



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 01:50 PM BST

PDB ID : 1C58  
Title : CRYSTAL STRUCTURE OF CYCLOAMYLOSE 26  
Authors : Gessler, K.; Saenger, W.; Nimz, O.  
Deposited on : 1999-11-04  
Resolution : 0.99 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
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) : 2.13.1

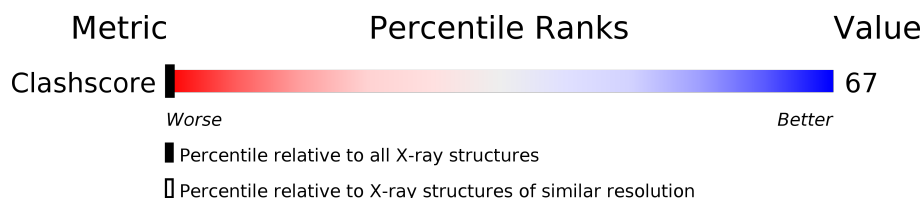
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 0.99 Å.

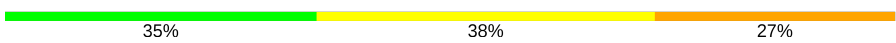
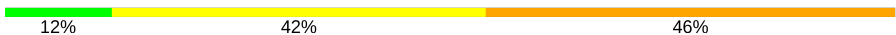
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1117 (1.06-0.94)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	26	 35% 38% 27%
1	B	26	 12% 42% 46%

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

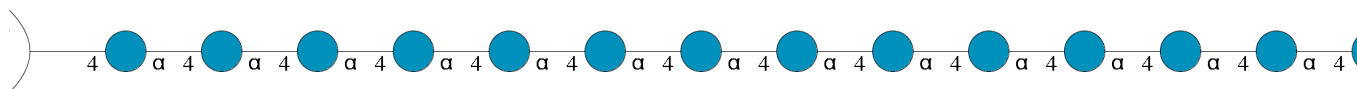
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	GLC	B	17	-	-	X	-
1	GLC	B	21	-	-	X	-
1	GLC	B	7	-	-	X	-
1	GLC	B	8	-	-	X	-

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1307 atoms, of which 571 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 an oligosaccharide called Cyclohexacosakis-(1-4)-(alpha-D-glucopyranose).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	26	Total	C	H	O	0	9	0
			582	156	287	139			
1	B	26	Total	C	H	O	0	8	0
			578	156	284	138			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	92	Total	O	0	0
			92	92		
2	B	55	Total	O	0	0
			55	55		

### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: Cyclohexacosakis-(1-4)-(alpha-D-glucopyranose)

Chain A: 



- Molecule 1: Cyclohexacosakis-(1-4)-(alpha-D-glucopyranose)

Chain B: 



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	21.84Å 22.92Å 29.05Å 87.36° 89.51° 61.98°	Depositor
Resolution (Å)	29.02 – 0.99	Depositor
% Data completeness (in resolution range)	96.7 (29.02-0.99)	Depositor
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.04	Depositor
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.082 , 0.100	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1307	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	9.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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 root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	295	287	206	11	0
1	B	294	284	209	63	0
2	A	92	0	0	6	0
2	B	55	0	0	10	0
All	All	736	571	415	69	0

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 67.

The worst 5 of 69 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2:GLC:C6	1:B:8:GLC:HO2	1.52	1.39
1:B:3:GLC:HO6	1:B:9:GLC:C4	0.89	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:GLC:O6	1:B:4:GLC:HO3	1.16	1.32
1:B:16[1]:GLC:O6	1:B:21:GLC:HO3	1.13	1.30
1:B:20:GLC:C6	1:B:26:GLC:HO3	1.59	1.30

