



Full wwPDB NMR Structure Validation Report ⓘ

Jun 6, 2023 – 05:02 pm BST

PDB ID : 6FGN
BMRB ID : 34231
Title : Solution Structure of p300Taz2-p63TA
Authors : Gebel, J.; Kazemi, S.; Lohr, F.; Guntert, P.; Dotsch, V.
Deposited on : 2018-01-11

This is a Full wwPDB NMR Structure Validation 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 ⓘ 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 : 4.02b-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

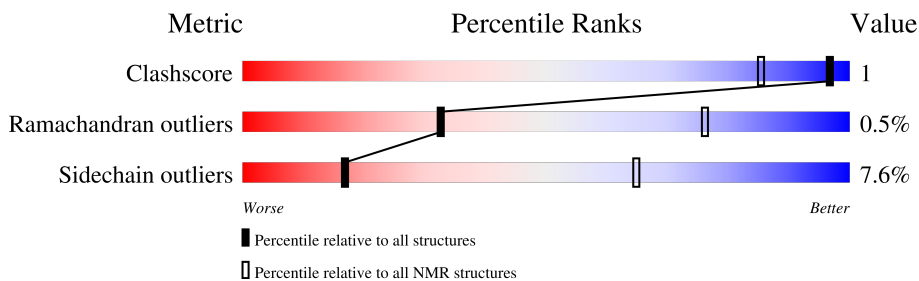
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 88%.

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	124	

2 Ensemble composition and analysis

This entry contains 20 models. Model 9 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:9-A:47, A:59-A:88, A:102-A:114 (82)	0.64	9

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 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1932 atoms, of which 966 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Histone acetyltransferase p300,Tumor protein 63.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	124	1929	597	966	184	172	10	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ALA	CYS	conflict	UNP Q09472
A	24	ALA	CYS	conflict	UNP Q09472
A	67	ALA	CYS	conflict	UNP Q09472
A	68	ALA	CYS	conflict	UNP Q09472
A	91	GLY	-	linker	UNP Q09472
A	92	THR	-	linker	UNP Q09472
A	93	ILE	-	linker	UNP Q09472
A	94	GLU	-	linker	UNP Q09472
A	95	GLY	-	linker	UNP Q09472
A	96	ARG	-	linker	UNP Q09472
A	97	GLY	-	linker	UNP Q09472
A	118	SER	CYS	conflict	UNP Q9H3D4

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

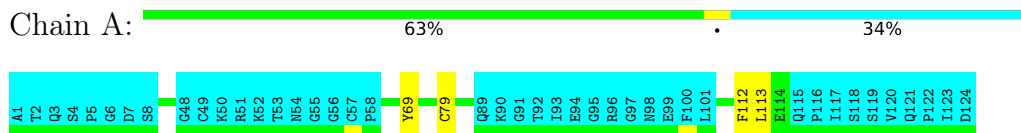
Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	3	3	3

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: Histone acetyltransferase p300,Tumor protein 63

