wwPDB NMR Structure Validation Summary Report (i)

Jun 6, 2023 – 06:44 pm BST

PDB ID	:	4A4E
BMRB ID	:	18005
Title	:	Solution structure of SMN Tudor domain in complex with symmetrically dimethylated arginine
Authors	:	Tripsianes, K.; Madl, T.; Machyna, M.; Fessas, D.; Englbrecht, C.; Fischer, U.; Neugebauer, K.M.; Sattler, M.
Deposited on	:	2011-10-12

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:

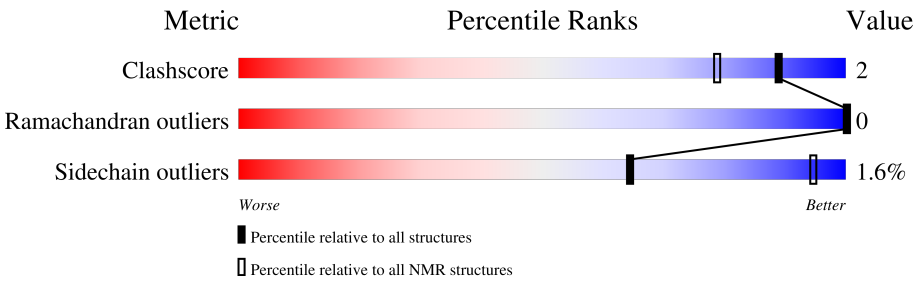
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	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 86%.

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	64	78% • 19%

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.

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:92-A:143 (52)	0.16	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. No single-model clusters were found.

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

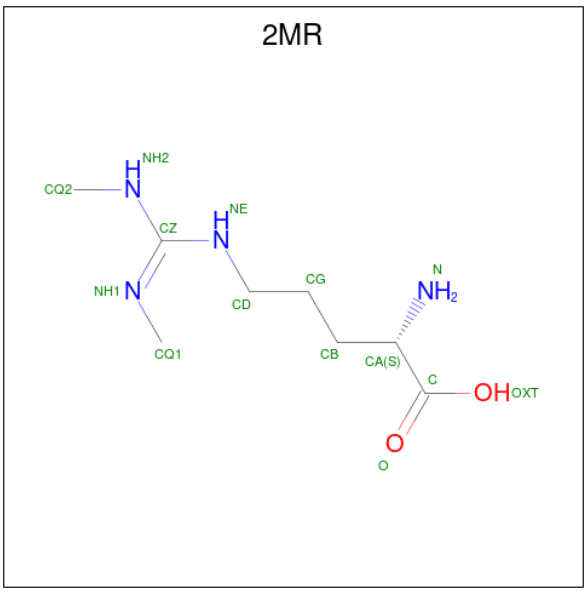
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1004 atoms, of which 494 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called SURVIVAL MOTOR NEURON PROTEIN.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	64	971	309	475	81	102	4	0

- Molecule 2 is N3, N4-DIMETHYLARGININE (three-letter code: 2MR) (formula: $C_8H_{18}N_4O_2$).



Mol	Chain	Residues	Atoms				
			Total	C	H	N	O
2	A	1	33	8	19	4	2

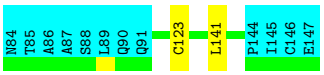
4 Residue-property plots (i)

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: SURVIVAL MOTOR NEURON PROTEIN

Chain A:

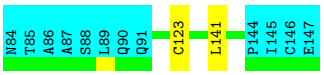


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

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

• Molecule 1: SURVIVAL MOTOR NEURON PROTEIN

Chain A:



5 Refinement protocol and experimental data overview (i)

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *LOWEST ENERGY*.

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

Software name	Classification	Version
CNS	refinement	
TALOS	structure solution	
CYANA	structure solution	
CNS	structure solution	

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	805
Number of shifts mapped to atoms	805
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 2MR

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	408	389	389	1±0
2	A	14	19	17	0±0
All	All	8440	8160	8120	30

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 2.

