wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2JUH
BMRB ID	:	15444
Title	:	Solution structure of DNA binding domain of ngTRF1
Authors	:	Lee, N.; Ko, S.
Deposited on	:	2007-08-27

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

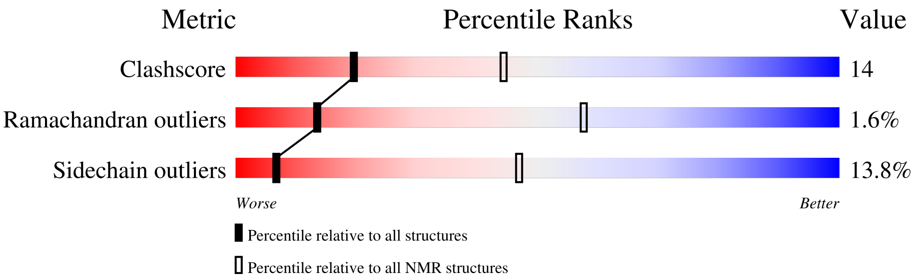
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal 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 81%.

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	A	121	

2 Ensemble composition and analysis (i)

This entry contains 20 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:581-A:608, A:616-A:633, A:641-A:659 (65)	0.54	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. No single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1802 atoms, of which 822 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Telomere binding protein TBP1.

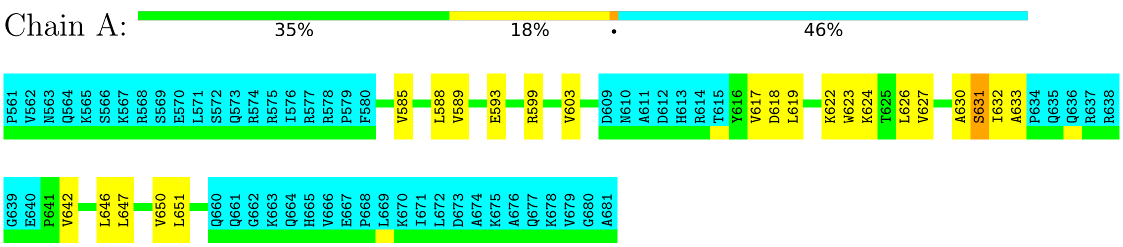
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	121	1802	612	822	192	175	1	0

4 Residue-property plots

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.

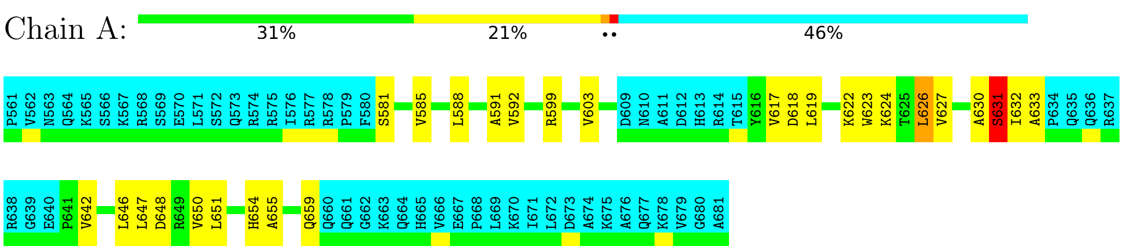
- Molecule 1: Telomere binding protein TBP1



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: Telomere binding protein TBP1



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	refinement	2.2.5
CYANA	structure solution	2.2.5

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	1087
Number of shifts mapped to atoms	1002
Number of unparsed shifts	0
Number of shifts with mapping errors	85
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

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	522	448	521	15±3
All	All	10440	8960	10420	292

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 14.