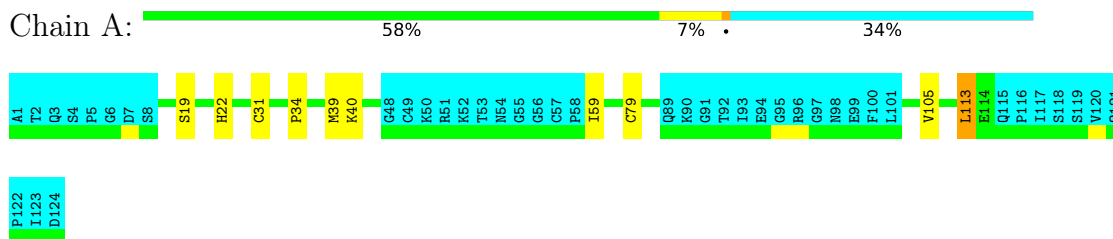


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

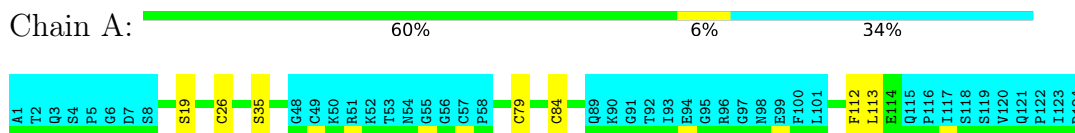
4.2.1 Score per residue for model 1

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



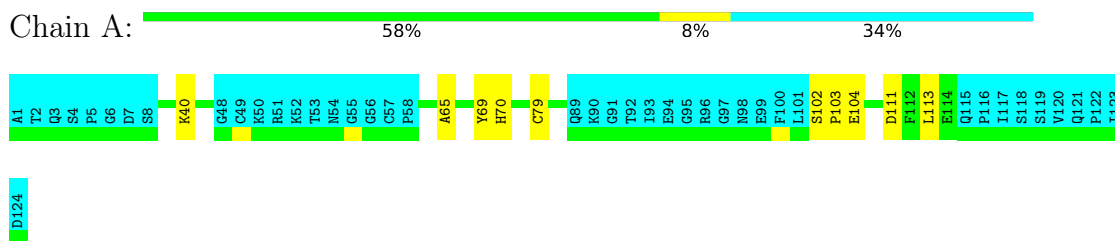
4.2.2 Score per residue for model 2

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



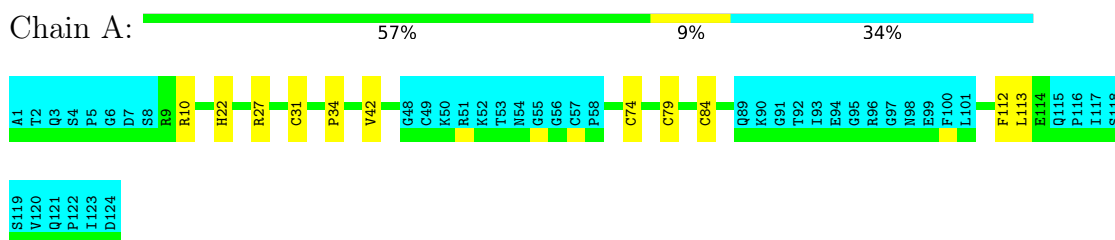
4.2.3 Score per residue for model 3

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



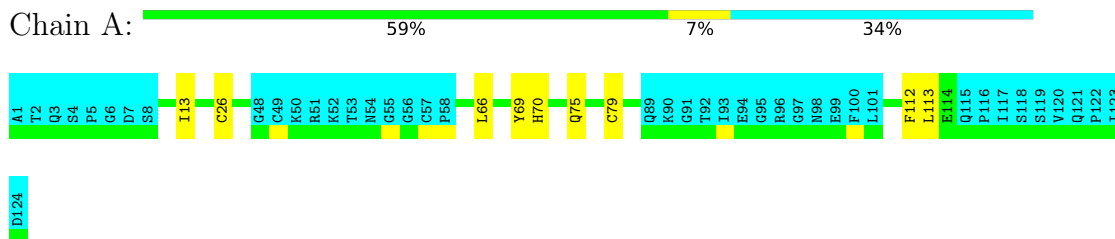
4.2.4 Score per residue for model 4

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



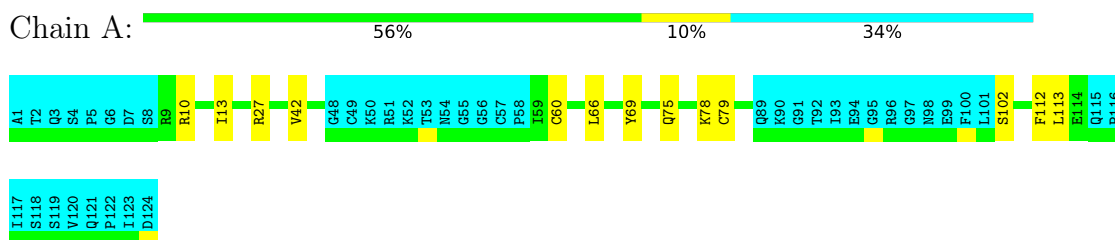
4.2.5 Score per residue for model 5

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



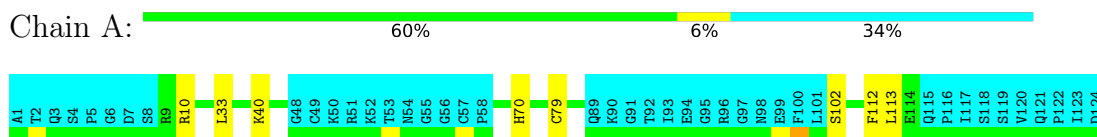
4.2.6 Score per residue for model 6

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



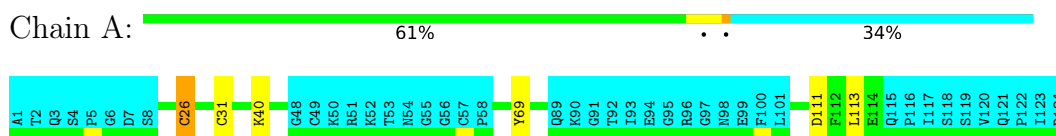
4.2.7 Score per residue for model 7

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



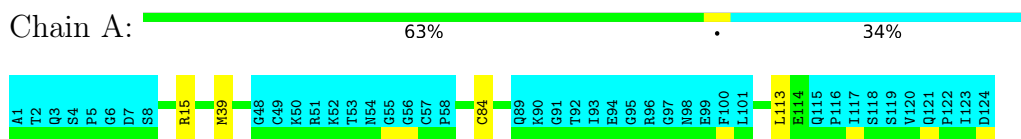
4.2.8 Score per residue for model 8

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



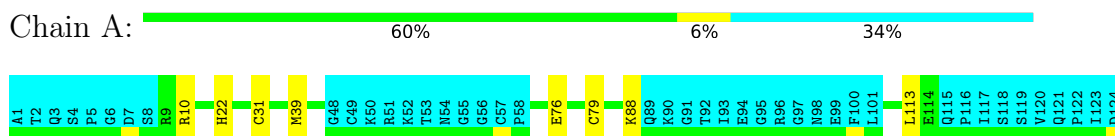
4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



