



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 2, 2023 – 10:07 AM EDT

PDB ID : 6N5E
Title : Broadly protective antibodies directed to a subdominant influenza hemagglutinin epitope
Authors : Bajic, G.; Schmidt, A.G.
Deposited on : 2018-11-21
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray 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/XrayValidationReportHelp>

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 : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16381 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	2188	1374	382	421	11	0	0	0
1	B	282	2188	1374	382	421	11	0	0	0
1	C	277	2153	1353	376	413	11	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	188	ASP	ASN	conflict	UNP P03437
B	188	ASP	ASN	conflict	UNP P03437
C	188	ASP	ASN	conflict	UNP P03437

- Molecule 2 is a protein called FL-1066 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	225	1707	1080	282	337	8	0	0	0
2	E	226	1715	1084	283	340	8	0	0	0
2	G	222	1687	1067	279	333	8	0	0	0

- Molecule 3 is a protein called FL-1066 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	I	211	1573	990	264	315	4	0	0	0
3	F	197	1457	915	245	293	4	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	0	0
			1573	990	264	315	4			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	2	Total	C	N	O	0	0	0	
			28	16	2	10				
4	K	2	Total	C	N	O	0	0	0	
			28	16	2	10				
4	L	2	Total	C	N	O	0	0	0	
			28	16	2	10				
4	M	2	Total	C	N	O	0	0	0	
			28	16	2	10				
4	N	2	Total	C	N	O	0	0	0	
			28	16	2	10				

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics i

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	153.56Å 153.56Å 91.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.33 – 3.00	Depositor
% Data completeness (in resolution range)	99.8 (44.33-3.00)	Depositor
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.249 , 0.287	Depositor
Wilson B-factor (Å ²)	60.7	Xtrriage
Anisotropy	0.316	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	0.088 for -h,-k,l 0.094 for h,-h-k,-l 0.398 for -k,-h,-l	Xtrriage
Reported twinning fraction	0.490 for -k,-h,-l	Depositor
Outliers	0 of 48395 reflections	Xtrriage
Total number of atoms	16381	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

10 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or 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 length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	J	1	1,4	14,14,15	0.27	0	17,19,21	1.46	2 (11%)
4	NAG	J	2	4	14,14,15	0.29	0	17,19,21	0.66	0
4	NAG	K	1	1,4	14,14,15	0.50	0	17,19,21	0.80	0
4	NAG	K	2	4	14,14,15	0.30	0	17,19,21	0.45	0
4	NAG	L	1	1,4	14,14,15	0.63	0	17,19,21	1.05	2 (11%)
4	NAG	L	2	4	14,14,15	0.79	1 (7%)	17,19,21	0.71	1 (5%)
4	NAG	M	1	1,4	14,14,15	0.27	0	17,19,21	0.74	0
4	NAG	M	2	4	14,14,15	0.73	0	17,19,21	0.59	0
4	NAG	N	1	1,4	14,14,15	0.43	0	17,19,21	2.47	2 (11%)
4	NAG	N	2	4	14,14,15	0.25	0	17,19,21	0.37	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
4	NAG	J	1	1,4	-	4/6/23/26	0/1/1/1
4	NAG	J	2	4	-	4/6/23/26	0/1/1/1
4	NAG	K	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	L	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	L	2	4	-	1/6/23/26	0/1/1/1
4	NAG	M	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	M	2	4	-	3/6/23/26	0/1/1/1
4	NAG	N	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	2	NAG	O5-C1	-2.38	1.39	1.43

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	1	NAG	C1-O5-C5	9.41	124.94	112.19
4	J	1	NAG	C2-N2-C7	4.50	129.31	122.90
4	L	1	NAG	C1-O5-C5	2.74	115.90	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	1	NAG	O5-C5-C6	-2.52	103.25	107.20
4	J	1	NAG	O4-C4-C5	-2.46	103.18	109.30

There are no chirality outliers.