5 of 7 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:123:CYS:SG	1:A:141:LEU:HD11	0.56	2.40	9	20
1:A:93:LYS:HG2	1:A:96:ASP:OD2	0.51	2.06	6	1
2:A:1148:2MR:HA	2:A:1148:2MR:HE	0.48	1.67	17	1
1:A:107:CYS:HB2	1:A:109:TYR:CE2	0.46	2.45	9	1
1:A:99:SER:HB2	1:A:142:LEU:HB2	0.43	1.90	8	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	52/64 (81%)	52±0 (100±1%)	0±0 (0±1%)	0±0 (0±0%)	100	100
All	All	1040/1280 (81%)	1036 (100%)	4 (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	A	45/55 (82%)	44±1 (98±2%)	1±1 (2±2%)	64	94
All	All	900/1100 (82%)	886 (98%)	14 (2%)	64	94

All 4 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	96	ASP	8
1	A	119	LYS	4
1	A	133	ARG	1
1	A	105	ASP	1

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)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	2MR	A	1148	-	11,13,13	0.78±0.05	0±0 (4±4%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	2MR	A	1148	-	11,15,15	1.46±0.07	2±0 (18±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MR	A	1148	-	-	0±0,13,15,15	-

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	1148	2MR	OXT-C	2.25	1.23	1.30	19	10

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	1148	2MR	CQ2-NH2-CZ	3.34	131.24	123.86	5	20
2	A	1148	2MR	NE-CZ-NH2	3.14	116.60	119.48	9	20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 86% for the well-defined parts and 86% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

7.1.1 Bookkeeping (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	805
Number of shifts mapped to atoms	805
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

The following errors were found when reading this chemical shift list.

- Chemical shift has been reported more than once. First 5 (of 0) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	85	THR	HG22	1.196	0.001	1
1	A	85	THR	HG23	1.196	0.001	1
1	A	86	ALA	HB2	1.388	0.020	1
1	A	86	ALA	HB3	1.388	0.020	1
1	A	87	ALA	HB2	1.384	0.020	1
1	A	87	ALA	HB3	1.384	0.020	1
1	A	89	LEU	HD12	0.905	0.001	2
1	A	89	LEU	HD13	0.905	0.001	2
1	A	89	LEU	HD22	0.863	0.020	2
1	A	89	LEU	HD23	0.863	0.020	2
1	A	94	VAL	HG12	0.879	0.001	2
1	A	94	VAL	HG13	0.879	0.001	2
1	A	94	VAL	HG22	0.974	0.020	2
1	A	94	VAL	HG23	0.974	0.020	2

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	100	ALA	HB2	1.171	0.020	1
1	A	100	ALA	HB3	1.171	0.020	1
1	A	101	ILE	HG22	0.614	0.011	1
1	A	101	ILE	HG23	0.614	0.011	1
1	A	101	ILE	HD12	0.851	0.020	1
1	A	101	ILE	HD13	0.851	0.020	1
1	A	108	ILE	HG22	0.748	0.001	1
1	A	108	ILE	HG23	0.748	0.001	1
1	A	108	ILE	HD12	0.808	0.003	1
1	A	108	ILE	HD13	0.808	0.003	1
1	A	111	ALA	HB2	0.876	0.020	1
1	A	111	ALA	HB3	0.876	0.020	1
1	A	112	THR	HG22	1.067	0.001	1
1	A	112	THR	HG23	1.067	0.001	1
1	A	113	ILE	HG22	0.596	0.013	1
1	A	113	ILE	HG23	0.596	0.013	1
1	A	113	ILE	HD12	0.566	0.001	1
1	A	113	ILE	HD13	0.566	0.001	1
1	A	114	ALA	HB2	1.233	0.020	1
1	A	114	ALA	HB3	1.233	0.020	1
1	A	116	ILE	HG22	0.033	0.003	1
1	A	116	ILE	HG23	0.033	0.003	1
1	A	116	ILE	HD12	0.656	0.012	1
1	A	116	ILE	HD13	0.656	0.012	1
1	A	122	THR	HG22	1.075	0.003	1
1	A	122	THR	HG23	1.075	0.003	1
1	A	124	VAL	HG12	0.674	0.008	2
1	A	124	VAL	HG13	0.674	0.008	2
1	A	124	VAL	HG22	0.764	0.001	2
1	A	124	VAL	HG23	0.764	0.001	2
1	A	125	VAL	HG12	0.435	0.002	2
1	A	125	VAL	HG13	0.435	0.002	2
1	A	125	VAL	HG22	0.226	0.012	2
1	A	125	VAL	HG23	0.226	0.012	2
1	A	126	VAL	HG12	0.678	0.002	2
1	A	126	VAL	HG13	0.678	0.002	2
1	A	126	VAL	HG22	0.702	0.001	2
1	A	126	VAL	HG23	0.702	0.001	2
1	A	128	THR	HG22	1.239	0.020	1
1	A	128	THR	HG23	1.239	0.020	1
1	A	138	LEU	HD12	0.790	0.005	2