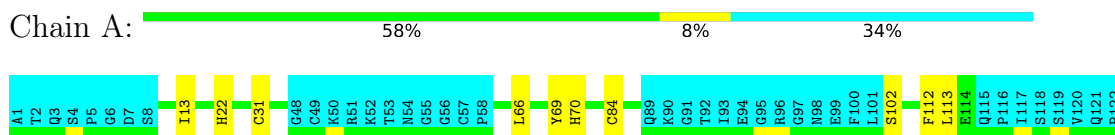
4.2.10 Score per residue for model 10

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



4.2.11 Score per residue for model 11

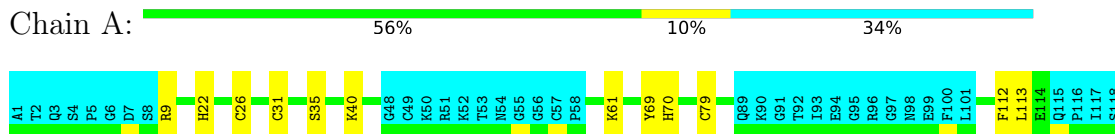
- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



I123
D124

4.2.12 Score per residue for model 12

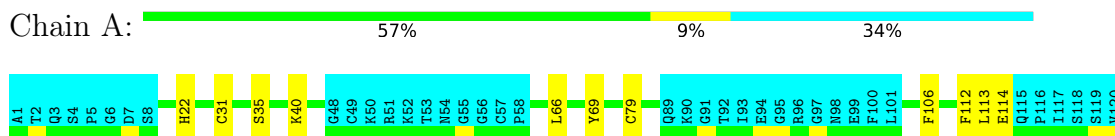
- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



S119
V120
Q121
P122
I123
D124

4.2.13 Score per residue for model 13

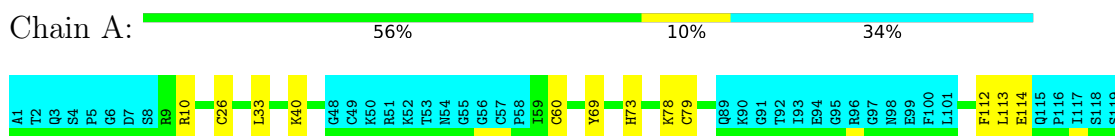
- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



Q121
P122
I123
D124

4.2.14 Score per residue for model 14

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



V120
Q121
P122
I123
D124

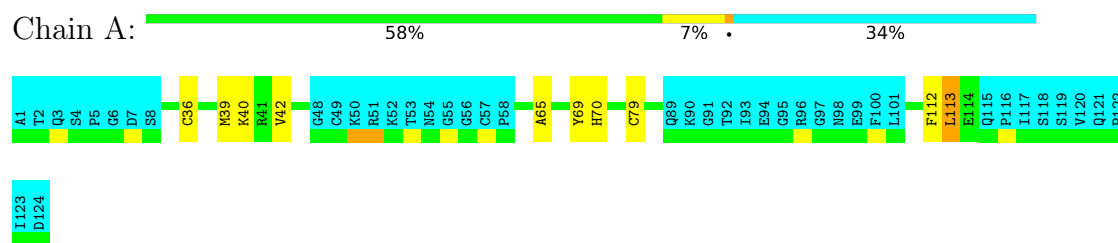
4.2.15 Score per residue for model 15

- Molecule 1: Histone acetyltransferase p300,Tumor protein 63



4.2.20 Score per residue for model 20

- Molecule 1: Histone acetyltransferase p300, Tumor protein 63



5 Refinement protocol and experimental data overview

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

Of the 200 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
OPAL	refinement	
CYANA	structure calculation	3.9

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	1471
Number of shifts mapped to atoms	1471
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

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:
ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.53±0.01	0±0/675 (0.0± 0.0%)	0.95±0.03	0±1/911 (0.0± 0.1%)
All	All	0.53	0/13500 (0.0%)	0.95	7/18220 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.1±1.1
All	All	0	22

There are no bond-length outliers.

