



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:02 PM UTC

PDB ID : 3BC9 / pdb\_00003bc9  
Title : Alpha-amylase B in complex with acarbose  
Authors : Tan, T.-C.; Mijts, B.N.; Swaminathan, K.; Patel, B.K.C.; Divne, C.  
Deposited on : 2007-11-12  
Resolution : 1.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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>.

---

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

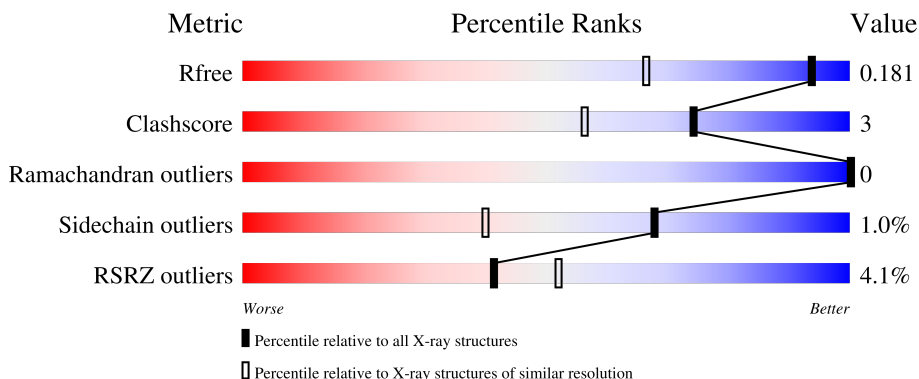
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.35 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))
$R_{free}$	180053	1216 (1.36-1.36)
Clashscore	190562	1232 (1.36-1.36)
Ramachandran outliers	187476	1220 (1.36-1.36)
Sidechain outliers	187428	1220 (1.36-1.36)
RSRZ outliers	180081	1214 (1.36-1.36)

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.

Mol	Chain	Length	Quality of chain
1	A	599	
2	B	2	
3	C	2	
4	D	3	
5	E	3	

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
5	GLC	E	1	X	-	-	-
9	GLC	A	1002	X	-	-	-

## 2 Entry composition i

There are 10 unique types of molecules in this entry. The entry contains 5566 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 Alpha amylase, catalytic region.

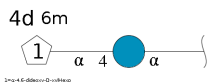
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	585	4822	3071	780	959	12	0	9	0

- Molecule 2 is an oligosaccharide called alpha-D-quinovopyranose-(1-4)-alpha-D-glucopyranose.



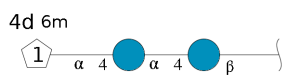
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	B	2	21	12	9	0	0	0

- Molecule 3 is an oligosaccharide called 4,6-dideoxy-alpha-D-xylo-hexopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
3	C	2	20	12	8	0	0	0

- Molecule 4 is an oligosaccharide called 4,6-dideoxy-alpha-D-xylo-hexopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	D	3	Total	C	O	0	0	0
			32	18	14			

- Molecule 5 is an oligosaccharide called 4,6-dideoxy-4-[[[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino]-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	3	Total	C	N	O	0	0	0
			44	25	1	18			

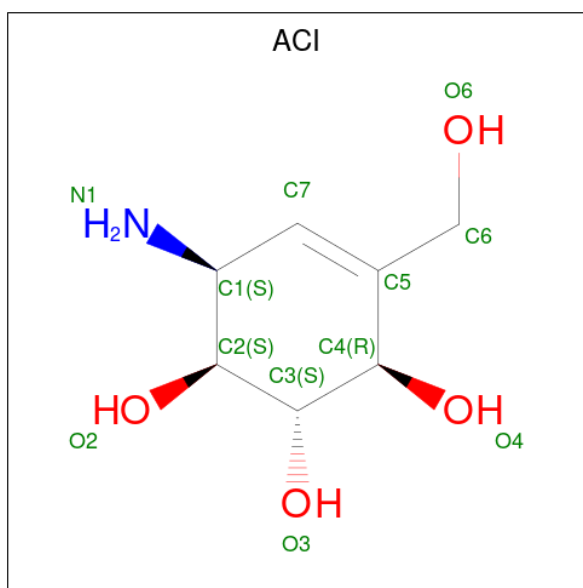
- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total	Ca	0	0
			4	4		

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

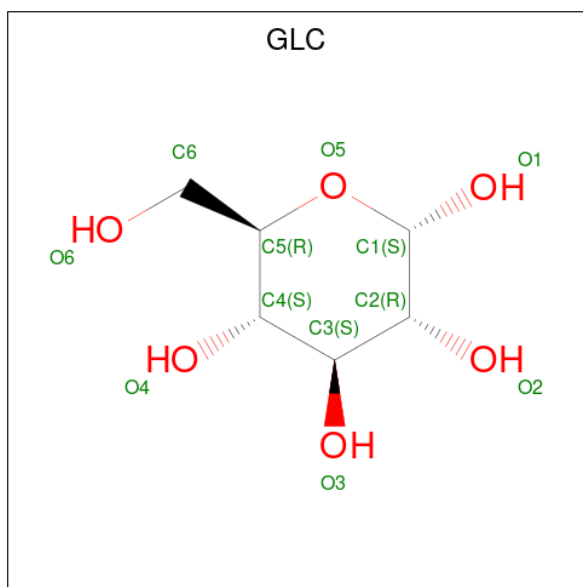
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Na	0	0
			1	1		

- Molecule 8 is 6-AMINO-4-HYDROXYMETHYL-CYCLOHEX-4-ENE-1,2,3-TRIOL (CCD ID: ACI) (formula: C<sub>7</sub>H<sub>13</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			12	7	1	4		
8	A	1	Total	C	N	O	0	0
			12	7	1	4		

- Molecule 9 is alpha-D-glucopyranose (CCD ID: GLC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			12	6	6		
9	A	1	Total	C	O	0	0
			12	6	6		