5 of 87 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:626:LEU:HD22	1:A:650:VAL:HG21	0.93	1.37	16	5
1:A:589:VAL:HG11	1:A:646:LEU:HD22	0.81	1.53	11	4
1:A:603:VAL:HG11	1:A:619:LEU:HD13	0.73	1.60	13	6
1:A:629:THR:HG21	1:A:642:VAL:HG21	0.69	1.64	18	1
1:A:627:VAL:HG23	1:A:651:LEU:HD12	0.69	1.65	8	3

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	65/121 (54%)	61±1 (94±1%)	3±1 (5±1%)	1±0 (2±0%)	13	57
All	All	1300/2420 (54%)	1218 (94%)	61 (5%)	21 (2%)	13	57

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	631	SER	20
1	A	616	TYR	1

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	54/103 (52%)	47±1 (86±3%)	7±1 (14±3%)	7	47
All	All	1080/2060 (52%)	931 (86%)	149 (14%)	7	47

5 of 25 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	618	ASP	17
1	A	626	LEU	16
1	A	623	TRP	13
1	A	588	LEU	12
1	A	593	GLU	11

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 81% for the well-defined parts and 63% 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	1087
Number of shifts mapped to atoms	1002
Number of unparsed shifts	0
Number of shifts with mapping errors	85
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

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 85) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	580	PHE	HB2	2.918	0.020	2
1	A	581	SER	HB2	4.425	0.020	2
1	A	584	GLU	HB2	2.695	0.020	2
1	A	584	GLU	HG2	2.658	0.020	2
1	A	586	GLU	HB2	2.163	0.020	2
1	A	586	GLU	HG2	2.269	0.020	2
1	A	588	LEU	HB2	1.853	0.020	2
1	A	590	GLU	HB2	2.134	0.020	2
1	A	590	GLU	HG2	2.484	0.020	2
1	A	593	GLU	HB2	2.646	0.020	2
1	A	593	GLU	HG2	2.597	0.020	2
1	A	594	HIS	HB2	3.037	0.020	2
1	A	595	LEU	HB2	1.416	0.020	2
1	A	599	ARG	HB2	1.932	0.020	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	599	ARG	HD2	2.969	0.020	2
1	A	599	ARG	HG2	1.372	0.020	2
1	A	600	TRP	HB2	3.6	0.020	2
1	A	601	ARG	HB2	1.215	0.020	2
1	A	601	ARG	HD2	2.86	0.020	2
1	A	601	ARG	HG2	1.58	0.020	2
1	A	602	ASP	HB2	2.656	0.020	2
1	A	604	LYS	HB2	2.365	0.020	2
1	A	605	MET	HB2	2.067	0.020	2
1	A	605	MET	HG2	2.667	0.020	2
1	A	606	ARG	HB2	1.611	0.020	2
1	A	606	ARG	HD2	2.835	0.020	2
1	A	606	ARG	HG2	1.595	0.020	2
1	A	608	PHE	HB2	3.569	0.020	2
1	A	609	ASP	HB2	2.951	0.020	2
1	A	610	ASN	HB2	2.808	0.020	2
1	A	612	ASP	HB2	2.608	0.020	2
1	A	613	HIS	HB2	3.182	0.020	2
1	A	616	TYR	HB2	3.001	0.020	2
1	A	618	ASP	HB2	2.897	0.020	2
1	A	619	LEU	HB2	1.981	0.020	2
1	A	621	ASP	HB2	2.509	0.020	2
1	A	622	LYS	HB2	1.517	0.020	2
1	A	623	TRP	HB2	3.255	0.020	2
1	A	624	LYS	HB2	1.884	0.020	2
1	A	624	LYS	HD2	1.617	0.020	2
1	A	624	LYS	HE2	2.905	0.020	2
1	A	624	LYS	HG2	1.351	0.020	2
1	A	626	LEU	HB2	0.882	0.020	2
1	A	628	HIS	HB2	3.117	0.020	2
1	A	631	SER	HB2	3.897	0.020	2
1	A	632	ILE	HG12	1.17	0.020	2
1	A	634	PRO	HB2	2.3	0.020	2
1	A	634	PRO	HD2	3.805	0.020	2
1	A	634	PRO	HG2	2.148	0.020	2
1	A	635	GLN	HB2	2.034	0.020	2
1	A	635	GLN	HG2	2.426	0.020	2
1	A	636	GLN	HB2	2.24	0.020	2
1	A	636	GLN	HG2	2.271	0.020	2
1	A	638	ARG	HB2	1.799	0.020	2
1	A	638	ARG	HD2	3.156	0.020	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	638	ARG	HG2	1.556	0.020	2
1	A	640	GLU	HB2	1.936	0.020	2
1	A	640	GLU	HG2	2.28	0.020	2
1	A	641	PRO	HB2	2.331	0.020	2
1	A	641	PRO	HD2	3.797	0.020	2
1	A	641	PRO	HG2	1.968	0.020	2
1	A	643	PRO	HB2	2.443	0.020	2
1	A	643	PRO	HD2	3.893	0.020	2
1	A	643	PRO	HG2	2.116	0.020	2
1	A	644	GLN	HB2	2.281	0.020	2
1	A	644	GLN	HG2	2.359	0.020	2
1	A	645	ASP	HB2	2.644	0.020	2
1	A	646	LEU	HB2	1.287	0.020	2
1	A	647	LEU	HB2	1.225	0.020	2
1	A	648	ASP	HB2	2.763	0.020	2
1	A	649	ARG	HB2	1.972	0.020	2
1	A	649	ARG	HD2	3.331	0.020	2
1	A	649	ARG	HG2	1.999	0.020	2
1	A	651	LEU	HB2	1.764	0.020	2
1	A	654	HIS	HB2	3.381	0.020	2
1	A	656	TYR	HB2	2.764	0.020	2
1	A	657	TRP	HB2	3.48	0.020	2
1	A	658	SER	HB2	3.793	0.020	2
1	A	659	GLN	HB2	2.073	0.020	2
1	A	659	GLN	HG2	2.351	0.020	2
1	A	660	GLN	HB2	2.079	0.020	2
1	A	660	GLN	HG2	1.938	0.020	2
1	A	665	HIS	HB2	3.045	0.020	2
1	A	667	GLU	HB2	1.967	0.020	2
1	A	667	GLU	HG2	2.236	0.020	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
$^{13}C_\alpha$	117	-0.29 ± 0.19	None needed (< 0.5 ppm)
$^{13}C_\beta$	113	0.40 ± 0.10	None needed (< 0.5 ppm)
$^{13}C'$	121	-0.32 ± 0.16	None needed (< 0.5 ppm)
^{15}N	111	-0.39 ± 0.30	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 81%, i.e. 743 atoms were assigned a chemical shift out of a possible 912. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	322/323 (100%)	129/130 (99%)	130/130 (100%)	63/63 (100%)
Sidechain	409/504 (81%)	284/331 (86%)	125/155 (81%)	0/18 (0%)
Aromatic	12/85 (14%)	9/43 (21%)	0/36 (0%)	3/6 (50%)
Overall	743/912 (81%)	422/504 (84%)	255/321 (79%)	66/87 (76%)

