wwPDB NMR Structure Validation Summary Report (i)

Jun 4, 2023 – 10:10 AM EDT

PDB ID	:	2N9I
BMRB ID	:	25907
Title	:	Solution structure of reduced human cytochrome c
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Deposited on	:	2015-11-24

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:

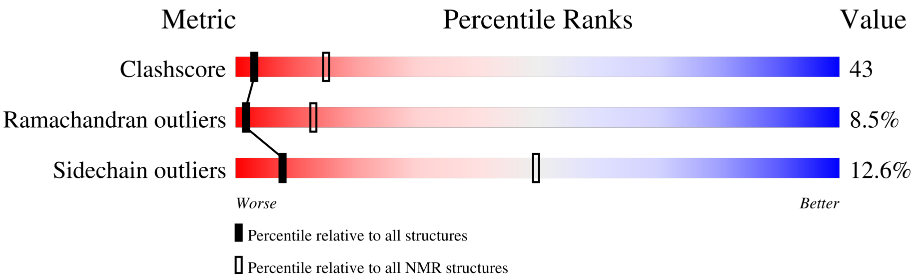
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints 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 94%.

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	104	

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:1-A:104 (104)	0.66	3

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 3 clusters. No single-model clusters were found.

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

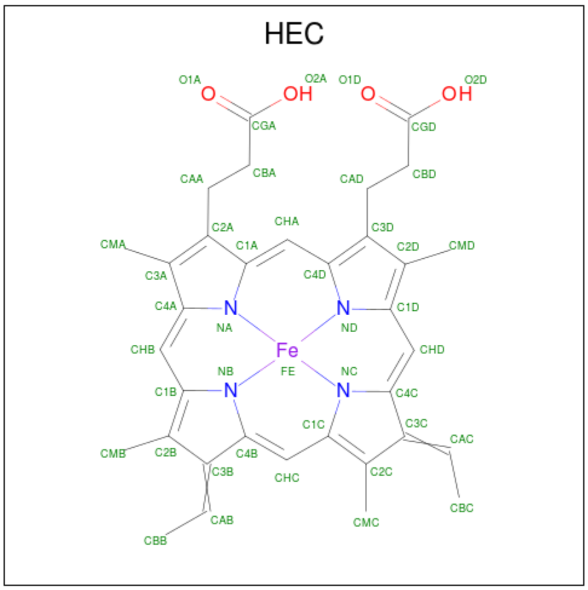
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1722 atoms, of which 864 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cytochrome c.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	104	1647	521	832	142	147	5	0

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



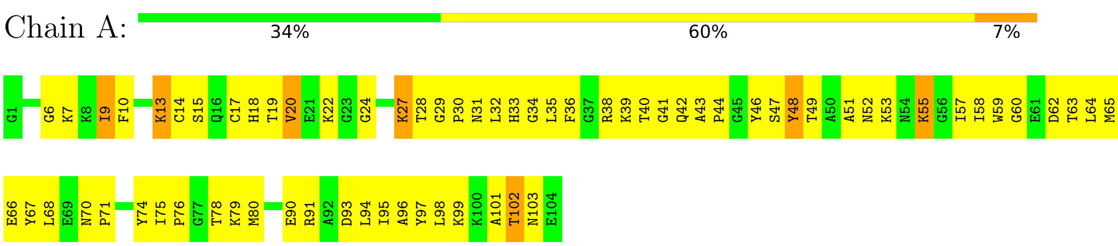
Mol	Chain	Residues	Atoms					
			Total	C	Fe	H	N	O
2	A	1	75	34	1	32	4	4

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.

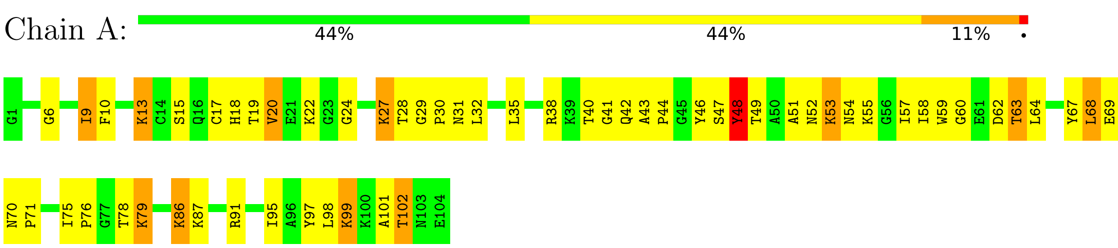
- Molecule 1: Cytochrome c



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

The representative model is number 3. Colouring as in section 4.1 above.