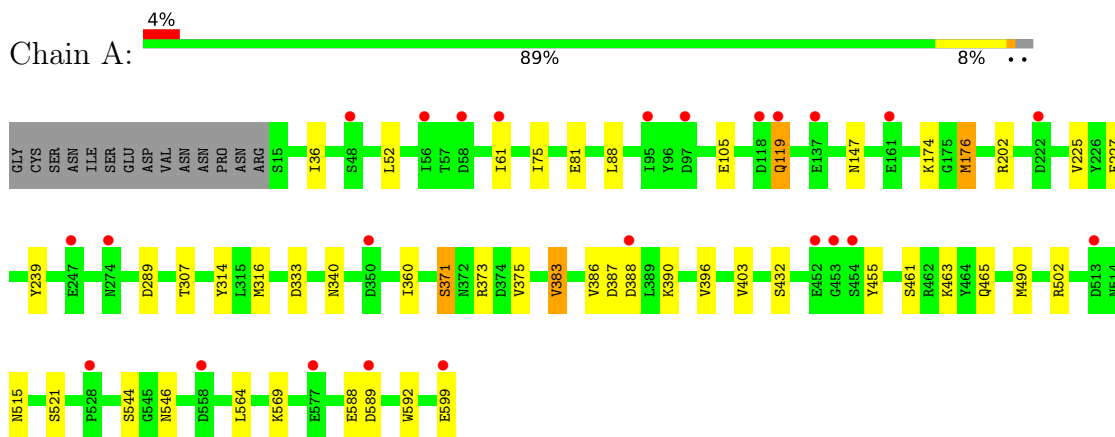
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	574	Total	O	0	0
			574	574		

### 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.

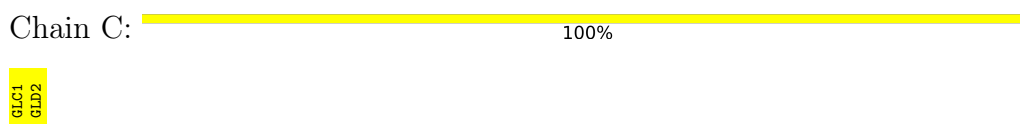
- Molecule 1: Alpha amylase, catalytic region



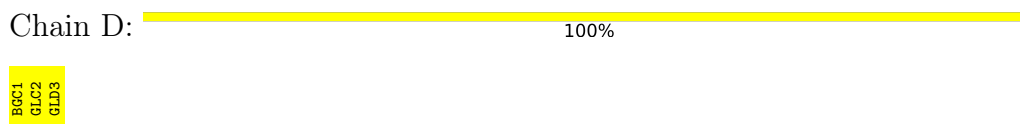
- Molecule 2: alpha-D-quinovopyranose-(1-4)-alpha-D-glucopyranose



- Molecule 3: 4,6-dideoxy-alpha-D-xylo-hexopyranose-(1-4)-alpha-D-glucopyranose



- Molecule 4: 4,6-dideoxy-alpha-D-xylo-hexopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranose



- Molecule 5: 4,6-dideoxy-4-[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain E:

100%

GLC1  
GLC2  
ACT13

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	227.85Å 77.24Å 50.38Å 90.00° 98.63° 90.00°	Depositor
Resolution (Å)	30.00 – 1.35 30.00 – 1.35	Depositor EDS
% Data completeness (in resolution range)	99.2 (30.00-1.35) 99.2 (30.00-1.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.96 (at 1.35Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.151 , 0.178 0.160 , 0.181	Depositor DCC
$R_{free}$ test set	1877 reflections (0.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.0	Xtrriage
Anisotropy	0.667	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 43.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5566	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% 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: GLC, CA, GLD, G6D, AC1, NA, ACI, 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	A	1.21	7/4955 (0.1%)	1.07	6/6751 (0.1%)

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 outliers	#Planarity outliers
1	A	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	225	VAL	CA-CB	5.61	1.61	1.54
1	A	316	MET	C-O	-5.32	1.17	1.23
1	A	227	PHE	C-O	5.23	1.30	1.23
1	A	174	LYS	N-CA	-5.11	1.39	1.46
1	A	375	VAL	CA-CB	-5.08	1.48	1.54
1	A	360	ILE	CA-CB	5.08	1.60	1.54
1	A	383	VAL	CA-CB	5.04	1.60	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	502	ARG	NE-CZ-NH2	6.85	125.36	119.20
1	A	396	VAL	N-CA-C	-6.40	104.26	110.72
1	A	403	VAL	CA-C-O	-5.93	114.99	121.28
1	A	455	TYR	N-CA-CB	-5.70	102.06	110.49
1	A	502	ARG	NE-CZ-NH1	-5.37	116.13	121.50
1	A	465	GLN	O-C-N	5.08	127.51	122.12

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	314	TYR	Sidechain

## 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	A	4822	0	4443	29	0
2	B	21	0	10	0	0
3	C	20	0	18	0	0
4	D	32	0	29	0	0
5	E	44	0	30	0	0
6	A	4	0	0	0	0
7	A	1	0	0	0	0
8	A	24	0	22	0	0
9	A	24	0	23	4	0
10	A	574	0	0	5	1
All	All	5566	0	4575	30	1

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 3.