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	138	LEU	HD13	0.790	0.005	2
1	A	138	LEU	HD22	0.664	0.008	2
1	A	138	LEU	HD23	0.664	0.008	2
1	A	141	LEU	HD12	-0.256	0.006	2
1	A	141	LEU	HD13	-0.256	0.006	2
1	A	141	LEU	HD22	0.260	0.002	2
1	A	141	LEU	HD23	0.260	0.002	2
1	A	142	LEU	HD12	0.850	0.020	2
1	A	142	LEU	HD13	0.850	0.020	2
1	A	142	LEU	HD22	0.905	0.013	2
1	A	142	LEU	HD23	0.905	0.013	2
1	A	145	ILE	HG22	0.895	0.020	1
1	A	145	ILE	HG23	0.895	0.020	1
1	A	145	ILE	HD12	0.832	0.002	1
1	A	145	ILE	HD13	0.832	0.002	1
1	A	1148	2MR	HQ12	2.415	0.020	1
1	A	1148	2MR	HQ13	2.415	0.020	1
1	A	1148	2MR	HQ22	2.415	0.020	1
1	A	1148	2MR	HQ23	2.415	0.020	1

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	-0.30 ± 0.23	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	60	-0.01 ± 0.17	None needed (< 0.5 ppm)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	60	0.60 ± 0.33	None needed (imprecise)

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 86%, i.e. 585 atoms were assigned a chemical shift out of a possible 678. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	207/262 (79%)	107/107 (100%)	50/104 (48%)	50/51 (98%)
Sidechain	320/355 (90%)	218/230 (95%)	99/113 (88%)	3/12 (25%)

Continued on next page...

Continued from previous page...

	Total	^{1}H	^{13}C	^{15}N
Aromatic	58/61 (95%)	29/29 (100%)	27/30 (90%)	2/2 (100%)
Overall	585/678 (86%)	354/366 (97%)	176/247 (71%)	55/65 (85%)

7.1.4 Statistically unusual chemical shifts (i)

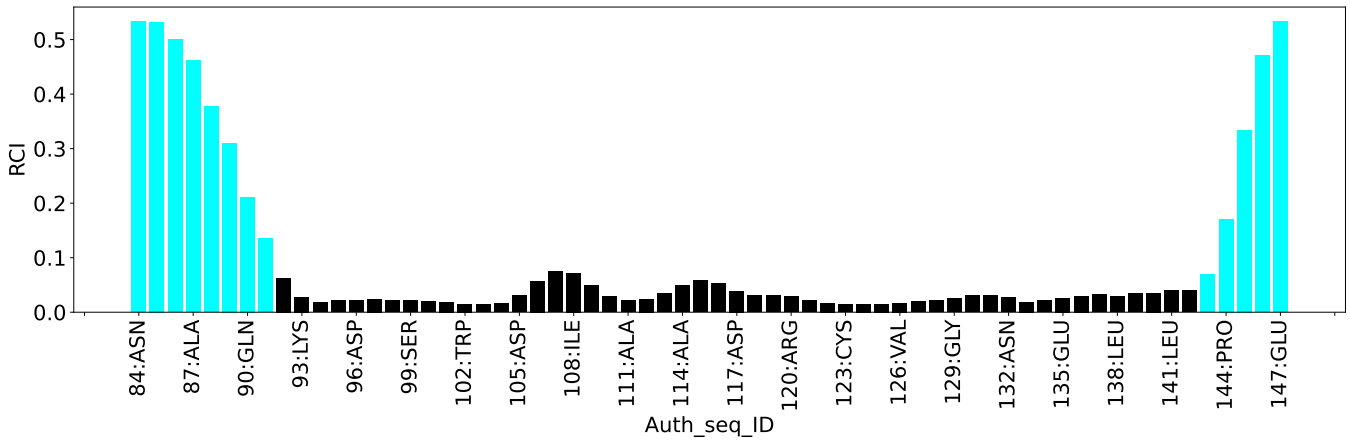
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	104	GLU	HB2	-0.50	1.00 – 3.05	-12.3
1	A	104	GLU	HB3	0.09	0.95 – 3.05	-9.1
1	A	132	ASN	HD22	4.15	4.69 – 9.61	-6.1
1	A	104	GLU	H	4.92	5.45 – 11.20	-5.9

