

wwPDB NMR Structure Validation Summary Report (i)

Jun 4, 2023 – 06:46 PM EDT

PDB ID : 2LHX BMRB ID : 17870

Title : Di-O-GalNAc glycosylated Mucin sequence based on MUC2 Mucin glycopro-

tein tandem repeat

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Deposited on : 2011-08-18

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 $\begin{array}{c} \text{A user guide is available at} \\ \text{https://www.wwpdb.org/validation/2017/NMRValidationReportHelp} \\ \text{with specific help available everywhere you see the (i) symbol.} \end{array}$

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

Mogul : 1.8.5 (274361), CSD as541be (2020)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

wwPDB-RCI : v 1n 11 5 13 A (Berjanski et al., 2005)

PANAV : Wang et al. (2010)

 $\begin{array}{ccc} wwPDB\text{-ShiftChecker} &:& v1.2\\ BMRB \ Restraints \ Analysis &:& v1.2 \end{array}$

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

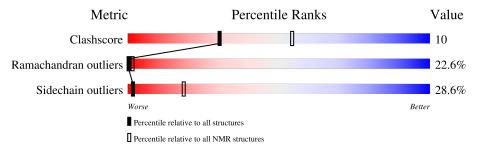
Validation Pipeline (wwPDB-VP) : 2.33

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

The overall completeness of chemical shifts assignment is 86%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive $(\# \mathrm{Entries})$	$egin{array}{c} { m NMR \ archive} \ (\#{ m Entries}) \end{array}$	
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	9	33%	67%	



2 Ensemble composition and analysis (i)

This entry contains 24 models.

Cyrange was unable to find well-defined residues.

Error message: The number of core atoms (4) was below the domain threshold value (8).

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust



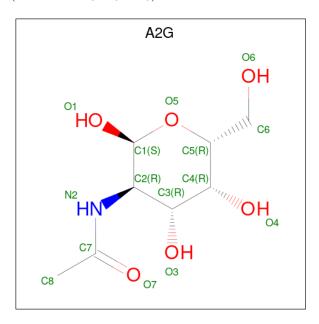
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 174 atoms, of which 90 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called MUC2 Mucin Domain Peptide.

Mol	Chain	Residues	Atoms			Trace		
1	Λ	0	Total	С	Н	N	О	1
1	A	9	118	36	62	9	11	1

• Molecule 2 is 2-acetamido-2-deoxy-alpha-D-galactopyranose (three-letter code: A2G) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				
2	٨	1	Total	С	Н	N	О
2	А	1	28	8	14	1	5
2	Λ	1	Total	С	Н	N	О
<i>Z</i>	А	1	28	8	14	1	5



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: MUC2 Mucin Domain Peptide

Chain A: 33% 67%

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

The representative model is number 1. Colouring as in section 4.1 above.

• Molecule 1: MUC2 Mucin Domain Peptide

Chain A: 56% 22% 22%



Refinement protocol and experimental data overview (i) 5



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

Of the 100 calculated structures, 24 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
CNS	structure solution	
XPLOR-NIH	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	118
Number of shifts mapped to atoms	118
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%



6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NH2, A2G, ACE

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	56	62	60	2±2
2	A	28	28	24	0±0
All	All	2016	2160	2016	40

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 10.

5 of 18 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	$Distance(\mathring{A})$	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:7:LEU:H	1:A:7:LEU:HD23	0.90	1.24	13	2
1:A:7:LEU:H	1:A:7:LEU:CD2	0.70	1.99	22	2
1:A:7:LEU:HD23	1:A:7:LEU:N	0.70	2.00	13	2
1:A:5:THR:O	1:A:7:LEU:N	0.62	2.32	5	5
1:A:8:LYS:O	2:A:11:A2G:H8	0.62	1.94	2	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	7/9 (78%)	4±1 (63±15%)	1±1 (14±12%)	2±1 (23±15%)	0 1
All	All	168/216 (78%)	106 (63%)	24 (14%)	38 (23%)	0 1

All 4 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	6	PRO	11
1	A	2	PRO	11
1	A	7	LEU	10
1	A	8	LYS	6

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	Perce	ntiles
1	A	7/7 (100%)	5±1 (71±13%)	2±1 (29±13%)	2	18
All	All	168/168 (100%)	120 (71%)	48 (29%)	2	18

All 5 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	5	THR	17
1	A	4	THR	13
1	A	3	THR	10
1	A	8	LYS	4
1	A	7	LEU	4



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)

2 ligands are 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	Trimo	Chain	Dag	Timle		Bond leng	ths
IVIOI	Type	Chain	nes	Lilik	Counts	RMSZ	#Z>2
2	A2G	A	11	1	14,14,15	0.64 ± 0.01	0±0 (0±0%)
2	A2G	A	10	1	14,14,15	0.64 ± 0.01	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.