All (30) 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:A:52:LEU:HD23	1:A:61[B]:ILE:HD12	1.48	0.95
1:A:105:GLU:OE1	1:A:569:LYS:HE2	1.89	0.72
1:A:599:GLU:O	10:A:1558:HOH:O	2.09	0.70
1:A:371:SER:HB3	10:A:1402:HOH:O	1.99	0.63
1:A:307:THR:H	9:A:1001:GLC:H62	1.67	0.59
1:A:52:LEU:CD2	1:A:61[B]:ILE:HD12	2.28	0.59
1:A:119:GLN:HG3	1:A:119:GLN:O	2.05	0.56
1:A:383:VAL:CG1	1:A:388:ASP:HB3	2.36	0.55
1:A:340:ASN:OD1	1:A:371:SER:HB2	2.05	0.55
1:A:371:SER:OG	1:A:373[A]:ARG:HB3	2.07	0.54

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ILE:HD13	1:A:88:LEU:HD21	1.92	0.52
1:A:307:THR:H	9:A:1001:GLC:C6	2.25	0.50
1:A:81:GLU:OE2	10:A:1471:HOH:O	2.19	0.49
1:A:36:ILE:HG21	1:A:88:LEU:HD22	1.96	0.48
1:A:515:ASN:HD21	1:A:521:SER:H	1.61	0.47
1:A:147:ASN:HD21	1:A:202:ARG:HH12	1.61	0.47
1:A:386[A]:VAL:HG13	10:A:1135:HOH:O	2.14	0.47
9:A:1001:GLC:O6	9:A:1001:GLC:O4	2.22	0.47
1:A:147:ASN:ND2	1:A:202:ARG:HH12	2.14	0.46
1:A:544:SER:OG	1:A:546:ASN:OD1	2.17	0.46
1:A:589:ASP:O	1:A:592[A]:TRP:CZ3	2.70	0.45
1:A:515:ASN:ND2	1:A:521:SER:H	2.14	0.45
1:A:176:MET:HE2	1:A:176:MET:HB2	1.78	0.43
1:A:239:TYR:CD1	9:A:1002:GLC:H2	2.53	0.43
1:A:333:ASP:OD1	10:A:1461:HOH:O	2.22	0.43
1:A:390:LYS:HD2	1:A:432[B]:SER:OG	2.19	0.43
1:A:386[A]:VAL:HG23	1:A:387:ASP:N	2.34	0.43
1:A:461:SER:OG	1:A:588:GLU:CD	2.63	0.41
1:A:36:ILE:HG21	1:A:88:LEU:CD2	2.49	0.41
1:A:463:LYS:HG2	1:A:490:MET:HE1	2.03	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1384:HOH:O	10:A:1405:HOH:O[4_555]	2.07	0.13

## 5.3 Torsion angles [i](#)

### 5.3.1 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 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	A	592/599 (99%)	577 (98%)	15 (2%)	0	<a href="#">100</a> <a href="#">100</a>

There are no Ramachandran outliers to report.

### 5.3.2 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 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	A	513/517 (99%)	508 (99%)	5 (1%)	68 40

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	GLN
1	A	176	MET
1	A	289	ASP
1	A	371	SER
1	A	564	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	101	GLN
1	A	127	GLN
1	A	147	ASN
1	A	197	GLN
1	A	248	ASN
1	A	515	ASN

### 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

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
2	GLC	B	1	2,8	11,11,12	1.08	0	15,15,17	1.95	5 (33%)
2	G6D	B	2	2	10,10,11	1.19	1 (10%)	14,14,16	1.41	4 (28%)
3	GLC	C	1	3,8	11,11,12	0.94	0	15,15,17	1.46	2 (13%)
3	GLD	C	2	3,8	9,9,10	1.52	2 (22%)	11,12,14	1.68	2 (18%)
4	BGC	D	1	4	12,12,12	1.13	0	17,17,17	1.38	2 (11%)
4	GLC	D	2	4	11,11,12	1.06	0	15,15,17	1.21	1 (6%)
4	GLD	D	3	4,8	9,9,10	1.43	1 (11%)	11,12,14	2.61	4 (36%)
5	GLC	E	1	5	12,12,12	0.82	0	17,17,17	1.38	3 (17%)
5	GLC	E	2	5	11,11,12	0.69	0	15,15,17	1.44	3 (20%)
5	AC1	E	3	5	21,22,23	0.62	0	22,32,34	1.29	2 (9%)

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	GLC	B	1	2,8	-	0/2/19/22	0/1/1/1
2	G6D	B	2	2	-	-	0/1/1/1
3	GLC	C	1	3,8	-	0/2/19/22	0/1/1/1
3	GLD	C	2	3,8	-	-	0/1/1/1
4	BGC	D	1	4	-	2/2/22/22	0/1/1/1
4	GLC	D	2	4	-	0/2/19/22	0/1/1/1
4	GLD	D	3	4,8	-	-	0/1/1/1
5	GLC	E	1	5	1/1/5/5	2/2/22/22	0/1/1/1
5	GLC	E	2	5	-	0/2/19/22	0/1/1/1
5	AC1	E	3	5	-	1/6/43/46	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	3	GLD	O5-C5	3.42	1.47	1.44
3	C	2	GLD	O5-C1	-3.28	1.38	1.43
3	C	2	GLD	O5-C5	2.58	1.46	1.44
2	B	2	G6D	O2-C2	-2.40	1.38	1.43

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	3	GLD	C3-C4-C5	-6.03	101.64	111.21
4	D	3	GLD	O5-C5-C4	-4.37	105.16	109.39
3	C	2	GLD	C1-O5-C5	4.23	118.02	111.80
4	D	1	BGC	C3-C4-C5	-3.29	104.26	110.23
2	B	1	GLC	C1-C2-C3	3.27	114.41	109.64
5	E	1	GLC	O2-C2-C1	3.12	116.44	109.25
4	D	3	GLD	O5-C5-C6	-3.05	103.43	107.72
4	D	2	GLC	C2-C3-C4	-3.04	105.52	110.86
3	C	1	GLC	C2-C3-C4	-3.00	105.58	110.86
3	C	1	GLC	C1-O5-C5	2.95	116.14	112.19
3	C	2	GLD	O5-C5-C6	2.86	111.75	107.72
2	B	1	GLC	C3-C4-C5	-2.83	105.11	110.23
4	D	1	BGC	C1-O5-C5	-2.81	108.21	113.65
2	B	1	GLC	O2-C2-C3	-2.81	104.33	110.15
2	B	2	G6D	O5-C5-C6	-2.73	101.48	107.40
2	B	1	GLC	O4-C4-C3	-2.73	103.95	110.38
5	E	2	GLC	C1-O5-C5	2.69	115.79	112.19
5	E	1	GLC	C4-C3-C2	2.52	115.25	110.83
5	E	3	AC1	C1-C2-C3	-2.44	106.09	109.64
4	D	3	GLD	C6-C5-C4	-2.40	109.64	113.27
5	E	1	GLC	O2-C2-C3	-2.38	104.76	110.38
5	E	2	GLC	O5-C1-C2	-2.34	105.21	110.79
2	B	2	G6D	C1-C2-C3	2.26	112.94	109.64
5	E	3	AC1	C7B-C1B-N4A	-2.19	107.45	110.68
2	B	2	G6D	O2-C2-C3	-2.14	105.71	110.15
5	E	2	GLC	C6-C5-C4	-2.05	108.00	113.02
2	B	1	GLC	O3-C3-C2	-2.03	105.91	110.05
2	B	2	G6D	O3-C3-C2	-2.01	105.94	110.05