7.1.4 Statistically unusual chemical shifts (i)

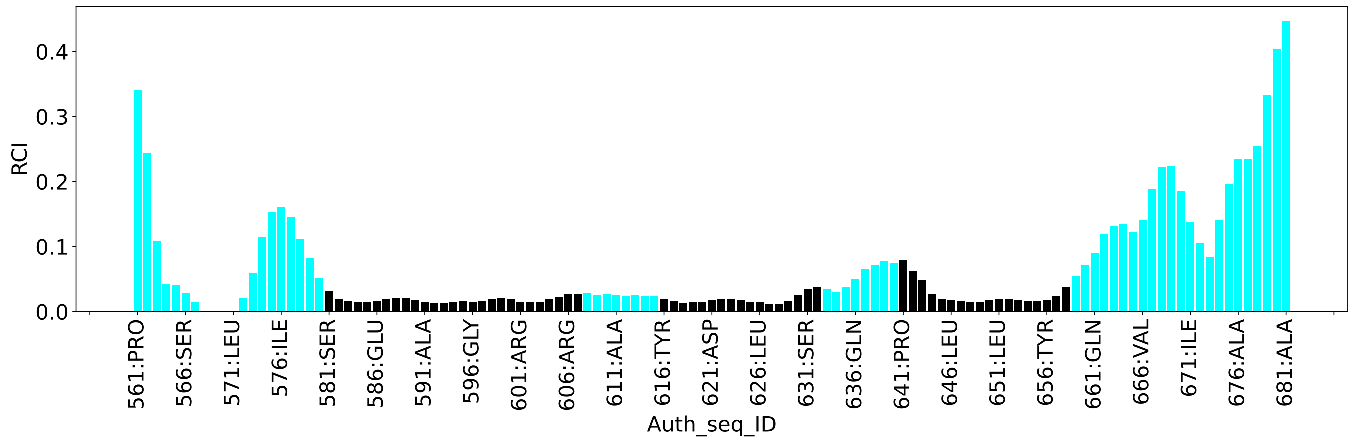
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	569	SER	HA	58.74	2.50 – 6.44	137.8
1	A	596	GLY	HA3	1.17	2.08 – 5.71	-7.5
1	A	637	ARG	CG	33.74	21.24 – 33.19	5.5
1	A	596	GLY	HA2	2.06	2.15 – 5.77	-5.3
1	A	592	VAL	HG11	-0.54	-0.48 – 2.12	-5.2
1	A	592	VAL	HG12	-0.54	-0.48 – 2.12	-5.2
1	A	592	VAL	HG13	-0.54	-0.48 – 2.12	-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:


RCI
0.0
0.1
0.2
0.3
0.4
561:PRO
566:SER
571:LEU
576:ILE
581:SER
586:GLU
591:ALA
596:GLY
601:ARG
606:ARG
611:ALA
616:TYR
621:ASP
626:LEU
631:SER
636:GLN
641:PRO
646:LEU
651:LEU
656:TYR
661:GLN
666:VAL
671:ILE
676:ALA
681:ALA
Auth_seq_ID

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	1259
Intra-residue (|i-j|=0)	300
Sequential (|i-j|=1)	315
Medium range (|i-j|>1 and |i-j|<5)	323
Long range (|i-j|≥5)	259
Inter-chain	0
Hydrogen bond restraints	62
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	365
Number of restraints per residue	10.4
Number of long range restraints per residue[1]	2.1

[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)	20.9	0.2
0.2-0.5 (Medium)	34.4	0.5
>0.5 (Large)	38.8	3.9

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)

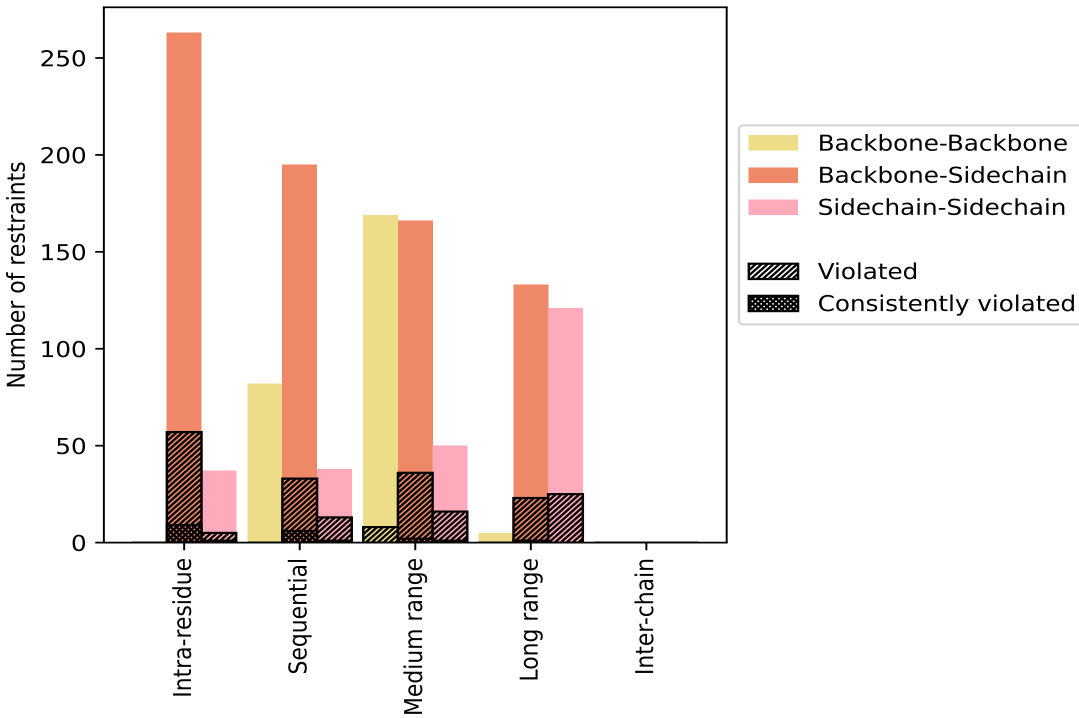
9.1 Summary of distance violations (i)