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 (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	1863
Intra-residue (|i-j|=0)	393
Sequential (|i-j|=1)	435
Medium range (|i-j|>1 and |i-j|<5)	235
Long range (|i-j|≥5)	800
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	29.1
Number of long range restraints per residue[1]	12.5

[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)	14.7	0.2
0.2-0.5 (Medium)	36.5	0.5
>0.5 (Large)	44.8	2.36

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)

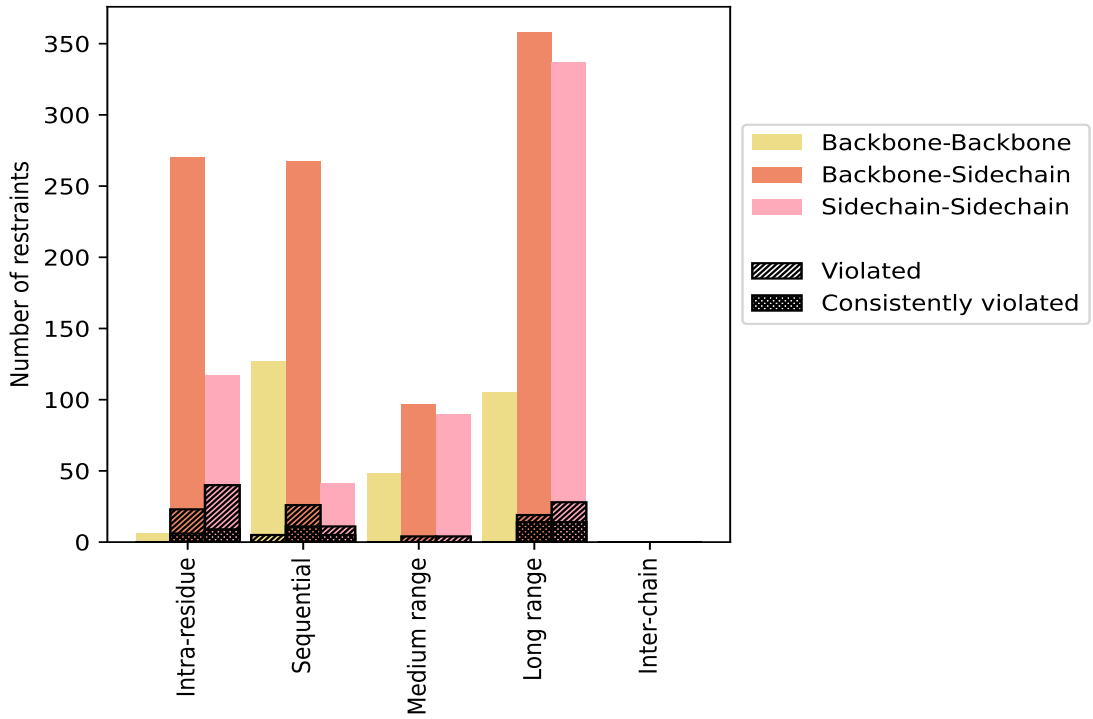
9.1 Summary of distance violations (i)

