wwPDB NMR Structure Validation Summary Report

Jun 3, 2023 – 11:03 PM EDT

PDB ID	:	7SA5
BMRB ID	:	27579
Title	:	Two-state solution NMR structure of Apo Pin1
Authors	:	Born, A.; Vogeli, B.
Deposited on	:	2021-09-22

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:

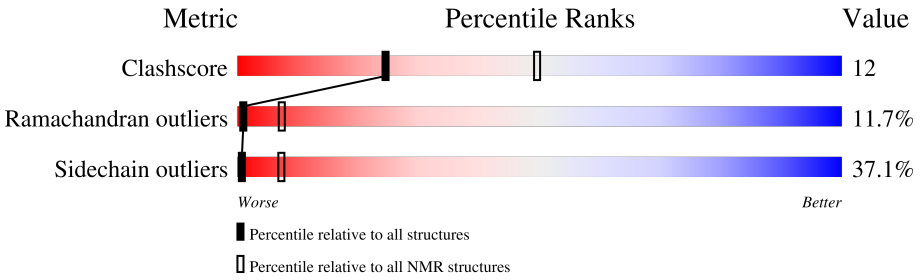
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal 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 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	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	163	37% 50% · 10%

2 Ensemble composition and analysis

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: *target function*.

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:5-A:39 (35)	1.19	2
2	A:53-A:163 (111)	1.18	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 4 clusters. No single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2519 atoms, of which 1238 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1.

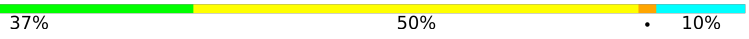
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	163	2519	786	1238	239	250	6	0

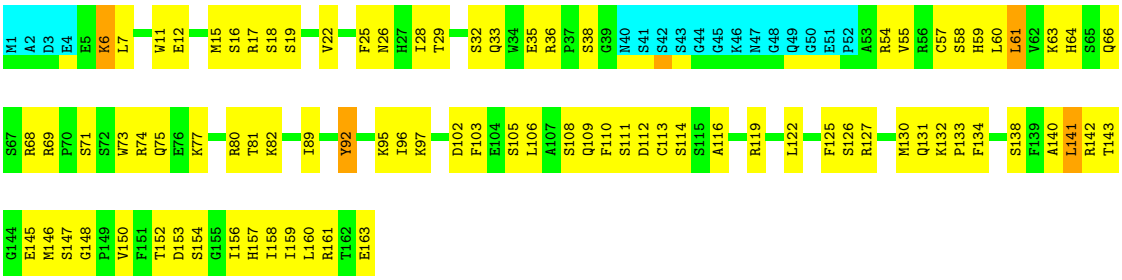
4 Residue-property plots (i)

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: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

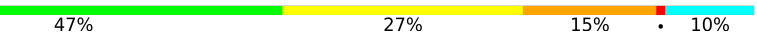
Chain A: 

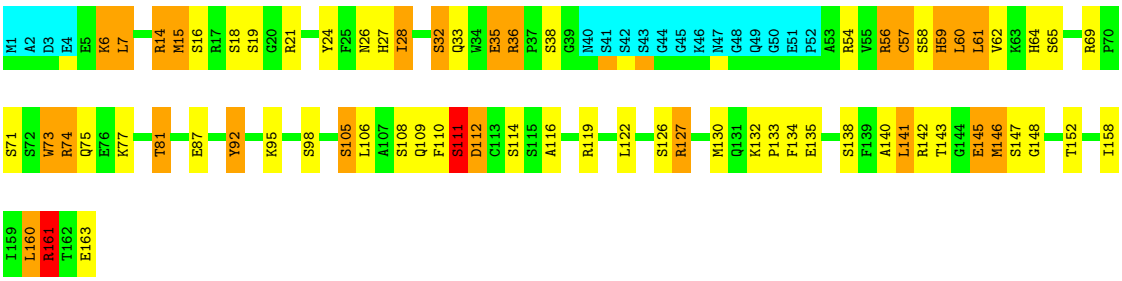


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

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

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A: 



5 Refinement protocol and experimental data overview

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

Of the 400 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	
CYANA	structure calculation	

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	1801
Number of shifts mapped to atoms	1801
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

6.1 Standard geometry

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

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	1167	1141	1141	27±8
All	All	23340	22820	22820	543

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 12.