Mal	Trino	Chain	Dec	Link		Bond ang	gles		
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	#Z>2		
2	A2G	A	11	1	17,19,21	0.83 ± 0.01	0±0 (0±1%)		
2	A2G	A	10	1	17,19,21	0.83 ± 0.01	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	ol Type Chain		Res	Link	Chirals	Torsions	Rings
2	A2G	A	11	1	-	$0\pm0,6,23,26$	$0 \pm 0,1,1,1$
2	A2G	A	10	1	-	$0\pm0,6,23,26$	$0\pm0,1,1,1$

There are no bond-length outliers.

All unique angle outliers are listed below.

	Mol	Chain	Ros	Type	Atoms	$f Z = f Observed(^o)$		Ideal(0)	Mod	dels
	WIOI	Chain	rtes	Type	Atoms		Observed()	ideai()	Worst	Total
ſ	2	A	11	A2G	O5-C1-C2	2.01	108.11	111.29	13	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 86% for the well-defined parts and 86% for the entire structure.

7.1 Chemical shift list 1

File name: working cs.cif

Chemical shift list name: assigned_chem_shift_list_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	118
Number of shifts mapped to atoms	118
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 86%, i.e. 80 atoms were assigned a chemical shift out of a possible 93. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	23/31 (74%)	12/12 (100%)	7/14 (50%)	4/5 (80%)
Sidechain	57/62 (92%)	41/41 (100%)	16/20 (80%)	0/1 (0%)
Overall	80/93 (86%)	53/53 (100%)	23/34 (68%)	4/6 (67%)

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 con-



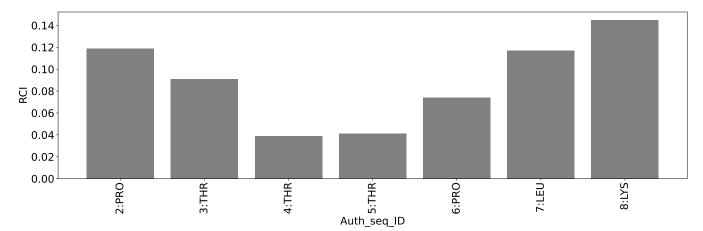
taining paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	4	THR	СВ	79.33	61.12 - 78.27	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:





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	119
Intra-residue ($ i-j =0$)	63
Sequential ($ i-j =1$)	25
Medium range ($ i-j >1$ and $ i-j <5$)	6
Long range (i-j ≥5)	25
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	4
Number of unmapped restraints	0
Number of restraints per residue	13.7
Number of long range restraints per residue ¹	2.8

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 (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)	0.0	0.11
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.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	0.0	1.2
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None



