



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 9, 2024 – 03:40 PM EST

PDB ID : 3CHB  
Title : CHOLERA TOXIN B-PENTAMER COMPLEXED WITH GM1 PEN-TASACCHARIDE  
Authors : Merritt, E.A.; Hol, W.G.J.  
Deposited on : 1998-03-24  
Resolution : 1.25 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	<b>FAILED</b>
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

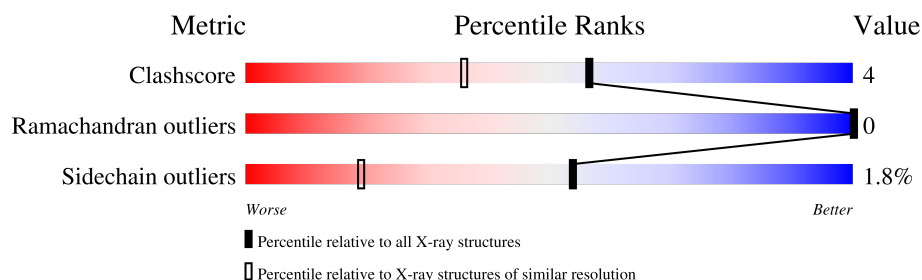
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.25 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	180529	1571 (1.28-1.24)
Ramachandran outliers	177936	1538 (1.28-1.24)
Sidechain outliers	177891	1537 (1.28-1.24)


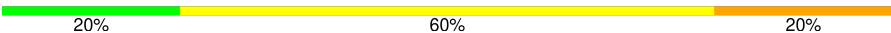

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	D	104	
1	E	104	
1	F	104	
1	G	104	
1	H	104	
2	A	5	
2	C	5	

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Mol	Chain	Length	Quality of chain
3	B	5	 20%80%
3	I	5	 20%60%20%
3	J	5	 20%80%

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5203 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 CHOLERA TOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	103	Total	C	N	O	S	0	3	0
			823	517	144	156	6			
1	E	103	Total	C	N	O	S	0	3	0
			823	517	144	156	6			
1	F	103	Total	C	N	O	S	0	1	0
			816	511	143	156	6			
1	G	103	Total	C	N	O	S	0	2	0
			818	513	143	156	6			
1	H	103	Total	C	N	O	S	0	2	0
			818	513	143	156	6			

There are 115 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	ILE	deletion	UNP P01556
D	?	-	LYS	deletion	UNP P01556
D	?	-	LEU	deletion	UNP P01556
D	?	-	LYS	deletion	UNP P01556
D	?	-	PHE	deletion	UNP P01556
D	?	-	GLY	deletion	UNP P01556
D	?	-	VAL	deletion	UNP P01556
D	?	-	PHE	deletion	UNP P01556
D	?	-	PHE	deletion	UNP P01556
D	?	-	THR	deletion	UNP P01556
D	?	-	VAL	deletion	UNP P01556
D	?	-	LEU	deletion	UNP P01556
D	?	-	LEU	deletion	UNP P01556
D	?	-	SER	deletion	UNP P01556
D	?	-	SER	deletion	UNP P01556
D	?	-	ALA	deletion	UNP P01556
D	?	-	TYR	deletion	UNP P01556
D	?	-	ALA	deletion	UNP P01556
D	?	-	HIS	deletion	UNP P01556

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	GLY	deletion	UNP P01556
D	18	HIS	TYR	conflict	UNP P01556
D	47	THR	ILE	conflict	UNP P01556
D	94	ARG	HIS	cloning artifact	UNP P01556
E	?	-	ILE	deletion	UNP P01556
E	?	-	LYS	deletion	UNP P01556
E	?	-	LEU	deletion	UNP P01556
E	?	-	LYS	deletion	UNP P01556
E	?	-	PHE	deletion	UNP P01556
E	?	-	GLY	deletion	UNP P01556
E	?	-	VAL	deletion	UNP P01556
E	?	-	PHE	deletion	UNP P01556
E	?	-	PHE	deletion	UNP P01556
E	?	-	THR	deletion	UNP P01556
E	?	-	VAL	deletion	UNP P01556
E	?	-	LEU	deletion	UNP P01556
E	?	-	LEU	deletion	UNP P01556
E	?	-	SER	deletion	UNP P01556
E	?	-	SER	deletion	UNP P01556
E	?	-	ALA	deletion	UNP P01556
E	?	-	TYR	deletion	UNP P01556
E	?	-	ALA	deletion	UNP P01556
E	?	-	HIS	deletion	UNP P01556
E	?	-	GLY	deletion	UNP P01556
E	18	HIS	TYR	conflict	UNP P01556
E	47	THR	ILE	conflict	UNP P01556
E	94	ARG	HIS	cloning artifact	UNP P01556
F	?	-	ILE	deletion	UNP P01556
F	?	-	LYS	deletion	UNP P01556
F	?	-	LEU	deletion	UNP P01556
F	?	-	LYS	deletion	UNP P01556
F	?	-	PHE	deletion	UNP P01556
F	?	-	GLY	deletion	UNP P01556
F	?	-	VAL	deletion	UNP P01556
F	?	-	PHE	deletion	UNP P01556
F	?	-	PHE	deletion	UNP P01556
F	?	-	THR	deletion	UNP P01556
F	?	-	VAL	deletion	UNP P01556
F	?	-	LEU	deletion	UNP P01556
F	?	-	LEU	deletion	UNP P01556
F	?	-	SER	deletion	UNP P01556
F	?	-	SER	deletion	UNP P01556

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Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	ALA	deletion	UNP P01556
F	?	-	TYR	deletion	UNP P01556
F	?	-	ALA	deletion	UNP P01556
F	?	-	HIS	deletion	UNP P01556
F	?	-	GLY	deletion	UNP P01556
F	18	HIS	TYR	conflict	UNP P01556
F	47	THR	ILE	conflict	UNP P01556
F	94	ARG	HIS	cloning artifact	UNP P01556
G	?	-	ILE	deletion	UNP P01556
G	?	-	LYS	deletion	UNP P01556
G	?	-	LEU	deletion	UNP P01556
G	?	-	LYS	deletion	UNP P01556
G	?	-	PHE	deletion	UNP P01556
G	?	-	GLY	deletion	UNP P01556
G	?	-	VAL	deletion	UNP P01556
G	?	-	PHE	deletion	UNP P01556
G	?	-	PHE	deletion	UNP P01556
G	?	-	THR	deletion	UNP P01556
G	?	-	VAL	deletion	UNP P01556
G	?	-	LEU	deletion	UNP P01556
G	?	-	LEU	deletion	UNP P01556
G	?	-	SER	deletion	UNP P01556
G	?	-	SER	deletion	UNP P01556
G	?	-	ALA	deletion	UNP P01556
G	?	-	TYR	deletion	UNP P01556
G	?	-	ALA	deletion	UNP P01556
G	?	-	HIS	deletion	UNP P01556
G	?	-	GLY	deletion	UNP P01556
G	18	HIS	TYR	conflict	UNP P01556
G	47	THR	ILE	conflict	UNP P01556
G	94	ARG	HIS	cloning artifact	UNP P01556
H	?	-	ILE	deletion	UNP P01556
H	?	-	LYS	deletion	UNP P01556
H	?	-	LEU	deletion	UNP P01556
H	?	-	LYS	deletion	UNP P01556
H	?	-	PHE	deletion	UNP P01556
H	?	-	GLY	deletion	UNP P01556
H	?	-	VAL	deletion	UNP P01556
H	?	-	PHE	deletion	UNP P01556
H	?	-	PHE	deletion	UNP P01556
H	?	-	THR	deletion	UNP P01556
H	?	-	VAL	deletion	UNP P01556

