wwPDB NMR Structure Validation Summary Report

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Title	:	CTLA-4, NMR, 20 STRUCTURES
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This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

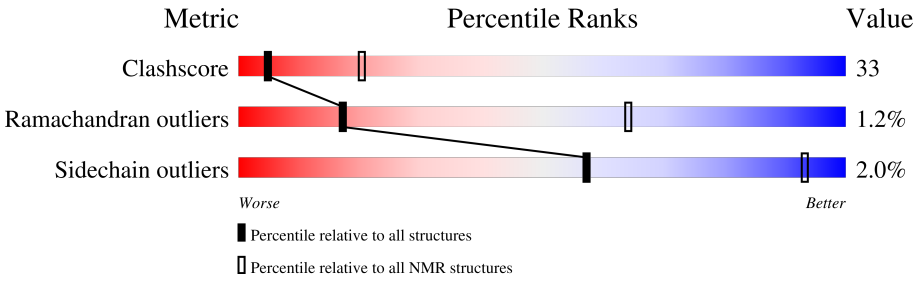
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 was not calculated.

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	129	42% 44% • 12%
2	B	4	25% 75%
3	C	4	25% 75%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	B	NAG	2	1	-

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models).

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:2-A:64, A:67-A:106, A:108-A:117 (113)	1.05	4

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2099 atoms, of which 1036 are hydrogens and 0 are deuteriums.

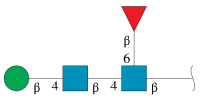
- Molecule 1 is a protein called CTLA-4.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	129	1907	604	942	157	194	10	0

There is a discrepancy between the modelled and reference sequences:

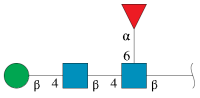
Chain	Residue	Modelled	Actual	Comment	Reference
A	113	THR	ALA	conflict	UNP P16410

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	B	4	96	28	47	2	19	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
3	C	4	96	28	47	2	19	0

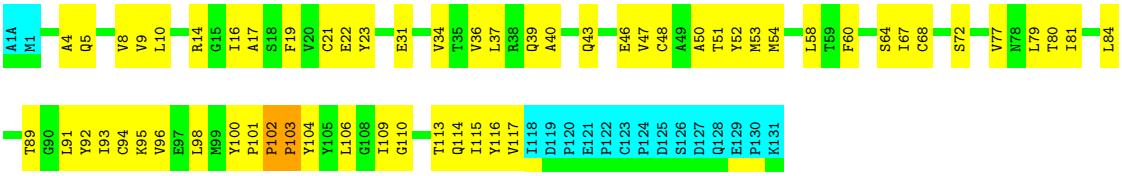
4 Residue-property plots

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.

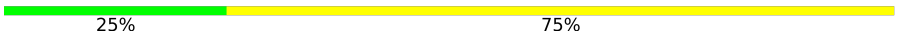
• Molecule 1: CTLA-4

Chain A:



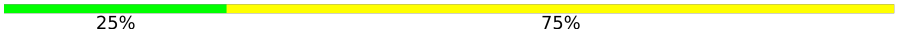
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:



• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:



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

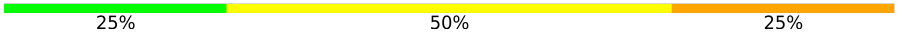
The representative model is number 4. Colouring as in section 4.1 above.

• Molecule 1: CTLA-4

Chain A:

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:



• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

5 Refinement protocol and experimental data overview

The models were refined using the following method: *DISTANCE GEOMETRY SIMULATED ANNEALING*.