9 Distance violation analysis (i)

9.1 Summary of distance violations (i)

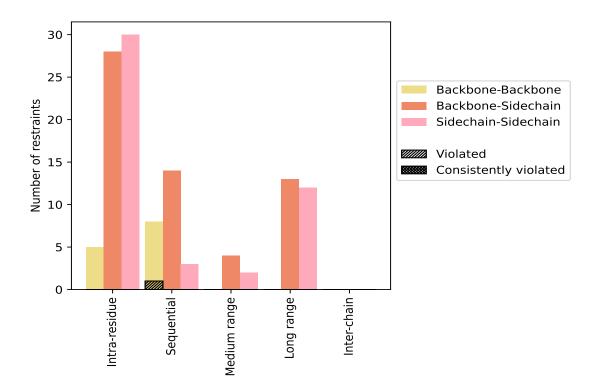
The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Dantuninta tema	Count	% ¹	Vic	lated ³	3	Consis	tentl	$\overline{ m y~Violated^4}$
Restraints type	Count	70	Count	$\%^2$	$ \%^1$	Count	$\%^2$	$\%^1$
Intra-residue (i-j =0)	63	52.9	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	5	4.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	28	23.5	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	30	25.2	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	25	21.0	1	4.0	0.8	0	0.0	0.0
Backbone-Backbone	8	6.7	1	12.5	0.8	0	0.0	0.0
Backbone-Sidechain	14	11.8	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	3	2.5	0	0.0	0.0	0	0.0	0.0
Medium range ($ i-j >1 \& i-j <5$)	6	5.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	4	3.4	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	2	1.7	0	0.0	0.0	0	0.0	0.0
Long range ($ i-j \ge 5$)	25	21.0	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	13	10.9	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	12	10.1	0	0.0	0.0	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	119	100.0	1	0.8	0.8	0	0.0	0.0
Backbone-Backbone	13	10.9	1	7.7	0.8	0	0.0	0.0
Backbone-Sidechain	59	49.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	47	39.5	0	0.0	0.0	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 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.

MadalID	Number of violations						M (8)	M (Å)	\mathbf{SD}^6 (Å)	Madian (Å)
Model ID	IR^1	SQ^2	MR^3	LR^4	IC^5	Total	Mean (Å)	Max (Å)	$SD^*(A)$	Median (Å)
1	0	0	0	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0	0	0	0.0	0.0	0.0	0.0
3	0	0	0	0	0	0	0.0	0.0	0.0	0.0
4	0	0	0	0	0	0	0.0	0.0	0.0	0.0
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

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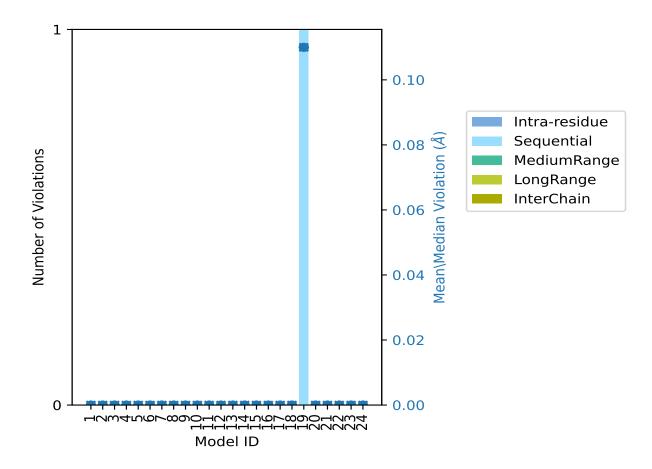
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Model ID	Number of violations						Mean (Å)	Max (Å)	${ m SD}^6$ (Å)	Median (Å)
Model 1D	IR^1	SQ^2	MR^3	LR^4	IC^5	Total	Mean (A)	Max (A)	$SD^*(A)$	Median (A)
12	0	0	0	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	0	0	0	0.0	0.0	0.0	0.0
15	0	0	0	0	0	0	0.0	0.0	0.0	0.0
16	0	0	0	0	0	0	0.0	0.0	0.0	0.0
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	1	0	0	0	1	0.11	0.11	0.0	0.11
20	0	0	0	0	0	0	0.0	0.0	0.0	0.0
21	0	0	0	0	0	0	0.0	0.0	0.0	0.0
22	0	0	0	0	0	0	0.0	0.0	0.0	0.0
23	0	0	0	0	0	0	0.0	0.0	0.0	0.0
24	0	0	0	0	0	0	0.0	0.0	0.0	0.0

 $^{^1{\}rm Intra-residue}$ restraints, $^2{\rm Sequential}$ restraints, $^3{\rm Medium}$ range restraints, $^4{\rm Long}$ range restraints, $^5{\rm Inter-chain}$ restraints, $^6{\rm Standard}$ 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, 118(IR:63, SQ:24, MR:6, LR:25, IC:0) restraints are not violated in the ensemble.