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)	393	21.1	63	16.0	3.4	15	3.8	0.8
Backbone-Backbone	6	0.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	270	14.5	23	8.5	1.2	6	2.2	0.3
Sidechain-Sidechain	117	6.3	40	34.2	2.1	9	7.7	0.5
Sequential (|i-j|=1)	435	23.3	42	9.7	2.3	16	3.7	0.9
Backbone-Backbone	127	6.8	5	3.9	0.3	0	0.0	0.0
Backbone-Sidechain	267	14.3	26	9.7	1.4	11	4.1	0.6
Sidechain-Sidechain	41	2.2	11	26.8	0.6	5	12.2	0.3
Medium range (|i-j|>1 & |i-j|<5)	235	12.6	8	3.4	0.4	0	0.0	0.0
Backbone-Backbone	48	2.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	97	5.2	4	4.1	0.2	0	0.0	0.0
Sidechain-Sidechain	90	4.8	4	4.4	0.2	0	0.0	0.0
Long range (|i-j|≥5)	800	42.9	47	5.9	2.5	28	3.5	1.5
Backbone-Backbone	105	5.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	358	19.2	19	5.3	1.0	14	3.9	0.8
Sidechain-Sidechain	337	18.1	28	8.3	1.5	14	4.2	0.8
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	1863	100.0	160	8.6	8.6	59	3.2	3.2
Backbone-Backbone	286	15.4	5	1.7	0.3	0	0.0	0.0
Backbone-Sidechain	992	53.2	72	7.3	3.9	31	3.1	1.7
Sidechain-Sidechain	585	31.4	83	14.2	4.5	28	4.8	1.5

[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 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	38	22	5	34	0	99	0.61	2.19	0.46	0.45
2	31	21	4	39	0	95	0.65	2.26	0.49	0.49
3	38	27	2	39	0	106	0.58	2.3	0.46	0.4
4	37	22	4	36	0	99	0.63	2.29	0.48	0.47
5	31	21	2	37	0	91	0.62	2.16	0.46	0.48
6	40	20	3	34	0	97	0.62	2.32	0.45	0.46
7	37	21	1	35	0	94	0.6	2.24	0.46	0.4
8	32	25	2	36	0	95	0.65	2.19	0.48	0.51
9	33	24	2	38	0	97	0.6	2.29	0.47	0.4
10	31	24	2	37	0	94	0.63	2.34	0.5	0.47
11	33	22	2	34	0	91	0.65	2.36	0.49	0.46

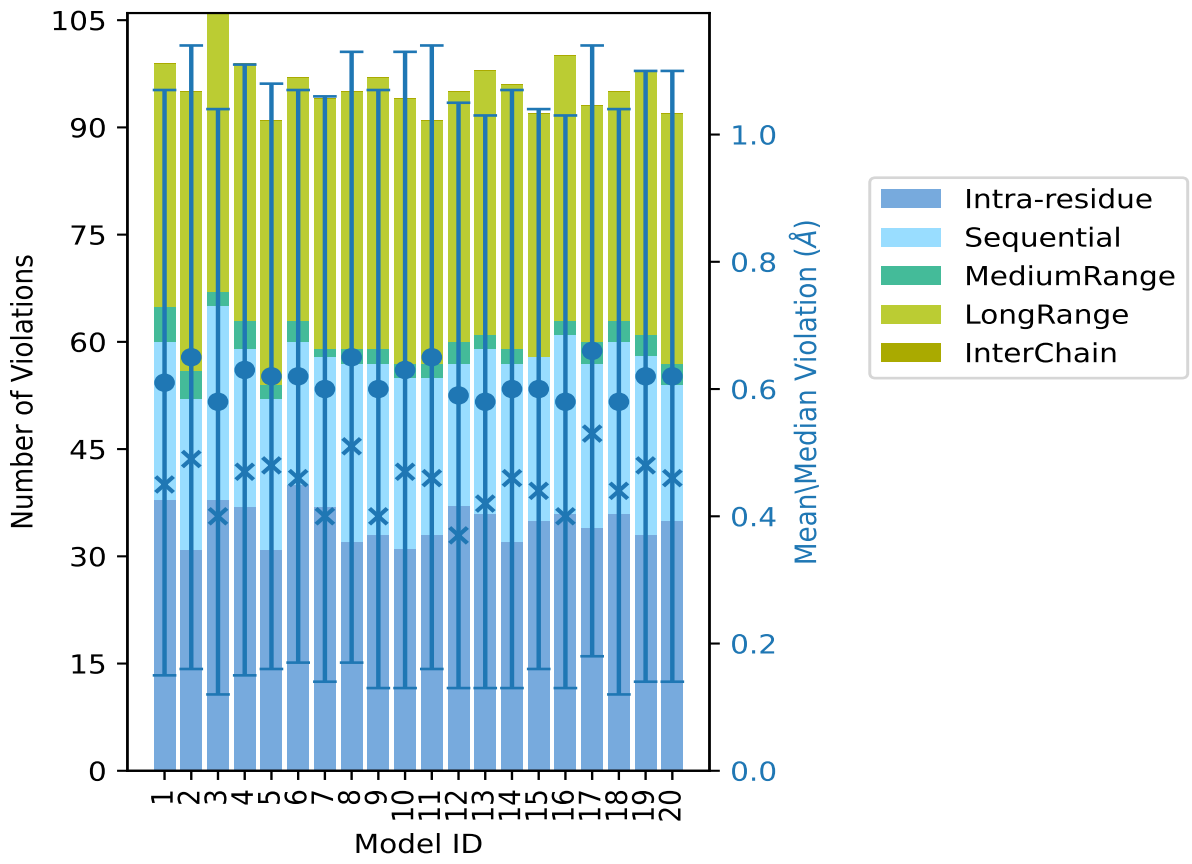
Continued on next page...