5 of 300 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:128:GLY:O	1:A:130:MET:N	0.95	1.99	9	3
1:A:28:ILE:HG22	1:A:140:ALA:HB1	0.91	1.41	12	1
1:A:29:THR:HG21	1:A:141:LEU:HD11	0.86	1.47	8	1
1:A:60:LEU:HD13	1:A:158:ILE:HD12	0.80	1.52	20	5
1:A:96:ILE:HD11	1:A:106:LEU:HD13	0.78	1.55	9	3

6.3 Torsion angles

6.3.1 Protein backbone

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	145/163 (89%)	91±6 (63±4%)	37±5 (26±4%)	17±3 (12±2%)	1 7
All	All	2900/3260 (89%)	1816 (63%)	744 (26%)	340 (12%)	1 7

5 of 82 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	153	ASP	16
1	A	127	ARG	13
1	A	61	LEU	12
1	A	110	PHE	12
1	A	111	SER	12

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	126/138 (91%)	79±4 (63±3%)	47±4 (37±3%)	1 7
All	All	2520/2760 (91%)	1585 (63%)	935 (37%)	1 7

5 of 112 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	92	TYR	20
1	A	105	SER	19
1	A	138	SER	19
1	A	141	LEU	19
1	A	38	SER	18

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

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_chem_shift_list_1*

7.1.1 Bookkeeping

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	1801
Number of shifts mapped to atoms	1801
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	9

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	163	-0.21 ± 0.10	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	148	-0.09 ± 0.13	None needed (< 0.5 ppm)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	152	0.12 ± 0.33	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

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. 1655 atoms were assigned a chemical shift out of a possible 1995. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	578/729 (79%)	295/297 (99%)	146/292 (50%)	137/140 (98%)
Sidechain	935/1105 (85%)	634/709 (89%)	291/335 (87%)	10/61 (16%)

Continued on next page...

Continued from previous page...

	Total	^{1}H	^{13}C	^{15}N
Aromatic	142/161 (88%)	71/81 (88%)	68/73 (93%)	3/7 (43%)
Overall	1655/1995 (83%)	1000/1087 (92%)	505/700 (72%)	150/208 (72%)

7.1.4 Statistically unusual chemical shifts (i)

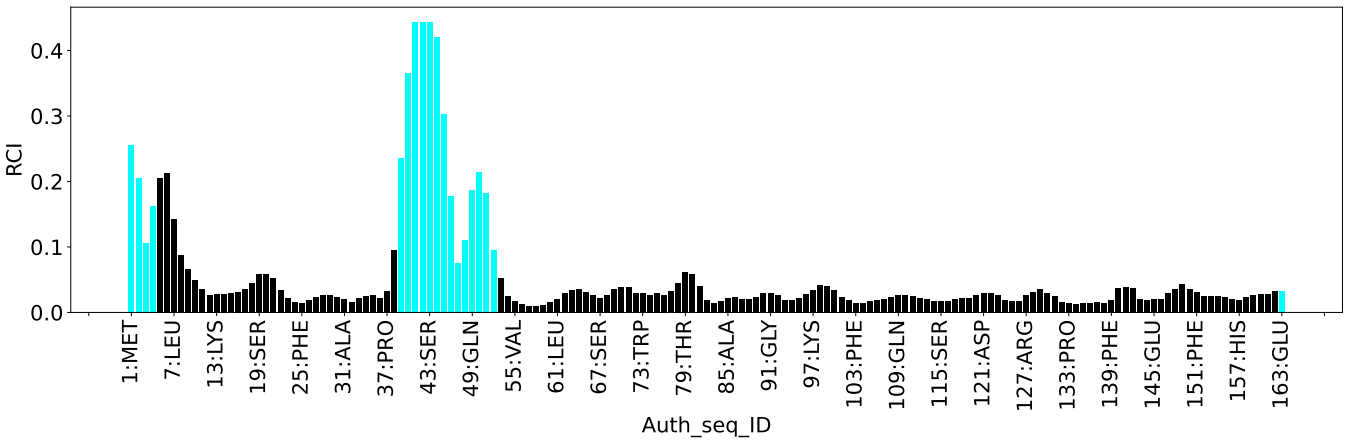
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	26	ASN	HB2	-0.69	1.27 – 4.34	-11.4
1	A	74	ARG	HG3	-0.64	0.15 – 2.94	-7.8
1	A	14	ARG	HB2	0.11	0.52 – 3.08	-6.6
1	A	26	ASN	HD22	4.06	4.69 – 9.61	-6.3
1	A	37	PRO	HG3	-0.04	0.33 – 3.48	-6.2
1	A	74	ARG	HG2	-0.02	0.26 – 2.87	-6.1
1	A	55	VAL	HG21	-0.63	-0.58 – 2.19	-5.2
1	A	55	VAL	HG22	-0.63	-0.58 – 2.19	-5.2
1	A	55	VAL	HG23	-0.63	-0.58 – 2.19	-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
1:MET
7:LEU
13:LYS
19:SER
25:PHE
31:ALA
37:PRO
43:SER
49:GLN
55:VAL
61:LEU
67:SER
73:TRP
79:THR
85:ALA
91:GLY
97:LYS
103:PHE
109:GLN
115:SER
121:ASP
127:ARG
133:PRO
139:PHE
145:GLU
151:PHE
157:HIS
163:GLU
Auth_seq_ID