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(°)	Ideal(°)	Models	
								Worst	Total
1	A	9	ARG	NE-CZ-NH2	-5.75	117.42	120.30	12	1
1	A	31	CYS	CA-CB-SG	-5.55	104.00	114.00	8	1
1	A	27	ARG	NE-CZ-NH2	-5.30	117.65	120.30	4	1
1	A	69	TYR	CB-CG-CD2	-5.17	117.90	121.00	16	1
1	A	15	ARG	NE-CZ-NH2	-5.11	117.75	120.30	9	1
1	A	10	ARG	NE-CZ-NH2	-5.02	117.79	120.30	18	1
1	A	15	ARG	NE-CZ-NH1	5.00	122.80	120.30	9	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	69	TYR	Sidechain	9
1	A	10	ARG	Sidechain	3
1	A	104	GLU	Sidechain	2
1	A	111	ASP	Sidechain	2
1	A	114	GLU	Sidechain	2
1	A	73	HIS	Sidechain	1
1	A	112	PHE	Sidechain	1
1	A	9	ARG	Sidechain	1
1	A	15	ARG	Sidechain	1

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	660	672	672	1±1
All	All	13260	13440	13440	18

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 1.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:ILE:HG23	1:A:66:LEU:HD22	0.54	1.78	5	3
1:A:39:MET:CE	1:A:113:LEU:HD22	0.49	2.37	20	2
1:A:22:HIS:CE1	1:A:31:CYS:SG	0.45	3.09	10	7
1:A:36:CYS:SG	1:A:40:LYS:HE3	0.44	2.53	20	1
1:A:79:CYS:HB3	1:A:84:CYS:SG	0.43	2.53	16	1
1:A:66:LEU:HD21	1:A:106:PHE:CE1	0.42	2.49	13	1
1:A:45:HIS:CD2	1:A:60:CYS:SG	0.42	3.13	16	1
1:A:26:CYS:SG	1:A:40:LYS:NZ	0.41	2.92	8	1
1:A:26:CYS:SG	1:A:40:LYS:HE3	0.40	2.55	14	1

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	82/124 (66%)	77±1 (94±2%)	5±1 (6±2%)	0±0 (0±1%)	32 76
All	All	1640/2480 (66%)	1536 (94%)	96 (6%)	8 (0%)	32 76

All 3 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	26	CYS	5
1	A	34	PRO	2
1	A	103	PRO	1

6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	74/108 (69%)	68±2 (92±2%)	6±2 (8±2%)	17 65
All	All	1480/2160 (69%)	1367 (92%)	113 (8%)	17 65

All 28 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	113	LEU	20
1	A	79	CYS	15
1	A	112	PHE	14
1	A	70	HIS	9
1	A	40	LYS	7
1	A	35	SER	4
1	A	84	CYS	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	102	SER	4
1	A	42	VAL	4
1	A	39	MET	4
1	A	60	CYS	3
1	A	33	LEU	3
1	A	19	SER	2
1	A	10	ARG	2
1	A	75	GLN	2
1	A	78	LYS	2
1	A	88	LYS	2
1	A	61	LYS	2
1	A	105	VAL	1
1	A	74	CYS	1
1	A	27	ARG	1
1	A	76	GLU	1
1	A	69	TYR	1
1	A	47	LYS	1
1	A	72	LYS	1
1	A	111	ASP	1
1	A	25	GLN	1
1	A	104	GLU	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](#)

Of 3 ligands modelled in this entry, 3 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 i

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 87% 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	1471
Number of shifts mapped to atoms	1471
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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
$^{13}\text{C}_\alpha$	124	-0.29 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	117	0.21 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	114	-0.31 ± 0.12	None needed (< 0.5 ppm)
^{15}N	115	-0.27 ± 0.27	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 88%, i.e. 1033 atoms were assigned a chemical shift out of a possible 1176. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	397/402 (99%)	159/160 (99%)	160/164 (98%)	78/78 (100%)
Sidechain	556/683 (81%)	381/444 (86%)	175/205 (85%)	0/34 (0%)

Continued on next page...

Continued from previous page...

	Total	¹ H	¹³ C	¹⁵ N
Aromatic	80/91 (88%)	35/45 (78%)	34/35 (97%)	11/11 (100%)
Overall	1033/1176 (88%)	575/649 (89%)	369/404 (91%)	89/123 (72%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 1470 atoms were assigned a chemical shift out of a possible 1687. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	594/611 (97%)	241/247 (98%)	238/248 (96%)	115/116 (99%)
Sidechain	786/975 (81%)	535/630 (85%)	251/296 (85%)	0/49 (0%)
Aromatic	90/101 (89%)	40/50 (80%)	39/40 (98%)	11/11 (100%)
Overall	1470/1687 (87%)	816/927 (88%)	528/584 (90%)	126/176 (72%)