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Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	LEU	deletion	UNP P01556
H	?	-	LEU	deletion	UNP P01556
H	?	-	SER	deletion	UNP P01556
H	?	-	SER	deletion	UNP P01556
H	?	-	ALA	deletion	UNP P01556
H	?	-	TYR	deletion	UNP P01556
H	?	-	ALA	deletion	UNP P01556
H	?	-	HIS	deletion	UNP P01556
H	?	-	GLY	deletion	UNP P01556
H	18	HIS	TYR	conflict	UNP P01556
H	47	THR	ILE	conflict	UNP P01556
H	94	ARG	HIS	cloning artifact	UNP P01556

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	A	5	Total	C	N	O	0	0	1
			57	31	2	24			
2	C	5	Total	C	N	O	0	0	1
			57	31	2	24			

- Molecule 3 is an oligosaccharide called beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose-(1-4)-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	5	Total	C	N	O	0	0	0
			68	37	2	29			
3	I	5	Total	C	N	O	0	0	0
			68	37	2	29			
3	J	5	Total	C	N	O	0	0	0
			68	37	2	29			

- Molecule 4 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

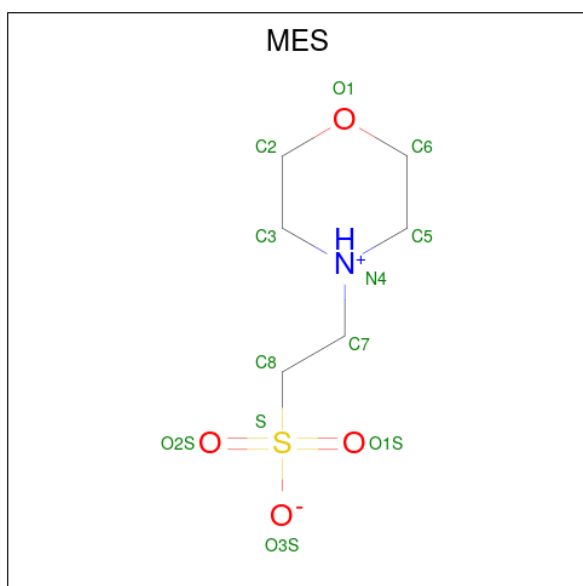
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	X	0	0
			1	1		
4	E	1	Total	X	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	1	Total	X	0	0
			1	1		
4	G	1	Total	X	0	0
			1	1		
4	H	1	Total	X	0	0
			1	1		

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	G	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
5	G	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	152	Total	O	0	0
			152	152		
6	E	145	Total	O	0	0
			145	145		
6	F	135	Total	O	0	0
			135	135		
6	G	161	Total	O	0	0
			161	161		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	165	Total 165	O 165	0	0

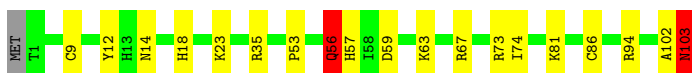
### 3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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 failed to run properly.

- Molecule 1: CHOLERA TOXIN

Chain D: 




- Molecule 1: CHOLERA TOXIN

Chain E: 




- Molecule 1: CHOLERA TOXIN

Chain F: 




- Molecule 1: CHOLERA TOXIN

Chain G: 



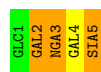
- Molecule 1: CHOLERA TOXIN

Chain H: 



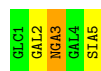
- Molecule 2: beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain A: 



- Molecule 2: beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain C: 



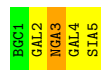
- Molecule 3: beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain B: 



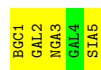
- Molecule 3: beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain I: 



- Molecule 3: beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain J: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.12Å 66.18Å 78.22Å 90.00° 106.33° 90.00°	Depositor
Resolution (Å)	22.00 – 1.25	Depositor
% Data completeness (in resolution range)	92.0 (22.00-1.25)	Depositor
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.49 (at 1.25Å)	Xtriage
Refinement program	SHELX-96	Depositor
R, $R_{free}$	0.133 , 0.180	Depositor
Wilson B-factor (Å <sup>2</sup> )	10.8	Xtriage
Anisotropy	0.324	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5203	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SIA, GLC, GAL, UNX, NGA, MES, BGC

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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	D	0.69	0/851	1.46	14/1147 (1.2%)
1	E	0.66	0/851	1.42	13/1147 (1.1%)
1	F	0.64	0/834	1.43	9/1125 (0.8%)
1	G	0.67	0/842	1.36	10/1136 (0.9%)
1	H	0.66	0/842	1.34	11/1136 (1.0%)
All	All	0.66	0/4220	1.40	57/5691 (1.0%)

There are no bond length outliers.

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	F	73	ARG	NE-CZ-NH2	17.87	129.24	120.30
1	H	73	ARG	NE-CZ-NH2	13.96	127.28	120.30
1	G	67	ARG	NE-CZ-NH2	-13.59	113.50	120.30
1	D	67	ARG	NE-CZ-NH1	12.84	126.72	120.30
1	H	67	ARG	NE-CZ-NH1	12.70	126.65	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 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	D	823	0	834	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	823	0	833	6	0
1	F	816	0	824	5	0
1	G	818	0	824	9	0
1	H	818	0	825	3	0
2	A	57	0	47	6	0
2	C	57	0	47	1	0
3	B	68	0	58	0	0
3	I	68	0	58	1	0
3	J	68	0	58	0	0
4	D	1	0	0	1	0
4	E	1	0	0	1	0
4	F	1	0	0	1	0
4	G	1	0	0	1	0
4	H	1	0	0	1	0
5	G	24	0	26	1	0
6	D	152	0	0	7	0
6	E	145	0	0	3	0
6	F	135	0	0	4	0
6	G	161	0	0	4	0
6	H	165	0	0	0	0
All	All	5203	0	4434	40	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 4.

