



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2L75 / pdb_00002l75
BMRB ID : 17344
Title : Solution structure of CHD4-PHD2 in complex with H3K9me3
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This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

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with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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)	:	2.49

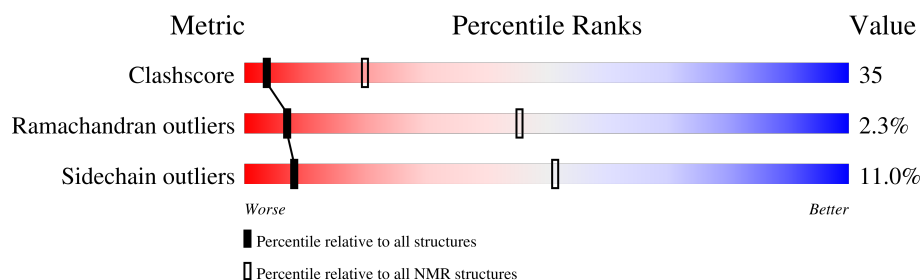
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 85%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	61	
2	B	14	

2 Ensemble composition and analysis

This entry contains 20 models. Model 8 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:89-A:135, B:145-B:151 (54)	0.39	8

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 and 2 single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1033 atoms, of which 510 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Chromodomain-helicase-DNA-binding protein 4.

Mol	Chain	Residues	Atoms						Trace
1	A	56	Total	C	H	N	O	S	0
			838	268	406	76	78	10	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	GLY	-	expression tag	UNP Q14839
A	83	PRO	-	expression tag	UNP Q14839
A	84	LEU	-	expression tag	UNP Q14839
A	85	GLY	-	expression tag	UNP Q14839
A	86	SER	-	expression tag	UNP Q14839

- Molecule 2 is a protein called 14-meric peptide from 1Histone H3.1.

Mol	Chain	Residues	Atoms					Trace
2	B	11	Total	C	H	N	O	0
			193	53	104	20	16	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	157	TYR	-	SEE REMARK 999	UNP P68431

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

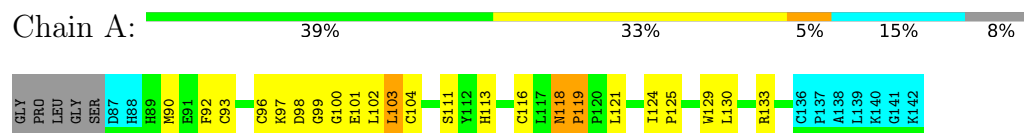
Mol	Chain	Residues	Atoms	
3	A	2	Total	Zn
			2	2

4 Residue-property plots [i](#)

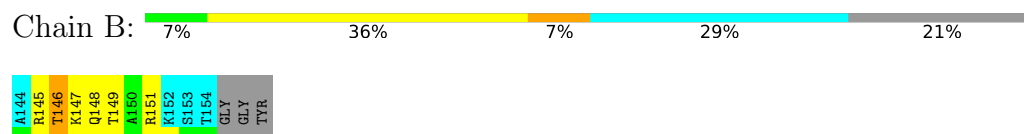
4.1 Average score per residue in the NMR ensemble

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: Chromodomain-helicase-DNA-binding protein 4



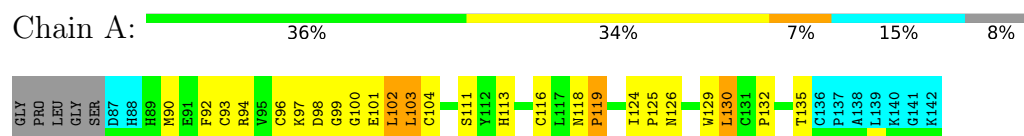
- Molecule 2: 14-meric peptide from 1Histone H3.1



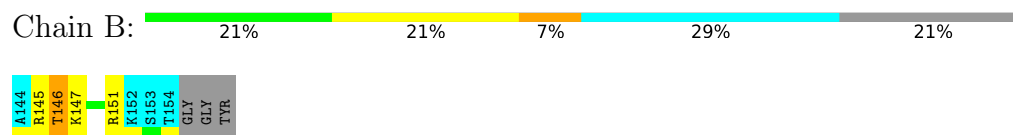
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 8. Colouring as in section 4.1 above.

- Molecule 1: Chromodomain-helicase-DNA-binding protein 4



- Molecule 2: 14-meric peptide from 1Histone H3.1



5 Refinement protocol and experimental data overview

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

Of the 1000 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
ARIA	structure solution	
ARIA	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	793
Number of shifts mapped to atoms	741
Number of unparsed shifts	0
Number of shifts with mapping errors	52
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, M3L

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	365	337	335	28±4
2	B	59	66	66	13±2
All	All	8520	8060	8020	576

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 35.