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)	300	23.8	62	20.7	4.9	10	3.3	0.8
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	263	20.9	57	21.7	4.5	9	3.4	0.7
Sidechain-Sidechain	37	2.9	5	13.5	0.4	1	2.7	0.1
Sequential (|i-j|=1)	315	25.0	46	14.6	3.7	7	2.2	0.6
Backbone-Backbone	82	6.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	195	15.5	33	16.9	2.6	6	3.1	0.5
Sidechain-Sidechain	38	3.0	13	34.2	1.0	1	2.6	0.1
Medium range (|i-j|>1 & |i-j|<5)	323	25.7	56	17.3	4.4	3	0.9	0.2
Backbone-Backbone	107	8.5	4	3.7	0.3	0	0.0	0.0
Backbone-Sidechain	166	13.2	36	21.7	2.9	2	1.2	0.2
Sidechain-Sidechain	50	4.0	16	32.0	1.3	1	2.0	0.1
Long range (|i-j|≥5)	259	20.6	48	18.5	3.8	1	0.4	0.1
Backbone-Backbone	5	0.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	133	10.6	23	17.3	1.8	1	0.8	0.1
Sidechain-Sidechain	121	9.6	25	20.7	2.0	0	0.0	0.0
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	62	4.9	4	6.5	0.3	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1259	100.0	216	17.2	17.2	21	1.7	1.7
Backbone-Backbone	256	20.3	8	3.1	0.6	0	0.0	0.0
Backbone-Sidechain	757	60.1	149	19.7	11.8	18	2.4	1.4
Sidechain-Sidechain	246	19.5	59	24.0	4.7	3	1.2	0.2

[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	33	25	22	15	0	95	0.54	3.14	0.44	0.48
2	33	24	24	22	0	103	0.56	3.08	0.45	0.47
3	30	26	17	17	0	90	0.53	3.18	0.46	0.39
4	32	22	18	23	0	95	0.52	3.05	0.45	0.38
5	31	21	21	14	0	87	0.57	3.12	0.49	0.4
6	34	27	25	15	0	101	0.55	3.62	0.48	0.38
7	32	25	14	11	0	82	0.53	3.07	0.47	0.38
8	32	24	22	21	0	99	0.49	2.99	0.42	0.38
9	29	22	20	19	0	90	0.54	3.11	0.46	0.42
10	36	25	22	23	0	106	0.52	3.01	0.45	0.38
11	28	20	17	20	0	85	0.54	3.16	0.44	0.44