- Molecule 1: Cytochrome c



5 Refinement protocol and experimental data overview (i)

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

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**
TALOS+	refinement	
TALOS+	geometry optimization	
CYANA	structure solution	
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	1368
Number of shifts mapped to atoms	1368
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	94%

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: HEC

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	815	832	843	72±6
2	A	43	32	30	11±3
All	All	17160	17280	17460	1494

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 43.

5 of 519 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:PHE:CE2	1:A:98:LEU:HD21	1.08	1.82	14	15
1:A:10:PHE:CE1	1:A:98:LEU:HD21	1.02	1.90	10	7
1:A:10:PHE:CZ	1:A:98:LEU:HD21	0.97	1.95	15	9
1:A:10:PHE:CE1	1:A:20:VAL:HG13	0.96	1.96	11	7
1:A:35:LEU:HD21	2:A:500:HEC:HMA3	0.94	1.38	13	7

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	102/104 (98%)	68±3 (67±3%)	25±3 (25±3%)	9±2 (9±2%)	2	13
All	All	2040/2080 (98%)	1364 (67%)	502 (25%)	174 (9%)	2	13

5 of 29 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	27	LYS	20
1	A	24	GLY	19
1	A	48	TYR	19
1	A	55	LYS	19
1	A	20	VAL	17

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	85/85 (100%)	74±3 (87±4%)	11±3 (13±4%)	8	50
All	All	1700/1700 (100%)	1486 (87%)	214 (13%)	8	50

5 of 42 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	53	LYS	20
1	A	102	THR	17
1	A	17	CYS	15
1	A	13	LYS	14
1	A	99	LYS	12

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	HEC	A	500	1	32,50,50	0.94±0.01	2±0 (6±0%)

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	HEC	A	500	1	24,82,82	1.09±0.00	0±0 (2±2%)

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	HEC	A	500	1	-	0±0,10,54,54	-

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	500	HEC	C3C-C2C	2.43	1.38	1.40	12	20
2	A	500	HEC	C2B-C3B	2.25	1.38	1.40	10	20

All unique angle outliers are listed below.

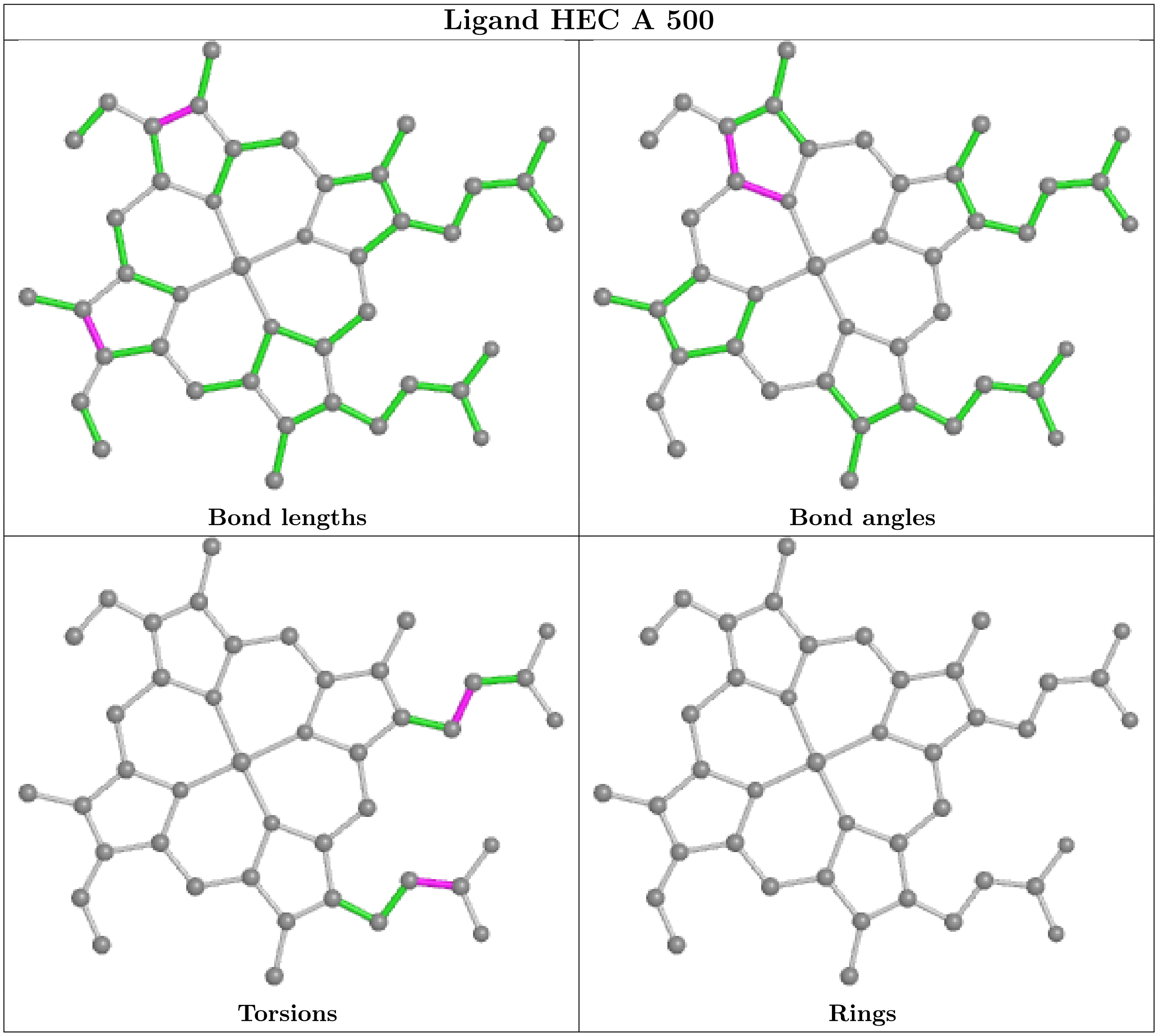
Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
2	A	500	HEC	C3B-C4B-NB	2.03	107.11	110.94	4	10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 94% for the well-defined parts and 94% 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	1368
Number of shifts mapped to atoms	1368
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	36