The worst 5 of 40 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:D:74[B]:ILE:HD12	6:D:9835:HOH:O	1.82	0.78
1:F:9[B]:CYS:SG	4:F:109:UNX:UNK	2.07	0.76
1:D:9[B]:CYS:SG	4:D:109:UNX:UNK	2.09	0.74
1:G:9[B]:CYS:SG	4:G:109:UNX:UNK	2.09	0.73
1:H:9[B]:CYS:SG	4:H:109:UNX:UNK	2.09	0.73

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	D	104/104 (100%)	103 (99%)	1 (1%)	0	100	100
1	E	104/104 (100%)	103 (99%)	1 (1%)	0	100	100
1	F	102/104 (98%)	101 (99%)	1 (1%)	0	100	100
1	G	103/104 (99%)	102 (99%)	1 (1%)	0	100	100
1	H	103/104 (99%)	102 (99%)	1 (1%)	0	100	100
All	All	516/520 (99%)	511 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	D	92/90 (102%)	89 (97%)	3 (3%)	33	4
1	E	92/90 (102%)	90 (98%)	2 (2%)	47	12
1	F	90/90 (100%)	89 (99%)	1 (1%)	70	36
1	G	91/90 (101%)	90 (99%)	1 (1%)	70	36
1	H	91/90 (101%)	90 (99%)	1 (1%)	70	36
All	All	456/450 (101%)	448 (98%)	8 (2%)	54	19

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	103	ASN
1	G	94	ARG
1	E	94	ARG
1	E	56	GLN
1	F	63	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	103	ASN
1	G	103	ASN
1	F	18	HIS
1	E	103	ASN
1	G	13	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

Of 25 monosaccharides modelled in this entry, 23 were used for Mogul analysis.

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	$\# Z  > 2$
2	GAL	A	2	2	11,11,12	0.48	0	15,15,17	1.31	3 (20%)
2	NGA	A	3	2	14,14,15	0.79	0	17,19,21	1.83	5 (29%)
2	GAL	A	4	2	11,11,12	0.56	0	15,15,17	1.09	1 (6%)
2	SIA	A	5	2	20,20,21	0.90	1 (5%)	21,28,31	1.78	6 (28%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	BGC	B	1	3	12,12,12	0.60	0	17,17,17	1.04	1 (5%)
3	GAL	B	2	3	11,11,12	0.55	0	15,15,17	1.13	1 (6%)
3	NGA	B	3	3	14,14,15	0.85	0	17,19,21	1.38	3 (17%)
3	GAL	B	4	3	11,11,12	0.29	0	15,15,17	0.77	0
3	SIA	B	5	3	20,20,21	1.03	1 (5%)	21,28,31	1.66	5 (23%)
2	GAL	C	2	2	11,11,12	0.49	0	15,15,17	1.43	1 (6%)
2	NGA	C	3	2	14,14,15	0.86	1 (7%)	17,19,21	1.97	5 (29%)
2	GAL	C	4	2	11,11,12	0.43	0	15,15,17	1.10	0
2	SIA	C	5	2	20,20,21	0.88	1 (5%)	21,28,31	1.86	6 (28%)
3	BGC	I	1	3	12,12,12	0.54	0	17,17,17	1.23	0
3	GAL	I	2	3	11,11,12	0.65	0	15,15,17	1.24	2 (13%)
3	NGA	I	3	3	14,14,15	0.82	0	17,19,21	1.35	2 (11%)
3	GAL	I	4	3	11,11,12	0.71	0	15,15,17	0.88	1 (6%)
3	SIA	I	5	3	20,20,21	1.04	1 (5%)	21,28,31	1.45	4 (19%)
3	BGC	J	1	3	12,12,12	0.66	0	17,17,17	1.59	3 (17%)
3	GAL	J	2	3	11,11,12	0.47	0	15,15,17	1.33	2 (13%)
3	NGA	J	3	3	14,14,15	0.80	0	17,19,21	1.66	4 (23%)
3	GAL	J	4	3	11,11,12	0.38	0	15,15,17	1.01	0
3	SIA	J	5	3	20,20,21	0.88	0	21,28,31	1.94	6 (28%)

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	GAL	A	2	2	-	2/2/19/22	0/1/1/1
2	NGA	A	3	2	-	1/6/23/26	0/1/1/1
2	GAL	A	4	2	-	0/2/19/22	0/1/1/1
2	SIA	A	5	2	-	3/18/34/38	0/1/1/1
3	BGC	B	1	3	-	0/2/22/22	0/1/1/1
3	GAL	B	2	3	-	0/2/19/22	0/1/1/1
3	NGA	B	3	3	-	0/6/23/26	0/1/1/1
3	GAL	B	4	3	-	0/2/19/22	0/1/1/1
3	SIA	B	5	3	-	2/18/34/38	0/1/1/1
2	GAL	C	2	2	-	0/2/19/22	0/1/1/1
2	NGA	C	3	2	-	1/6/23/26	0/1/1/1
2	GAL	C	4	2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SIA	C	5	2	-	3/18/34/38	0/1/1/1
3	BGC	I	1	3	-	0/2/22/22	0/1/1/1
3	GAL	I	2	3	-	0/2/19/22	0/1/1/1
3	NGA	I	3	3	-	1/6/23/26	0/1/1/1
3	GAL	I	4	3	-	0/2/19/22	0/1/1/1
3	SIA	I	5	3	-	3/18/34/38	0/1/1/1
3	BGC	J	1	3	-	0/2/22/22	0/1/1/1
3	GAL	J	2	3	-	0/2/19/22	0/1/1/1
3	NGA	J	3	3	-	2/6/23/26	0/1/1/1
3	GAL	J	4	3	-	0/2/19/22	0/1/1/1
3	SIA	J	5	3	-	2/18/34/38	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5	SIA	C11-C10	2.33	1.55	1.50
3	B	5	SIA	C11-C10	2.26	1.55	1.50
3	I	5	SIA	O1A-C1	2.06	1.28	1.22
2	C	3	NGA	C8-C7	2.05	1.54	1.50
2	C	5	SIA	O1B-C1	-2.02	1.24	1.30

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3	NGA	O7-C7-C8	4.93	130.83	122.05
2	C	5	SIA	O10-C10-C11	4.88	130.74	122.05
3	J	1	BGC	C1-O5-C5	4.73	122.79	113.65
2	C	2	GAL	C1-O5-C5	4.70	118.48	112.19
2	A	5	SIA	O10-C10-C11	4.48	130.03	122.05