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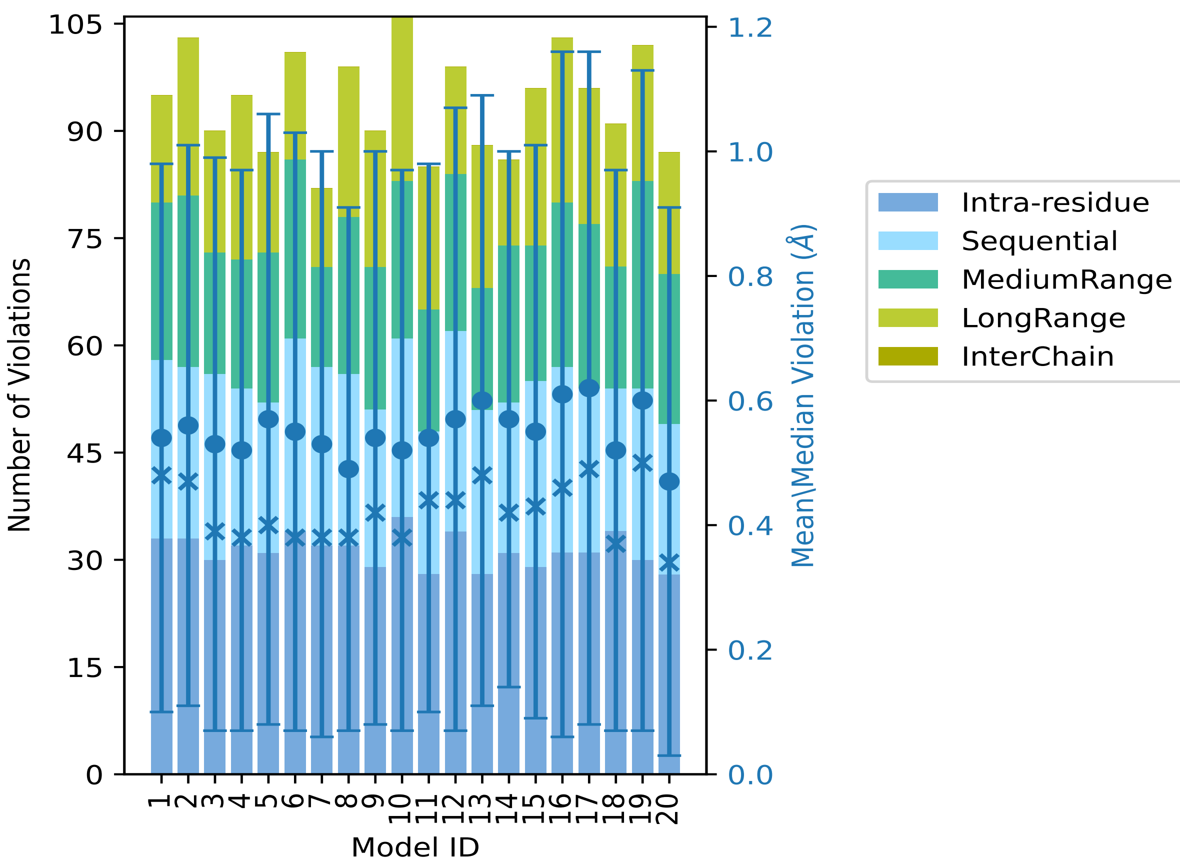
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	34	28	22	15	0	99	0.57	3.34	0.5	0.44
13	28	23	17	20	0	88	0.6	3.03	0.49	0.48
14	31	21	22	12	0	86	0.57	3.01	0.43	0.42
15	29	26	19	22	0	96	0.55	3.11	0.46	0.43
16	31	26	23	23	0	103	0.61	3.84	0.55	0.46
17	31	23	23	19	0	96	0.62	3.9	0.54	0.49
18	34	20	17	20	0	91	0.52	3.02	0.45	0.37
19	30	24	29	19	0	102	0.6	3.89	0.53	0.5
20	28	21	21	17	0	87	0.47	2.81	0.44	0.34

[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

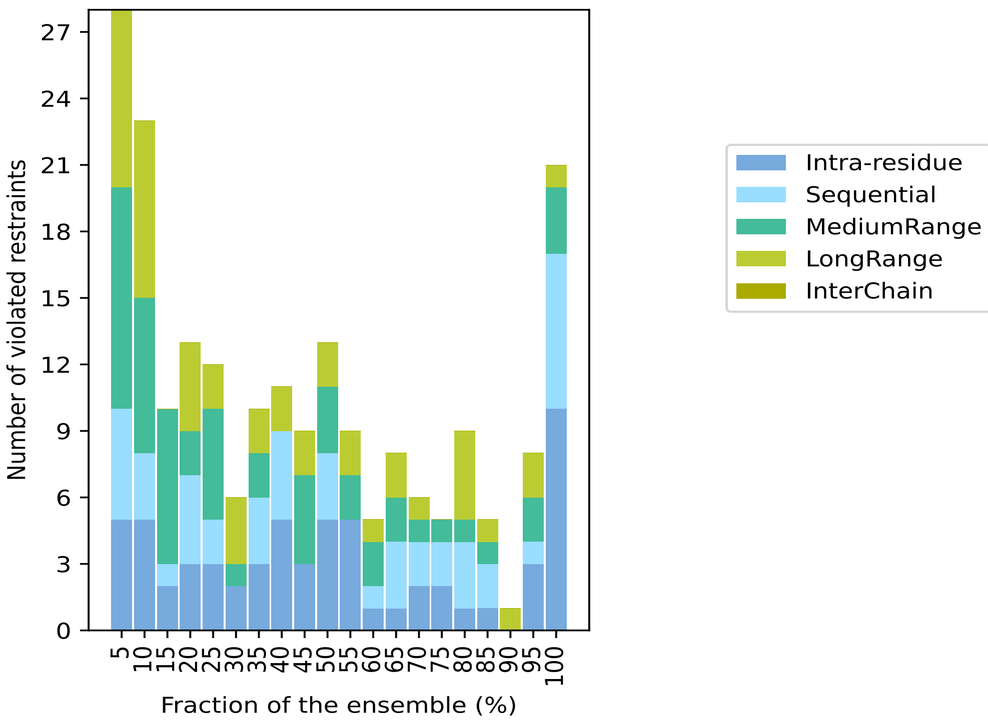
9.3 Distance violation statistics for the ensemble (i)