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	37	20	3	35	0	95	0.59	2.32	0.46	0.37
13	36	23	2	37	0	98	0.58	2.27	0.45	0.42
14	32	25	2	37	0	96	0.6	2.31	0.47	0.46
15	35	23	0	34	0	92	0.6	2.17	0.44	0.44
16	36	25	2	37	0	100	0.58	2.25	0.45	0.4
17	34	23	3	33	0	93	0.66	2.23	0.48	0.53
18	36	24	3	32	0	95	0.58	2.27	0.46	0.44
19	33	25	3	37	0	98	0.62	2.26	0.48	0.48
20	35	19	3	35	0	92	0.62	2.19	0.48	0.46

[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

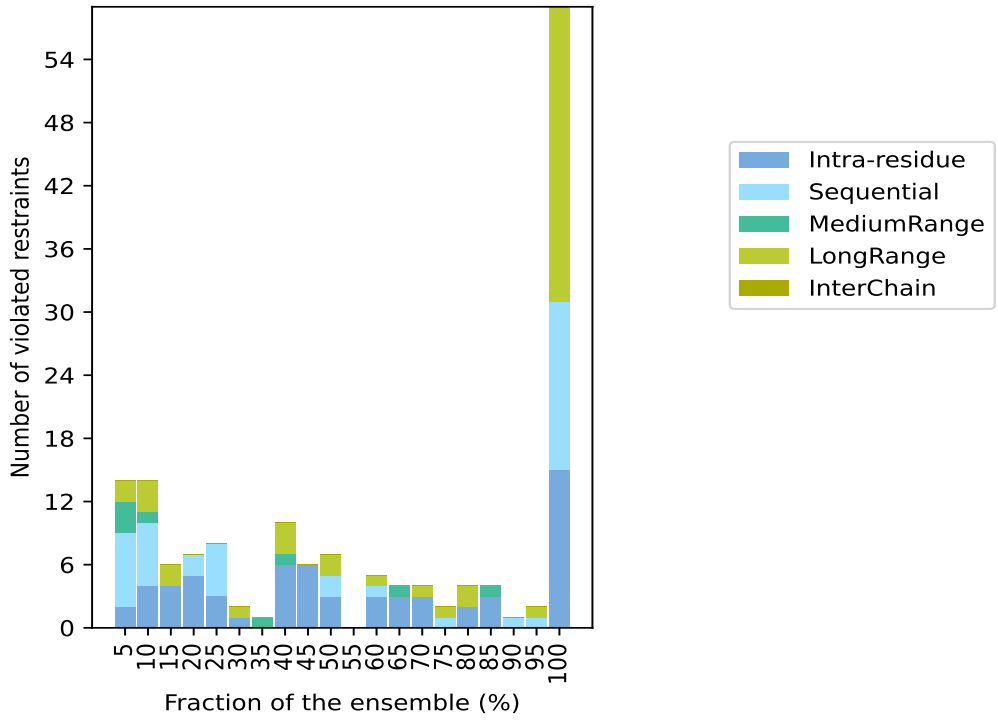
9.3 Distance violation statistics for the ensemble (i)