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

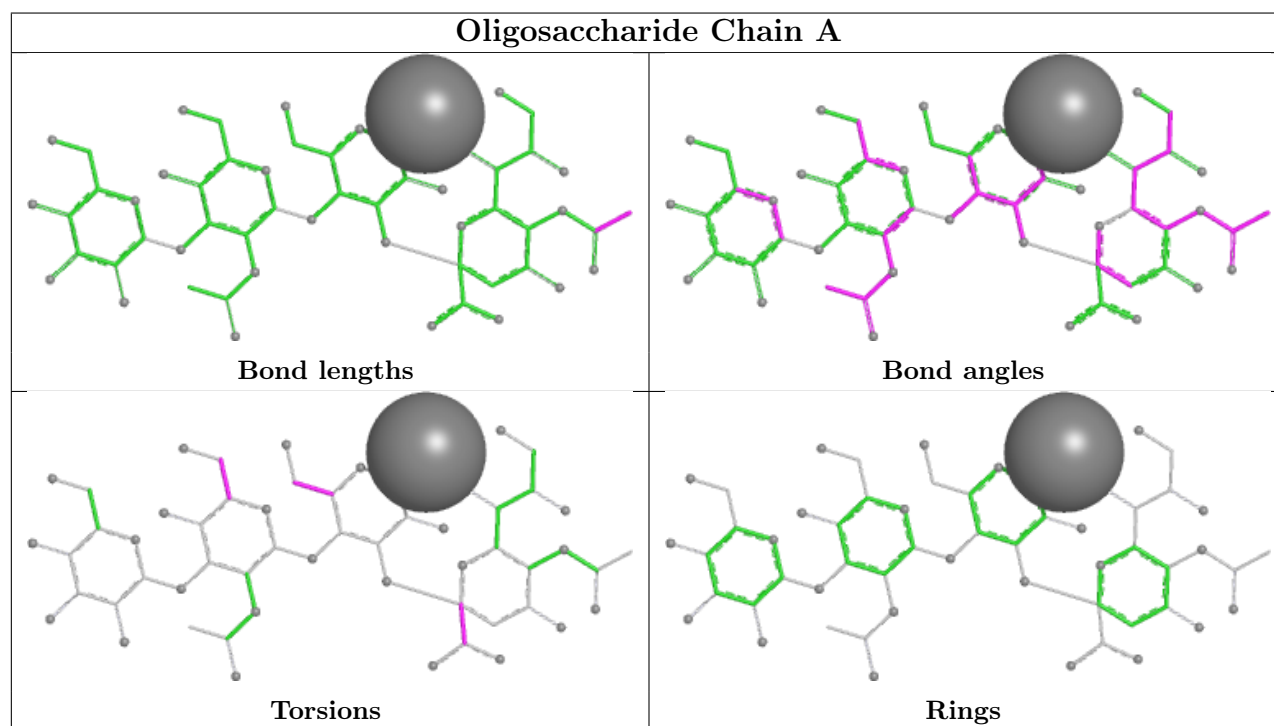
Mol	Chain	Res	Type	Atoms
2	C	5	SIA	O1A-C1-C2-O6
3	B	5	SIA	O1A-C1-C2-O6
3	I	5	SIA	O1A-C1-C2-O6
3	J	5	SIA	O1A-C1-C2-O6
3	J	3	NGA	O5-C5-C6-O6

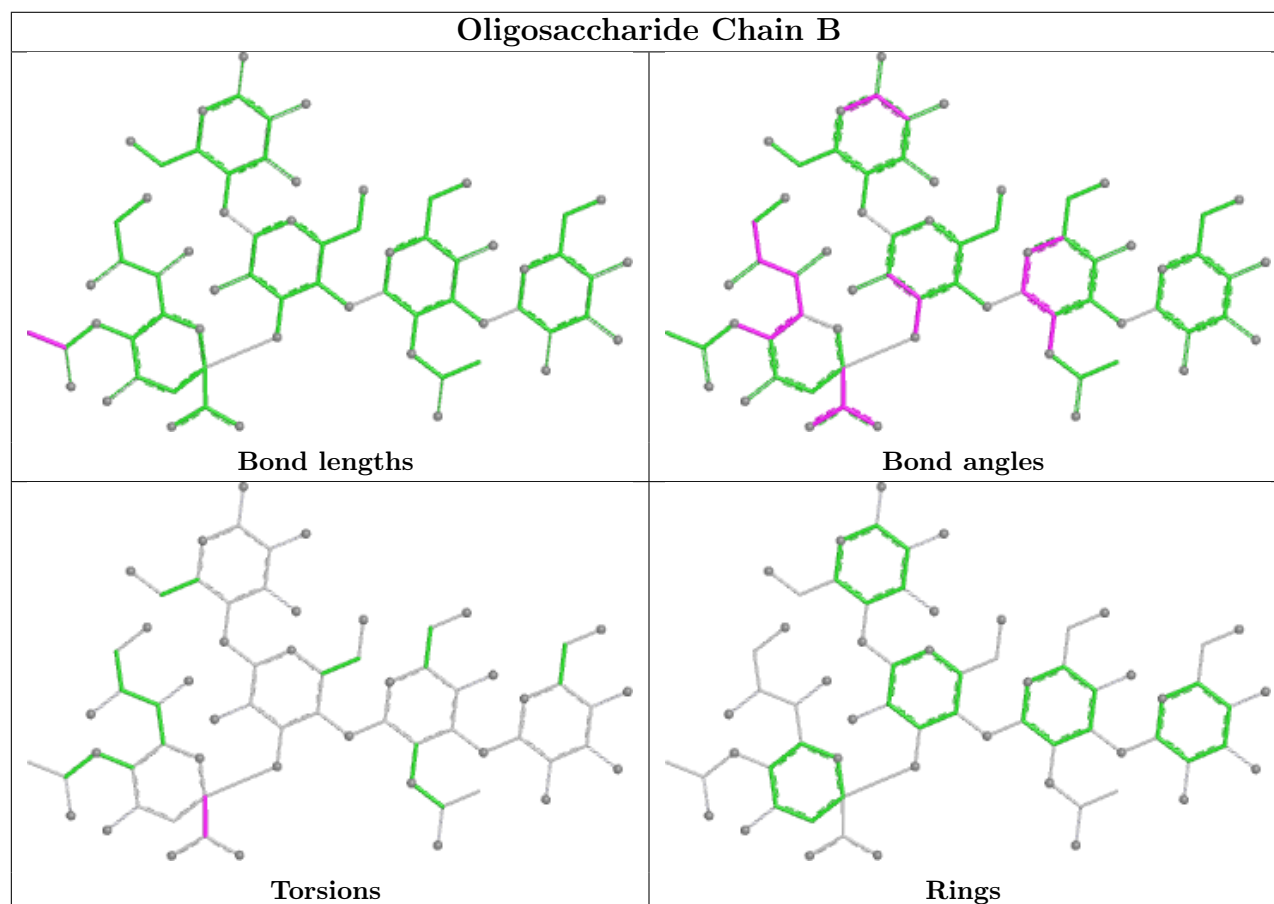
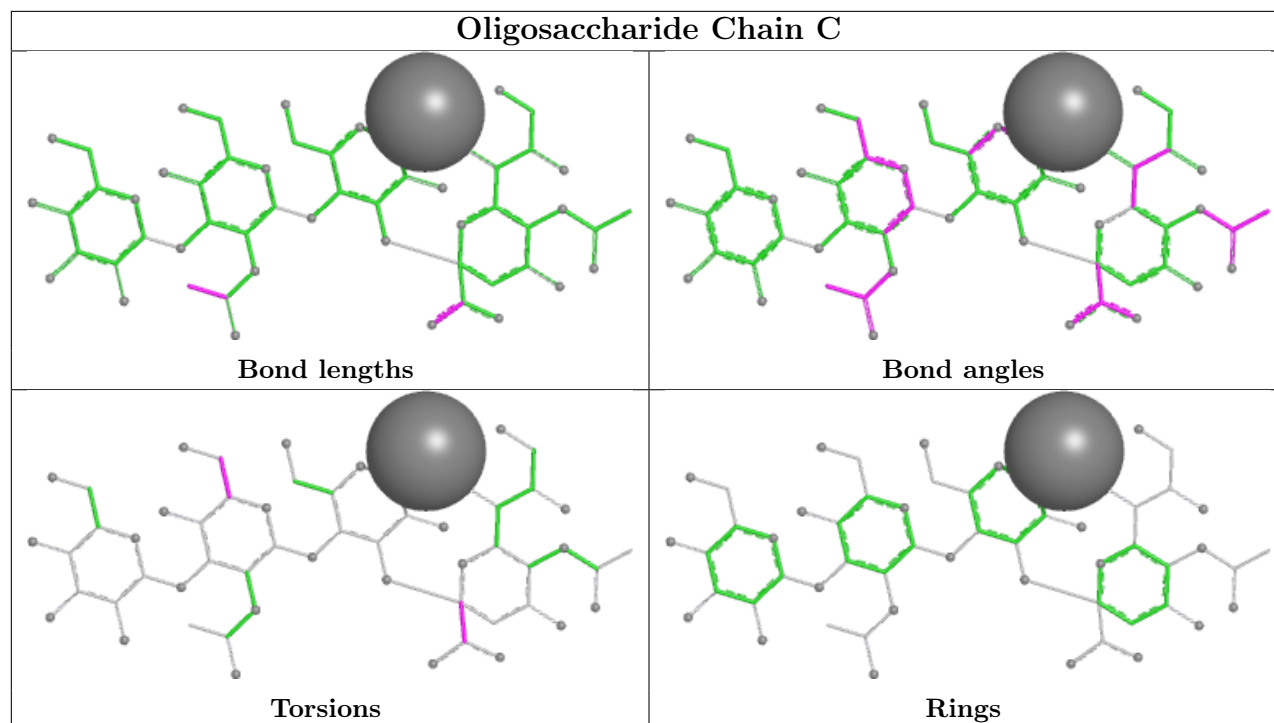
There are no ring outliers.