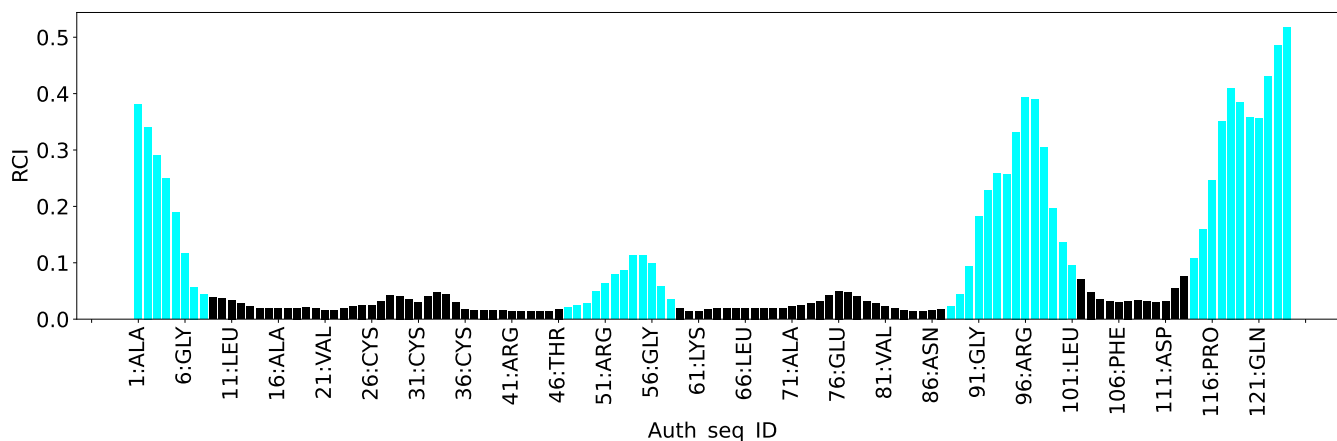
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

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	1461
Intra-residue ($ i-j =0$)	365
Sequential ($ i-j =1$)	458
Medium range ($ i-j >1$ and $ i-j <5$)	369
Long range ($ i-j \geq 5$)	269
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	1
Number of restraints per residue	11.8
Number of long range restraints per residue ¹	2.2

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)	0.2	0.12
0.2-0.5 (Medium)	None	None
>0.5 (Large)	None	None

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

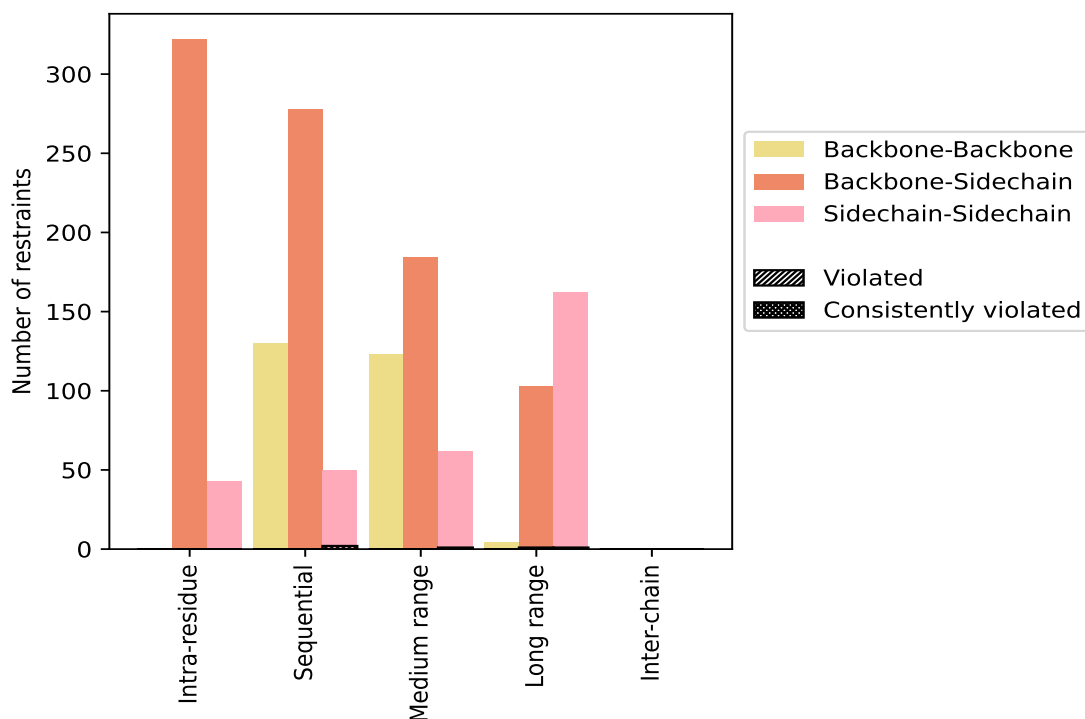
9.1 Summary of distance violations

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.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	365	25.0	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	322	22.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	43	2.9	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	458	31.3	2	0.4	0.1	0	0.0	0.0
Backbone-Backbone	130	8.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	278	19.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	50	3.4	2	4.0	0.1	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	369	25.3	1	0.3	0.1	0	0.0	0.0
Backbone-Backbone	123	8.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	184	12.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	62	4.2	1	1.6	0.1	0	0.0	0.0
Long range ($i-j \geq 5$)	269	18.4	2	0.7	0.1	0	0.0	0.0
Backbone-Backbone	4	0.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	103	7.0	1	1.0	0.1	0	0.0	0.0
Sidechain-Sidechain	162	11.1	1	0.6	0.1	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	1461	100.0	5	0.3	0.3	0	0.0	0.0
Backbone-Backbone	257	17.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	887	60.7	1	0.1	0.1	0	0.0	0.0
Sidechain-Sidechain	317	21.7	4	1.3	0.3	0	0.0	0.0