Nu	mber	of vio	lated	Fraction of the ensemble			
IR^1	SQ^2	MR^3	LR^4	$ IC^5 $	Total	Count ⁶	%
0	1	0	0	0	1	1	4.2
0	0	0	0	0	0	2	8.3
0	0	0	0	0	0	3	12.5
0	0	0	0	0	0	4	16.7
0	0	0	0	0	0	5	20.8
0	0	0	0	0	0	6	25.0

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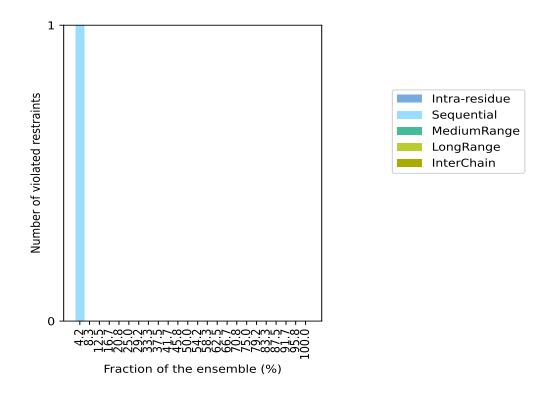
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Nu	mber	of vio	lated	Fraction of the ensemble			
IR^1	SQ^2	MR^3	LR^4	IC^5	Total	Count ⁶	%
0	0	0	0	0	0	7	29.2
0	0	0	0	0	0	8	33.3
0	0	0	0	0	0	9	37.5
0	0	0	0	0	0	10	41.7
0	0	0	0	0	0	11	45.8
0	0	0	0	0	0	12	50.0
0	0	0	0	0	0	13	54.2
0	0	0	0	0	0	14	58.3
0	0	0	0	0	0	15	62.5
0	0	0	0	0	0	16	66.7
0	0	0	0	0	0	17	70.8
0	0	0	0	0	0	18	75.0
0	0	0	0	0	0	19	79.2
0	0	0	0	0	0	20	83.3
0	0	0	0	0	0	21	87.5
0	0	0	0	0	0	22	91.7
0	0	0	0	0	0	23	95.8
0	0	0	0	0	0	24	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)

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.

Data insufficient to plot histogram

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.

\mathbf{Key}	Atom-1	Atom-2	Model ID	Violation (A)
(1,34)	1:A:7:LEU:HA	1:A:8:LYS:H	19	0.11



10 Dihedral-angle violation analysis (i)

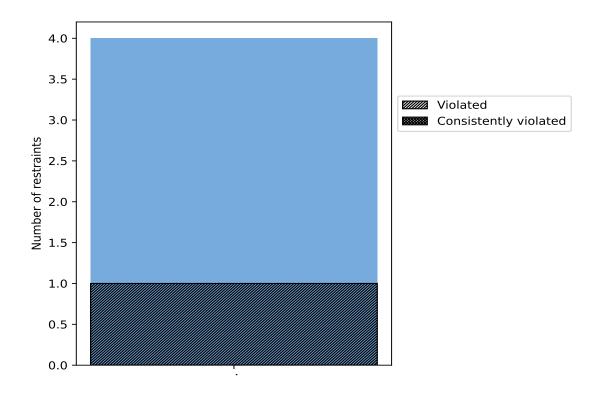
10.1 Summary of dihedral-angle violations (i)

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

A l - A	C	$\%^{1}$	${f Violated}^3$			Consistently Violated ⁴		
Angle type	Count	70	Count	$\%^2$	$\%^1$	Count	$\%^2$	% ¹
	4	100.0	1	25.0	25.0	0	0.0	0.0
Total	4	100.0	1	25.0	25.0	0	0.0	0.0

 $^{^1}$ percentage calculated with respect to total number of dihedral-angle restraints, 2 percentage calculated with respect to number of restraints in a particular dihedral-angle type, 3 violated in at least one model, 4 violated in all the models

10.1.1 Bar chart: Distribution of dihedral-angles and violations (i)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories



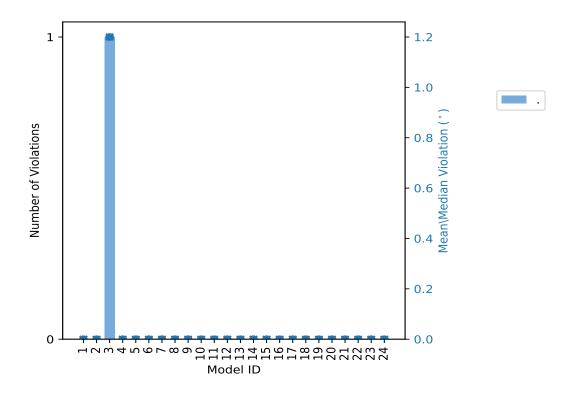
10.2 Dihedral-angle violation statistics for each model (i)