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

69 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	$\# Z  > 2$
1	GLC	A	1	1	11,11,12	0.76	0	15,15,17	0.97	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	GLC	A	10[1]	-	11,11,12	0.91	1 (9%)	15,15,17	0.77	0
1	GLC	A	10[2]	-	11,11,12	0.89	1 (9%)	15,15,17	0.74	0
1	GLC	A	11[1]	-	11,11,12	1.29	1 (9%)	15,15,17	0.87	0
1	GLC	A	11[2]	-	11,11,12	1.28	1 (9%)	15,15,17	0.87	0
1	GLC	A	12	1	11,11,12	0.76	0	15,15,17	0.80	1 (6%)
1	GLC	A	13	1	11,11,12	0.90	1 (9%)	15,15,17	0.84	0
1	GLC	A	14	1	11,11,12	0.97	1 (9%)	15,15,17	1.39	1 (6%)
1	GLC	A	15	1	11,11,12	1.25	1 (9%)	15,15,17	1.28	1 (6%)
1	GLC	A	16[1]	-	11,11,12	0.99	1 (9%)	15,15,17	0.98	2 (13%)
1	GLC	A	16[2]	-	11,11,12	0.98	1 (9%)	15,15,17	0.97	2 (13%)
1	GLC	A	17	1	11,11,12	0.69	0	15,15,17	0.66	0
1	GLC	A	18	1	11,11,12	1.00	1 (9%)	15,15,17	0.85	0
1	GLC	A	19	1	11,11,12	0.79	0	15,15,17	0.72	0
1	GLC	A	2	1	11,11,12	0.90	1 (9%)	15,15,17	1.32	2 (13%)
1	GLC	A	20	1	11,11,12	0.68	0	15,15,17	0.71	0
1	GLC	A	21	1	11,11,12	0.88	1 (9%)	15,15,17	0.77	1 (6%)
1	GLC	A	22[1]	-	11,11,12	0.72	0	15,15,17	0.87	0
1	GLC	A	22[2]	-	11,11,12	0.70	0	15,15,17	0.87	0
1	GLC	A	23[1]	-	11,11,12	0.81	0	15,15,17	0.77	0
1	GLC	A	23[2]	-	11,11,12	0.90	0	15,15,17	0.85	0
1	GLC	A	24[1]	-	11,11,12	0.91	1 (9%)	15,15,17	0.70	0
1	GLC	A	24[2]	-	11,11,12	0.91	1 (9%)	15,15,17	0.70	0
1	GLC	A	25	1	11,11,12	0.72	0	15,15,17	0.75	0
1	GLC	A	26	1	11,11,12	0.74	0	15,15,17	1.08	1 (6%)
1	GLC	A	3	1	11,11,12	1.01	0	15,15,17	0.97	0
1	GLC	A	4[1]	-	11,11,12	1.11	1 (9%)	15,15,17	0.87	0
1	GLC	A	4[2]	-	11,11,12	1.13	1 (9%)	15,15,17	0.88	0
1	GLC	A	5[1]	-	11,11,12	0.86	1 (9%)	15,15,17	0.77	0
1	GLC	A	5[2]	-	11,11,12	0.89	1 (9%)	15,15,17	0.76	0
1	GLC	A	6	1	11,11,12	0.83	0	15,15,17	0.79	0
1	GLC	A	7	1	11,11,12	0.75	0	15,15,17	0.75	0
1	GLC	A	8	1	11,11,12	0.71	0	15,15,17	0.85	0
1	GLC	A	9[1]	-	11,11,12	0.90	0	15,15,17	0.78	0
1	GLC	A	9[2]	-	11,11,12	0.91	0	15,15,17	0.85	0
1	GLC	B	1	1	11,11,12	1.06	1 (9%)	15,15,17	0.83	0
1	GLC	B	10	1	11,11,12	0.87	1 (9%)	15,15,17	0.83	0
1	GLC	B	11[1]	-	11,11,12	0.79	0	15,15,17	0.86	0
1	GLC	B	11[2]	-	11,11,12	0.78	0	15,15,17	0.85	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	GLC	B	12[1]	-	11,11,12	0.88	0	15,15,17	0.76	0
1	GLC	B	12[2]	-	11,11,12	0.80	0	15,15,17	0.68	0