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	104	-0.35 ± 0.34	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	91	0.05 ± 0.14	None needed (< 0.5 ppm)
$^{13}C'$	95	-0.32 ± 0.30	None needed (< 0.5 ppm)
^{15}N	97	0.25 ± 0.79	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 94%, i.e. 1334 atoms were assigned a chemical shift out of a possible 1418. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	511/525 (97%)	215/217 (99%)	199/208 (96%)	97/100 (97%)
Sidechain	739/785 (94%)	499/506 (99%)	231/248 (93%)	9/31 (29%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	84/108 (78%)	46/53 (87%)	36/51 (71%)	2/4 (50%)
Overall	1334/1418 (94%)	760/776 (98%)	466/507 (92%)	108/135 (80%)

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	49	THR	HG1	8.79	0.08 – 2.19	36.2
1	A	78	THR	HG1	8.49	0.08 – 2.19	34.8
1	A	38	ARG	NE	121.28	76.53 – 92.65	22.8
1	A	91	ARG	NE	120.00	76.53 – 92.65	22.0
1	A	40	THR	HG1	4.89	0.08 – 2.19	17.8
1	A	80	MET	HG2	-3.74	0.65 – 4.19	-17.4
1	A	67	TYR	HE1	3.01	5.59 – 7.82	-16.6
1	A	63	THR	HG1	4.62	0.08 – 2.19	16.5
1	A	67	TYR	HE2	3.01	5.58 – 7.83	-16.4
1	A	18	HIS	HD2	0.12	4.65 – 9.35	-14.6
1	A	80	MET	HB2	-2.57	0.42 – 3.63	-14.3
1	A	80	MET	HE1	-3.28	-0.03 – 3.80	-13.5
1	A	80	MET	HE2	-3.28	-0.03 – 3.80	-13.5
1	A	80	MET	HE3	-3.28	-0.03 – 3.80	-13.5
1	A	18	HIS	HE1	0.51	5.13 – 10.76	-13.2
1	A	80	MET	HG3	-1.89	0.54 – 4.26	-11.5
1	A	29	GLY	HA2	-0.01	2.15 – 5.77	-11.0
1	A	67	TYR	CE1	132.09	111.24 – 124.66	10.5
1	A	55	LYS	HE2	1.29	1.95 – 3.88	-8.4
1	A	46	TYR	HD2	4.84	5.48 – 8.39	-7.2
1	A	30	PRO	HD2	1.21	1.93 – 5.38	-7.1
1	A	38	ARG	CZ	184.50	141.81 – 177.93	6.8
1	A	41	GLY	HA2	1.50	2.15 – 5.77	-6.8
1	A	82	PHE	HB2	0.56	1.20 – 4.80	-6.8
1	A	18	HIS	HB2	0.77	1.36 – 4.85	-6.7
1	A	80	MET	HB3	-0.23	0.33 – 3.66	-6.7
1	A	84	GLY	H	4.48	5.23 – 11.42	-6.2
1	A	71	PRO	HG2	0.10	0.41 – 3.45	-6.0
1	A	32	LEU	HD11	-0.78	-0.61 – 2.12	-5.6
1	A	32	LEU	HD12	-0.78	-0.61 – 2.12	-5.6
1	A	32	LEU	HD13	-0.78	-0.61 – 2.12	-5.6
1	A	22	LYS	HB2	0.50	0.58 – 2.97	-5.4