5 of 125 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:104:CYS:HB2	2:B:145:ARG:HB2	1.01	1.32	3	1
1:A:104:CYS:HB3	2:B:145:ARG:HB3	0.96	1.37	17	13
1:A:118:ASN:HB3	1:A:119:PRO:HD2	0.90	1.42	14	1
1:A:100:GLY:HA2	2:B:151:ARG:HD2	0.89	1.41	12	15
1:A:104:CYS:HB2	2:B:145:ARG:HB3	0.83	1.47	18	5

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	47/61 (77%)	41±1 (86±3%)	6±2 (12±4%)	1±1 (1±1%)	11	57
2	B	7/14 (50%)	4±1 (60±14%)	2±1 (32±13%)	1±1 (8±10%)	1	14
All	All	1080/1500 (72%)	897 (83%)	158 (15%)	25 (2%)	7	45

5 of 6 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	119	PRO	12
2	B	145	ARG	6
2	B	148	GLN	3
2	B	149	THR	2
1	A	89	HIS	1

6.3.2 Protein sidechains

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	44/54 (81%)	40±1 (91±2%)	4±1 (9±2%)	11	56
2	B	6/9 (67%)	5±1 (77±11%)	1±1 (23±11%)	2	27
All	All	1000/1260 (79%)	890 (89%)	110 (11%)	8	51

5 of 17 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	103	LEU	20
2	B	146	THR	20

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Mol	Chain	Res	Type	Models (Total)
1	A	130	LEU	19
1	A	118	ASN	10
1	A	102	LEU	9

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue 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	M3L	B	152	2	10,11,12	0.69±0.03	0±0 (0±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	M3L	B	152	2	9,14,16	0.45±0.05	0±0 (0±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	M3L	B	152	2	-	0±0,9,10,12	-

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 85% for the well-defined parts and 84% 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	793
Number of shifts mapped to atoms	741
Number of unparsed shifts	0
Number of shifts with mapping errors	52
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

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 52) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	82	GLY	HA2	3.97	0.005	2
1	A	82	GLY	HA3	3.981	0.005	2
1	A	82	GLY	CA	43.506	0.000	1
1	A	83	PRO	HA	4.48	0.002	1
1	A	83	PRO	HB2	2.304	0.006	2
1	A	83	PRO	HB3	1.945	0.002	2
1	A	83	PRO	HD2	3.57	0.006	2
1	A	83	PRO	HD3	3.57	0.006	2
1	A	83	PRO	HG2	1.989	0.018	2
1	A	83	PRO	HG3	1.989	0.018	2
1	A	83	PRO	C	176.981	0.000	1
1	A	83	PRO	CA	63.144	0.043	1
1	A	83	PRO	CB	32.339	0.020	1
1	A	83	PRO	CD	49.579	0.062	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	83	PRO	CG	27.105	0.048	1
1	A	84	LEU	H	8.507	0.005	1
1	A	84	LEU	HA	4.372	0.004	1
1	A	84	LEU	HB2	1.665	0.003	2
1	A	84	LEU	HB3	1.572	0.004	2
1	A	84	LEU	HD11	0.886	0.012	.
1	A	84	LEU	HD12	0.886	0.012	.
1	A	84	LEU	HD13	0.886	0.012	.
1	A	84	LEU	HD21	0.844	0.004	.
1	A	84	LEU	HD22	0.844	0.004	.
1	A	84	LEU	HD23	0.844	0.004	.
1	A	84	LEU	HG	1.642	0.011	1
1	A	84	LEU	C	177.939	0.000	1
1	A	84	LEU	CA	55.206	0.062	1
1	A	84	LEU	CB	42.459	0.003	1
1	A	84	LEU	CD1	24.855	0.014	2
1	A	84	LEU	CD2	23.461	0.039	2
1	A	84	LEU	CG	27.042	0.053	1
1	A	84	LEU	N	122.453	0.037	1
1	A	85	GLY	H	8.42	0.002	1
1	A	85	GLY	HA2	4.018	0.002	2
1	A	85	GLY	HA3	4.018	0.002	2
1	A	85	GLY	CA	45.177	0.087	1
1	A	85	GLY	N	110.001	0.046	1
1	A	86	SER	H	8.333	0.005	1
1	A	86	SER	HA	4.465	0.022	1
1	A	86	SER	HB2	3.83	0.010	2
1	A	86	SER	HB3	3.745	0.012	2
1	A	86	SER	CA	58.42	0.130	1
1	A	86	SER	CB	63.913	0.094	1
1	A	86	SER	N	116.008	0.051	1
1	B	156	GLY	H	8.175	0.002	1
1	B	156	GLY	HA2	3.857	0.002	2
1	B	156	GLY	HA3	3.857	0.002	2
1	B	157	TYR	H	7.574	0.001	1
1	B	157	TYR	HA	4.379	0.003	1
1	B	157	TYR	HB2	3.056	0.001	2
1	B	157	TYR	HB3	2.843	0.004	2