1	GLC	B	13[1]	-	11,11,12	1.07	0	15,15,17	1.00	0
1	GLC	B	13[2]	-	11,11,12	1.02	0	15,15,17	0.96	0
1	GLC	B	14	1	11,11,12	0.80	0	15,15,17	1.18	0
1	GLC	B	15	1	11,11,12	0.82	0	15,15,17	0.87	0
1	GLC	B	16[1]	-	11,11,12	1.07	1 (9%)	15,15,17	1.00	1 (6%)
1	GLC	B	16[2]	-	11,11,12	1.03	1 (9%)	15,15,17	0.99	1 (6%)
1	GLC	B	17	1	11,11,12	0.75	0	15,15,17	0.65	0
1	GLC	B	18[1]	-	11,11,12	1.03	1 (9%)	15,15,17	0.82	0
1	GLC	B	18[2]	-	11,11,12	1.03	1 (9%)	15,15,17	0.78	0
1	GLC	B	19	1	11,11,12	0.90	1 (9%)	15,15,17	0.80	0
1	GLC	B	2	1	11,11,12	1.34	2 (18%)	15,15,17	1.34	1 (6%)
1	GLC	B	20	1	11,11,12	0.86	0	15,15,17	0.65	0
1	GLC	B	21	1	11,11,12	0.79	0	15,15,17	0.86	0
1	GLC	B	22	1	11,11,12	0.91	0	15,15,17	1.06	1 (6%)
1	GLC	B	23[1]	-	11,11,12	1.25	1 (9%)	15,15,17	0.79	1 (6%)
1	GLC	B	23[2]	-	11,11,12	1.22	1 (9%)	15,15,17	0.84	1 (6%)
1	GLC	B	24[1]	-	11,11,12	0.81	1 (9%)	15,15,17	0.82	1 (6%)
1	GLC	B	24[2]	-	11,11,12	0.81	1 (9%)	15,15,17	0.82	1 (6%)
1	GLC	B	25[1]	-	11,11,12	1.04	1 (9%)	15,15,17	0.58	0
1	GLC	B	25[2]	-	11,11,12	1.04	1 (9%)	15,15,17	0.58	0
1	GLC	B	26	1	11,11,12	1.10	1 (9%)	15,15,17	1.17	0
1	GLC	B	3	1	11,11,12	1.04	1 (9%)	15,15,17	0.97	1 (6%)
1	GLC	B	4	1	11,11,12	0.79	1 (9%)	15,15,17	0.68	0
1	GLC	B	5	1	11,11,12	0.85	0	15,15,17	0.81	0
1	GLC	B	6	1	11,11,12	0.83	0	15,15,17	0.83	1 (6%)
1	GLC	B	7	1	11,11,12	0.83	0	15,15,17	0.70	0
1	GLC	B	8	1	11,11,12	1.16	1 (9%)	15,15,17	1.03	1 (6%)
1	GLC	B	9	1	11,11,12	0.95	1 (9%)	15,15,17	0.89	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
1	GLC	A	1	1	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	GLC	A	10[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	10[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	11[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	11[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	12	1	-	0/2/19/22	0/1/1/1
1	GLC	A	13	1	-	0/2/19/22	0/1/1/1
1	GLC	A	14	1	-	0/2/19/22	0/1/1/1
1	GLC	A	15	1	-	0/2/19/22	0/1/1/1
1	GLC	A	16[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	16[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	17	1	-	0/2/19/22	0/1/1/1
1	GLC	A	18	1	-	0/2/19/22	0/1/1/1
1	GLC	A	19	1	-	0/2/19/22	0/1/1/1
1	GLC	A	2	1	-	0/2/19/22	0/1/1/1
1	GLC	A	20	1	-	0/2/19/22	0/1/1/1
1	GLC	A	21	1	-	0/2/19/22	0/1/1/1