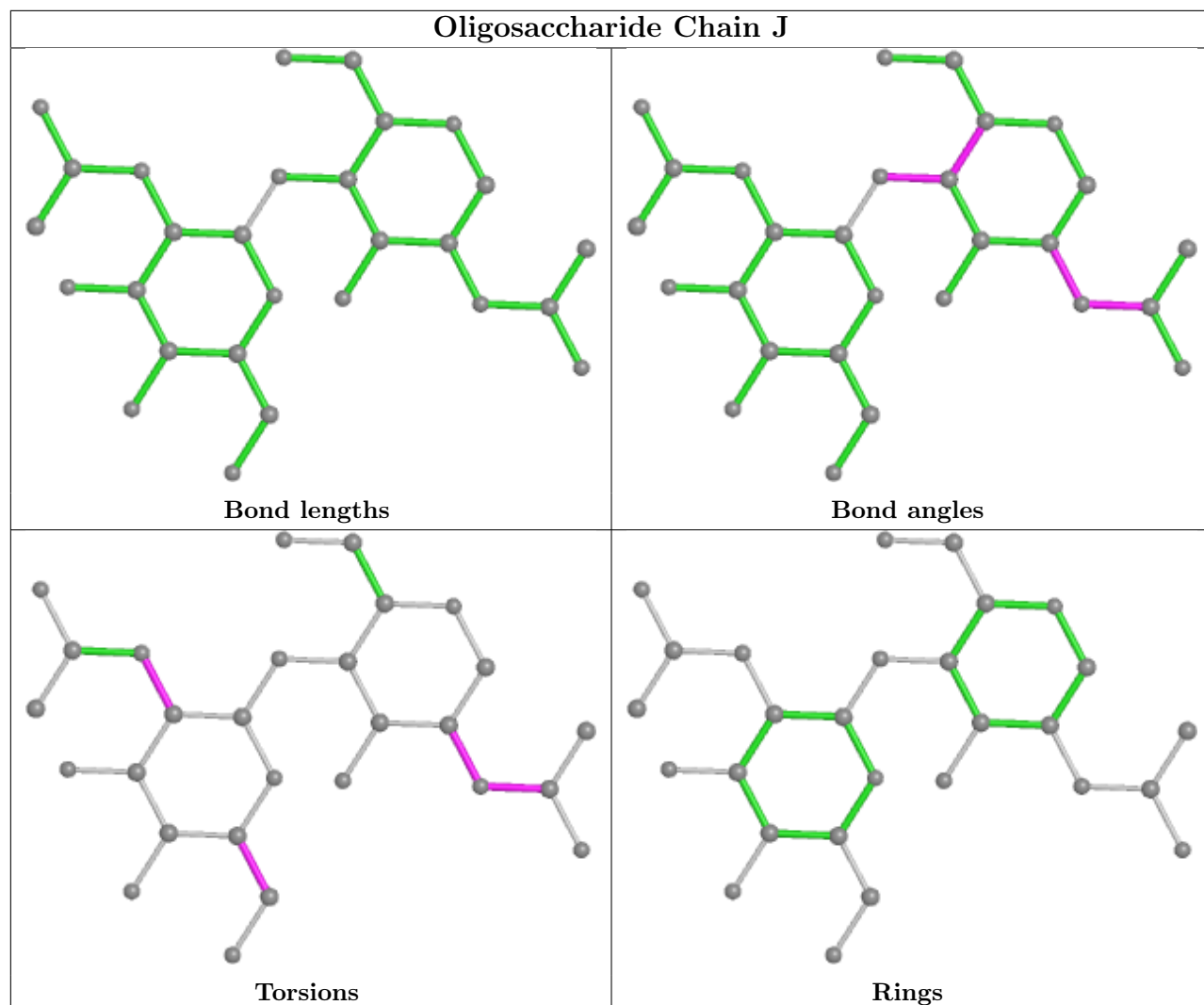
5 of 26 torsion outliers are listed below:

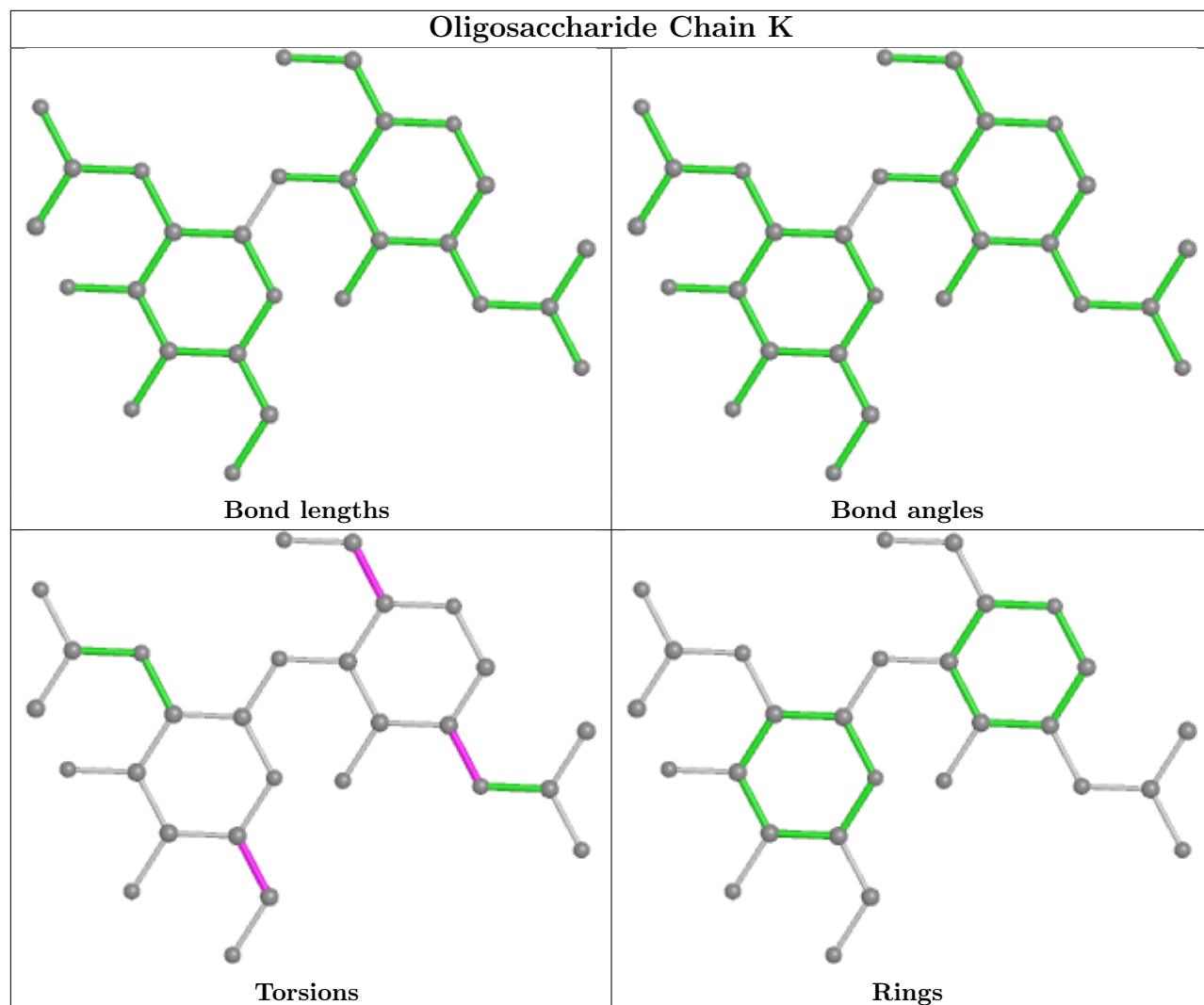
Mol	Chain	Res	Type	Atoms
4	K	1	NAG	C4-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6
4	M	2	NAG	C4-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6
4	J	2	NAG	O5-C5-C6-O6