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	E	1	GLC	C1

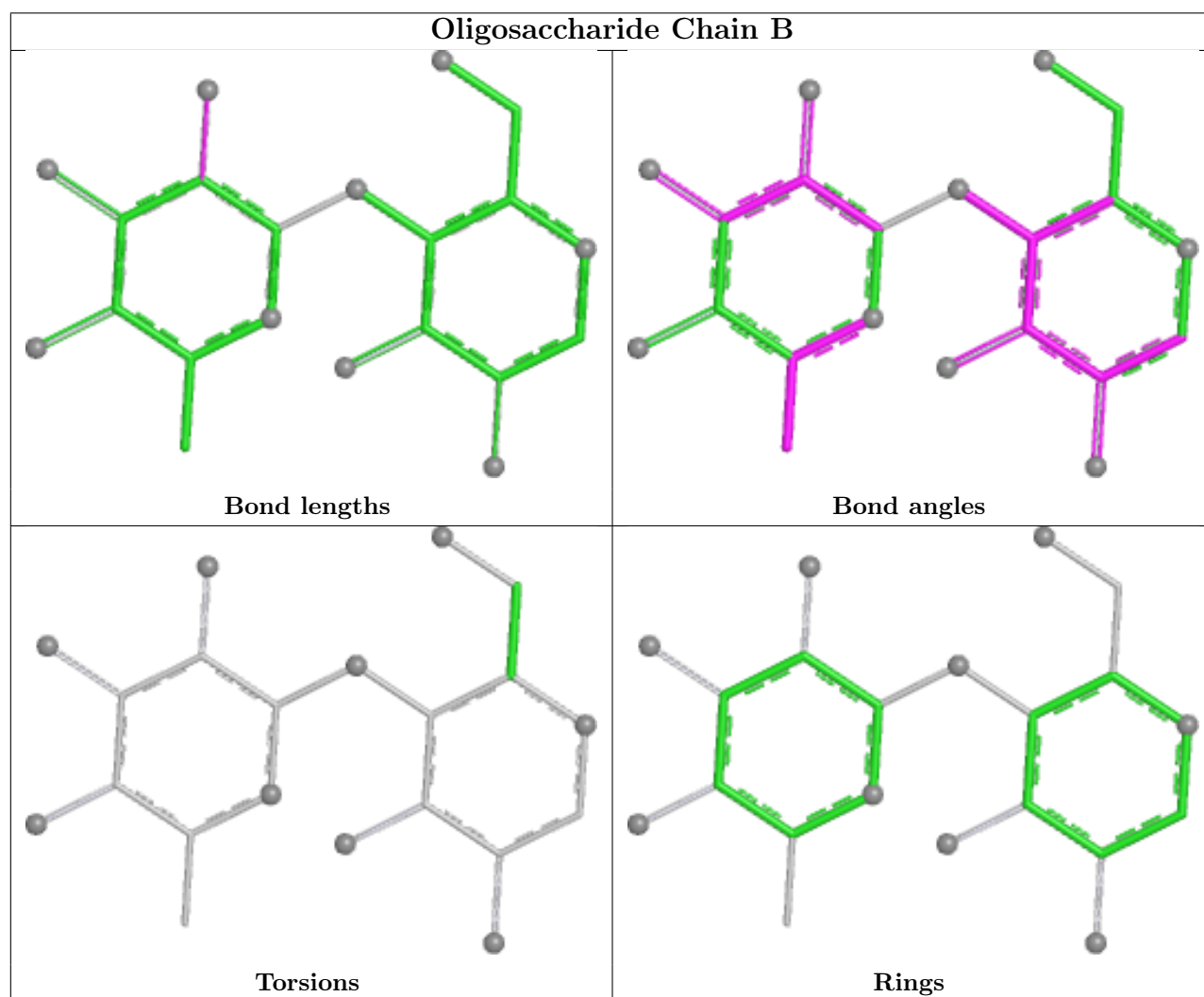
All (5) torsion outliers are listed below:

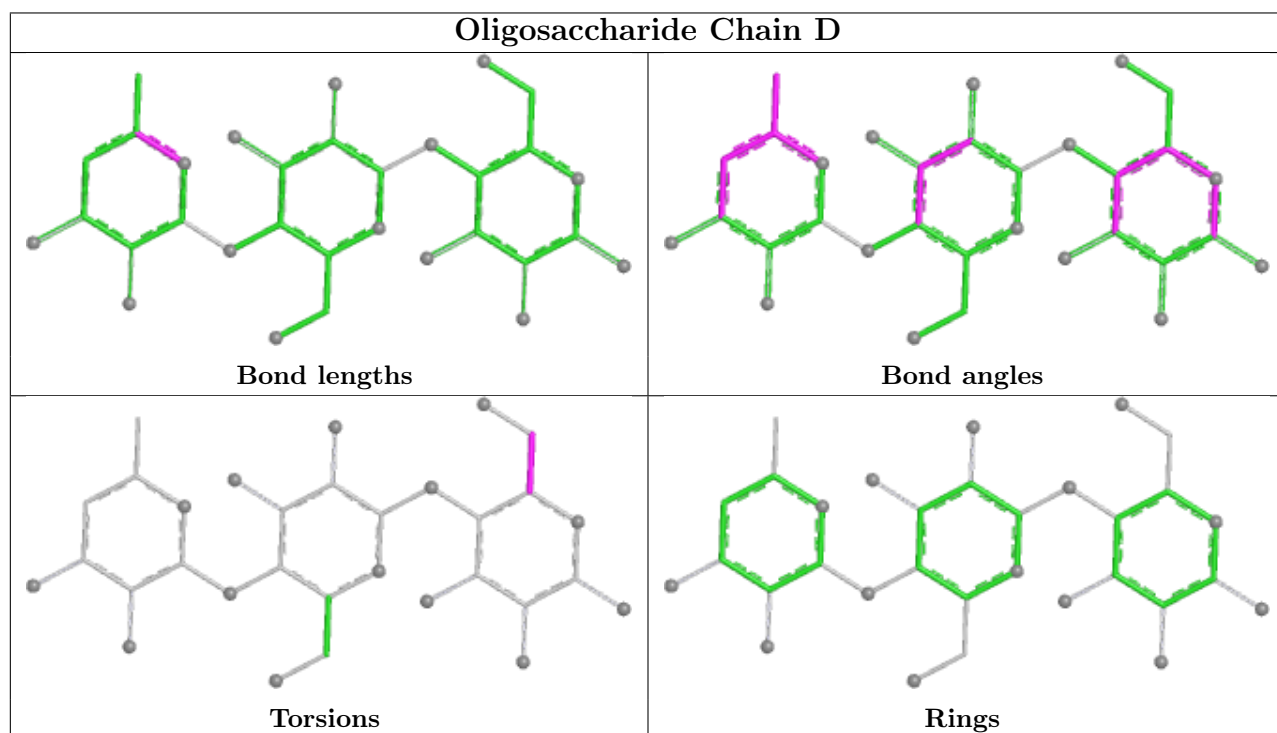
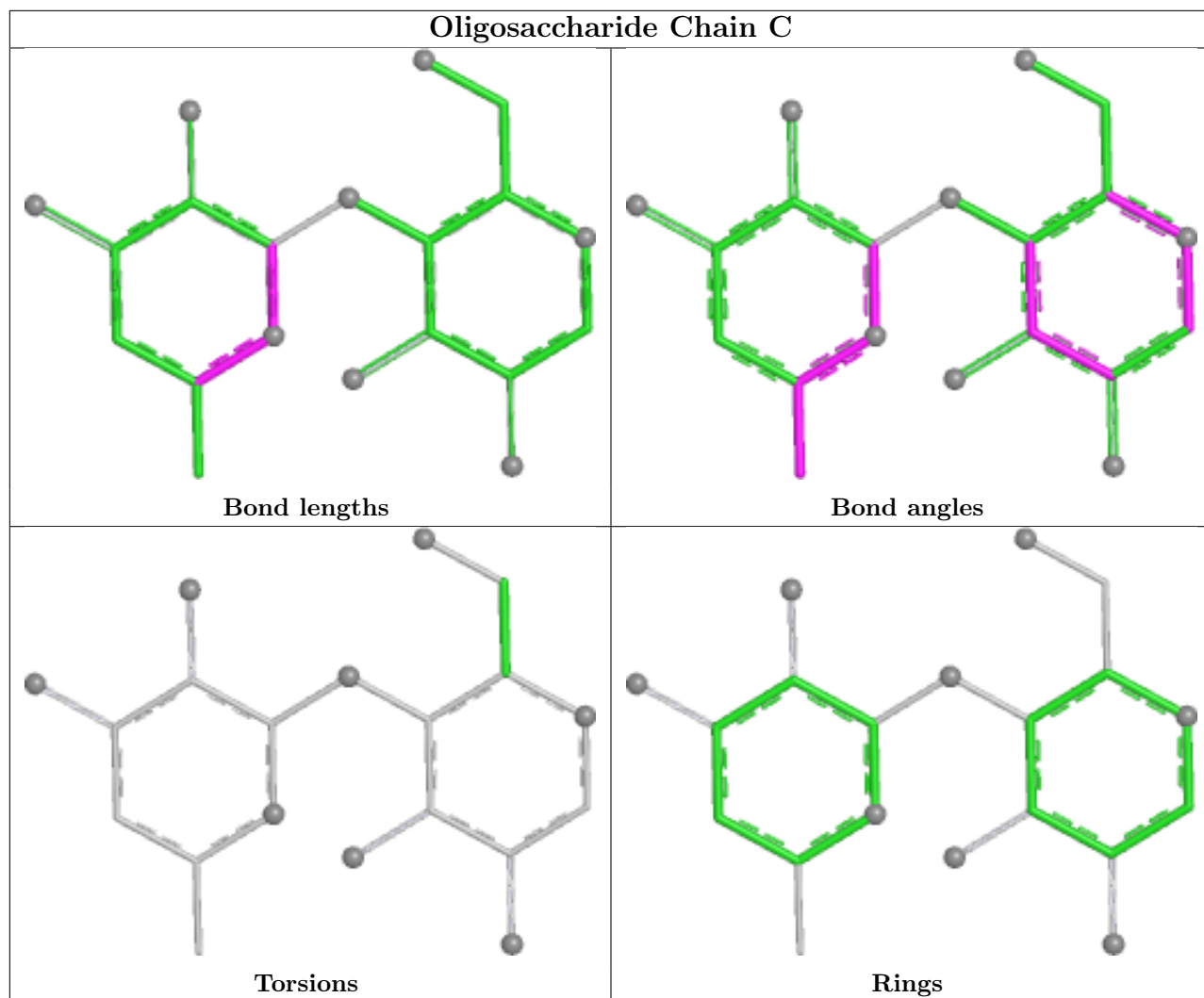
Mol	Chain	Res	Type	Atoms
4	D	1	BGC	O5-C5-C6-O6
4	D	1	BGC	C4-C5-C6-O6
5	E	1	GLC	C4-C5-C6-O6
5	E	1	GLC	O5-C5-C6-O6
5	E	3	AC1	C3-C4-N4A-C1B