1	GLC	A	22[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	22[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	23[1]	-	-	2/2/19/22	0/1/1/1
1	GLC	A	23[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	24[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	24[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	25	1	-	0/2/19/22	0/1/1/1
1	GLC	A	26	1	-	0/2/19/22	0/1/1/1
1	GLC	A	3	1	-	0/2/19/22	0/1/1/1
1	GLC	A	4[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	4[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	5[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	5[2]	-	-	1/2/19/22	0/1/1/1
1	GLC	A	6	1	-	0/2/19/22	0/1/1/1
1	GLC	A	7	1	-	0/2/19/22	0/1/1/1
1	GLC	A	8	1	-	0/2/19/22	0/1/1/1
1	GLC	A	9[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	A	9[2]	-	-	1/2/19/22	0/1/1/1
1	GLC	B	1	1	-	0/2/19/22	0/1/1/1
1	GLC	B	10	1	-	0/2/19/22	0/1/1/1
1	GLC	B	11[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	11[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	12[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	12[2]	-	-	1/2/19/22	0/1/1/1
1	GLC	B	13[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	13[2]	-	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	GLC	B	14	1	-	0/2/19/22	0/1/1/1
1	GLC	B	15	1	-	0/2/19/22	0/1/1/1
1	GLC	B	16[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	16[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	17	1	-	0/2/19/22	0/1/1/1
1	GLC	B	18[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	18[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	19	1	-	0/2/19/22	0/1/1/1
1	GLC	B	2	1	-	0/2/19/22	0/1/1/1
1	GLC	B	20	1	-	0/2/19/22	0/1/1/1
1	GLC	B	21	1	-	0/2/19/22	0/1/1/1
1	GLC	B	22	1	-	0/2/19/22	0/1/1/1
1	GLC	B	23[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	23[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	24[1]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	24[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	25[1]	-	-	1/2/19/22	0/1/1/1
1	GLC	B	25[2]	-	-	0/2/19/22	0/1/1/1
1	GLC	B	26	1	-	0/2/19/22	0/1/1/1
1	GLC	B	3	1	-	0/2/19/22	0/1/1/1
1	GLC	B	4	1	-	0/2/19/22	0/1/1/1
1	GLC	B	5	1	-	0/2/19/22	0/1/1/1
1	GLC	B	6	1	-	0/2/19/22	0/1/1/1
1	GLC	B	7	1	-	0/2/19/22	0/1/1/1
1	GLC	B	8	1	-	0/2/19/22	0/1/1/1
1	GLC	B	9	1	-	0/2/19/22	0/1/1/1