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	N	umber of violations	Moon (°)	Mor (°)	SD (°)	Modian (°)
Model 1D		Total	$\mathbf{Mean} (^{\circ})$	$\mathbf{Max} \ (^{\circ})$	\mathbf{SD} (°)	\mid Median (°) \mid
1	0	0	0.0	0.0	0.0	0.0
2	0	0	0.0	0.0	0.0	0.0
3	1	1	1.2	1.2	0.0	1.2
4	0	0	0.0	0.0	0.0	0.0
5	0	0	0.0	0.0	0.0	0.0
6	0	0	0.0	0.0	0.0	0.0
7	0	0	0.0	0.0	0.0	0.0
8	0	0	0.0	0.0	0.0	0.0
9	0	0	0.0	0.0	0.0	0.0
10	0	0	0.0	0.0	0.0	0.0
11	0	0	0.0	0.0	0.0	0.0
12	0	0	0.0	0.0	0.0	0.0
13	0	0	0.0	0.0	0.0	0.0
14	0	0	0.0	0.0	0.0	0.0
15	0	0	0.0	0.0	0.0	0.0
16	0	0	0.0	0.0	0.0	0.0
17	0	0	0.0	0.0	0.0	0.0
18	0	0	0.0	0.0	0.0	0.0
19	0	0	0.0	0.0	0.0	0.0
20	0	0	0.0	0.0	0.0	0.0
21	0	0	0.0	0.0	0.0	0.0
22	0	0	0.0	0.0	0.0	0.0
23	0	0	0.0	0.0	0.0	0.0
24	0	0	0.0	0.0	0.0	0.0



10.2.1 Bar graph: Dihedral 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

10.3 Dihedral-angle violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in very 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 ensemble.

N	umber of violated restraints	Fractio	n of the ensemble
	Total	Count ¹	%
1	1	1	4.2
0	0	2	8.3
0	0	3	12.5
0	0	4	16.7
0	0	5	20.8
0	0	6	25.0
0	0	7	29.2
0	0	8	33.3
0	0	9	37.5
0	0	10	41.7
0	0	11	45.8

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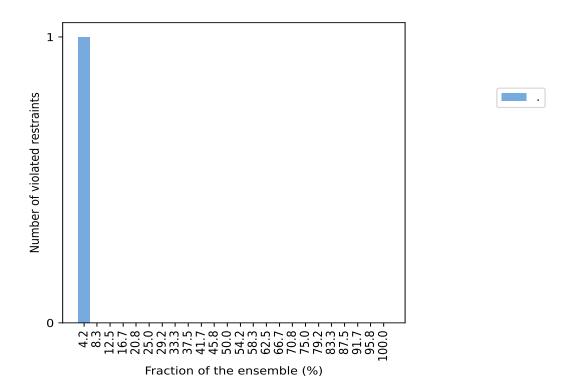


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N	umber of violated restraints	Fraction	n of the ensemble
	Total	Count ¹	%
0	0	12	50.0
0	0	13	54.2
0	0	14	58.3
0	0	15	62.5
0	0	16	66.7
0	0	17	70.8
0	0	18	75.0
0	0	19	79.2
0	0	20	83.3
0	0	21	87.5
0	0	22	91.7
0	0	23	95.8
0	0	24	100.0

 $^{^{1}}$ Number of models with violations

10.3.1 Bar graph: Dihedral-angle Violation statistics for the ensemble (i)





10.4 Most violated dihedral-angle restraints in the ensemble (i)

No violations found

10.5 All violated dihedral-angle restraints (i)

10.5.1 Histogram: Distribution of violations (i)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.

Data insufficient to plot histogram

10.5.2 Table: All violated dihedral-angle restraints (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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,1)	1:A:4:THR:HA	1:A:4:THR:CA	1:A:4:THR:CB	1:A:4:THR:HB	3	1.2