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	11609
Intra-residue (|i-j|=0)	2768
Sequential (|i-j|=1)	3004
Medium range (|i-j|>1 and |i-j|<5)	2002
Long range (|i-j|≥5)	3835
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	5639
Number of restraints per residue	71.2
Number of long range restraints per residue[1]	23.5

[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

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)	238.2	0.2
0.2-0.5 (Medium)	537.5	0.5
>0.5 (Large)	2376.3	42.83

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)

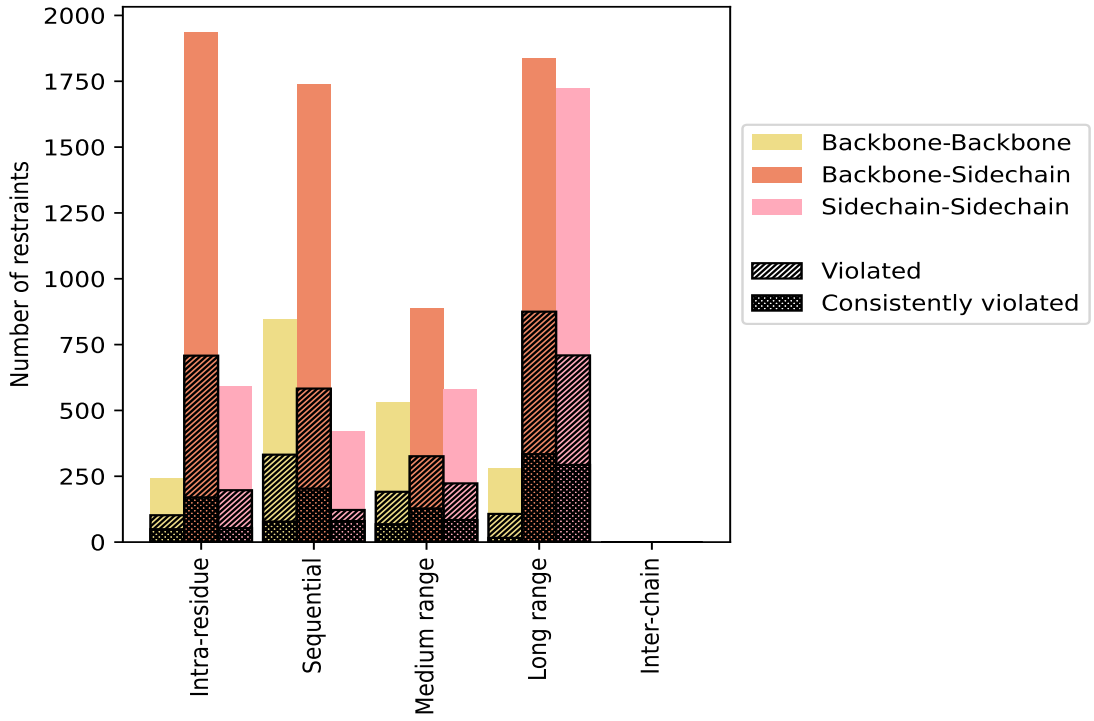
9.1 Summary of distance violations (i)