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2	GLC	O5-C1	-3.46	1.38	1.43
1	B	23[2]	GLC	O5-C1	-3.22	1.38	1.43
1	B	23[1]	GLC	O5-C1	-3.22	1.38	1.43
1	A	15	GLC	O5-C1	-3.18	1.38	1.43
1	A	11[2]	GLC	O5-C1	-3.11	1.38	1.43

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	14	GLC	C1-C2-C3	3.91	114.47	109.67
1	A	15	GLC	C1-O5-C5	3.39	116.79	112.19
1	B	2	GLC	C1-O5-C5	2.81	116.00	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2	GLC	C1-C2-C3	2.66	112.94	109.67
1	B	23[2]	GLC	C1-O5-C5	2.38	115.41	112.19

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	23[1]	GLC	O5-C5-C6-O6
1	B	25[1]	GLC	O5-C5-C6-O6
1	B	12[2]	GLC	O5-C5-C6-O6
1	A	23[1]	GLC	C4-C5-C6-O6
1	A	9[2]	GLC	O5-C5-C6-O6

There are no ring outliers.

29 monomers are involved in 67 short contacts:

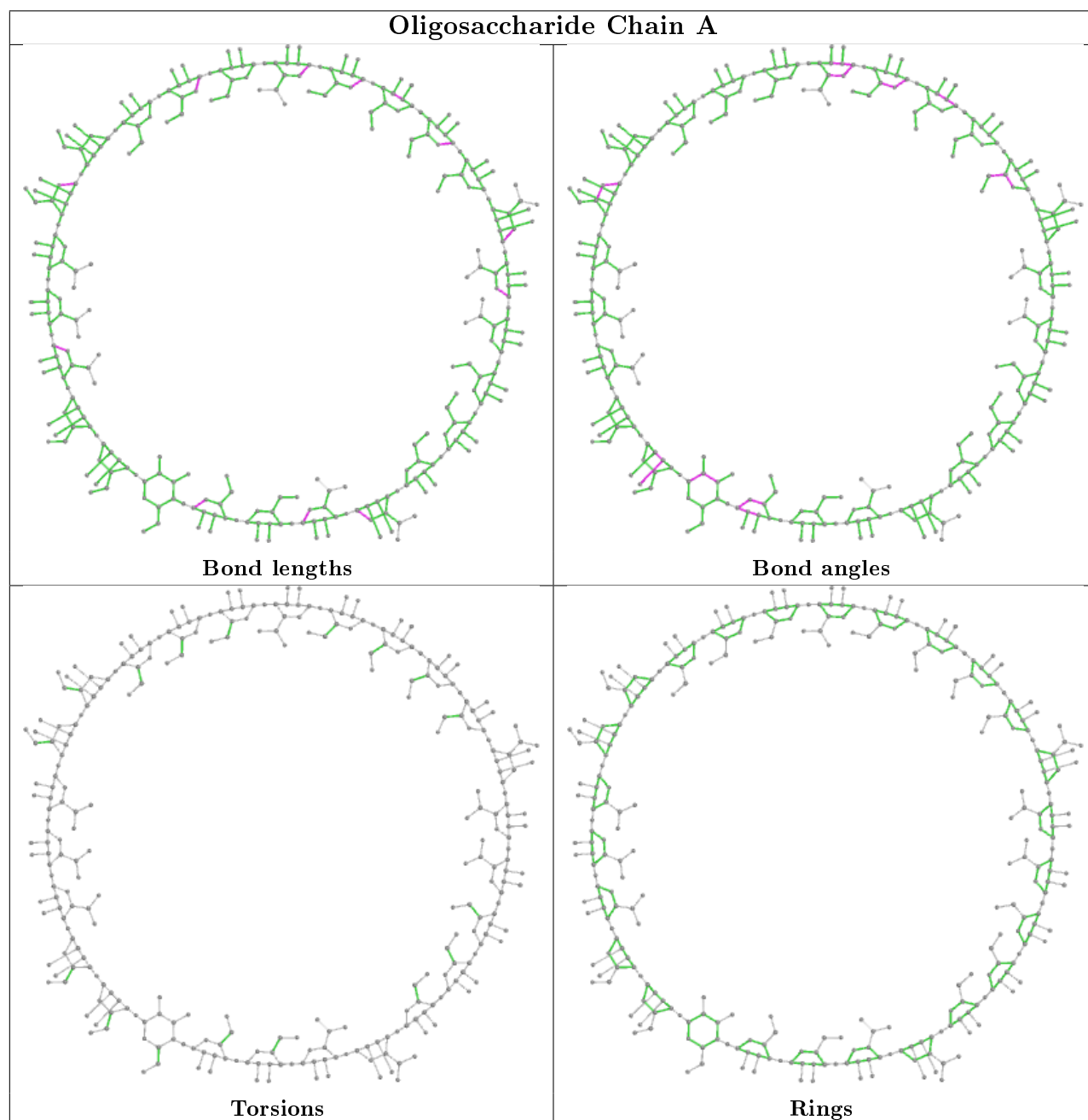
Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	10[1]	GLC	1	0
1	A	16[1]	GLC	1	0
1	B	1	GLC	5	0
1	A	2	GLC	1	0
1	B	11[2]	GLC	2	0
1	B	8	GLC	9	0
1	B	7	GLC	11	0
1	B	26	GLC	3	0
1	B	16[2]	GLC	1	0
1	A	5[2]	GLC	1	0
1	B	16[1]	GLC	2	0
1	A	8	GLC	1	0
1	B	21	GLC	11	0
1	B	3	GLC	5	0
1	B	2	GLC	5	0
1	B	10	GLC	4	0
1	B	15	GLC	4	0
1	B	4	GLC	3	0
1	B	9	GLC	5	0
1	B	17	GLC	6	0
1	B	24[1]	GLC	1	0
1	A	18	GLC	3	0
1	A	14	GLC	1	0
1	A	12	GLC	1	0