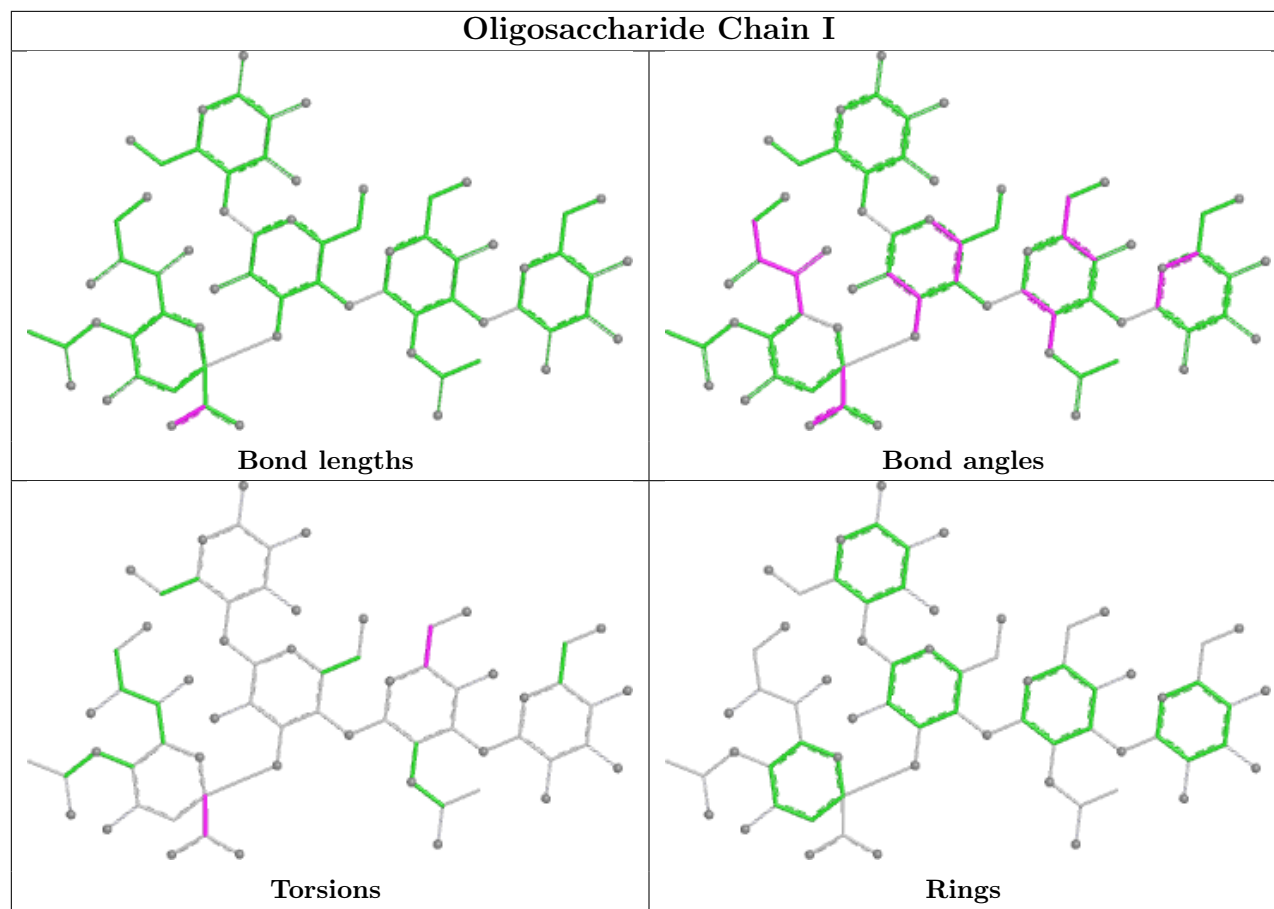
5 monomers are involved in 8 short contacts:

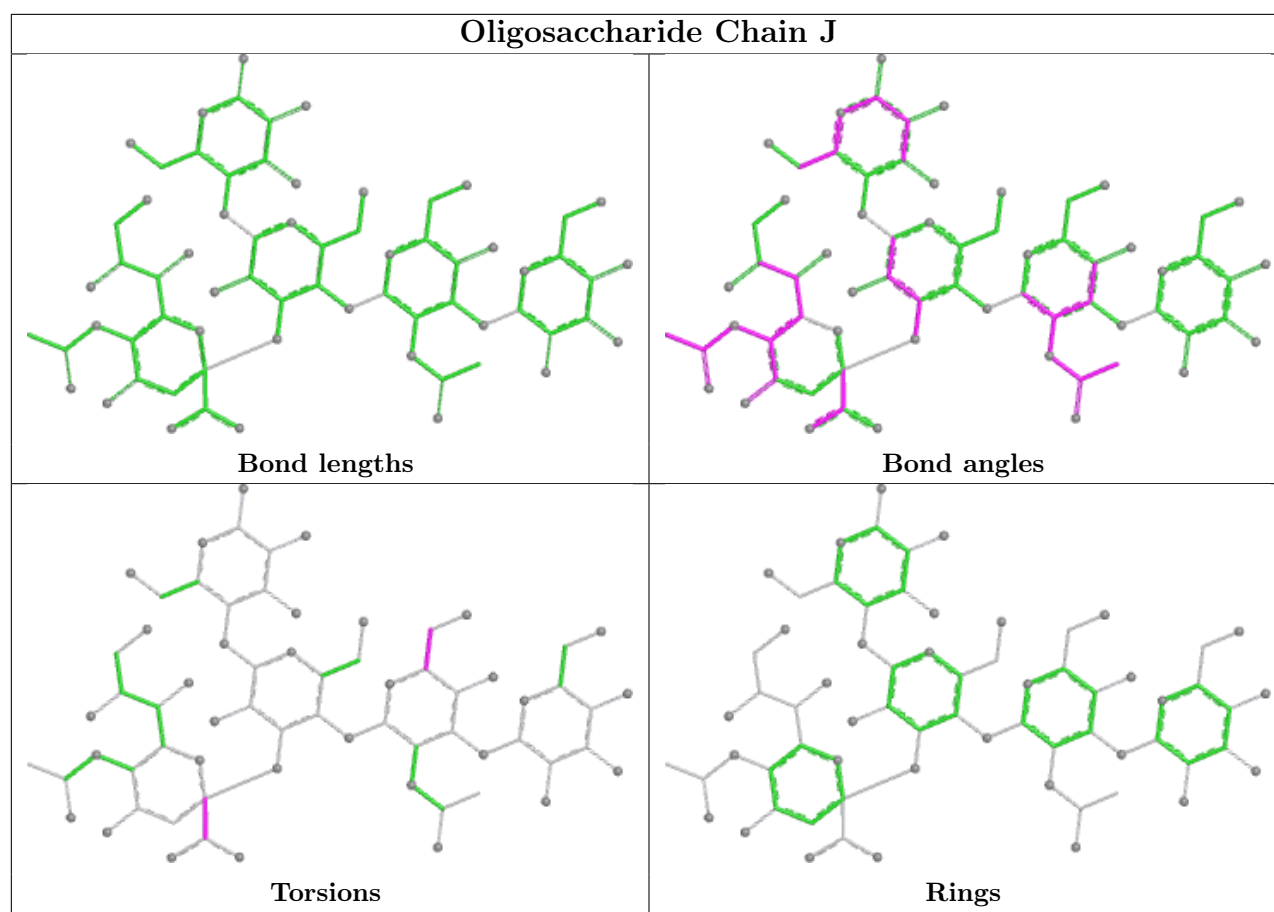
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3	NGA	3	0
2	C	3	NGA	1	0
2	A	5	SIA	3	0
3	I	3	NGA	1	0
2	A	2	GAL	1	0

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](#)

Of 7 ligands modelled in this entry, 5 are unknown - leaving 2 for Mogul analysis.

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$
5	MES	G	6002	-	12,12,12	1.36	3 (25%)	15,16,16	1.45	2 (13%)
5	MES	G	6001	-	12,12,12	1.09	1 (8%)	15,16,16	0.70	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
5	MES	G	6002	-	-	0/6/14/14	0/1/1/1
5	MES	G	6001	-	-	0/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	6002	MES	C7-N4	2.66	1.53	1.47
5	G	6002	MES	C5-N4	2.26	1.53	1.46
5	G	6001	MES	C5-N4	2.03	1.52	1.46
5	G	6002	MES	C8-S	2.01	1.80	1.77

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	6002	MES	O2S-S-C8	-2.85	102.42	106.73
5	G	6002	MES	C6-C5-N4	-2.24	106.72	110.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	6001	MES	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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

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

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

### 6.3 Carbohydrates

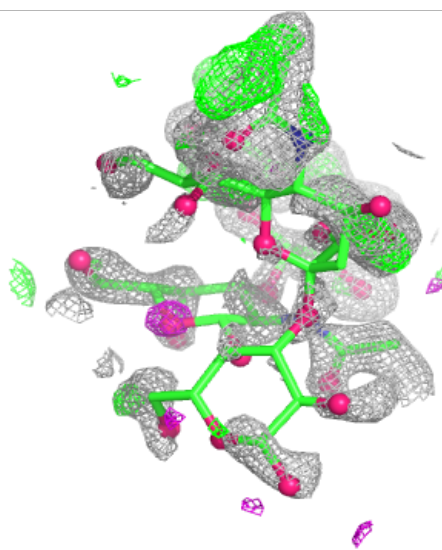
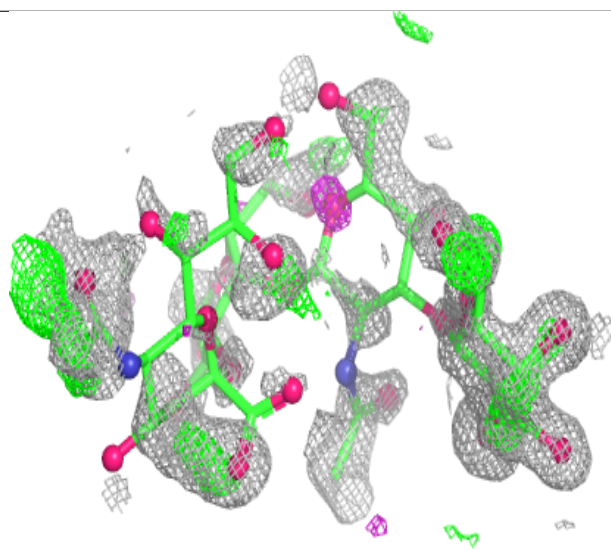
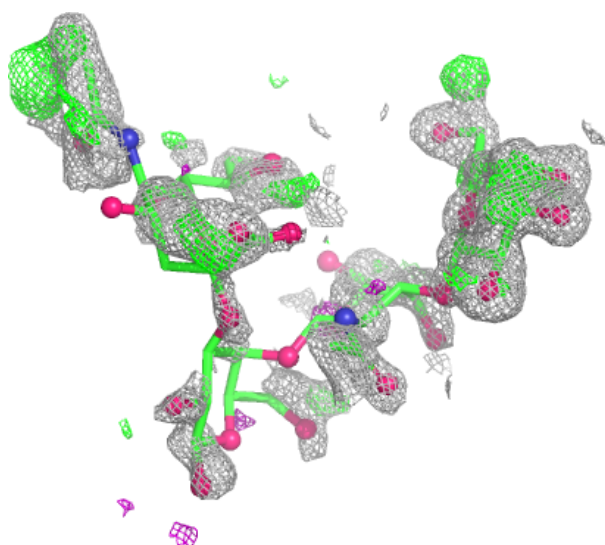
EDS failed to run properly - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