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	61	-0.11 ± 0.40	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	54	-0.31 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}'$	54	0.24 ± 0.27	None needed (< 0.5 ppm)
^{15}N	51	-0.73 ± 0.38	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 85%, i.e. 608 atoms were assigned a chemical shift out of a possible 715. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	237/261 (91%)	104/105 (99%)	92/108 (85%)	41/48 (85%)
Sidechain	332/399 (83%)	236/258 (91%)	94/124 (76%)	2/17 (12%)
Aromatic	39/55 (71%)	20/27 (74%)	13/21 (62%)	6/7 (86%)
Overall	608/715 (85%)	360/390 (92%)	199/253 (79%)	49/72 (68%)

7.1.4 Statistically unusual chemical shifts [i](#)

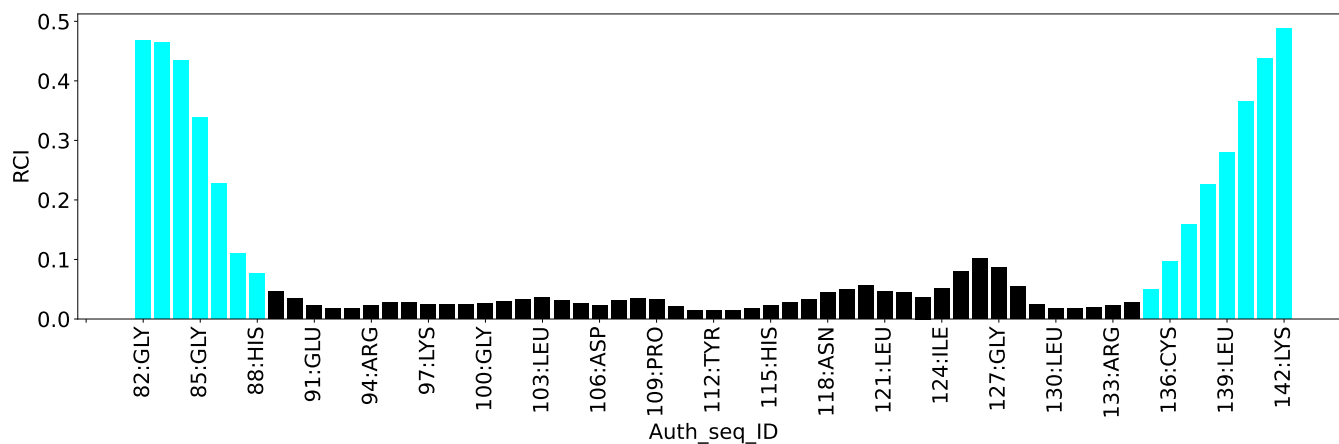
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	103	LEU	HD11	-0.78	-0.61 – 2.12	-5.6
1	A	103	LEU	HD12	-0.78	-0.61 – 2.12	-5.6
1	A	103	LEU	HD13	-0.78	-0.61 – 2.12	-5.6

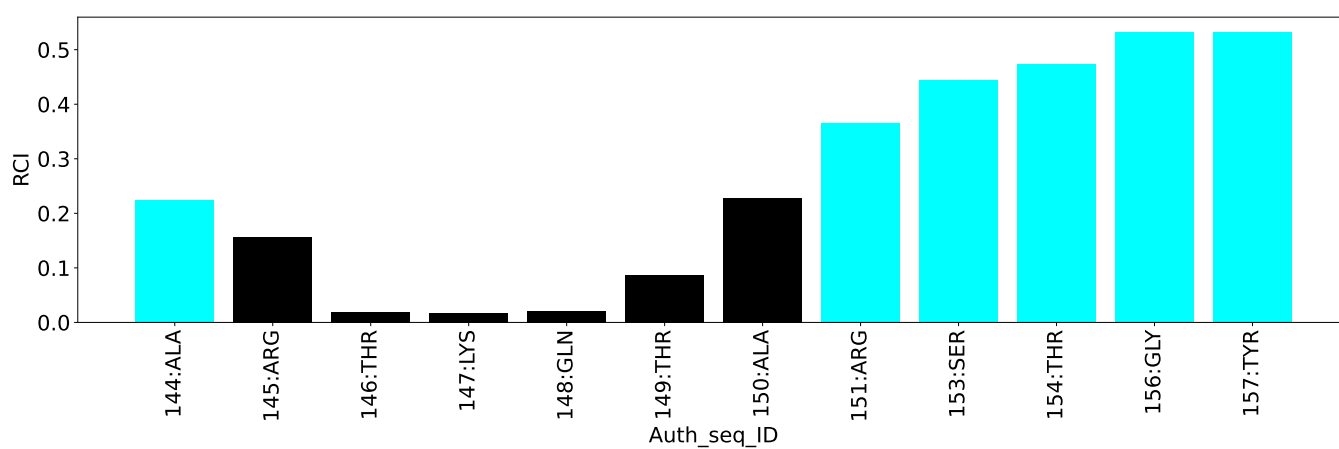
7.1.5 Random Coil Index (RCI) plots [i](#)