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 disulfid 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	0	0	0	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	1	0	1	0.11	0.11	0.0	0.11
3	0	1	0	0	0	1	0.12	0.12	0.0	0.12
4	0	0	1	0	0	1	0.11	0.11	0.0	0.11
5	0	0	0	0	0	0	0.0	0.0	0.0	0.0
6	0	0	0	0	0	0	0.0	0.0	0.0	0.0
7	0	0	0	0	0	0	0.0	0.0	0.0	0.0
8	0	0	0	0	0	0	0.0	0.0	0.0	0.0
9	0	0	0	0	0	0	0.0	0.0	0.0	0.0
10	0	0	0	0	0	0	0.0	0.0	0.0	0.0
11	0	0	0	0	0	0	0.0	0.0	0.0	0.0

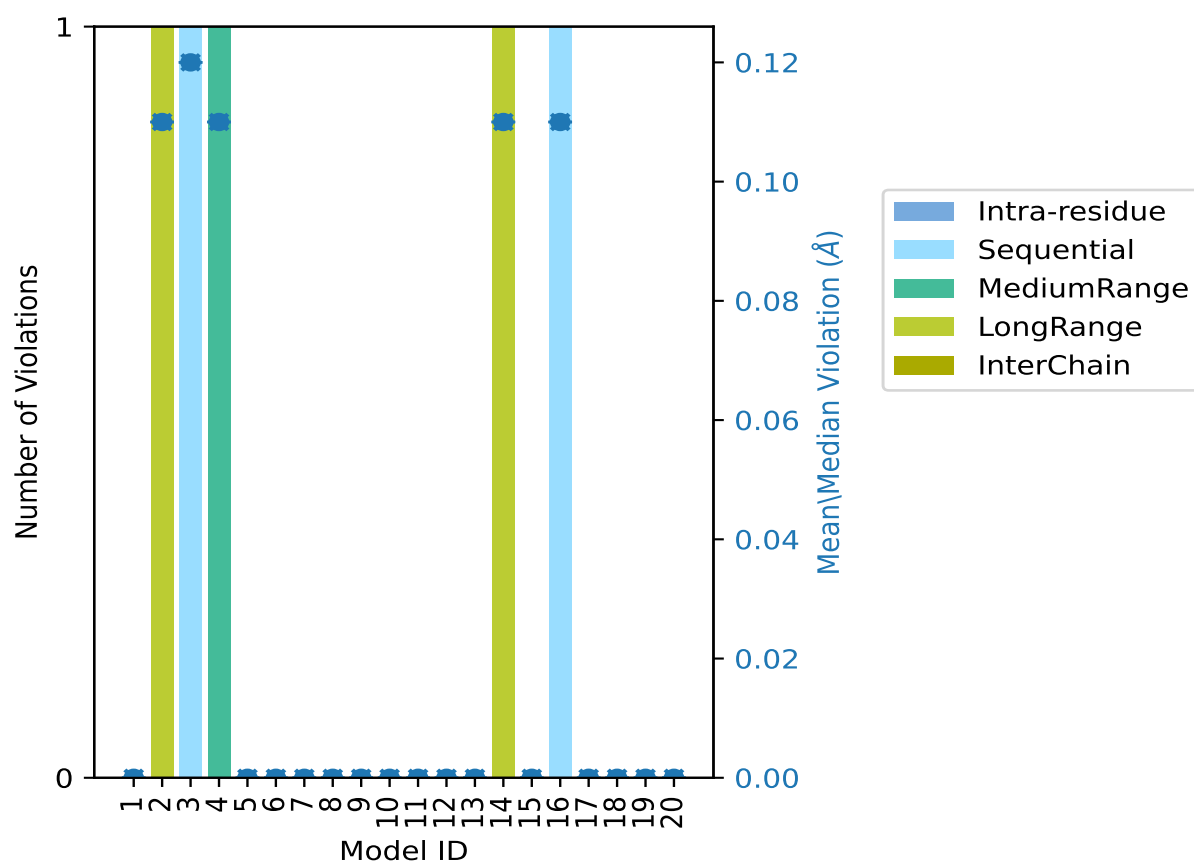
Continued on next page...

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	0	0	0	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	1	0	1	0.11	0.11	0.0	0.11
15	0	0	0	0	0	0	0.0	0.0	0.0	0.0
16	0	1	0	0	0	1	0.11	0.11	0.0	0.11
17	0	0	0	0	0	0	0.0	0.0	0.0	0.0
18	0	0	0	0	0	0	0.0	0.0	0.0	0.0
19	0	0	0	0	0	0	0.0	0.0	0.0	0.0
20	0	0	0	0	0	0	0.0	0.0	0.0	0.0

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 [\(i\)](#)