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)	2768	23.8	1007	36.4	8.7	272	9.8	2.3
Backbone-Backbone	242	2.1	102	42.1	0.9	49	20.2	0.4
Backbone-Sidechain	1936	16.7	708	36.6	6.1	170	8.8	1.5
Sidechain-Sidechain	590	5.1	197	33.4	1.7	53	9.0	0.5
Sequential (|i-j|=1)	3004	25.9	1037	34.5	8.9	361	12.0	3.1
Backbone-Backbone	846	7.3	332	39.2	2.9	78	9.2	0.7
Backbone-Sidechain	1737	15.0	583	33.6	5.0	203	11.7	1.7
Sidechain-Sidechain	421	3.6	122	29.0	1.1	80	19.0	0.7
Medium range (|i-j|>1 & |i-j|<5)	2002	17.2	740	37.0	6.4	280	14.0	2.4
Backbone-Backbone	532	4.6	191	35.9	1.6	68	12.8	0.6
Backbone-Sidechain	889	7.7	326	36.7	2.8	128	14.4	1.1
Sidechain-Sidechain	581	5.0	223	38.4	1.9	84	14.5	0.7
Long range (|i-j|≥5)	3835	33.0	1691	44.1	14.6	643	16.8	5.5
Backbone-Backbone	278	2.4	107	38.5	0.9	16	5.8	0.1
Backbone-Sidechain	1835	15.8	875	47.7	7.5	334	18.2	2.9
Sidechain-Sidechain	1722	14.8	709	41.2	6.1	293	17.0	2.5
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	11609	100.0	4475	38.5	38.5	1556	13.4	13.4
Backbone-Backbone	1898	16.3	732	38.6	6.3	211	11.1	1.8
Backbone-Sidechain	6397	55.1	2492	39.0	21.5	835	13.1	7.2
Sidechain-Sidechain	3314	28.5	1251	37.7	10.8	510	15.4	4.4

[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



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

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	698	731	508	1259	0	3196	3.03	42.83	5.88	1.25
2	662	738	496	1172	0	3068	2.08	23.19	2.89	1.18
3	665	749	480	1217	0	3111	2.84	34.85	5.22	1.2
4	708	739	530	1217	0	3194	2.18	24.75	2.91	1.27
5	698	739	492	1192	0	3121	2.06	23.38	2.75	1.2
6	677	751	496	1253	0	3177	3.03	40.58	5.7	1.22
7	675	748	508	1229	0	3160	2.79	40.14	4.99	1.23
8	670	740	502	1220	0	3132	2.14	24.6	3.01	1.24
9	673	728	539	1219	0	3159	2.15	24.0	2.94	1.21
10	681	752	465	1246	0	3144	3.05	38.47	5.73	1.25
11	692	740	497	1230	0	3159	2.69	34.45	4.6	1.22

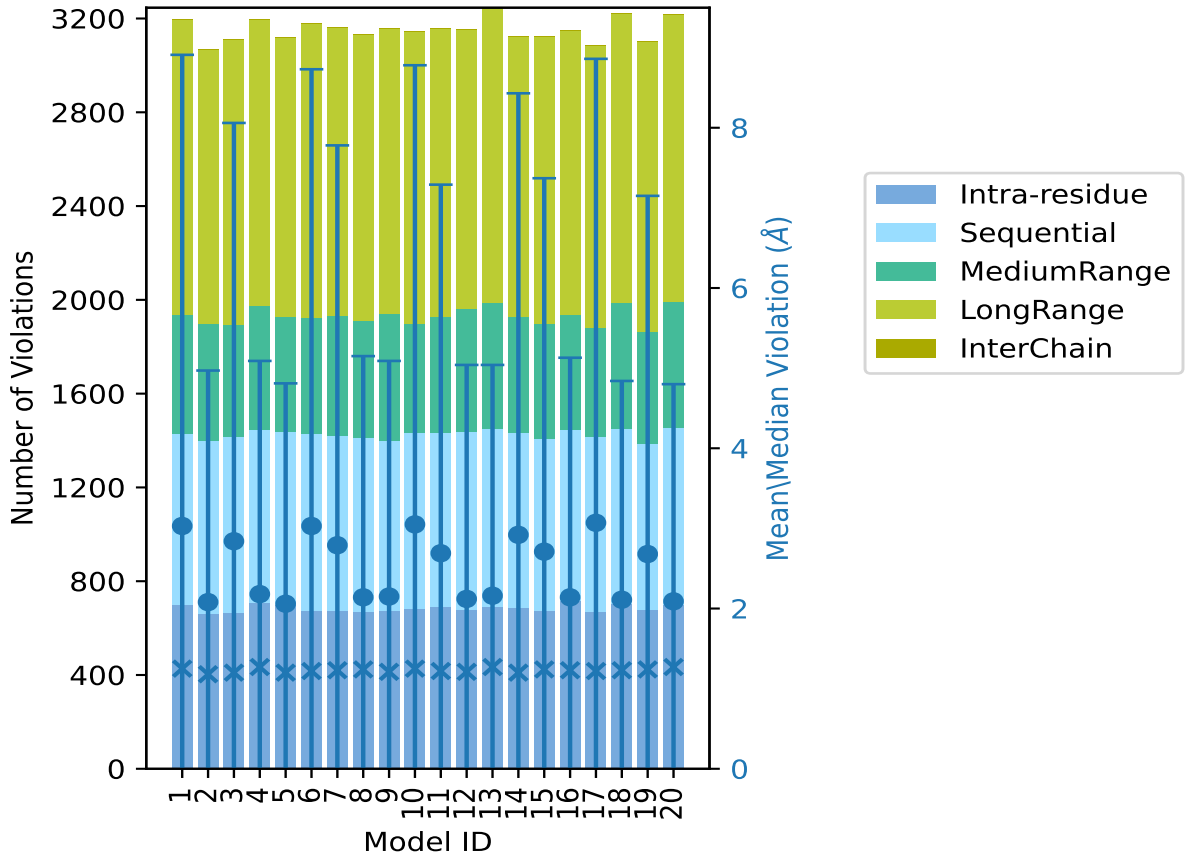
Continued on next page...