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:



Random coil index (RCI) for chain B:



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	1006
Intra-residue ($ i-j =0$)	178
Sequential ($ i-j =1$)	271
Medium range ($ i-j >1$ and $ i-j <5$)	143
Long range ($ i-j \geq 5$)	292
Inter-chain	122
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	11
Number of restraints per residue	13.1
Number of long range restraints per residue ¹	3.8

¹Long 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)	32.5	0.2
0.2-0.5 (Medium)	52.6	0.5
>0.5 (Large)	81.0	5.3

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 ⓘ

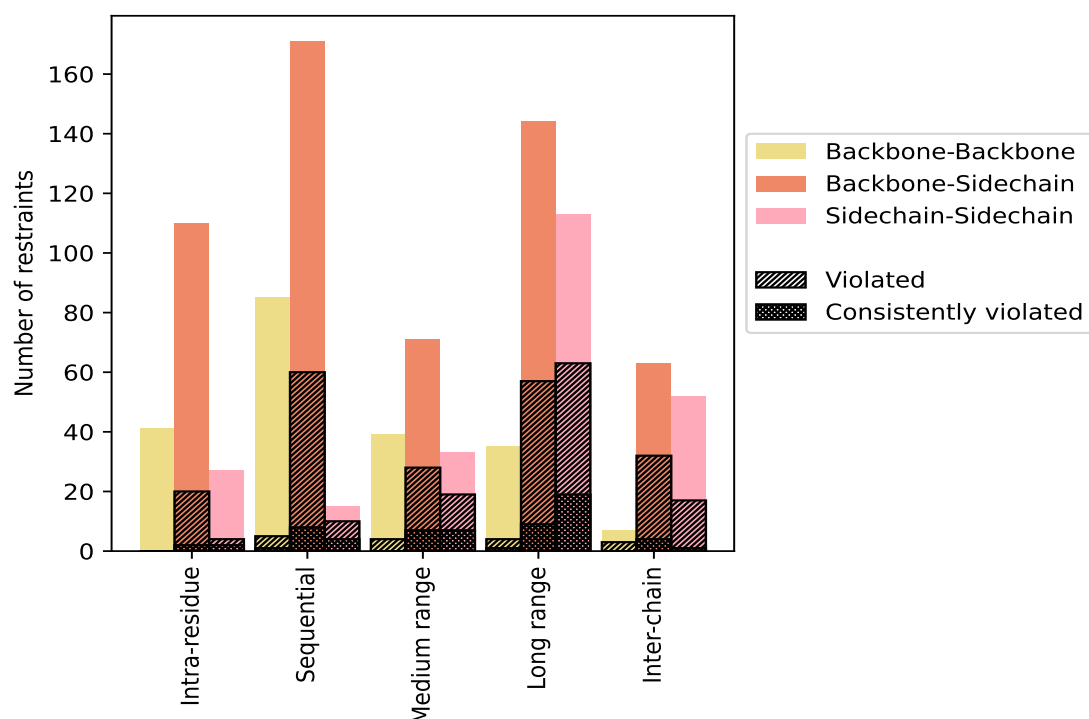
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	178	17.7	24	13.5	2.4	4	2.2	0.4
Backbone-Backbone	41	4.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	110	10.9	20	18.2	2.0	2	1.8	0.2
Sidechain-Sidechain	27	2.7	4	14.8	0.4	2	7.4	0.2
Sequential ($i-j =1$)	271	26.9	75	27.7	7.5	13	4.8	1.3
Backbone-Backbone	85	8.4	5	5.9	0.5	1	1.2	0.1
Backbone-Sidechain	171	17.0	60	35.1	6.0	8	4.7	0.8
Sidechain-Sidechain	15	1.5	10	66.7	1.0	4	26.7	0.4
Medium range ($i-j >1$ & $i-j <5$)	143	14.2	51	35.7	5.1	14	9.8	1.4
Backbone-Backbone	39	3.9	4	10.3	0.4	0	0.0	0.0
Backbone-Sidechain	71	7.1	28	39.4	2.8	7	9.9	0.7
Sidechain-Sidechain	33	3.3	19	57.6	1.9	7	21.2	0.7
Long range ($i-j \geq 5$)	292	29.0	124	42.5	12.3	29	9.9	2.9
Backbone-Backbone	35	3.5	4	11.4	0.4	1	2.9	0.1
Backbone-Sidechain	144	14.3	57	39.6	5.7	9	6.2	0.9
Sidechain-Sidechain	113	11.2	63	55.8	6.3	19	16.8	1.9
Inter-chain	122	12.1	52	42.6	5.2	5	4.1	0.5
Backbone-Backbone	7	0.7	3	42.9	0.3	0	0.0	0.0
Backbone-Sidechain	63	6.3	32	50.8	3.2	4	6.3	0.4
Sidechain-Sidechain	52	5.2	17	32.7	1.7	1	1.9	0.1
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	1006	100.0	326	32.4	32.4	65	6.5	6.5
Backbone-Backbone	207	20.6	16	7.7	1.6	2	1.0	0.2
Backbone-Sidechain	559	55.6	197	35.2	19.6	30	5.4	3.0
Sidechain-Sidechain	240	23.9	113	47.1	11.2	33	13.8	3.3