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

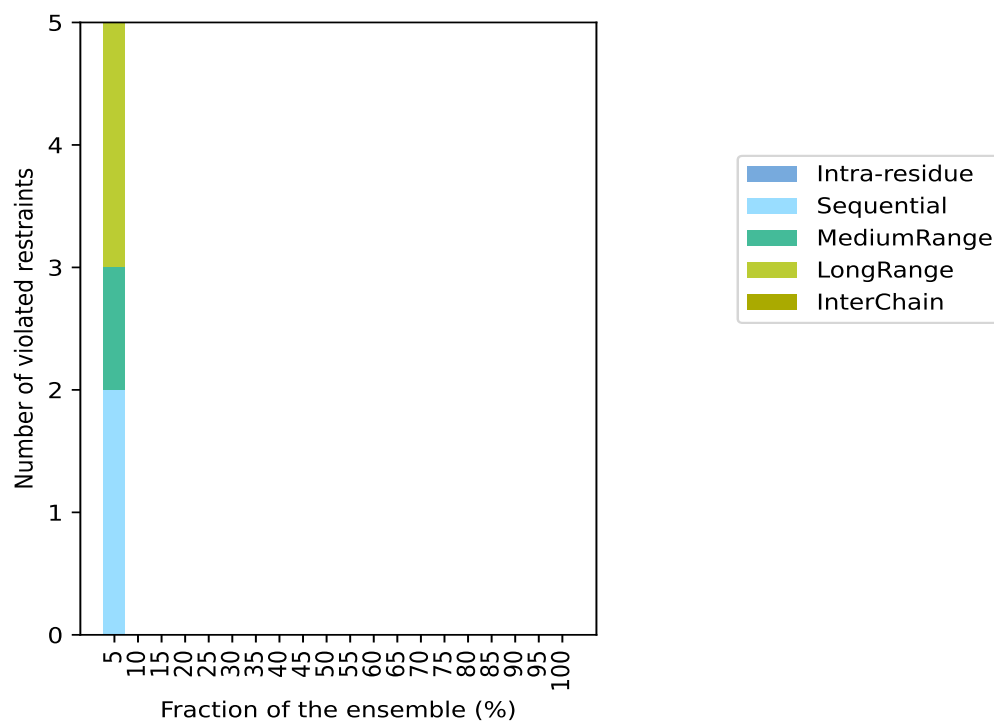
9.3 Distance violation statistics for the ensemble

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, 1456(IR:365, SQ:456, MR:368, LR:267, 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	%
0	2	1	2	0	5	1	5.0
0	0	0	0	0	0	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	0	0	0	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	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](#)



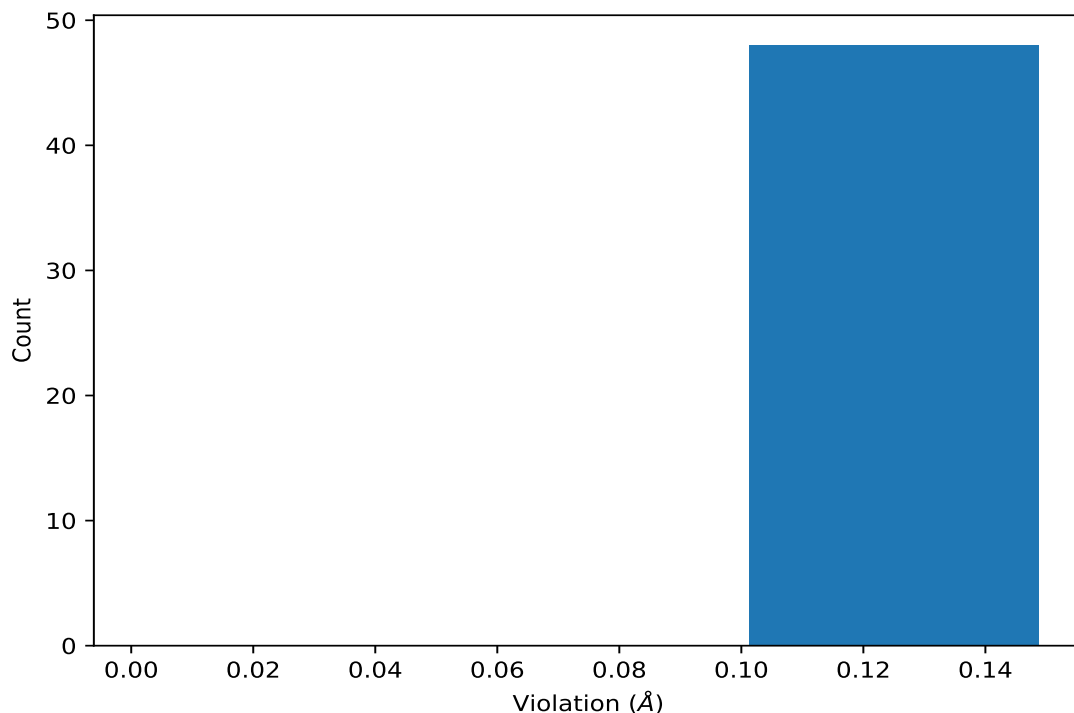
9.4 Most violated distance restraints in the ensemble [i](#)