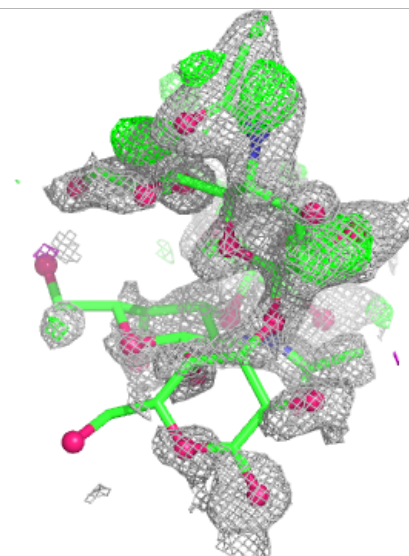
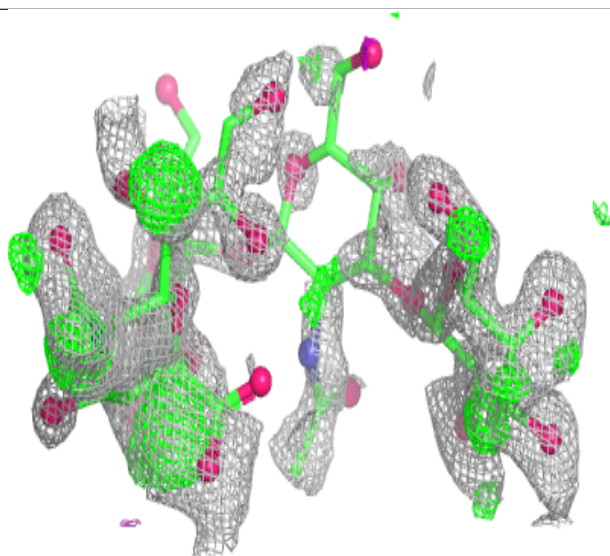
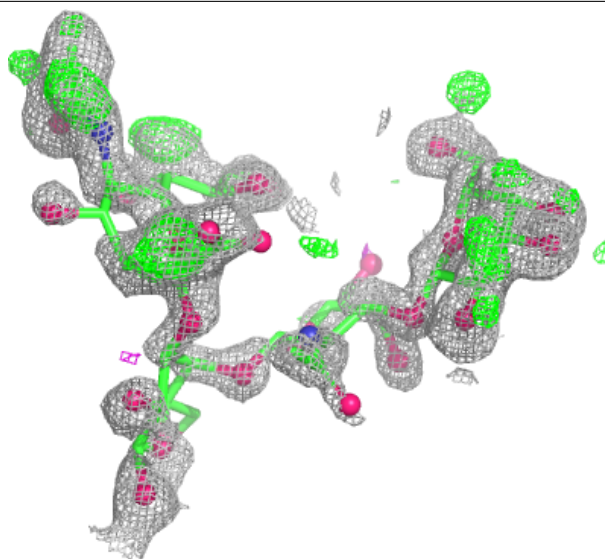
**Electron density around Chain A:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



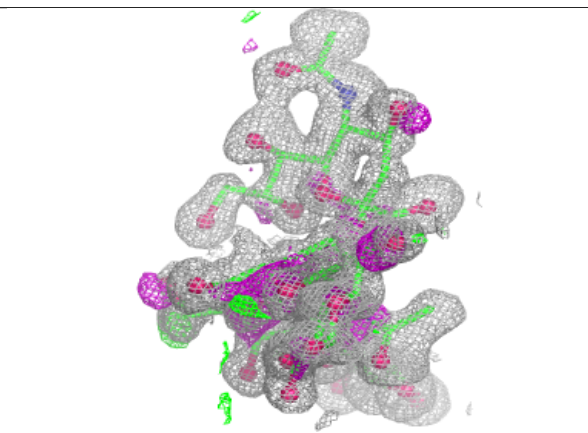
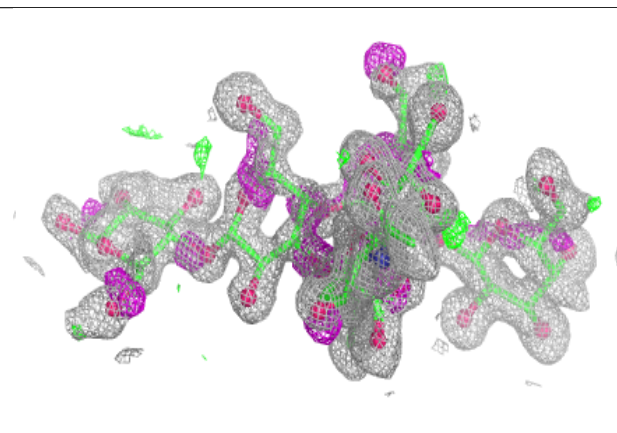
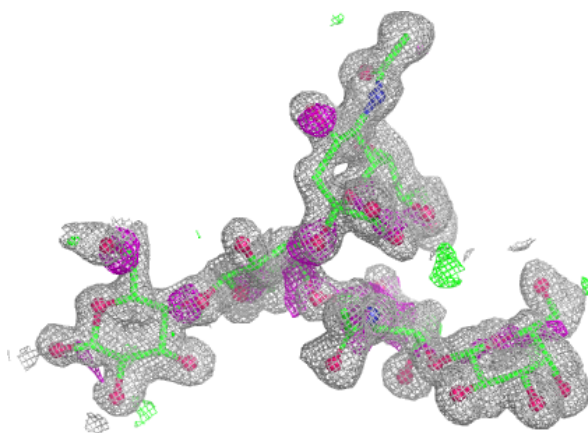
**Electron density around Chain C:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