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	14	38	32	76	26	186	0.9	4.0	0.9	0.52
2	15	37	34	78	22	186	1.02	4.79	0.98	0.63
3	11	37	38	66	23	175	0.78	3.63	0.77	0.47
4	9	33	26	62	20	150	0.8	3.82	0.8	0.48
5	12	36	29	66	24	167	0.81	4.18	0.82	0.47
6	14	43	27	68	22	174	0.82	5.06	0.9	0.46
7	11	37	28	61	23	160	0.84	5.3	0.93	0.42
8	9	38	27	56	20	150	0.6	3.15	0.59	0.38
9	12	37	29	62	24	164	0.8	4.11	0.82	0.45
10	10	38	27	60	22	157	0.78	3.84	0.77	0.45

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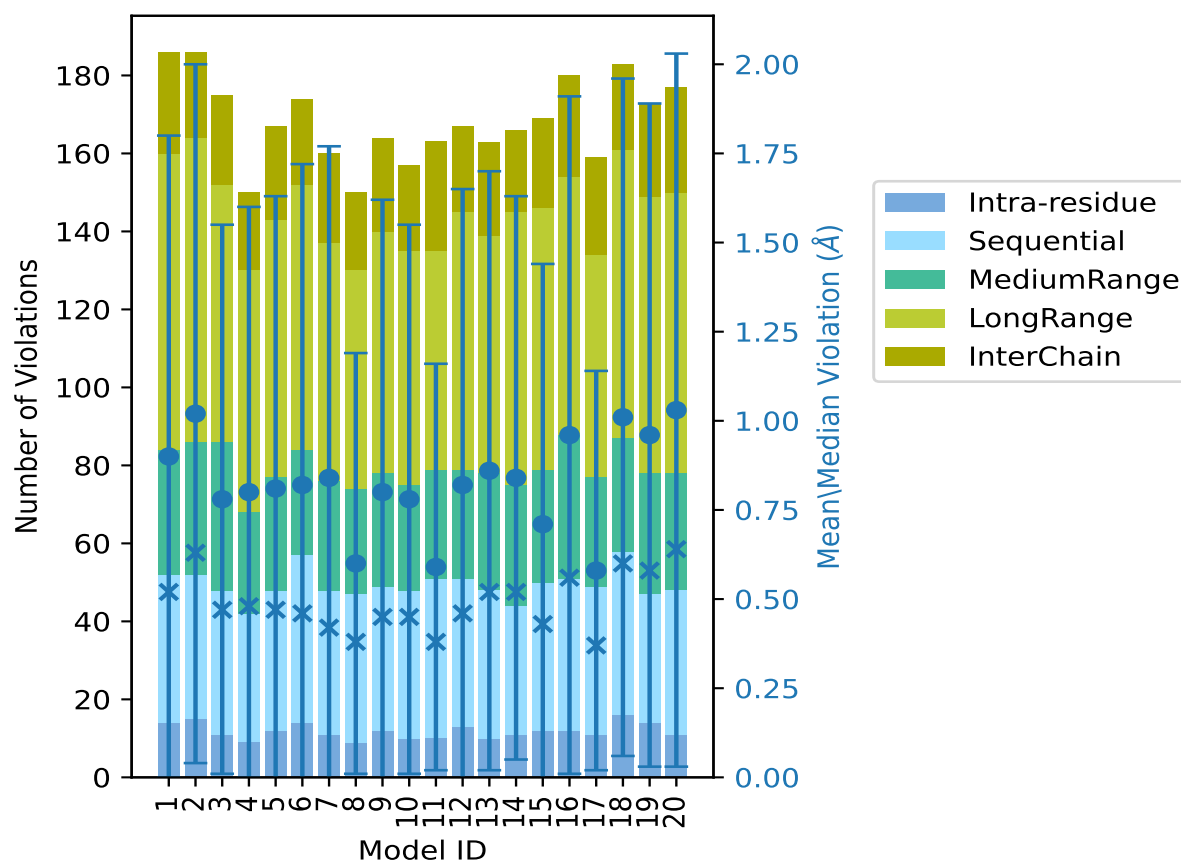
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	10	41	28	56	28	163	0.59	3.15	0.57	0.38
12	13	38	28	66	22	167	0.82	3.98	0.83	0.46
13	10	38	30	61	24	163	0.86	3.74	0.84	0.52
14	11	33	31	70	21	166	0.84	4.1	0.79	0.52
15	12	38	29	67	23	169	0.71	3.76	0.73	0.43
16	12	39	37	66	26	180	0.96	4.34	0.95	0.56
17	11	38	28	57	25	159	0.58	2.86	0.56	0.37
18	16	42	29	74	22	183	1.01	4.06	0.95	0.6
19	14	33	31	71	24	173	0.96	3.98	0.93	0.58
20	11	37	30	72	27	177	1.03	4.91	1.0	0.64