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	679	758	522	1194	0	3153	2.12	25.14	2.92	1.21
13	690	759	540	1257	0	3246	2.16	25.4	2.88	1.27
14	687	746	494	1196	0	3123	2.92	36.19	5.51	1.2
15	675	735	487	1228	0	3125	2.71	36.26	4.66	1.24
16	715	731	493	1208	0	3147	2.14	25.11	2.99	1.23
17	668	749	465	1202	0	3084	3.07	40.46	5.79	1.22
18	704	747	536	1235	0	3222	2.11	23.65	2.73	1.23
19	679	708	476	1241	0	3104	2.68	32.6	4.47	1.24
20	701	752	537	1226	0	3216	2.09	22.41	2.71	1.27

[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



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

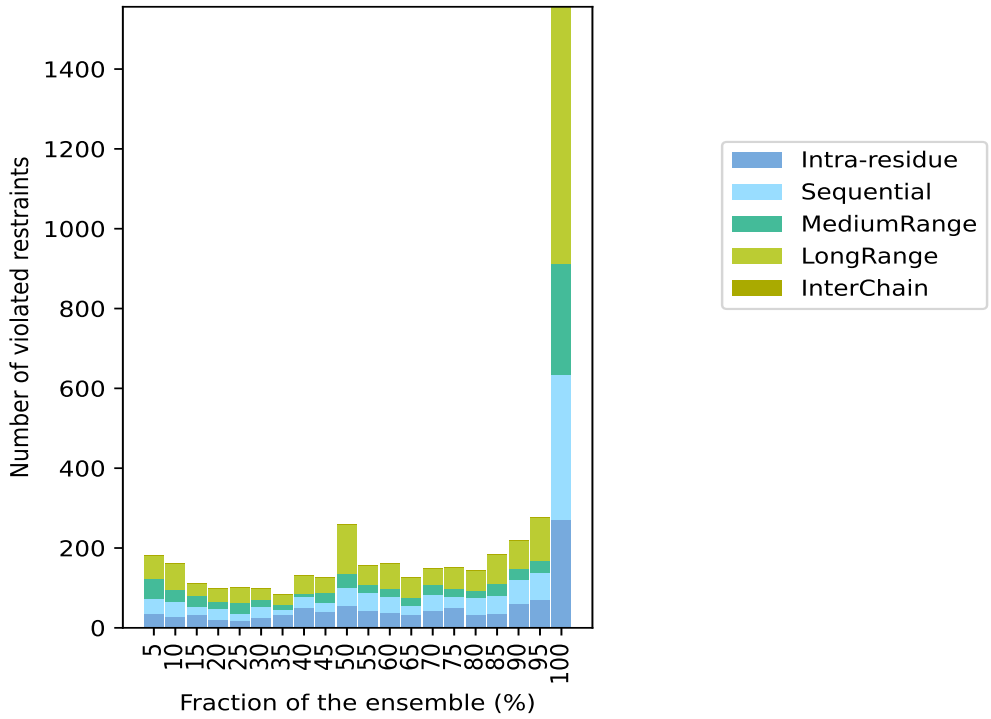
9.3 Distance violation statistics for the ensemble (i)

