



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2020 – 08:09 PM JST

PDB ID : 7C67
Title : Crystal structure of beta-glycosides-binding protein of ABC transporter in a closed state bound to cellotriose
Authors : Kanaujia, S.P.; Chandravanshi, M.; Samanta, R.
Deposited on : 2020-05-21
Resolution : 2.00 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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) : 1.13
EDS : 2.14.6
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.6

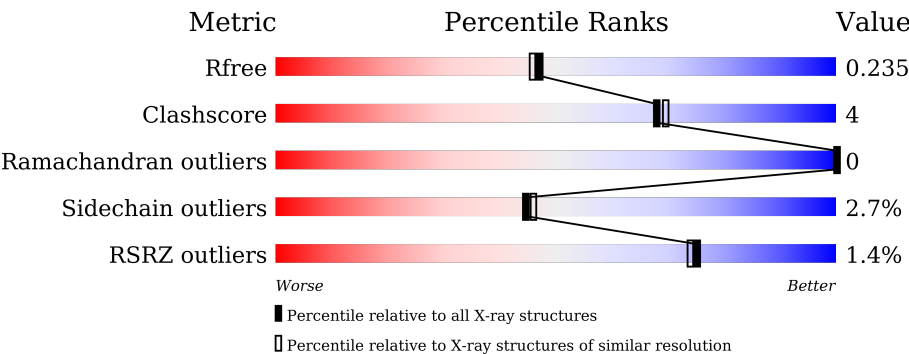
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 ≥ 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	423	
1	B	423	
2	C	3	
2	D	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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLC	C	1	X	-	-	-

2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 6949 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.

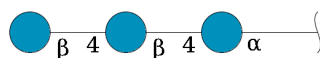
- Molecule 1 is a protein called Sugar ABC transporter, periplasmic sugar-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	6	0
			3216	2069	554	583	10			
1	B	417	Total	C	N	O	S	0	2	0
			3204	2060	554	580	10			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q53W80
A	417	HIS	-	expression tag	UNP Q53W80
A	418	HIS	-	expression tag	UNP Q53W80
A	419	HIS	-	expression tag	UNP Q53W80
A	420	HIS	-	expression tag	UNP Q53W80
A	421	HIS	-	expression tag	UNP Q53W80
A	422	HIS	-	expression tag	UNP Q53W80
B	0	MET	-	initiating methionine	UNP Q53W80
B	417	HIS	-	expression tag	UNP Q53W80
B	418	HIS	-	expression tag	UNP Q53W80
B	419	HIS	-	expression tag	UNP Q53W80
B	420	HIS	-	expression tag	UNP Q53W80
B	421	HIS	-	expression tag	UNP Q53W80
B	422	HIS	-	expression tag	UNP Q53W80

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	3	Total	C	O	0	0	0
			34	18	16			
2	D	3	Total	C	O	0	0	0
			34	18	16			

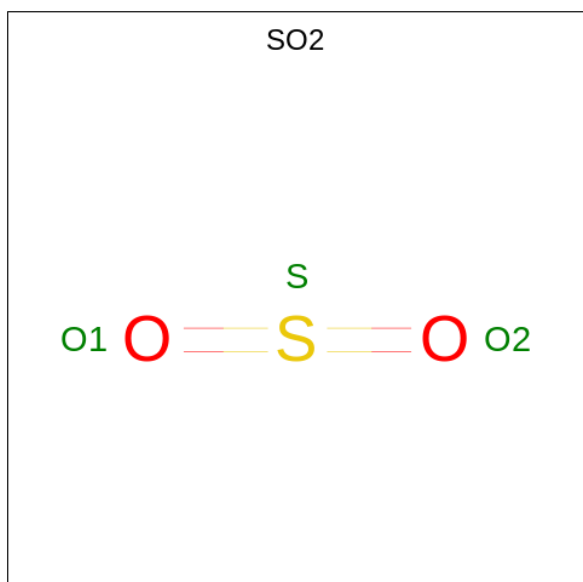
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	2	Total	Cl	0	0
			2	2		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