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, 1703(IR:330, SQ:393, MR:227, LR:753, 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]	%
2	7	3	2	0	14	1	5.0
4	6	1	3	0	14	2	10.0
4	0	0	2	0	6	3	15.0
5	2	0	0	0	7	4	20.0
3	5	0	0	0	8	5	25.0
1	0	0	1	0	2	6	30.0
0	0	1	0	0	1	7	35.0
6	0	1	3	0	10	8	40.0
6	0	0	0	0	6	9	45.0
3	2	0	2	0	7	10	50.0
0	0	0	0	0	0	11	55.0
3	1	0	1	0	5	12	60.0
3	0	1	0	0	4	13	65.0
3	0	0	1	0	4	14	70.0
0	1	0	1	0	2	15	75.0
2	0	0	2	0	4	16	80.0
3	0	1	0	0	4	17	85.0
0	1	0	0	0	1	18	90.0
0	1	0	1	0	2	19	95.0
15	16	0	28	0	59	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

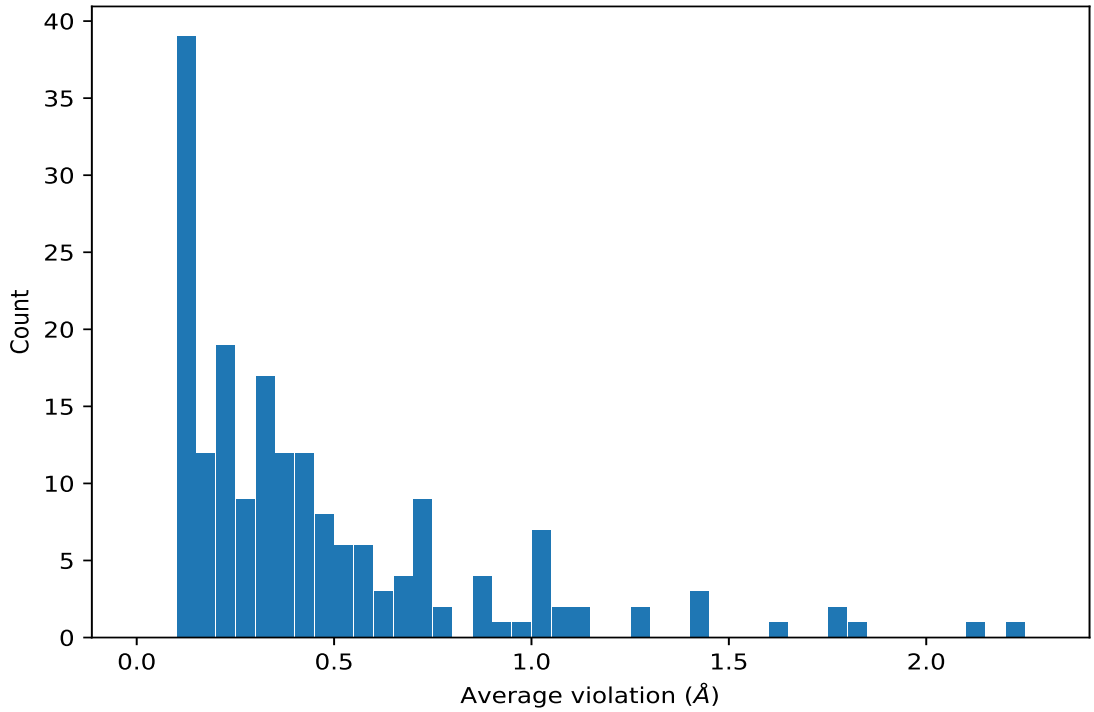
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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.