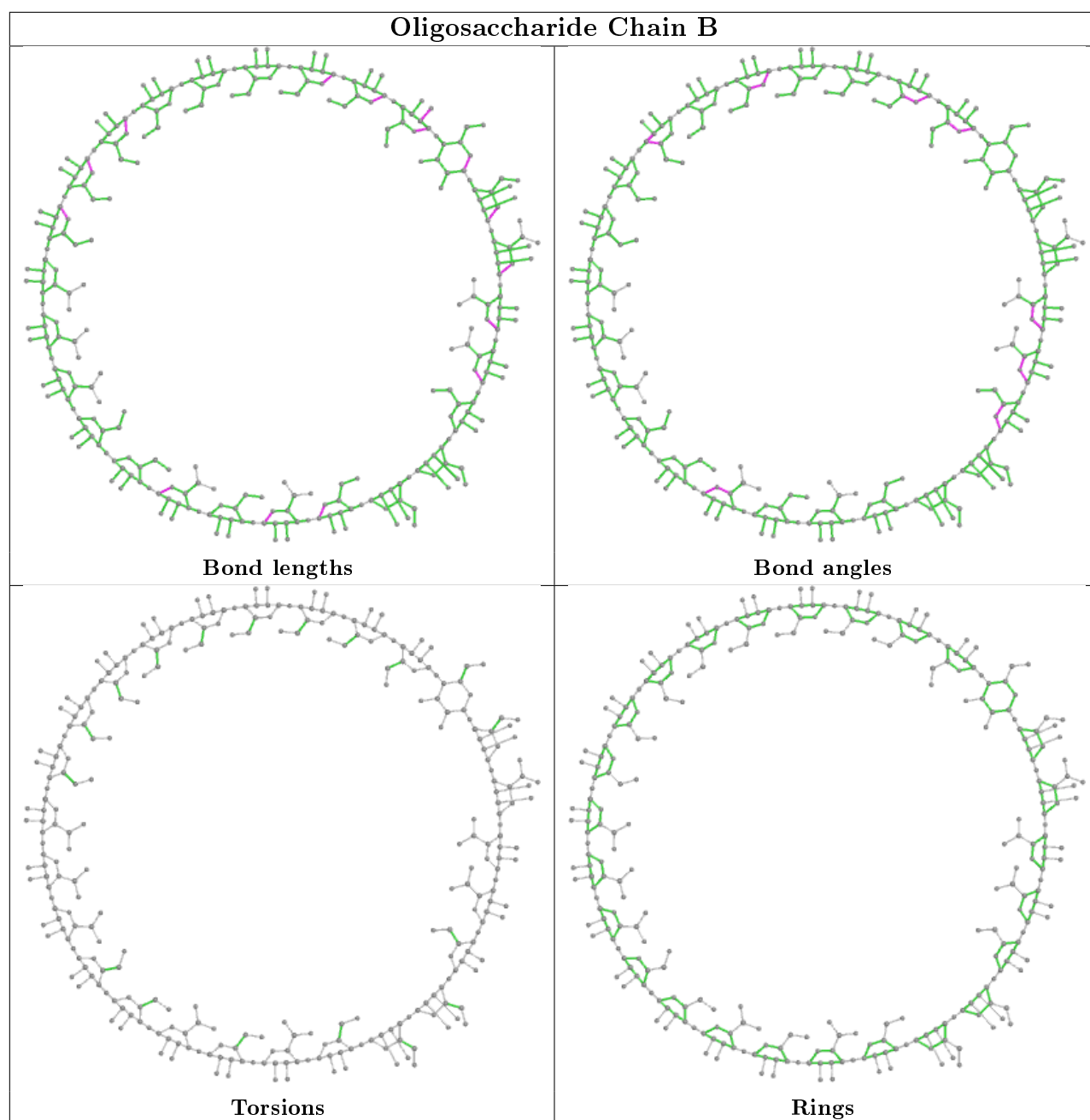
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	7	GLC	2	0
1	B	23[1]	GLC	1	0
1	B	14	GLC	2	0
1	B	19	GLC	2	0
1	B	20	GLC	4	0

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





## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.