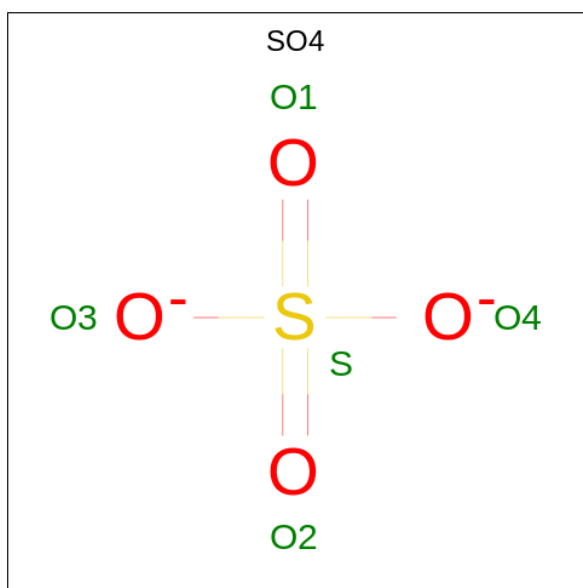
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Na	0	0
			1	1		
4	A	1	Total	Na	0	0
			1	1		

- Molecule 5 is SULFUR DIOXIDE (three-letter code: SO2) (formula: O₂S).



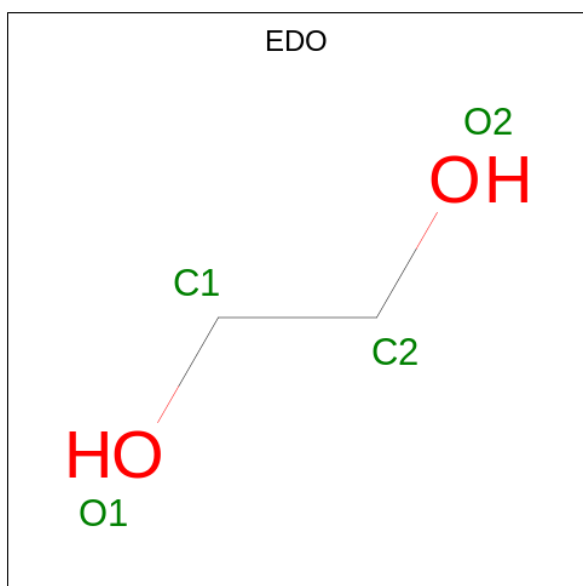
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			3	2	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



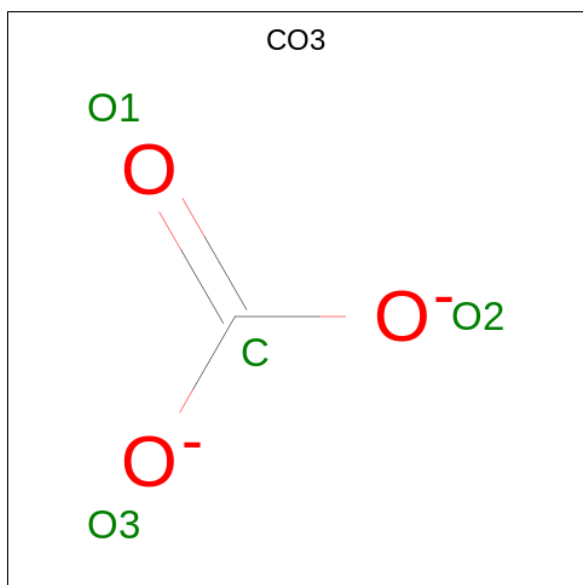
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	1	3		
8	A	1	Total	C	O	0	0
			4	1	3		
8	A	1	Total	C	O	0	0
			4	1	3		