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints,

⁵Inter-chain restraints, ⁶Standard 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

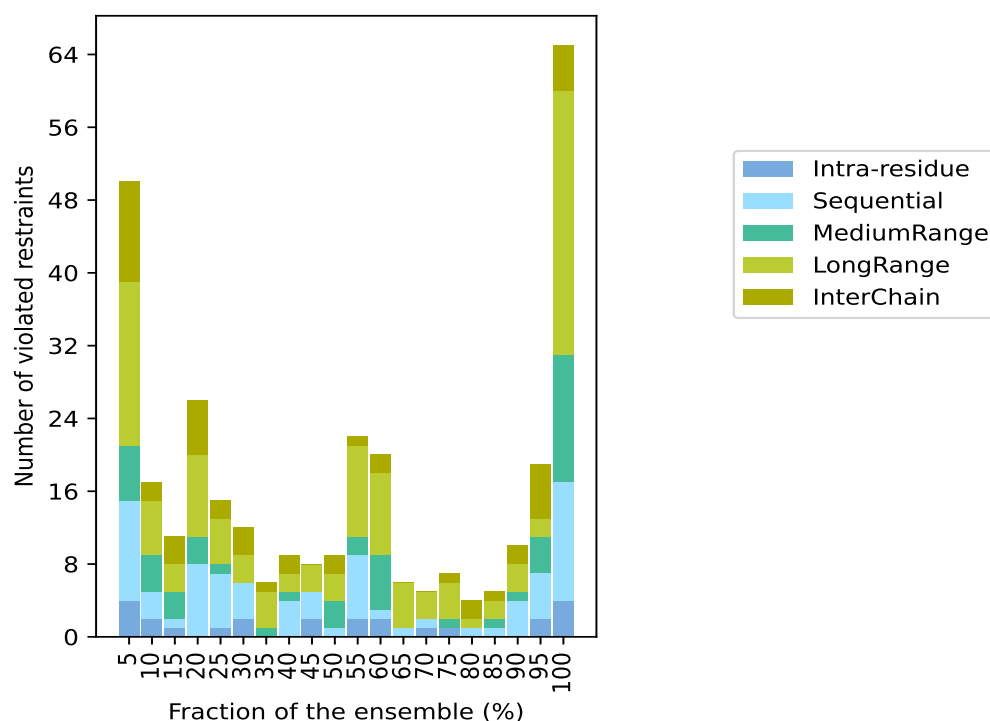
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 680(IR:154, SQ:196, MR:92, LR:168, IC:70) restraints are 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	%
4	11	6	18	11	50	1	5.0
2	3	4	6	2	17	2	10.0
1	1	3	3	3	11	3	15.0
0	8	3	9	6	26	4	20.0
1	6	1	5	2	15	5	25.0
2	4	0	3	3	12	6	30.0
0	0	1	4	1	6	7	35.0
0	4	1	2	2	9	8	40.0
2	3	0	3	0	8	9	45.0
0	1	3	3	2	9	10	50.0
2	7	2	10	1	22	11	55.0
2	1	6	9	2	20	12	60.0
0	1	0	5	0	6	13	65.0
1	1	0	3	0	5	14	70.0
1	0	1	4	1	7	15	75.0
0	1	0	1	2	4	16	80.0
0	1	1	2	1	5	17	85.0
0	4	1	3	2	10	18	90.0
2	5	4	2	6	19	19	95.0
4	13	14	29	5	65	20	100.0