Of the 50 calculated structures, 20 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATION*.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
X-PLOR3.1	structure solution	

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA, FUC, FUL

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	1.28±0.03	3±1/859 (0.4± 0.1%)	1.47±0.03	4±1/1172 (0.3± 0.1%)
All	All	1.28	63/17180 (0.4%)	1.47	78/23440 (0.3%)

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	0.1±0.4
All	All	0	3

5 of 7 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
1	A	103	PRO	N-CD	12.20	1.65	1.47	15	16
1	A	103	PRO	N-CA	10.33	1.64	1.47	14	8
1	A	102	PRO	C-N	9.81	1.52	1.34	17	16
1	A	102	PRO	CA-C	9.19	1.71	1.52	1	16
1	A	102	PRO	C-O	-7.64	1.07	1.23	2	3

5 of 11 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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	103	PRO	CA-N-CD	-23.58	78.49	111.50	12	20
1	A	102	PRO	C-N-CD	17.09	164.29	128.40	8	20
1	A	103	PRO	N-CA-CB	8.47	113.47	103.30	18	8

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	102	PRO	C-N-CA	-7.82	89.17	122.00	18	20
1	A	103	PRO	N-CD-CG	-7.39	92.12	103.20	13	4

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	102	PRO	Mainchain	3

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	844	832	830	61±8
2	B	49	47	43	2±1
3	C	49	47	43	2±2
All	All	18840	18520	18331	1241

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 33.

5 of 425 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:47:VAL:HG12	1:A:68:CYS:SG	1.22	1.73	8	1
1:A:48:CYS:SG	1:A:60:PHE:CG	1.22	2.33	13	1
1:A:5:GLN:NE2	1:A:94:CYS:SG	1.13	2.20	3	8
1:A:48:CYS:SG	1:A:68:CYS:N	1.12	2.22	3	1
1:A:60:PHE:CB	1:A:68:CYS:SG	1.11	2.38	13	2

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	113/129 (88%)	102±2 (90±2%)	9±2 (8±2%)	1±1 (1±1%)	17 64
All	All	2260/2580 (88%)	2043 (90%)	189 (8%)	28 (1%)	17 64

5 of 8 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	64	SER	10
1	A	67	ILE	7
1	A	104	TYR	5
1	A	47	VAL	2
1	A	62	ASP	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	93/108 (86%)	91±1 (98±1%)	2±1 (2±1%)	57 93
All	All	1860/2160 (86%)	1823 (98%)	37 (2%)	57 93

5 of 14 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	106	LEU	6
1	A	53	MET	6
1	A	54	MET	5
1	A	5	GLN	4
1	A	14	ARG	2

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)

8 monosaccharides 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	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	NAG	B	1	1,2	14,14,15	0.56±0.05	0±0 (0±0%)
2	NAG	B	2	2	14,14,15	0.50±0.02	0±0 (0±0%)
2	BMA	B	3	2	11,11,12	0.27±0.01	0±0 (0±0%)
2	FUL	B	4	2	10,10,11	0.44±0.10	0±0 (0±0%)
3	NAG	C	1	1,3	14,14,15	0.57±0.03	0±0 (0±0%)
3	NAG	C	2	3	14,14,15	0.50±0.02	0±0 (0±0%)
3	BMA	C	3	3	11,11,12	0.28±0.01	0±0 (0±0%)
3	FUC	C	4	3	10,10,11	0.59±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	NAG	B	1	1,2	17,19,21	0.61±0.06	0±0 (0±2%)
2	NAG	B	2	2	17,19,21	0.54±0.06	0±0 (1±2%)
2	BMA	B	3	2	15,15,17	0.27±0.01	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	FUL	B	4	2	14,14,16	0.68±0.23	0±1 (3±6%)
3	NAG	C	1	1,3	17,19,21	0.68±0.04	0±0 (2±2%)
3	NAG	C	2	3	17,19,21	0.58±0.05	1±0 (3±2%)
3	BMA	C	3	3	15,15,17	0.29±0.02	0±0 (0±0%)
3	FUC	C	4	3	14,14,16	0.96±0.07	1±1 (8±3%)

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	NAG	B	1	1,2	-	0±0,6,23,26	0±0,1,1,1
2	NAG	B	2	2	-	0±0,6,23,26	0±0,1,1,1
2	BMA	B	3	2	-	0±0,2,19,22	0±0,1,1,1
2	FUL	B	4	2	-	-	0±0,1,1,1
3	NAG	C	1	1,3	-	0±0,6,23,26	0±0,1,1,1
3	NAG	C	2	3	-	2±0 ,6,23,26	0±0,1,1,1
3	BMA	C	3	3	-	0±0,2,19,22	0±0,1,1,1
3	FUC	C	4	3	-	-	0±0,1,1,1

There are no bond-length outliers.