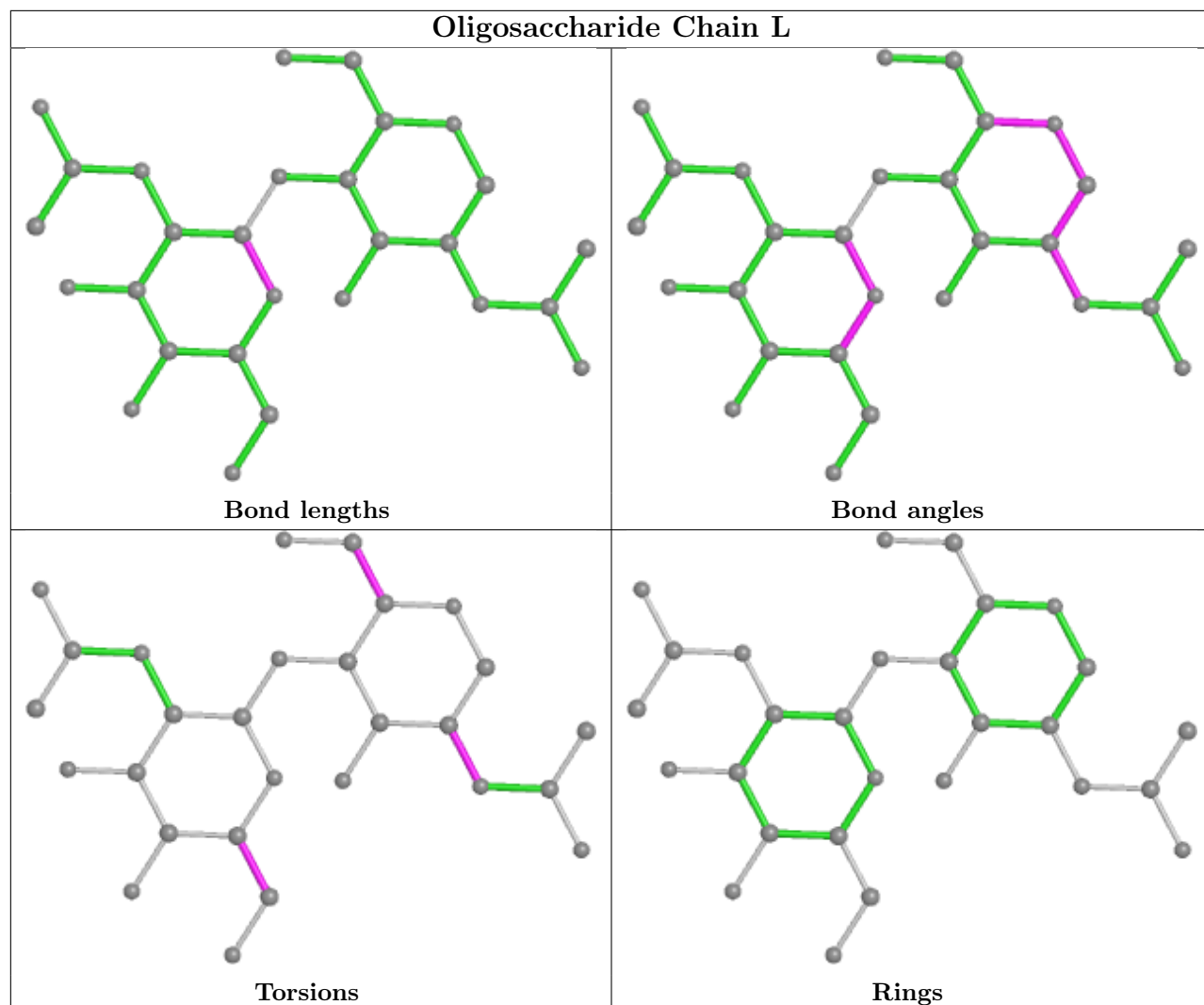
There are no ring outliers.