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, 985(IR:238, SQ:269, MR:267, LR:211, 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]	%
5	5	10	8	0	28	1	5.0
5	3	7	8	0	23	2	10.0
2	1	7	0	0	10	3	15.0
3	4	2	4	0	13	4	20.0
3	2	5	2	0	12	5	25.0
2	0	1	3	0	6	6	30.0
3	3	2	2	0	10	7	35.0
5	4	0	2	0	11	8	40.0
3	0	4	2	0	9	9	45.0
5	3	3	2	0	13	10	50.0
5	0	2	2	0	9	11	55.0
1	1	2	1	0	5	12	60.0
1	3	2	2	0	8	13	65.0
2	2	1	1	0	6	14	70.0
2	2	1	0	0	5	15	75.0
1	3	1	4	0	9	16	80.0
1	2	1	1	0	5	17	85.0
0	0	0	1	0	1	18	90.0
3	1	2	2	0	8	19	95.0
10	7	3	1	0	21	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

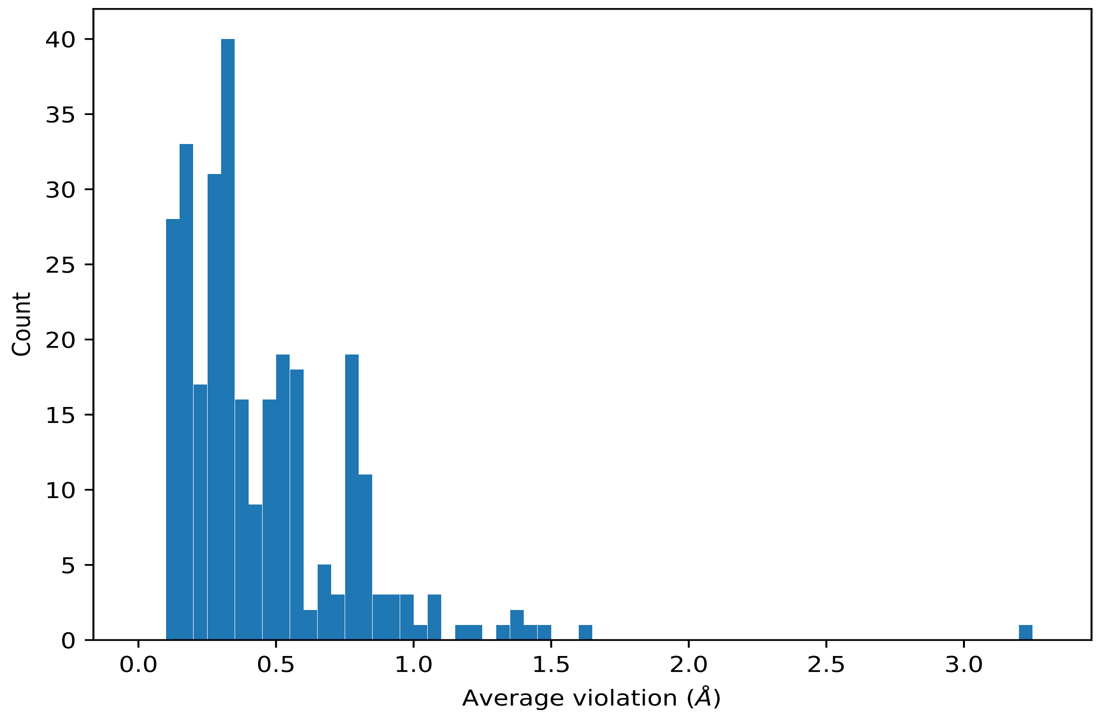
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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.