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, 7134(IR:1761, SQ:1967, MR:1262, LR:2144, 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]	%
36	36	50	60	0	182	1	5.0
27	37	32	66	0	162	2	10.0
32	22	26	32	0	112	3	15.0
19	27	20	33	0	99	4	20.0
16	20	27	38	0	101	5	25.0
24	30	16	29	0	99	6	30.0
32	14	13	24	0	83	7	35.0
49	30	6	46	0	131	8	40.0
41	22	24	40	0	127	9	45.0
55	47	33	125	0	260	10	50.0
42	47	19	49	0	157	11	55.0
38	40	20	62	0	160	12	60.0
31	25	21	48	0	125	13	65.0
44	38	27	39	0	148	14	70.0
51	26	21	53	0	151	15	75.0
32	44	16	51	0	143	16	80.0
36	43	30	75	0	184	17	85.0
60	61	27	70	0	218	18	90.0
70	67	32	108	0	277	19	95.0
272	361	280	643	0	1556	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

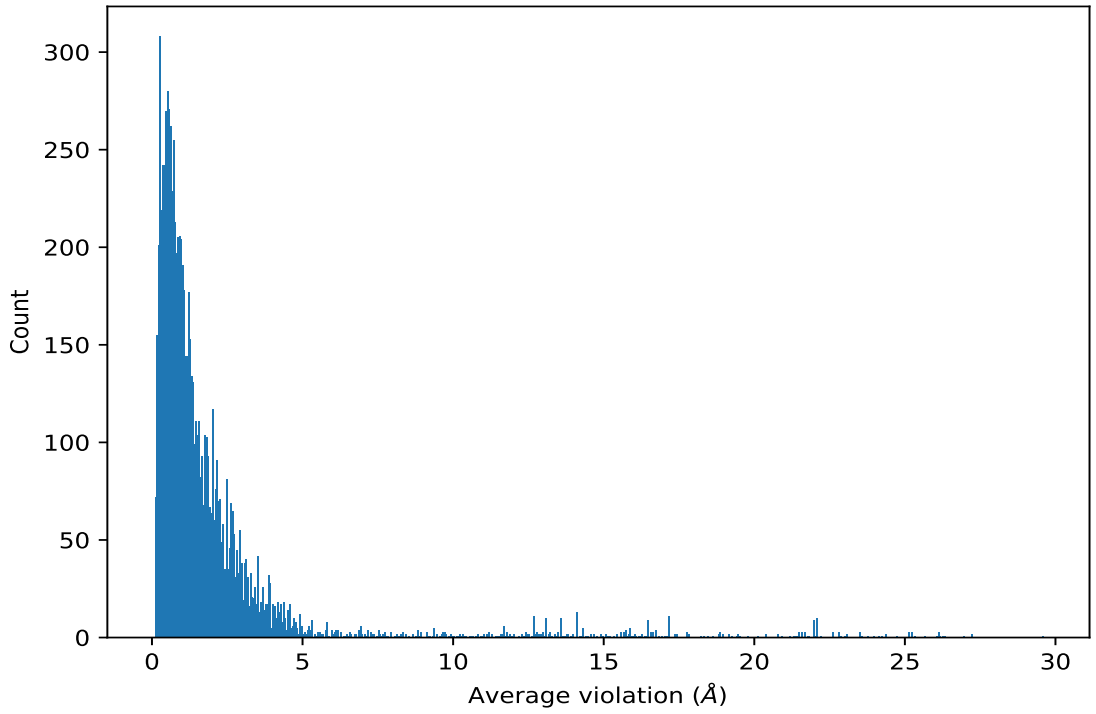
9.3.1 Bar graph : Distance violation statistics for the ensemble



9.4 Most violated distance restraints in the ensemble

9.4.1 Histogram : Distribution of mean distance violations

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.