5 of 9 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(^{o})	Ideal(^{o})	Models	
								Worst	Total
3	C	4	FUC	C1-C2-C3	2.57	106.51	109.67	1	19
2	B	4	FUL	C1-C2-C3	2.54	106.54	109.67	17	5
3	C	4	FUC	C3-C4-C5	2.39	113.50	109.77	5	1
3	C	4	FUC	O5-C1-C2	2.34	107.16	110.77	16	4
2	B	4	FUL	O5-C1-C2	2.29	107.24	110.77	11	5

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
2	B	2	NAG	C1	1

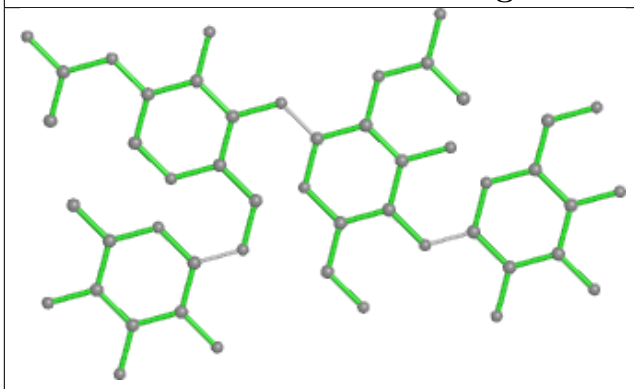
5 of 6 unique torsion outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
3	C	2	NAG	C8-C7-N2-C2	2
3	C	2	NAG	O7-C7-N2-C2	2
2	B	1	NAG	C8-C7-N2-C2	1
2	B	1	NAG	O7-C7-N2-C2	1
2	B	2	NAG	C8-C7-N2-C2	1

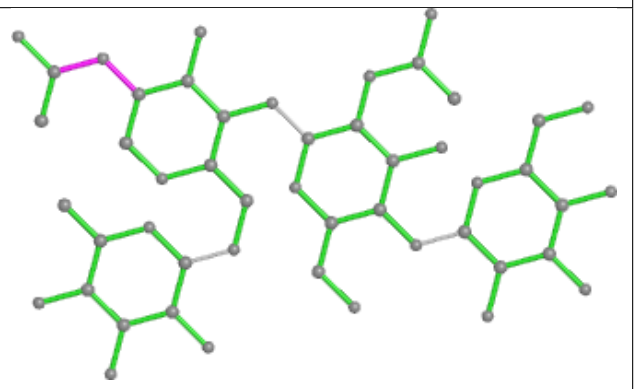
There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