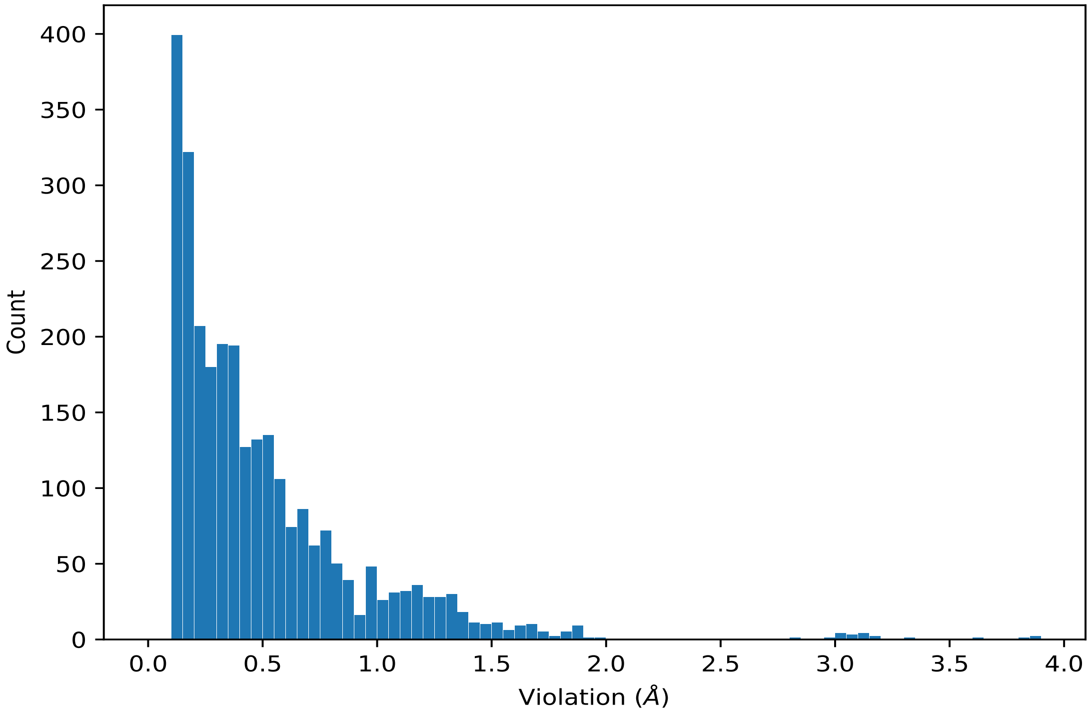
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	20	3.22	0.31	3.11
(1,702)	1:A:656:TYR:HD1	1:A:657:TRP:H	20	1.63	0.08	1.65
(1,1015)	1:A:604:LYS:HA	1:A:608:PHE:HB3	20	1.05	0.19	1.0
(1,1117)	1:A:633:ALA:HA	1:A:636:GLN:HB3	20	0.82	0.29	0.7
(1,81)	1:A:611:ALA:HA	1:A:612:ASP:HB3	20	0.79	0.39	0.88
(1,965)	1:A:593:GLU:HG3	1:A:652:ALA:H	20	0.78	0.18	0.72
(1,1113)	1:A:632:ILE:HG21	1:A:636:GLN:HB3	20	0.76	0.34	0.76
(1,1113)	1:A:632:ILE:HG22	1:A:636:GLN:HB3	20	0.76	0.34	0.76
(1,1113)	1:A:632:ILE:HG23	1:A:636:GLN:HB3	20	0.76	0.34	0.76
(1,860)	1:A:585:VAL:HA	1:A:586:GLU:HB3	20	0.76	0.43	1.06
(1,807)	1:A:633:ALA:H	1:A:634:PRO:HD3	20	0.55	0.07	0.56
(1,999)	1:A:600:TRP:H	1:A:600:TRP:HB3	20	0.54	0.01	0.54

[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)
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	17	3.9
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	19	3.89
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	16	3.84
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	6	3.62
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	12	3.34
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	3	3.18
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	11	3.16
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	1	3.14
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	5	3.12
(1,822)	1:A:656:TYR:HD1	1:A:657:TRP:HE1	9	3.11

10 Dihedral-angle violation analysis (i)

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