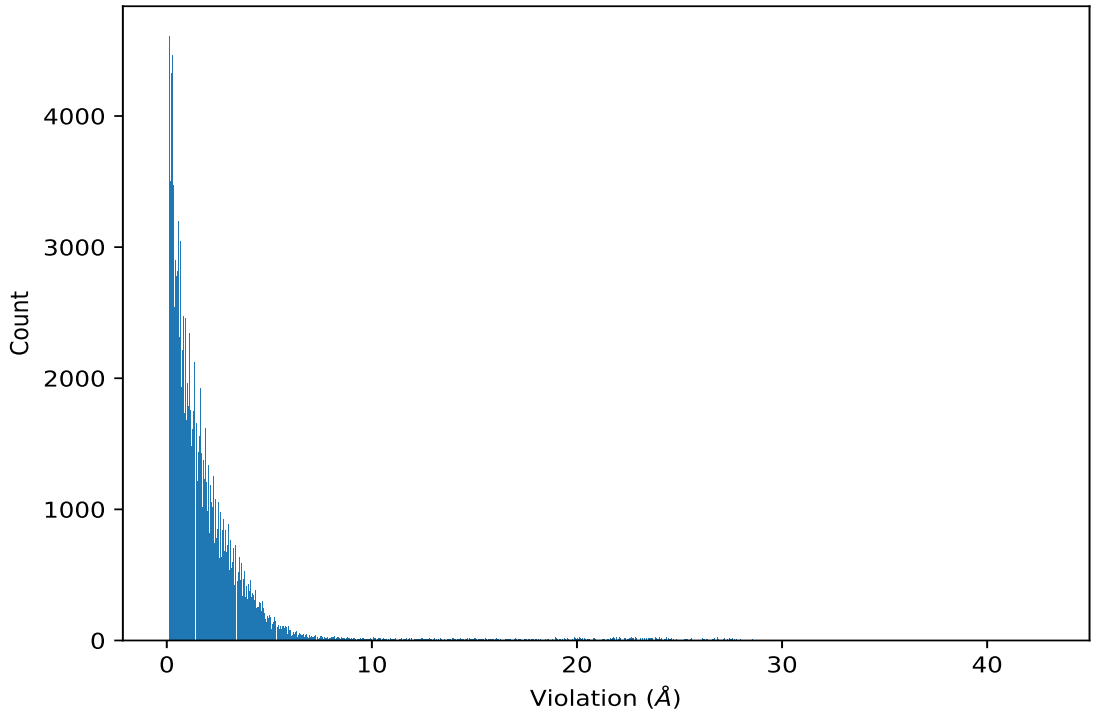
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(4,149)	1:A:98:SER:CB	1:A:10:GLY:H	20	20.9	12.56	18.42
(4,143)	1:A:98:SER:CB	1:A:2:ALA:H	20	19.5	10.25	16.81
(4,103)	1:A:90:ASN:CB	1:A:2:ALA:H	20	19.43	6.68	16.92
(4,109)	1:A:90:ASN:CB	1:A:10:GLY:H	20	19.15	11.37	17.74
(1,3465)	1:A:28:ILE:HG12	1:A:141:LEU:HG	20	18.84	16.72	18.05
(1,3461)	1:A:28:ILE:HG12	1:A:140:ALA:H	20	18.33	15.13	17.1
(4,164)	1:A:98:SER:CB	1:A:28:ILE:H	20	18.2	14.85	12.94
(4,166)	1:A:98:SER:CB	1:A:30:ASN:H	20	17.83	15.54	12.16
(4,165)	1:A:98:SER:CB	1:A:29:THR:H	20	17.44	15.34	11.56
(4,148)	1:A:98:SER:CB	1:A:7:LEU:H	20	17.38	10.57	15.62

[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)
(4,166)	1:A:98:SER:CB	1:A:30:ASN:H	1	42.83
(4,167)	1:A:98:SER:CB	1:A:31:ALA:H	1	42.69
(4,165)	1:A:98:SER:CB	1:A:29:THR:H	1	42.18
(4,164)	1:A:98:SER:CB	1:A:28:ILE:H	1	40.76
(4,166)	1:A:98:SER:CB	1:A:30:ASN:H	6	40.58
(4,166)	1:A:98:SER:CB	1:A:30:ASN:H	17	40.46
(1,3465)	1:A:28:ILE:HG12	1:A:141:LEU:HG	7	40.14
(4,164)	1:A:98:SER:CB	1:A:28:ILE:H	6	39.91
(4,162)	1:A:98:SER:CB	1:A:26:ASN:H	1	39.85
(4,167)	1:A:98:SER:CB	1:A:31:ALA:H	17	39.68

10 Dihedral-angle violation analysis (i)

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