:ALA:HB2	1:X:464:LYS:HB3	20	0.88	0.12	0.86
(1,986)	1:X:461:ALA:HB3	1:X:464:LYS:HB3	20	0.88	0.12	0.86
(1,43)	1:X:455:LYS:HD3	1:X:459:ILE:HD11	20	0.83	0.12	0.82
(1,43)	1:X:455:LYS:HD3	1:X:459:ILE:HD12	20	0.83	0.12	0.82
(1,43)	1:X:455:LYS:HD3	1:X:459:ILE:HD13	20	0.83	0.12	0.82
(1,566)	1:X:456:LYS:H	1:X:456:LYS:HB3	20	0.81	0.02	0.82
(1,211)	1:X:473:ALA:HB1	1:X:480:LEU:HB3	20	0.8	0.09	0.82
(1,211)	1:X:473:ALA:HB2	1:X:480:LEU:HB3	20	0.8	0.09	0.82
(1,211)	1:X:473:ALA:HB3	1:X:480:LEU:HB3	20	0.8	0.09	0.82
(1,1086)	1:X:494:LEU:HB3	1:X:495:LYS:H	20	0.77	0.08	0.8

[1]Number of violated models, [2]Standard 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)
(1,96)	1:X:448:LYS:HB3	1:X:449:PHE:HB3	10	2.41
(1,953)	1:X:455:LYS:HE3	1:X:456:LYS:HB3	17	2.23
(1,953)	1:X:455:LYS:HE3	1:X:456:LYS:HB3	11	2.19
(1,953)	1:X:455:LYS:HE3	1:X:456:LYS:HB3	16	2.14
(1,953)	1:X:455:LYS:HE3	1:X:456:LYS:HB3	20	2.12
(1,883)	1:X:432:LEU:HB3	1:X:434:GLU:H	20	2.06
(1,948)	1:X:454:GLU:HG3	1:X:486:ARG:HD3	8	1.98
(1,1092)	1:X:495:LYS:HB3	1:X:496:LYS:HB3	5	1.94

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1092)	1:X:495:LYS:HB3	1:X:496:LYS:HB3	9	1.94
(1,1092)	1:X:495:LYS:HB3	1:X:496:LYS:HB3	20	1.92

10 Dihedral-angle violation analysis (i)

Dihedral angle analysis failed due to data error in the dihedral angle restraints, possibly missing target value