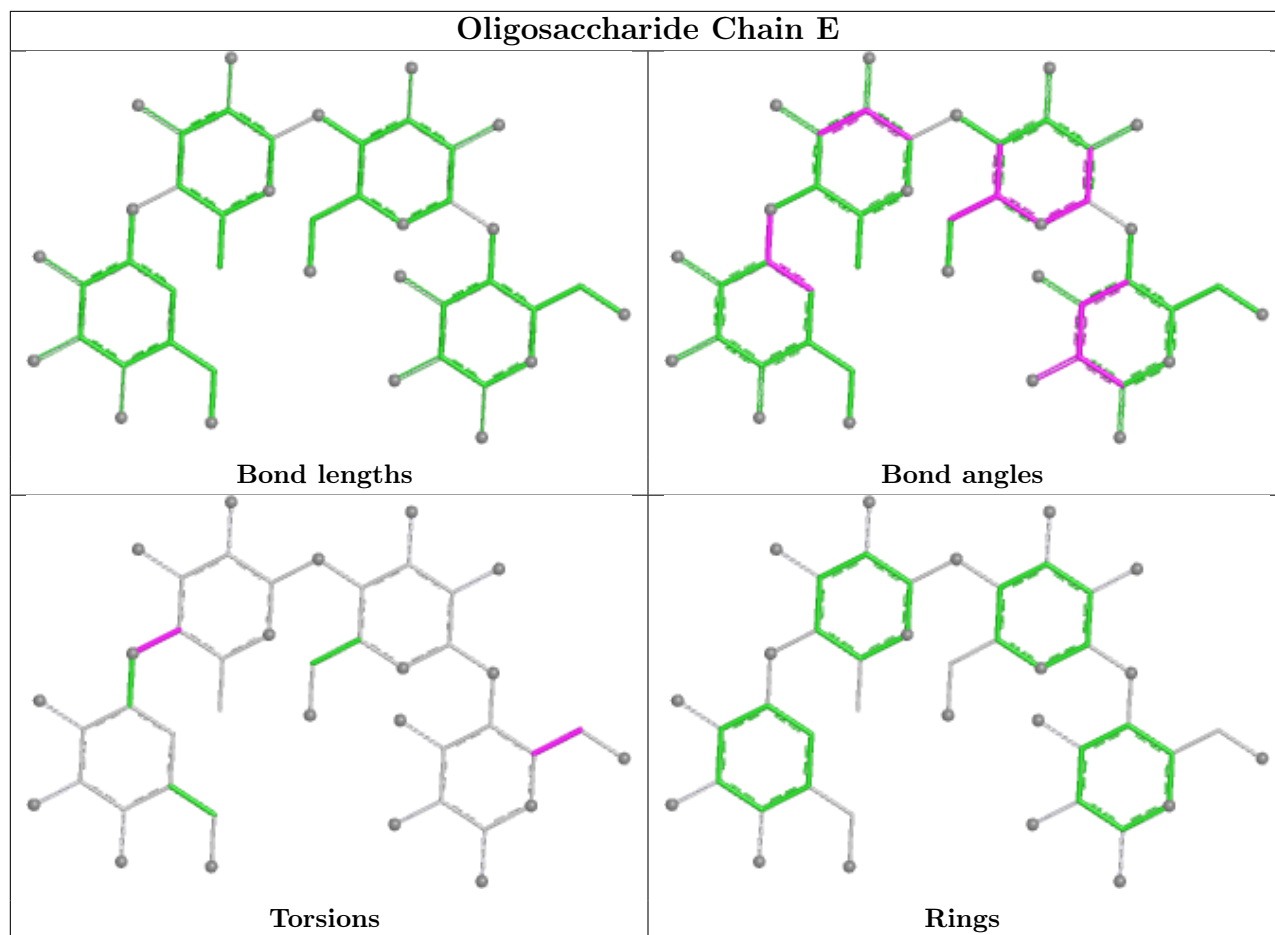
There are no ring outliers.

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.







## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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$
9	GLC	A	1002	-	12,12,12	0.51	0	17,17,17	2.18	6 (35%)
8	ACI	A	803	2,3	12,12,12	1.73	3 (25%)	11,17,17	1.52	1 (9%)
9	GLC	A	1001	-	12,12,12	0.99	0	17,17,17	2.67	5 (29%)
8	ACI	A	806	4,3	12,12,12	2.61	7 (58%)	11,17,17	2.08	3 (27%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GLC	A	1002	-	1/1/5/5	2/2/22/22	0/1/1/1
8	ACI	A	803	2,3	-	0/2/22/22	0/1/1/1
9	GLC	A	1001	-	-	1/2/22/22	0/1/1/1
8	ACI	A	806	4,3	-	2/2/22/22	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	806	ACI	C1-N1	4.10	1.59	1.47
8	A	806	ACI	C2-C1	3.85	1.58	1.52
8	A	806	ACI	C7-C5	3.71	1.38	1.32
8	A	803	ACI	O4-C4	3.40	1.48	1.42
8	A	806	ACI	C3-C4	-3.36	1.48	1.53
8	A	803	ACI	C2-C1	2.82	1.56	1.52
8	A	806	ACI	O6-C6	2.81	1.50	1.41
8	A	803	ACI	C7-C5	2.79	1.36	1.32
8	A	806	ACI	O2-C2	2.69	1.49	1.43
8	A	806	ACI	C1-C7	2.26	1.55	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1001	GLC	C4-C3-C2	-6.87	98.78	110.83
9	A	1001	GLC	C6-C5-C4	-5.89	98.55	113.02
8	A	806	ACI	O6-C6-C5	-5.04	96.90	112.74
9	A	1002	GLC	O1-C1-C2	4.71	122.65	108.98
9	A	1002	GLC	O1-C1-O5	4.46	123.67	110.41
9	A	1001	GLC	O5-C5-C4	4.38	117.58	109.70
8	A	806	ACI	C2-C1-N1	3.24	117.98	111.40
8	A	803	ACI	O4-C4-C5	-3.21	104.63	110.75
9	A	1002	GLC	O5-C5-C4	3.11	115.30	109.70
9	A	1002	GLC	C4-C3-C2	-2.88	105.77	110.83
9	A	1001	GLC	O3-C3-C4	-2.61	104.23	110.38
9	A	1002	GLC	O5-C5-C6	2.39	112.36	106.44
9	A	1001	GLC	O2-C2-C1	2.23	114.40	109.25
8	A	806	ACI	C2-C3-C4	-2.17	106.78	110.22
9	A	1002	GLC	C1-O5-C5	2.09	117.70	113.65