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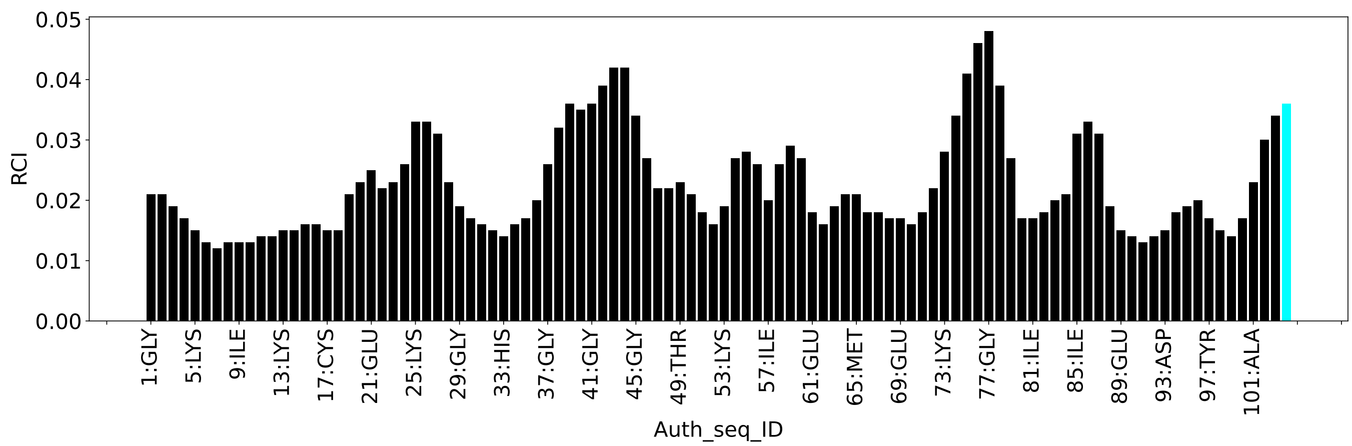
List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	46	TYR	HB2	0.98	1.09 – 4.72	-5.3
1	A	17	CYS	HB3	0.57	0.69 – 5.10	-5.3
1	A	18	HIS	HB3	1.10	1.18 – 4.91	-5.2
1	A	97	TYR	HE2	5.56	5.58 – 7.83	-5.1

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	1677
Intra-residue (|i-j|=0)	526
Sequential (|i-j|=1)	376
Medium range (|i-j|>1 and |i-j|<5)	292
Long range (|i-j|≥5)	483
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	7
Number of restraints per residue	16.1
Number of long range restraints per residue[1]	4.6

[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)	0.7	0.2
0.2-0.5 (Medium)	1.4	0.49
>0.5 (Large)	6.5	4.26

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)

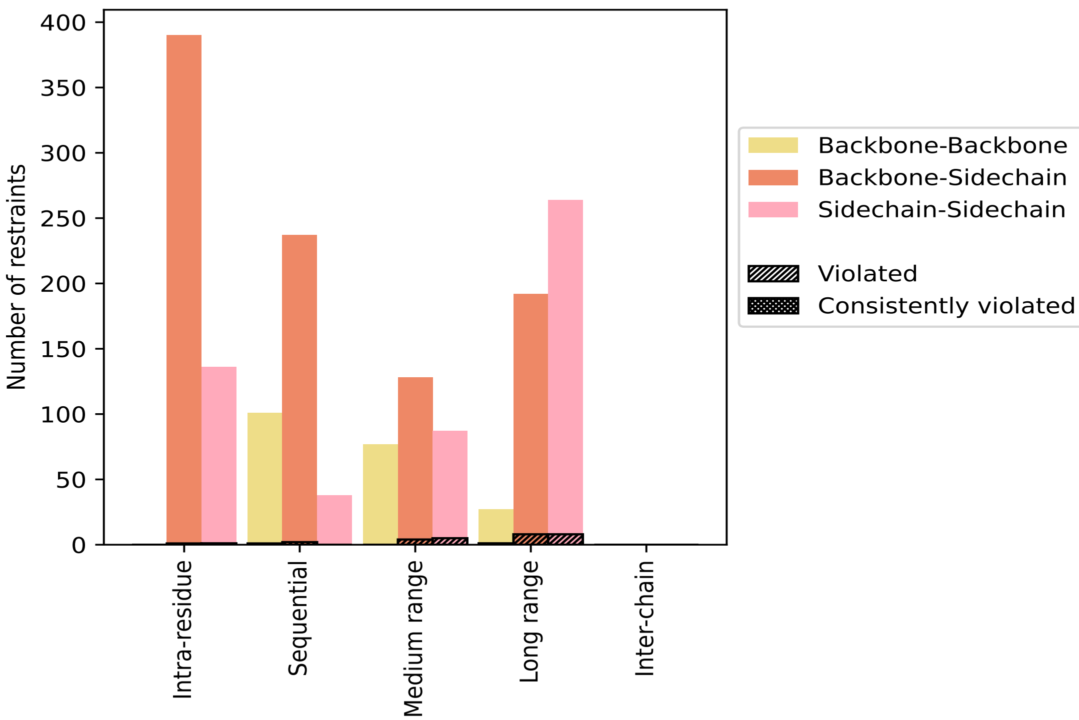
9.1 Summary of distance violations (i)