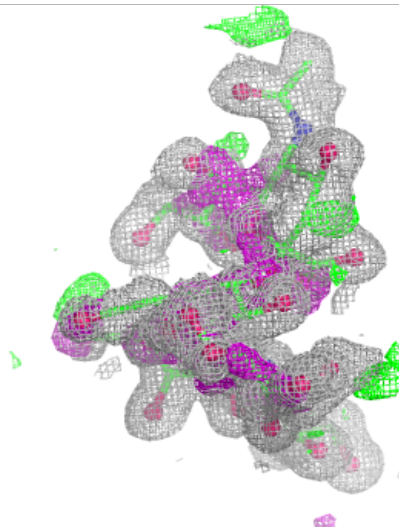
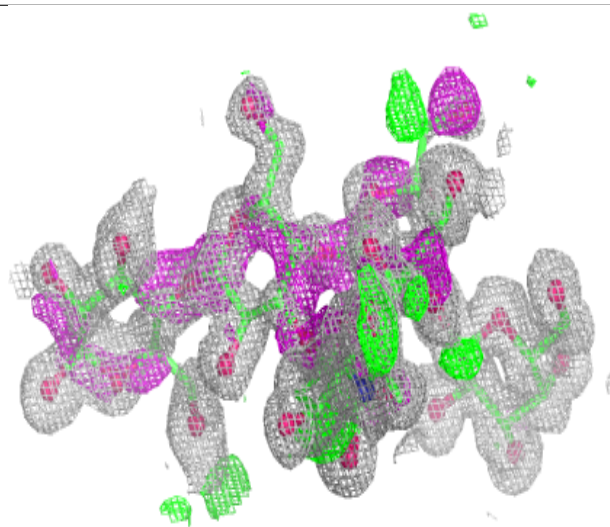
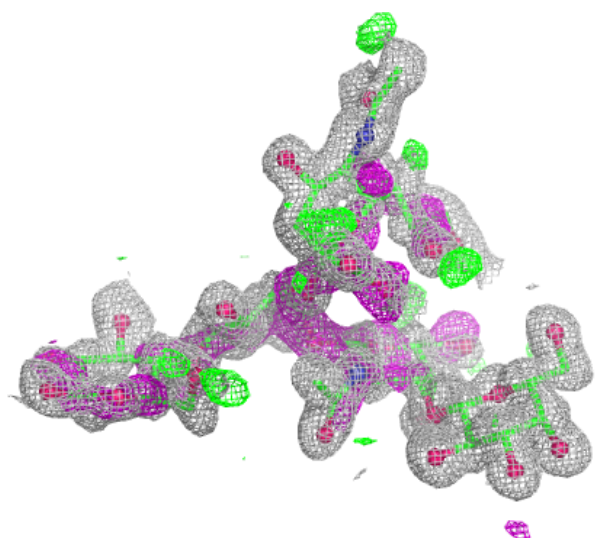
**Electron density around Chain B:**

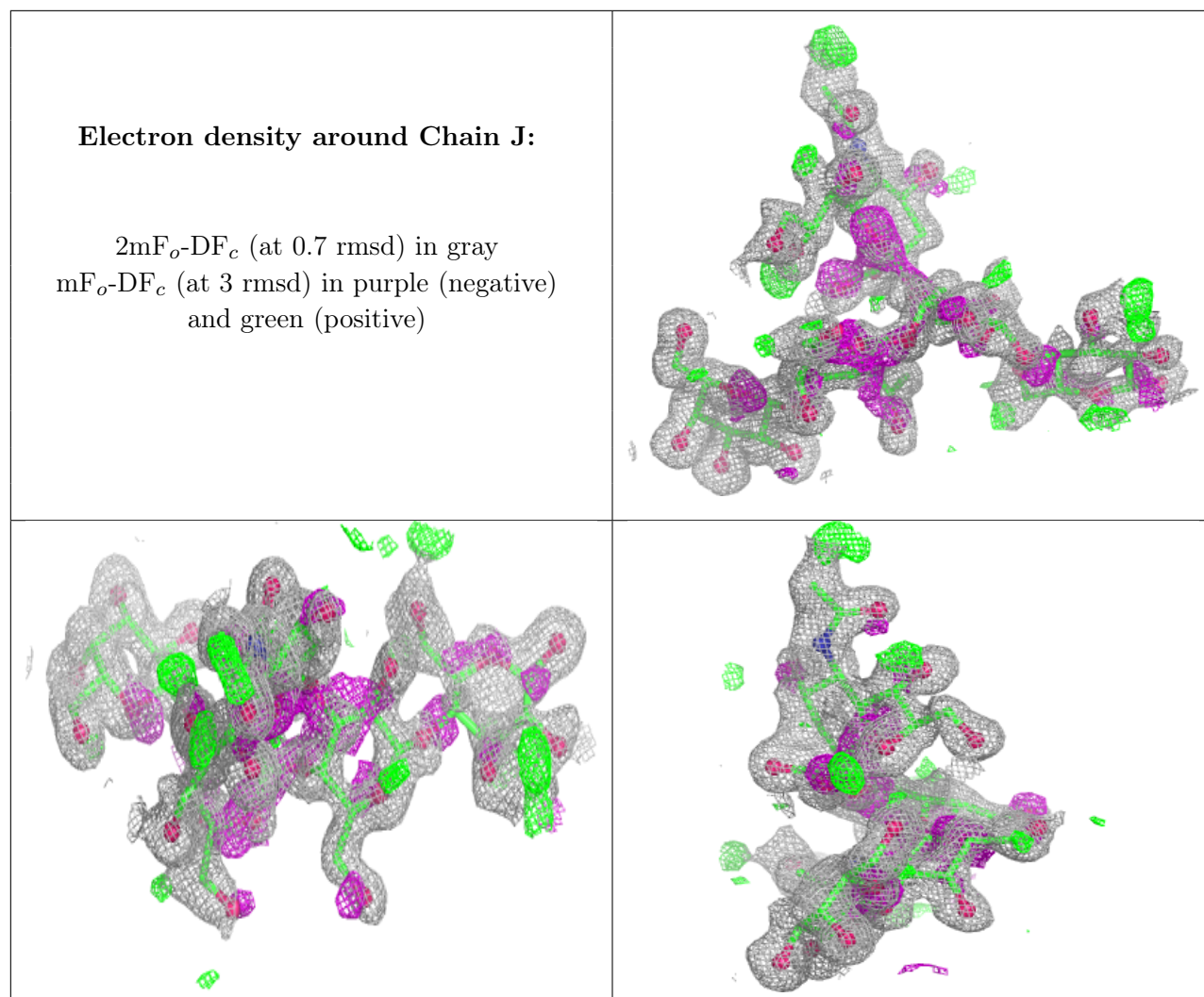
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain I:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.4 Ligands [i](#)

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

## 6.5 Other polymers [i](#)

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