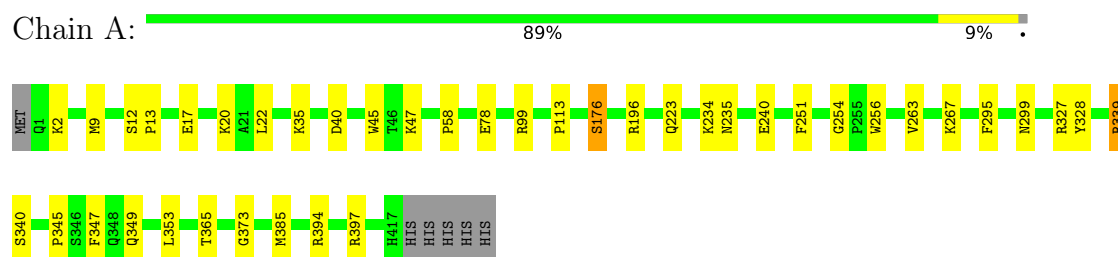
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	246	Total	O	0	0
			246	246		
9	B	173	Total	O	0	0
			173	173		

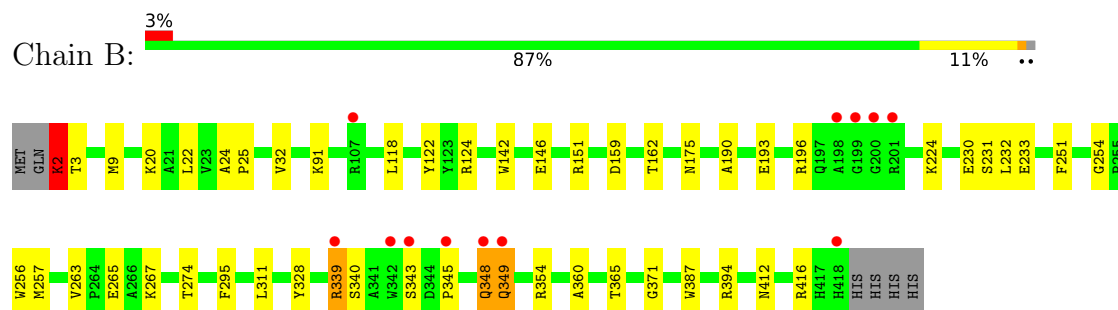
3 Residue-property plots

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 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.

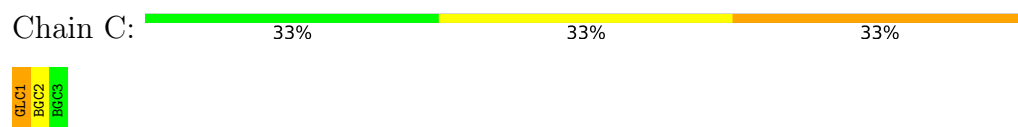
- Molecule 1: Sugar ABC transporter, periplasmic sugar-binding protein



- Molecule 1: Sugar ABC transporter, periplasmic sugar-binding protein



- Molecule 2: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranos e



- Molecule 2: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-alpha-D-glucopyranos e



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.67Å 109.88Å 110.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	55.00 – 2.00 54.94 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (55.00-2.00) 99.3 (54.94-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.170 , 0.231 0.178 , 0.235	Depositor DCC
R_{free} test set	2515 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6949	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CO3, BGC, CL, NA, GLC, EDO, SO2, SO4

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	0.87	5/3323 (0.2%)	0.98	5/4523 (0.1%)
1	B	0.78	1/3300 (0.0%)	0.93	3/4493 (0.1%)
All	All	0.82	6/6623 (0.1%)	0.95	8/9016 (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	B	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	233	GLU	CD-OE1	6.36	1.32	1.25
1	A	78	GLU	CD-OE1	6.25	1.32	1.25
1	A	176[A]	SER	C-O	5.57	1.33	1.23
1	A	176[B]	SER	C-O	5.57	1.33	1.23
1	A	17	GLU	CD-OE1	5.35	1.31	1.25
1	A	240	GLU	CD-OE1	5.07	1.31	1.25

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	354	ARG	NE-CZ-NH2	-10.58	115.01	120.30
1	B	354	ARG	NE-CZ-NH1	8.14	124.37	120.30
1	A	327	ARG	NE-CZ-NH2	-6.83	116.89	120.30
1	A	397	ARG	NE-CZ-NH2	-6.72	116.94	120.30
1	A	394	ARG	NE-CZ-NH1	5.21	122.91	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	394	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	A	394	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	A	385	MET	CG-SD-CE	5.08	108.32	100.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	2	LYS	Peptide
1	B	371	GLY	Peptide

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	3216	0	3199	18	0
1	B	3204	0	3166	30	0
2	C	34	0	30	0	0
2	D	34	0	30	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	3	0	0	0	0
6	A	5	0	0	0	0
6	B	5	0	0	0	0
7	A	8	0	12	0	0
7	B	4	0	6	1	0
8	A	12	0	0	1	0
9	A	246	0	0	6	1
9	B	173	0	0	7	0
All	All	6949	0	6443	49	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 4.