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)	526	31.4	2	0.4	0.1	1	0.2	0.1
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	390	23.3	1	0.3	0.1	0	0.0	0.0
Sidechain-Sidechain	136	8.1	1	0.7	0.1	1	0.7	0.1
Sequential (|i-j|=1)	376	22.4	3	0.8	0.2	0	0.0	0.0
Backbone-Backbone	101	6.0	1	1.0	0.1	0	0.0	0.0
Backbone-Sidechain	237	14.1	2	0.8	0.1	0	0.0	0.0
Sidechain-Sidechain	38	2.3	0	0.0	0.0	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	292	17.4	9	3.1	0.5	0	0.0	0.0
Backbone-Backbone	77	4.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	128	7.6	4	3.1	0.2	0	0.0	0.0
Sidechain-Sidechain	87	5.2	5	5.7	0.3	0	0.0	0.0
Long range (|i-j|≥5)	483	28.8	17	3.5	1.0	1	0.2	0.1
Backbone-Backbone	27	1.6	1	3.7	0.1	1	3.7	0.1
Backbone-Sidechain	192	11.4	8	4.2	0.5	0	0.0	0.0
Sidechain-Sidechain	264	15.7	8	3.0	0.5	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	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	1677	100.0	31	1.8	1.8	2	0.1	0.1
Backbone-Backbone	205	12.2	2	1.0	0.1	1	0.5	0.1
Backbone-Sidechain	947	56.5	15	1.6	0.9	0	0.0	0.0
Sidechain-Sidechain	525	31.3	14	2.7	0.8	1	0.2	0.1

[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	1	0	1	6	0	8	0.92	1.56	0.42	0.68
2	1	0	1	6	0	8	1.24	2.73	0.85	1.12
3	1	0	3	5	0	9	1.23	3.09	0.94	0.64
4	1	0	2	7	0	10	0.7	1.7	0.47	0.62
5	1	0	3	4	0	8	1.32	2.83	0.75	1.1
6	1	0	3	5	0	9	1.19	2.33	0.78	1.21
7	1	0	3	4	0	8	1.31	3.5	0.97	1.35
8	1	0	1	3	0	5	0.81	1.61	0.56	0.64
9	1	0	3	3	0	7	1.58	3.57	1.0	1.51
10	1	0	1	6	0	8	0.97	1.75	0.57	0.92
11	1	0	1	2	0	4	0.71	1.06	0.23	0.68