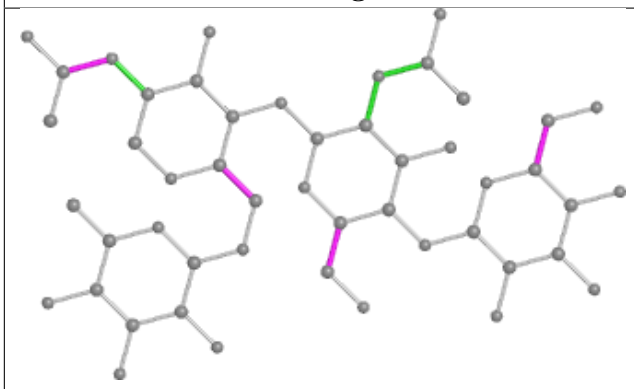
Oligosaccharide Chain B



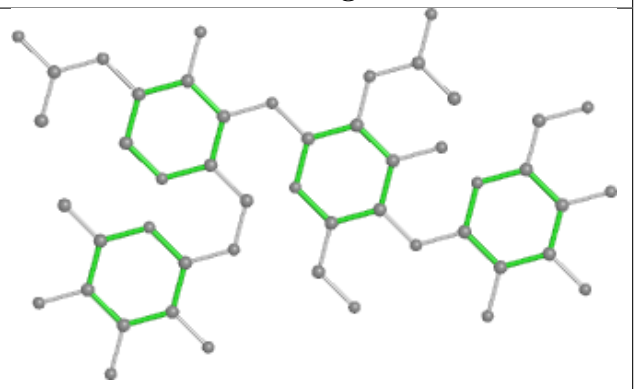
Bond lengths



Bond angles

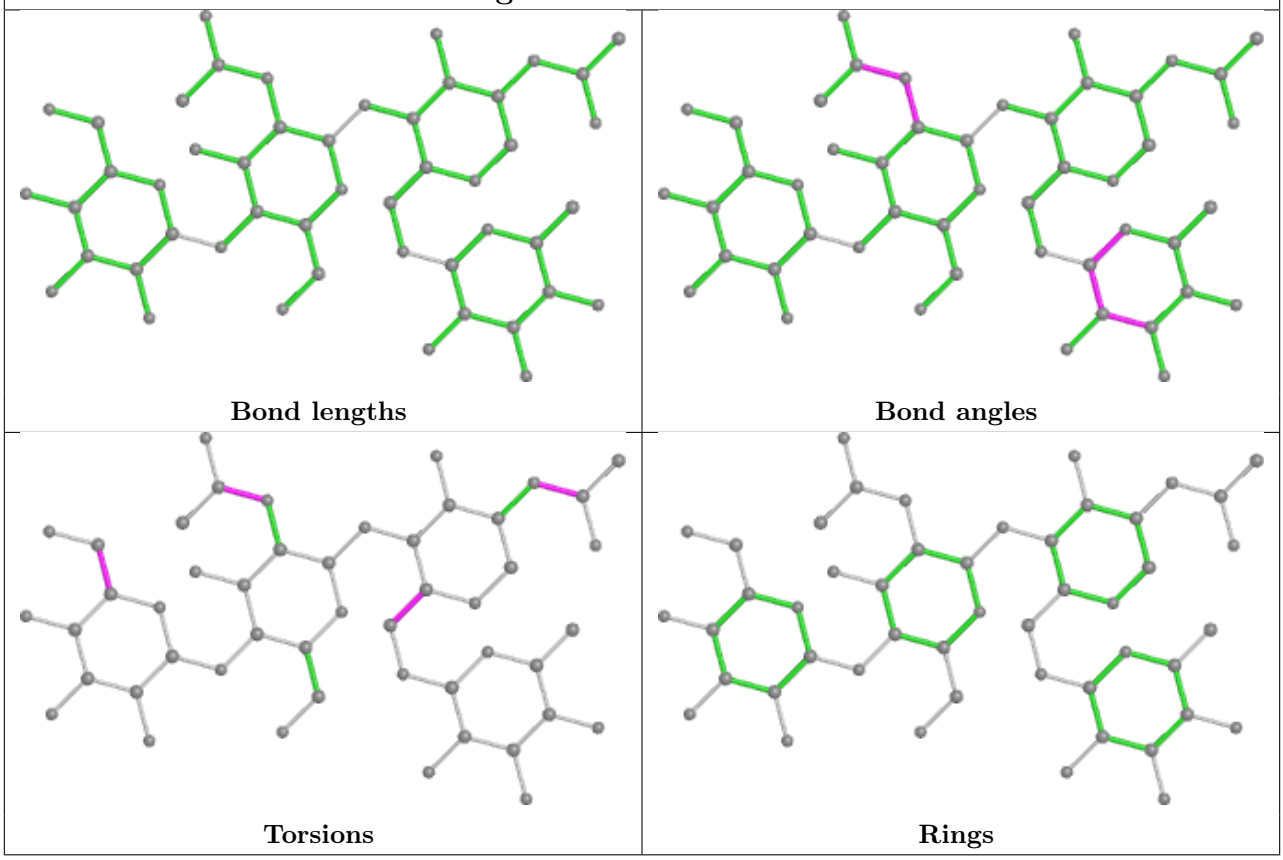


Torsions



Rings

Oligosaccharide Chain C



6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

No chemical shift data were provided