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints,

⁵Inter-chain restraints, ⁶ Number of models with violations

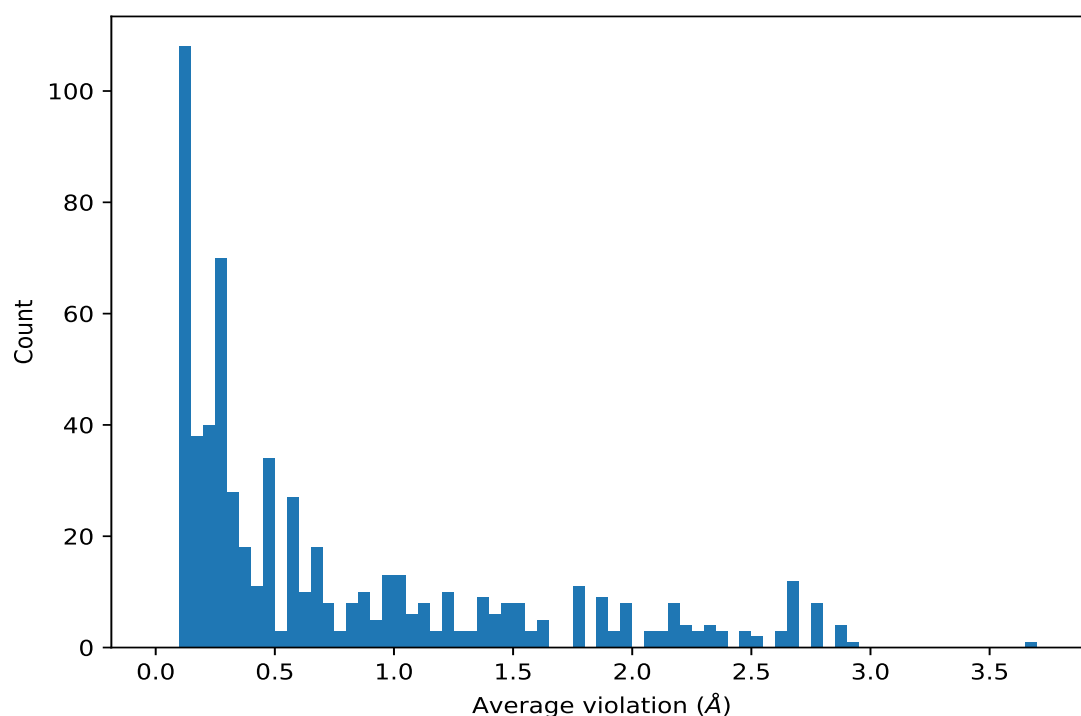
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,617)	1:114:A:ILE:HA	1:103:A:LEU:HD12	20	2.89	0.15	2.92
(1,617)	1:114:A:ILE:HA	1:103:A:LEU:HD11	20	2.89	0.15	2.92
(1,617)	1:114:A:ILE:HA	1:103:A:LEU:HD13	20	2.89	0.15	2.92
(1,532)	1:103:A:LEU:HD11	1:129:A:TRP:HZ2	20	2.8	0.05	2.82
(1,532)	1:103:A:LEU:HD13	1:129:A:TRP:HZ2	20	2.8	0.05	2.82
(1,532)	1:103:A:LEU:HD12	1:129:A:TRP:HZ2	20	2.8	0.05	2.82
(1,675)	1:97:A:LYS:HG3	1:92:A:PHE:HD1	20	2.8	1.47	3.77
(1,62)	1:121:A:LEU:HD12	1:103:A:LEU:HD11	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD11	1:103:A:LEU:HD11	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD13	1:103:A:LEU:HD13	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD12	1:103:A:LEU:HD13	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD13	1:103:A:LEU:HD11	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD11	1:103:A:LEU:HD12	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD13	1:103:A:LEU:HD12	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD12	1:103:A:LEU:HD12	20	2.69	1.17	2.14
(1,62)	1:121:A:LEU:HD11	1:103:A:LEU:HD13	20	2.69	1.17	2.14