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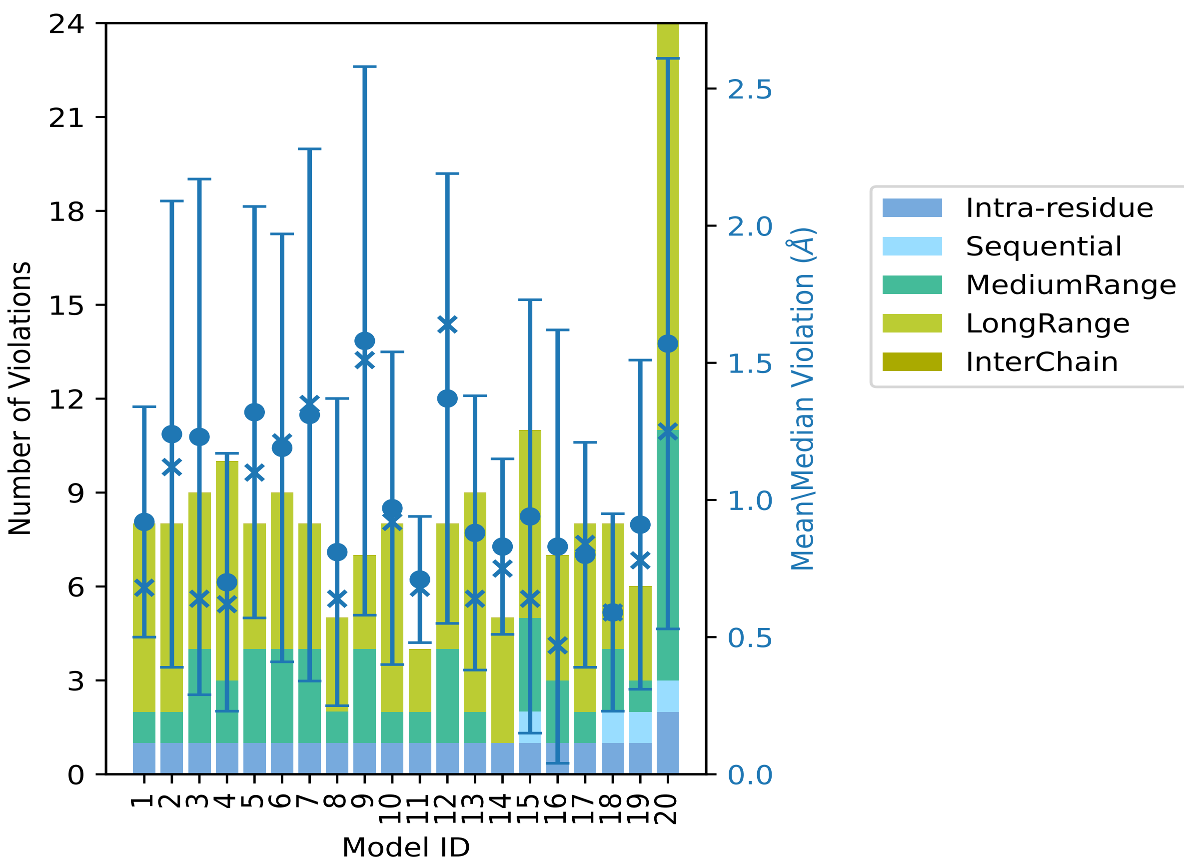
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	1	0	3	4	0	8	1.37	2.62	0.82	1.64
13	1	0	1	7	0	9	0.88	1.8	0.5	0.64
14	1	0	0	4	0	5	0.83	1.22	0.32	0.75
15	1	1	3	6	0	11	0.94	2.72	0.79	0.64
16	1	0	2	4	0	7	0.83	2.58	0.79	0.47
17	1	0	1	6	0	8	0.8	1.31	0.41	0.84
18	1	1	2	4	0	8	0.59	1.22	0.36	0.59
19	1	1	1	3	0	6	0.91	2.12	0.6	0.78
20	2	1	8	13	0	24	1.57	4.26	1.04	1.25

[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

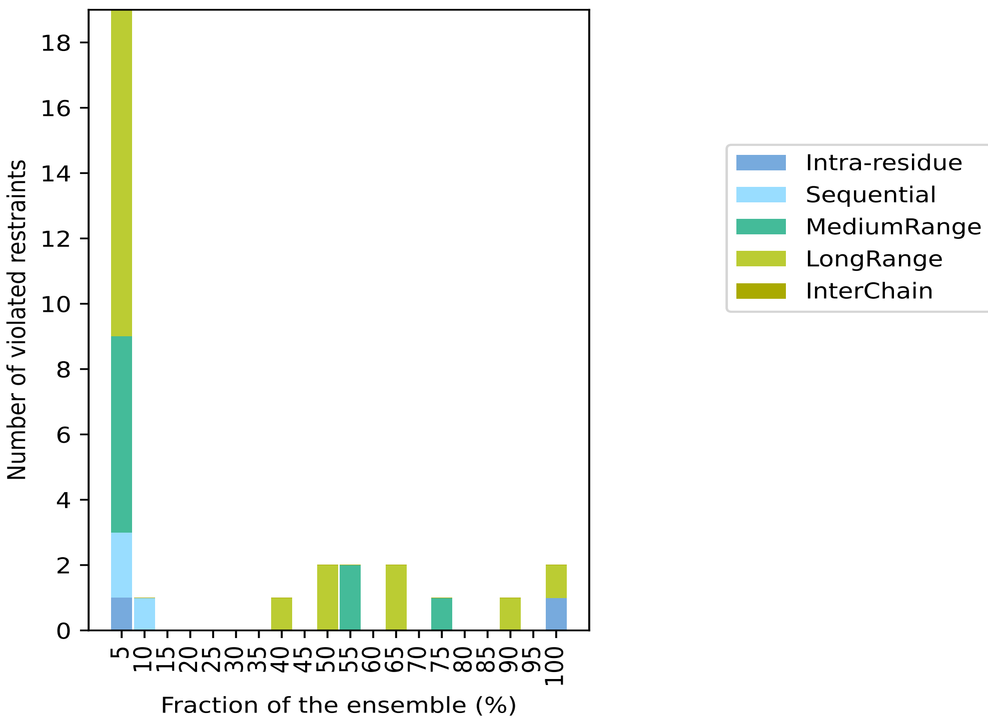
9.3 Distance violation statistics for the ensemble (i)