No violations found

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 lists the absolute value of the violation for each restraint in the ensemble sorted by its 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)
(1,1428)	1:A:104:GLU:HG2	1:A:105:VAL:HG11	3	0.12
(1,1428)	1:A:104:GLU:HG2	1:A:105:VAL:HG12	3	0.12
(1,1428)	1:A:104:GLU:HG2	1:A:105:VAL:HG13	3	0.12
(1,1428)	1:A:104:GLU:HG2	1:A:105:VAL:HG21	3	0.12
(1,1428)	1:A:104:GLU:HG2	1:A:105:VAL:HG22	3	0.12
(1,1428)	1:A:104:GLU:HG2	1:A:105:VAL:HG23	3	0.12
(1,1428)	1:A:104:GLU:HG3	1:A:105:VAL:HG11	3	0.12
(1,1428)	1:A:104:GLU:HG3	1:A:105:VAL:HG12	3	0.12
(1,1428)	1:A:104:GLU:HG3	1:A:105:VAL:HG13	3	0.12
(1,1428)	1:A:104:GLU:HG3	1:A:105:VAL:HG21	3	0.12
(1,1428)	1:A:104:GLU:HG3	1:A:105:VAL:HG22	3	0.12
(1,1428)	1:A:104:GLU:HG3	1:A:105:VAL:HG23	3	0.12
(1,563)	1:A:60:CYS:H	1:A:120:VAL:HG11	14	0.11
(1,563)	1:A:60:CYS:H	1:A:120:VAL:HG12	14	0.11
(1,563)	1:A:60:CYS:H	1:A:120:VAL:HG13	14	0.11
(1,563)	1:A:60:CYS:H	1:A:120:VAL:HG21	14	0.11

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,563)	1:A:60:CYS:H	1:A:120:VAL:HG22	14	0.11
(1,563)	1:A:60:CYS:H	1:A:120:VAL:HG23	14	0.11
(1,1260)	1:A:11:LEU:HD11	1:A:12:SER:HB2	16	0.11
(1,1260)	1:A:11:LEU:HD11	1:A:12:SER:HB3	16	0.11
(1,1260)	1:A:11:LEU:HD12	1:A:12:SER:HB2	16	0.11
(1,1260)	1:A:11:LEU:HD12	1:A:12:SER:HB3	16	0.11
(1,1260)	1:A:11:LEU:HD13	1:A:12:SER:HB2	16	0.11
(1,1260)	1:A:11:LEU:HD13	1:A:12:SER:HB3	16	0.11
(1,1260)	1:A:11:LEU:HD21	1:A:12:SER:HB2	16	0.11
(1,1260)	1:A:11:LEU:HD21	1:A:12:SER:HB3	16	0.11
(1,1260)	1:A:11:LEU:HD22	1:A:12:SER:HB2	16	0.11
(1,1260)	1:A:11:LEU:HD22	1:A:12:SER:HB3	16	0.11
(1,1260)	1:A:11:LEU:HD23	1:A:12:SER:HB2	16	0.11
(1,1260)	1:A:11:LEU:HD23	1:A:12:SER:HB3	16	0.11
(1,1142)	1:A:64:ILE:HD11	1:A:100:PHE:HD1	2	0.11
(1,1142)	1:A:64:ILE:HD11	1:A:100:PHE:HD2	2	0.11
(1,1142)	1:A:64:ILE:HD12	1:A:100:PHE:HD1	2	0.11
(1,1142)	1:A:64:ILE:HD12	1:A:100:PHE:HD2	2	0.11
(1,1142)	1:A:64:ILE:HD13	1:A:100:PHE:HD1	2	0.11
(1,1142)	1:A:64:ILE:HD13	1:A:100:PHE:HD2	2	0.11
(1,1128)	1:A:66:LEU:HD11	1:A:69:TYR:HD1	4	0.11
(1,1128)	1:A:66:LEU:HD11	1:A:69:TYR:HD2	4	0.11
(1,1128)	1:A:66:LEU:HD12	1:A:69:TYR:HD1	4	0.11
(1,1128)	1:A:66:LEU:HD12	1:A:69:TYR:HD2	4	0.11
(1,1128)	1:A:66:LEU:HD13	1:A:69:TYR:HD1	4	0.11
(1,1128)	1:A:66:LEU:HD13	1:A:69:TYR:HD2	4	0.11
(1,1128)	1:A:66:LEU:HD21	1:A:69:TYR:HD1	4	0.11
(1,1128)	1:A:66:LEU:HD21	1:A:69:TYR:HD2	4	0.11
(1,1128)	1:A:66:LEU:HD22	1:A:69:TYR:HD1	4	0.11
(1,1128)	1:A:66:LEU:HD22	1:A:69:TYR:HD2	4	0.11
(1,1128)	1:A:66:LEU:HD23	1:A:69:TYR:HD1	4	0.11
(1,1128)	1:A:66:LEU:HD23	1:A:69:TYR:HD2	4	0.11

10 Dihedral-angle violation analysis

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