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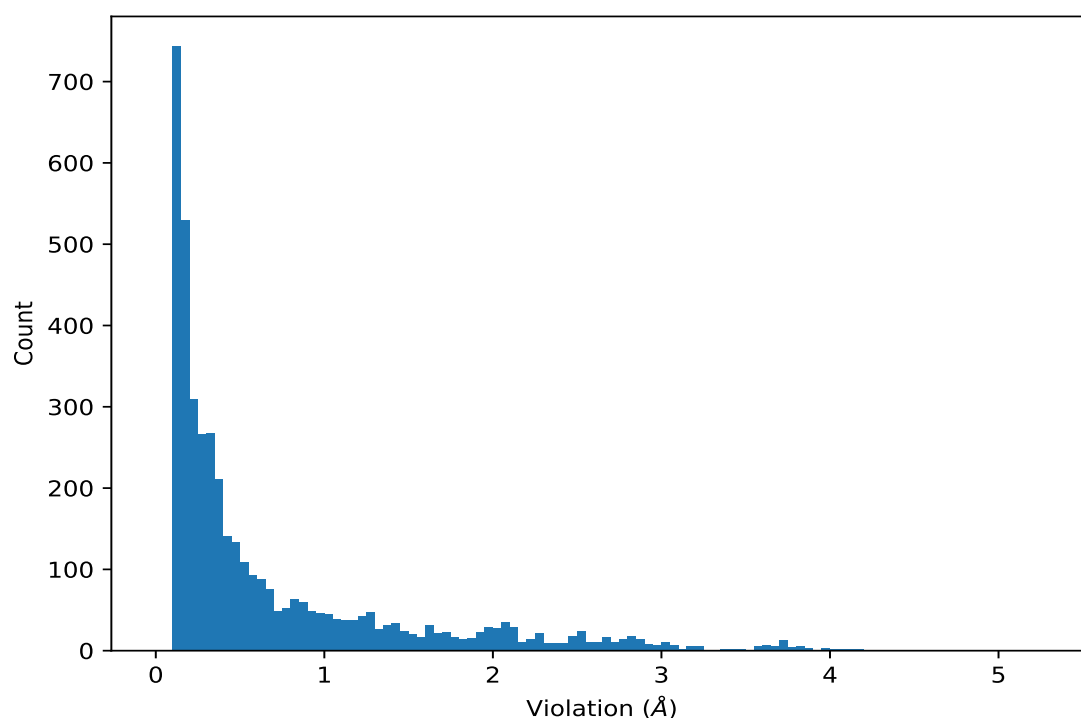
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,208)	1:103:A:LEU:HD23	1:104:A:CYS:H	20	2.47	0.07	2.5
(1,208)	1:103:A:LEU:HD22	1:104:A:CYS:H	20	2.47	0.07	2.5
(1,208)	1:103:A:LEU:HD21	1:104:A:CYS:H	20	2.47	0.07	2.5
(1,229)	1:114:A:ILE:H	1:102:A:LEU:HD13	20	2.36	1.56	3.7
(1,229)	1:114:A:ILE:H	1:102:A:LEU:HD11	20	2.36	1.56	3.7
(1,229)	1:114:A:ILE:H	1:102:A:LEU:HD12	20	2.36	1.56	3.7
(1,57)	1:103:A:LEU:HD21	1:104:A:CYS:HB3	20	2.31	0.56	2.02
(1,57)	1:103:A:LEU:HD22	1:104:A:CYS:HB3	20	2.31	0.56	2.02
(1,57)	1:103:A:LEU:HD23	1:104:A:CYS:HB3	20	2.31	0.56	2.02
(1,101)	1:113:A:HIS:HA	1:102:A:LEU:HD13	20	2.2	1.62	3.58
(1,101)	1:113:A:HIS:HA	1:102:A:LEU:HD11	20	2.2	1.62	3.58
(1,101)	1:113:A:HIS:HA	1:102:A:LEU:HD12	20	2.2	1.62	3.58
(1,61)	1:117:A:LEU:HD11	1:103:A:LEU:HD11	20	2.15	0.11	2.17
(1,61)	1:117:A:LEU:HD12	1:103:A:LEU:HD13	20	2.15	0.11	2.17
(1,61)	1:117:A:LEU:HD13	1:103:A:LEU:HD11	20	2.15	0.11	2.17
(1,61)	1:117:A:LEU:HD13	1:103:A:LEU:HD12	20	2.15	0.11	2.17
(1,61)	1:117:A:LEU:HD11	1:103:A:LEU:HD13	20	2.15	0.11	2.17
(1,61)	1:117:A:LEU:HD13	1:103:A:LEU:HD13	20	2.15	0.11	2.17
(1,61)	1:117:A:LEU:HD12	1:103:A:LEU:HD12	20	2.15	0.11	2.17
(1,61)	1:117:A:LEU:HD12	1:103:A:LEU:HD11	20	2.15	0.11	2.17
(1,1)	1:121:A:LEU:HD12	1:124:A:ILE:HG13	20	1.99	1.0	1.55

¹Number of violated models, ²Standard 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)
(1,62)	1:121:A:LEU:HD11	1:103:A:LEU:HD12	7	5.3
(1,62)	1:121:A:LEU:HD11	1:103:A:LEU:HD12	6	5.06
(1,62)	1:121:A:LEU:HD13	1:103:A:LEU:HD12	20	4.91
(1,62)	1:121:A:LEU:HD11	1:103:A:LEU:HD11	2	4.79
(1,675)	1:97:A:LYS:HG3	1:92:A:PHE:HD1	16	4.34
(1,675)	1:97:A:LYS:HG3	1:92:A:PHE:HD1	5	4.18
(1,1)	1:121:A:LEU:HD13	1:124:A:ILE:HG13	6	4.17
(1,675)	1:97:A:LYS:HG3	1:92:A:PHE:HD1	9	4.11
(1,675)	1:97:A:LYS:HG3	1:92:A:PHE:HD1	14	4.1
(1,675)	1:97:A:LYS:HG3	1:92:A:PHE:HD1	20	4.07

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found