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, 1646(IR:524, SQ:373, MR:283, LR:466, 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	2	6	10	0	19	1	5.0
0	1	0	0	0	1	2	10.0
0	0	0	0	0	0	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	7	35.0
0	0	0	1	0	1	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	2	0	2	10	50.0
0	0	2	0	0	2	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	2	0	2	13	65.0
0	0	0	0	0	0	14	70.0
0	0	1	0	0	1	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	1	0	1	18	90.0
0	0	0	0	0	0	19	95.0
1	0	0	1	0	2	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

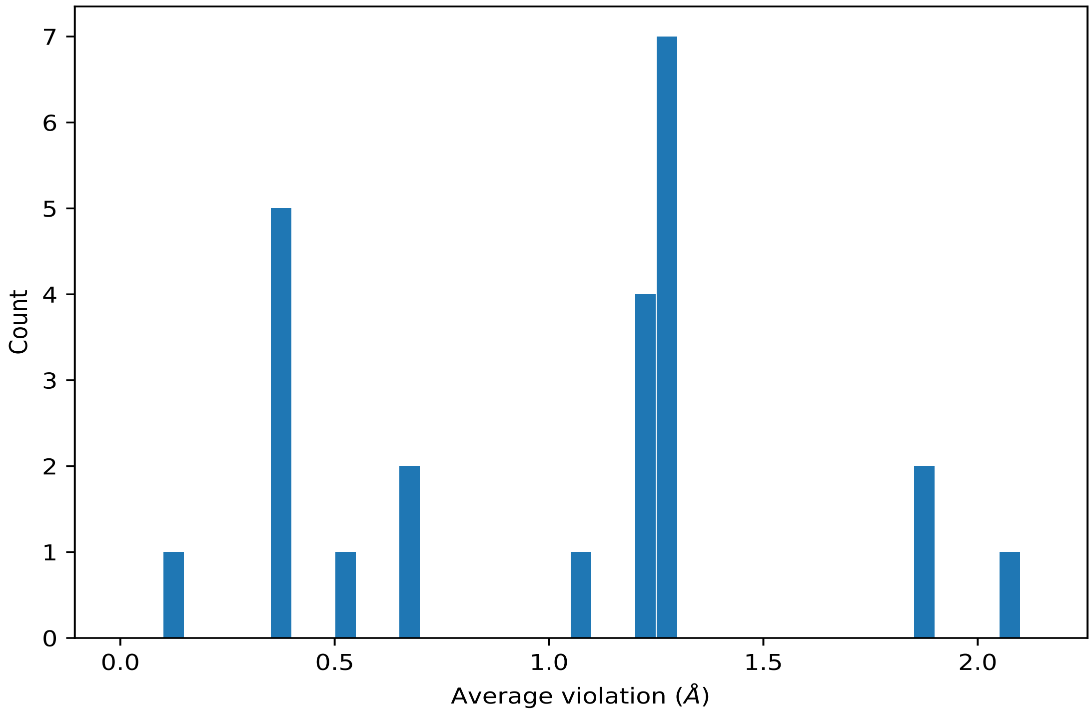
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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)
(1,852)	1:A:38:ARG:HD2	1:A:38:ARG:HH22	20	0.65	0.04	0.64
(1,852)	1:A:38:ARG:HD3	1:A:38:ARG:HH22	20	0.65	0.04	0.64
(1,1014)	1:A:41:GLY:HA2	1:A:53:LYS:HA	20	0.5	0.23	0.48
(1,1220)	1:A:41:GLY:HA3	1:A:48:TYR:HD1	18	1.25	0.16	1.27
(1,1397)	1:A:35:LEU:HD11	1:A:38:ARG:HH22	15	1.25	0.52	1.21
(1,1397)	1:A:35:LEU:HD12	1:A:38:ARG:HH22	15	1.25	0.52	1.21
(1,1397)	1:A:35:LEU:HD13	1:A:38:ARG:HH22	15	1.25	0.52	1.21
(1,1397)	1:A:35:LEU:HD21	1:A:38:ARG:HH22	15	1.25	0.52	1.21
(1,1397)	1:A:35:LEU:HD22	1:A:38:ARG:HH22	15	1.25	0.52	1.21
(1,1397)	1:A:35:LEU:HD23	1:A:38:ARG:HH22	15	1.25	0.52	1.21
(1,876)	1:A:32:LEU:HA	1:A:38:ARG:HH22	13	2.09	1.03	2.33
(1,859)	1:A:41:GLY:HA2	1:A:53:LYS:HB2	13	0.39	0.19	0.44
(1,859)	1:A:41:GLY:HA2	1:A:53:LYS:HB3	13	0.39	0.19	0.44
(1,1387)	1:A:34:GLY:HA2	1:A:38:ARG:HH22	11	1.89	0.51	1.99
(1,1387)	1:A:34:GLY:HA3	1:A:38:ARG:HH22	11	1.89	0.51	1.99
(1,944)	1:A:35:LEU:HA	1:A:38:ARG:HH22	11	1.21	0.64	1.38