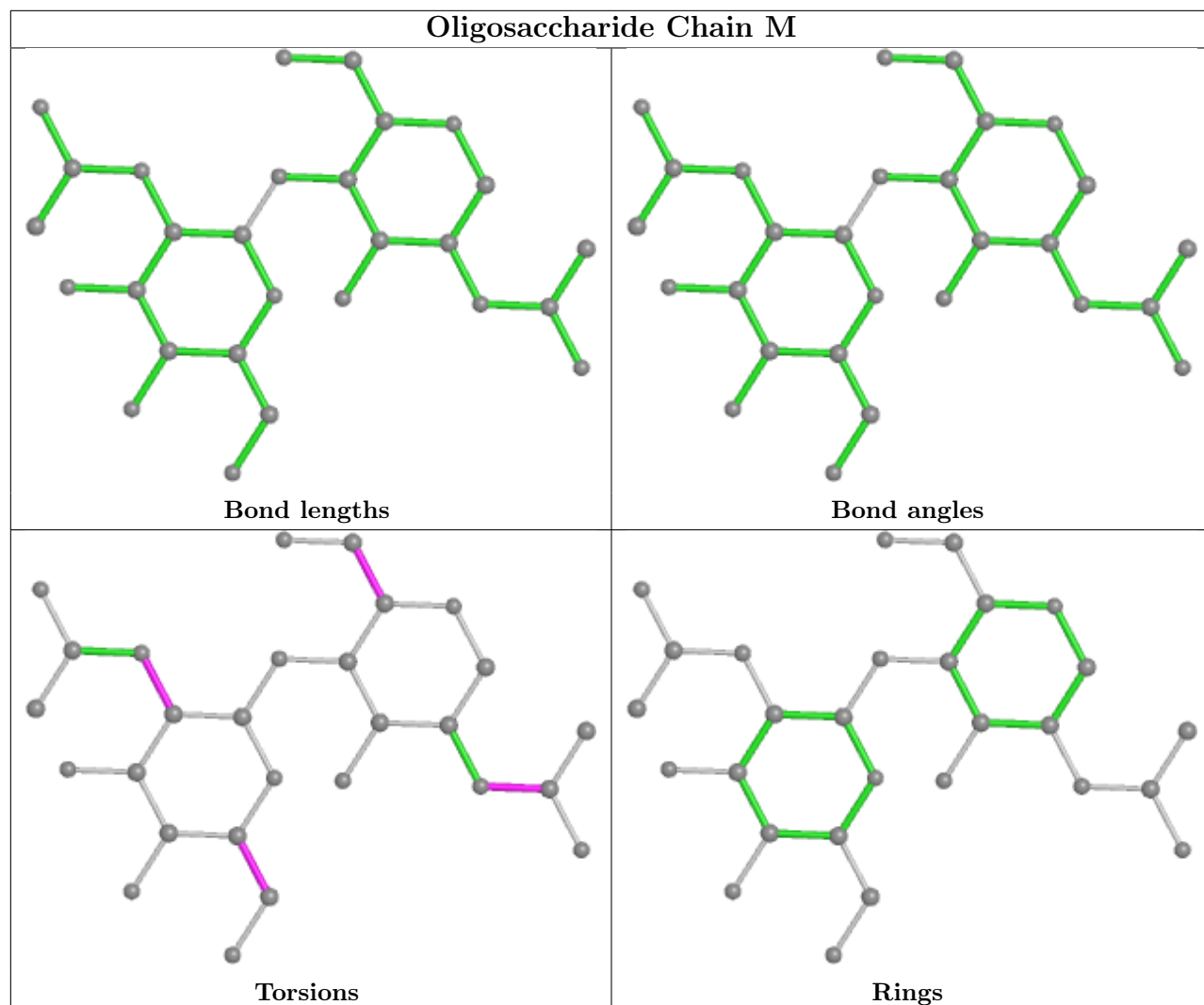
No monomer is involved in short contacts.