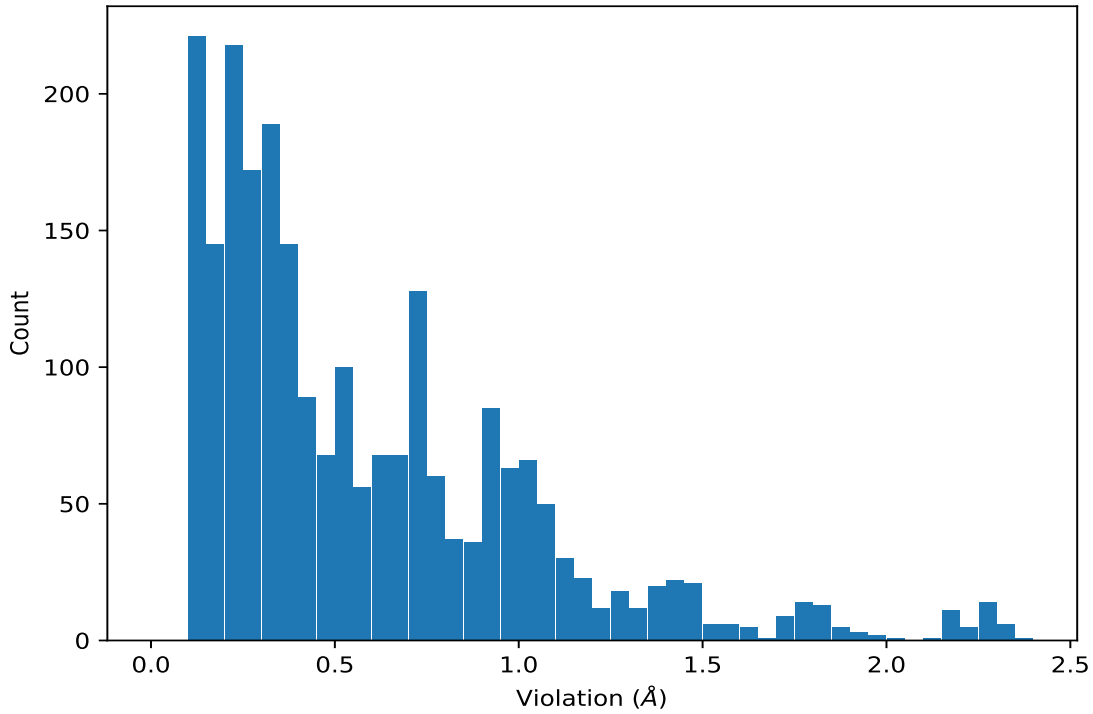
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,1798)	1:A:132:ASN:H	2:A:1148:2MR:HH2	20	2.24	0.05	2.25
(1,1849)	1:A:143:SER:HB2	1:A:144:PRO:HG3	20	2.11	0.42	2.24
(1,1451)	1:A:142:LEU:HB2	1:A:98:CYS:HB3	20	1.78	0.08	1.8
(1,1797)	1:A:132:ASN:HD21	2:A:1148:2MR:HH2	20	1.44	0.04	1.42
(1,91)	1:A:100:ALA:H	1:A:142:LEU:HB3	20	1.42	0.1	1.45
(1,636)	1:A:98:CYS:HB2	1:A:113:ILE:H	20	1.42	0.03	1.41
(1,1388)	1:A:99:SER:HA	1:A:142:LEU:HB3	20	1.29	0.09	1.28
(1,436)	1:A:142:LEU:H	1:A:98:CYS:HB3	20	1.29	0.06	1.29
(1,449)	1:A:142:LEU:HB2	1:A:143:SER:H	20	1.12	0.03	1.12
(1,1400)	1:A:144:PRO:HD2	1:A:98:CYS:HB3	20	1.11	0.1	1.1

[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)
(1,1798)	1:A:132:ASN:H	2:A:1148:2MR:HH2	11	2.36
(1,1849)	1:A:143:SER:HB2	1:A:144:PRO:HG3	10	2.34
(1,1849)	1:A:143:SER:HB2	1:A:144:PRO:HG3	6	2.32
(1,1849)	1:A:143:SER:HB2	1:A:144:PRO:HG3	12	2.32
(1,1798)	1:A:132:ASN:H	2:A:1148:2MR:HH2	14	2.31
(1,1849)	1:A:143:SER:HB2	1:A:144:PRO:HG3	3	2.3
(1,1798)	1:A:132:ASN:H	2:A:1148:2MR:HH2	12	2.3
(1,1849)	1:A:143:SER:HB2	1:A:144:PRO:HG3	9	2.29
(1,1798)	1:A:132:ASN:H	2:A:1148:2MR:HH2	4	2.29
(1,1849)	1:A:143:SER:HB2	1:A:144:PRO:HG3	4	2.28

10 Dihedral-angle violation analysis (i)

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