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	A	1002	GLC	C1

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	806	ACI	C4-C5-C6-O6
8	A	806	ACI	C7-C5-C6-O6
9	A	1002	GLC	O5-C5-C6-O6
9	A	1002	GLC	C4-C5-C6-O6
9	A	1001	GLC	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1002	GLC	1	0
9	A	1001	GLC	3	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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	585/599 (97%)	0.23	24 (4%) <span style="border: 1px solid red; padding: 2px;">41</span> <span style="border: 1px solid gray; padding: 2px;">52</span>	7, 17, 28, 39	9 (1%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	454	SER	5.5
1	A	577	GLU	3.8
1	A	513	ASP	3.8
1	A	48	SER	3.2
1	A	452	GLU	3.0
1	A	61[A]	ILE	2.9
1	A	58	ASP	2.9
1	A	599	GLU	2.8
1	A	97	ASP	2.8
1	A	247	GLU	2.5
1	A	222	ASP	2.5
1	A	118	ASP	2.4
1	A	119	GLN	2.4
1	A	589	ASP	2.4
1	A	350	ASP	2.3
1	A	274	ASN	2.3
1	A	453	GLY	2.3
1	A	388	ASP	2.3
1	A	161	GLU	2.2
1	A	137	GLU	2.2
1	A	558	ASP	2.1
1	A	56	ILE	2.1
1	A	528	PRO	2.0
1	A	95	ILE	2.0

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

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

## 6.3 Carbohydrates [i](#)

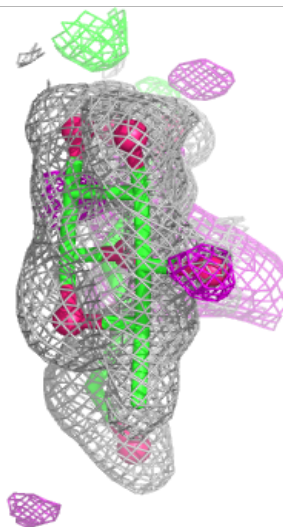
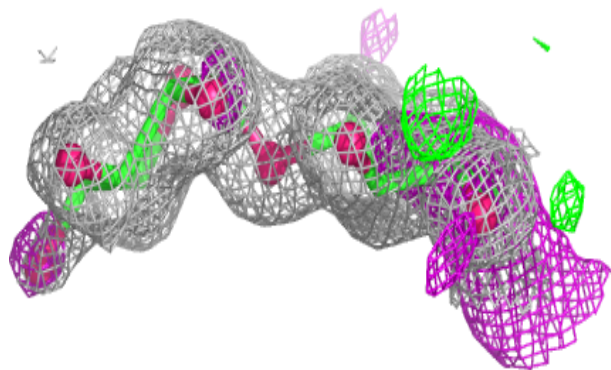
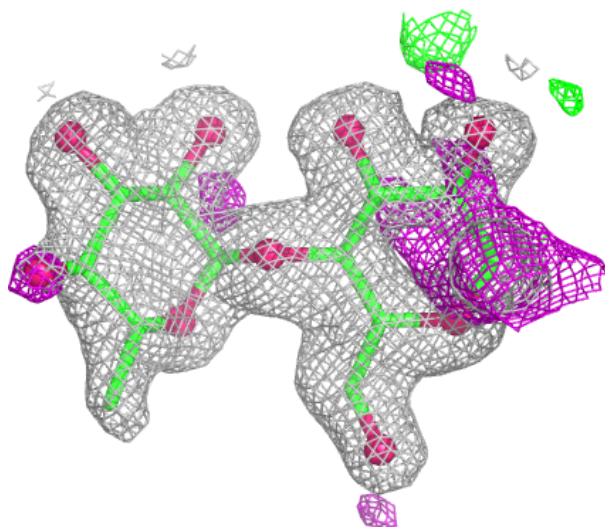
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	GLC	E	1	12/12	0.65	0.19	35,46,50,52	0
4	BGC	D	1	12/12	0.81	0.15	26,38,43,47	0
2	G6D	B	2	10/11	0.86	0.12	26,35,41,41	0
2	GLC	B	1	11/12	0.90	0.11	25,26,30,35	0
3	GLD	C	2	9/10	0.93	0.08	21,22,28,28	0
4	GLC	D	2	11/12	0.96	0.07	17,20,24,29	0
5	AC1	E	3	21/22	0.96	0.07	14,17,27,36	0
3	GLC	C	1	11/12	0.97	0.06	15,17,21,24	0
5	GLC	E	2	11/12	0.97	0.07	16,22,28,31	0
4	GLD	D	3	9/10	0.97	0.06	13,14,17,19	0

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.