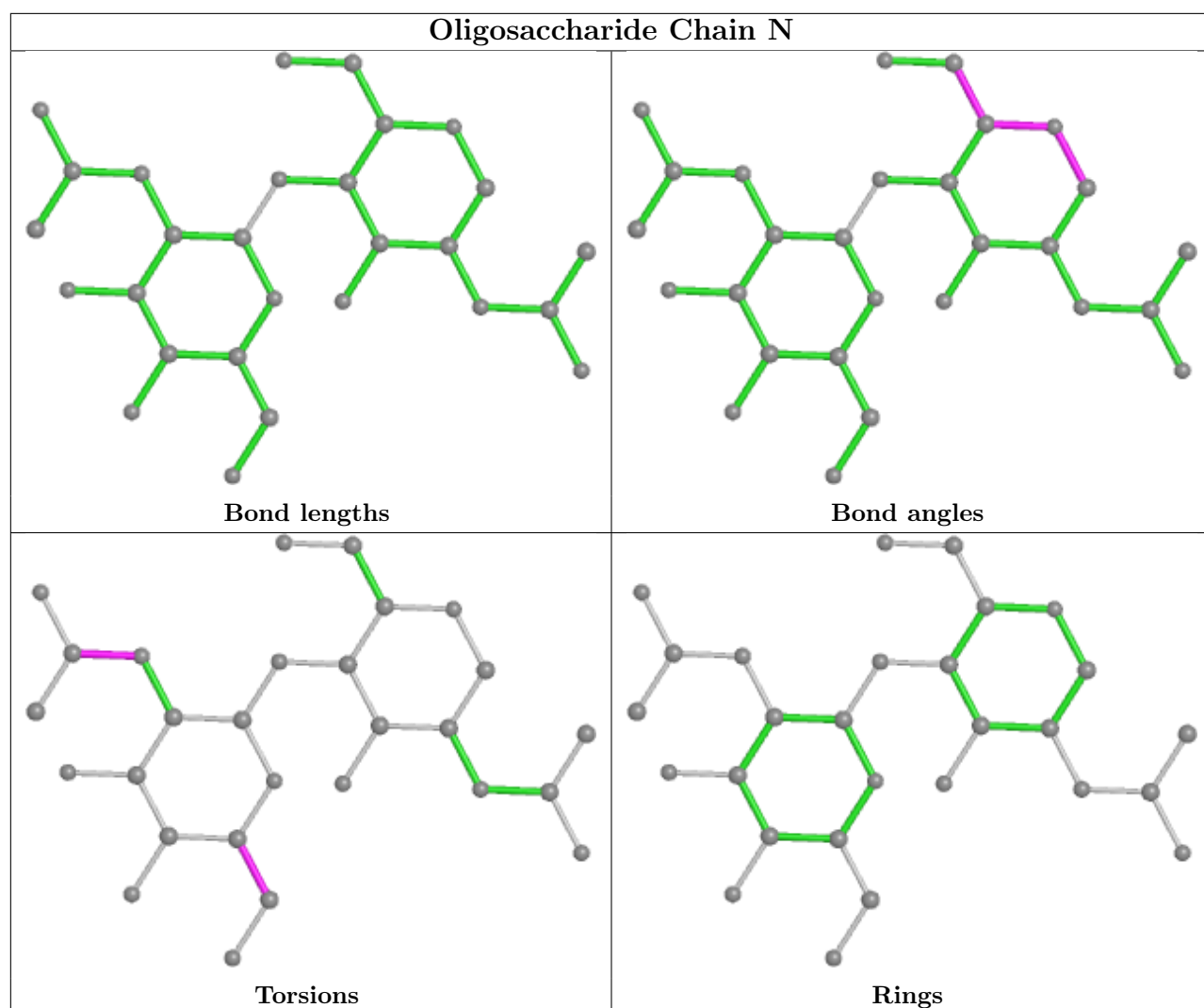
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.