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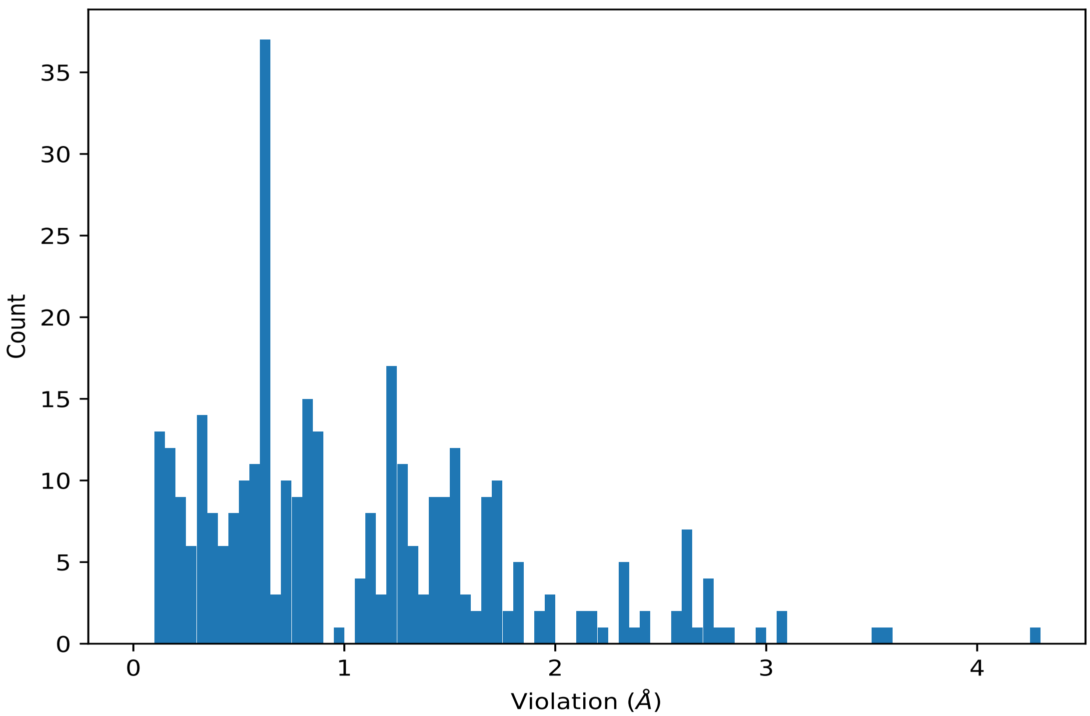
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,564)	1:A:38:ARG:HH22	1:A:43:ALA:HB1	10	1.2	0.73	1.1
(1,564)	1:A:38:ARG:HH22	1:A:43:ALA:HB2	10	1.2	0.73	1.1
(1,564)	1:A:38:ARG:HH22	1:A:43:ALA:HB3	10	1.2	0.73	1.1
(1,871)	1:A:38:ARG:HH22	1:A:43:ALA:HA	10	1.09	0.69	1.09

[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)
(1,1126)	1:A:44:PRO:HA	1:A:48:TYR:HE2	20	4.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,876)	1:A:32:LEU:HA	1:A:38:ARG:HH22	9	3.57
(1,876)	1:A:32:LEU:HA	1:A:38:ARG:HH22	7	3.5
(1,876)	1:A:32:LEU:HA	1:A:38:ARG:HH22	3	3.09
(1,1102)	1:A:48:TYR:HE1	2:A:500:HEC:HBA2	20	3.08
(1,1221)	1:A:48:TYR:HD1	1:A:52:ASN:HA	20	2.95
(1,876)	1:A:32:LEU:HA	1:A:38:ARG:HH22	5	2.83
(1,24)	1:A:48:TYR:HE1	1:A:52:ASN:HD21	20	2.79
(1,564)	1:A:38:ARG:HH22	1:A:43:ALA:HB1	2	2.73
(1,564)	1:A:38:ARG:HH22	1:A:43:ALA:HB2	2	2.73
(1,564)	1:A:38:ARG:HH22	1:A:43:ALA:HB3	2	2.73
(1,876)	1:A:32:LEU:HA	1:A:38:ARG:HH22	15	2.72

10 Dihedral-angle violation analysis (i)

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