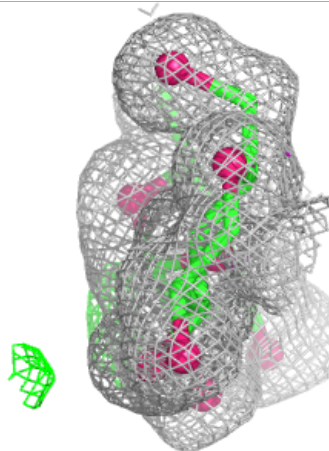
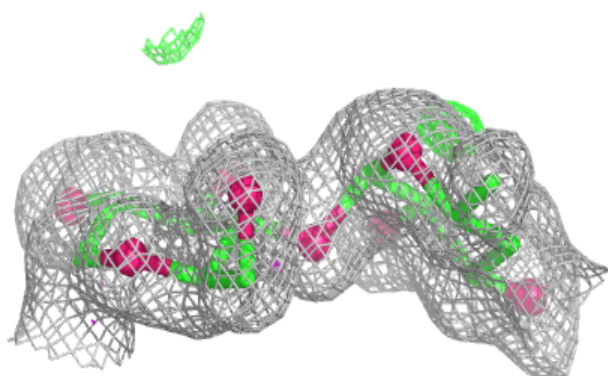
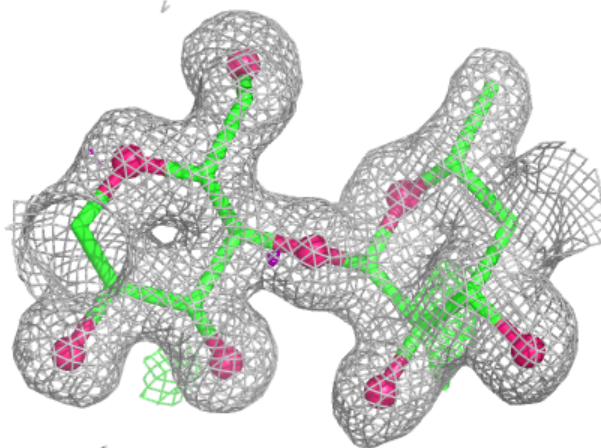
**Electron density around Chain B:**

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



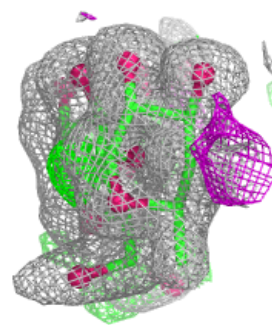
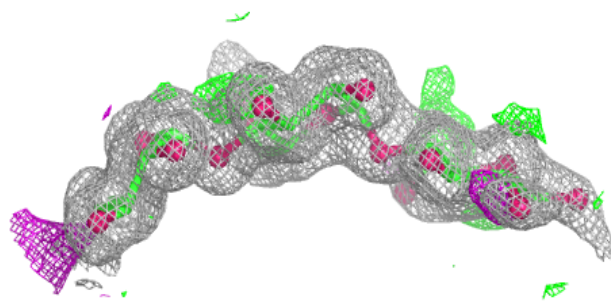
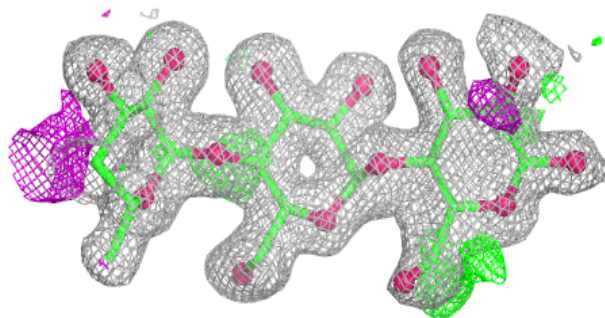
**Electron density around Chain C:**

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

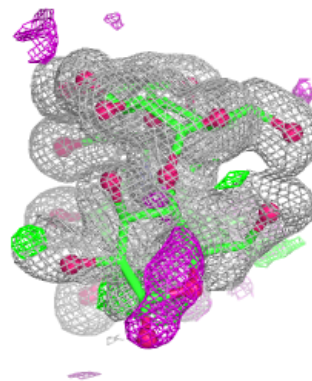
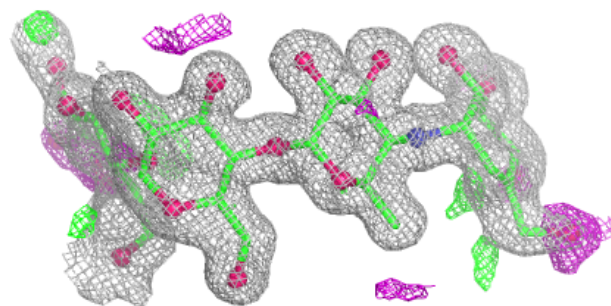
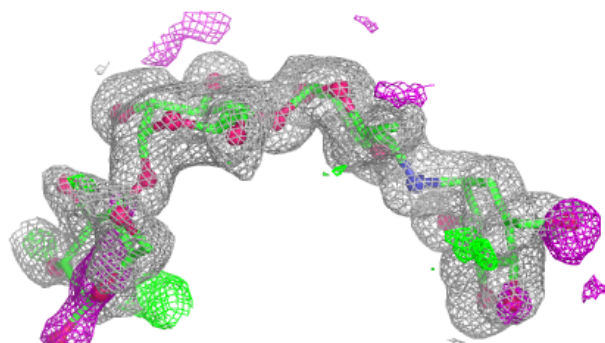


**Electron density around Chain D:**

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

**Electron density around Chain E:**

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



## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
9	GLC	A	1002	12/12	0.73	0.21	72,74,74,75	0
9	GLC	A	1001	12/12	0.83	0.15	26,40,42,46	0
8	ACI	A	803	12/12	0.92	0.10	20,22,29,38	0
8	ACI	A	806	12/12	0.94	0.09	14,18,24,30	0
6	CA	A	705	1/1	0.99	0.22	30,30,30,30	0
6	CA	A	702	1/1	1.00	0.01	10,10,10,10	0
6	CA	A	703	1/1	1.00	0.03	14,14,14,14	0
6	CA	A	701	1/1	1.00	0.02	11,11,11,11	0
7	NA	A	704	1/1	1.00	0.03	10,10,10,10	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.