All (49) 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:265:GLU:HG3	9:B:741:HOH:O	1.84	0.77
1:B:193[A]:GLU:OE2	9:B:601:HOH:O	2.05	0.73
1:B:2:LYS:O	1:B:32:VAL:HG23	1.87	0.73
1:B:339:ARG:HG3	1:B:340:SER:N	2.10	0.65
1:B:345:PRO:O	1:B:349:GLN:HG2	1.99	0.63
1:B:146:GLU:OE2	1:B:224:LYS:HE3	2.00	0.62
1:A:345:PRO:O	1:A:349:GLN:HB2	2.01	0.60
1:B:263:VAL:HG13	1:B:267:LYS:HB2	1.82	0.59
1:A:20[A]:LYS:HE2	9:A:602:HOH:O	2.01	0.59
1:B:343:SER:O	1:B:348:GLN:NE2	2.36	0.59
1:A:196:ARG:HD3	9:A:690:HOH:O	2.02	0.58
1:B:32:VAL:HG21	1:B:311:LEU:HD21	1.89	0.55
1:A:347:PHE:HA	1:A:353:LEU:HD23	1.88	0.54
1:B:274[A]:THR:HG22	9:B:675:HOH:O	2.08	0.54
1:B:412:ASN:O	1:B:416:ARG:HG3	2.08	0.54
1:A:99:ARG:NH2	9:A:606:HOH:O	2.41	0.53
1:B:3:THR:CG2	9:B:768:HOH:O	2.56	0.53
1:B:193[B]:GLU:OE2	1:B:196:ARG:HB3	2.08	0.53
1:B:274[A]:THR:HG22	9:B:644:HOH:O	2.10	0.52
1:A:40:ASP:HB3	9:A:753:HOH:O	2.09	0.52
1:B:3:THR:HG22	9:B:768:HOH:O	2.10	0.51
1:B:295:PHE:O	1:B:365:THR:HB	2.10	0.51
1:A:339:ARG:HG2	9:A:660:HOH:O	2.09	0.51
1:A:339:ARG:HG3	1:A:340:SER:N	2.25	0.49
1:B:159:ASP:OD1	1:B:274[A]:THR:HG21	2.12	0.49
1:A:254:GLY:HA3	1:A:256:TRP:CZ3	2.47	0.49
1:B:232:LEU:HD22	1:B:387:TRP:CE3	2.50	0.47
7:B:504:EDO:O1	9:B:602:HOH:O	2.19	0.47
1:B:254:GLY:HA3	1:B:256:TRP:CZ3	2.49	0.47
1:B:230:GLU:HG2	1:B:231:SER:N	2.31	0.46
1:B:124:ARG:NH2	1:B:274[B]:THR:HG22	2.31	0.46
1:A:13:PRO:HB2	1:A:267:LYS:O	2.16	0.46
1:A:47:LYS:NZ	9:A:618:HOH:O	2.50	0.45
1:A:176[B]:SER:OG	1:A:235:ASN:HB2	2.17	0.44
1:B:118:LEU:HD13	1:B:360:ALA:HA	2.00	0.43
1:B:122:TYR:CZ	1:B:257:MET:HB2	2.53	0.43
1:A:22:LEU:HD22	1:A:328:TYR:CD1	2.54	0.42
1:A:295:PHE:O	1:A:365:THR:HG22	2.19	0.42
1:B:22:LEU:HD22	1:B:328:TYR:CD1	2.55	0.42
1:A:234:LYS:NZ	8:A:510:CO3:O2	2.53	0.41
1:B:20:LYS:HA	1:B:20:LYS:CE	2.50	0.41
1:A:45:TRP:CH2	1:A:373:GLY:HA3	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:TRP:HH2	1:B:190:ALA:HB2	1.86	0.41
1:B:343:SER:HA	1:B:348:GLN:HE22	1.85	0.41
1:A:12:SER:HB2	1:A:13:PRO:HD2	2.02	0.41
1:B:159:ASP:HB3	1:B:162:THR:OG1	2.20	0.41
1:A:113:PRO:HA	1:A:299:ASN:OD1	2.21	0.40
1:B:339:ARG:CG	1:B:340:SER:N	2.82	0.40
1:B:24:ALA:HB3	1:B:25:PRO:HD3	2.03	0.40

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)
9:A:761:HOH:O	9:A:829:HOH:O[3_544]	2.08	0.12

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	421/423 (100%)	418 (99%)	3 (1%)	0	100	100
1	B	417/423 (99%)	411 (99%)	6 (1%)	0	100	100
All	All	838/846 (99%)	829 (99%)	9 (1%)	0	100	100

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	322/322 (100%)	314 (98%)	8 (2%)	47	49
1	B	318/322 (99%)	309 (97%)	9 (3%)	43	44
All	All	640/644 (99%)	623 (97%)	17 (3%)	44	46

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	9	MET
1	A	35	LYS
1	A	58	PRO
1	A	223	GLN
1	A	251	PHE
1	A	263	VAL
1	A	339	ARG
1	B	2	LYS
1	B	9	MET
1	B	91	LYS
1	B	151	ARG
1	B	175	ASN
1	B	251	PHE
1	B	339	ARG
1	B	348	GLN
1	B	349	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	348	GLN

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 ⓘ

6 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	C	1	2	12,12,12	0.67	0	17,17,17	2.16	6 (35%)
2	BGC	C	2	2	11,11,12	0.54	0	15,15,17	1.05	1 (6%)
2	BGC	C	3	2	11,11,12	0.50	0	15,15,17	0.69	0
2	GLC	D	1	2	12,12,12	0.48	0	17,17,17	2.14	6 (35%)
2	BGC	D	2	2	11,11,12	0.54	0	15,15,17	1.51	4 (26%)
2	BGC	D	3	2	11,11,12	0.59	0	15,15,17	0.74	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
2	GLC	C	1	2	2/2/5/5	2/2/22/22	0/1/1/1
2	BGC	C	2	2	-	0/2/19/22	0/1/1/1
2	BGC	C	3	2	-	0/2/19/22	0/1/1/1
2	GLC	D	1	2	-	0/2/22/22	0/1/1/1
2	BGC	D	2	2	-	0/2/19/22	0/1/1/1
2	BGC	D	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	GLC	O4-C4-C3	4.84	121.53	110.35
2	C	1	GLC	O3-C3-C4	4.26	120.21	110.35
2	D	1	GLC	O4-C4-C5	-3.85	99.74	109.30
2	D	1	GLC	O3-C3-C4	3.75	119.01	110.35
2	C	1	GLC	O4-C4-C5	-3.51	100.58	109.30
2	D	2	BGC	O3-C3-C2	-3.24	103.78	109.99

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	GLC	O4-C4-C3	3.13	117.59	110.35
2	D	1	GLC	C3-C4-C5	-3.01	104.88	110.24
2	C	1	GLC	O5-C1-C2	-2.97	104.99	110.28
2	C	1	GLC	C6-C5-C4	2.90	119.79	113.00
2	D	2	BGC	O2-C2-C1	2.57	114.42	109.15
2	D	2	BGC	C1-C2-C3	2.36	112.57	109.67
2	C	1	GLC	C3-C4-C5	2.35	114.43	110.24
2	C	2	BGC	O2-C2-C1	2.11	113.47	109.15
2	D	1	GLC	O5-C1-C2	-2.02	106.68	110.28
2	D	1	GLC	O3-C3-C2	-2.01	105.69	110.35
2	D	2	BGC	C1-O5-C5	2.01	114.91	112.19

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	1	GLC	C5
2	C	1	GLC	C3

All (2) torsion outliers are listed below:

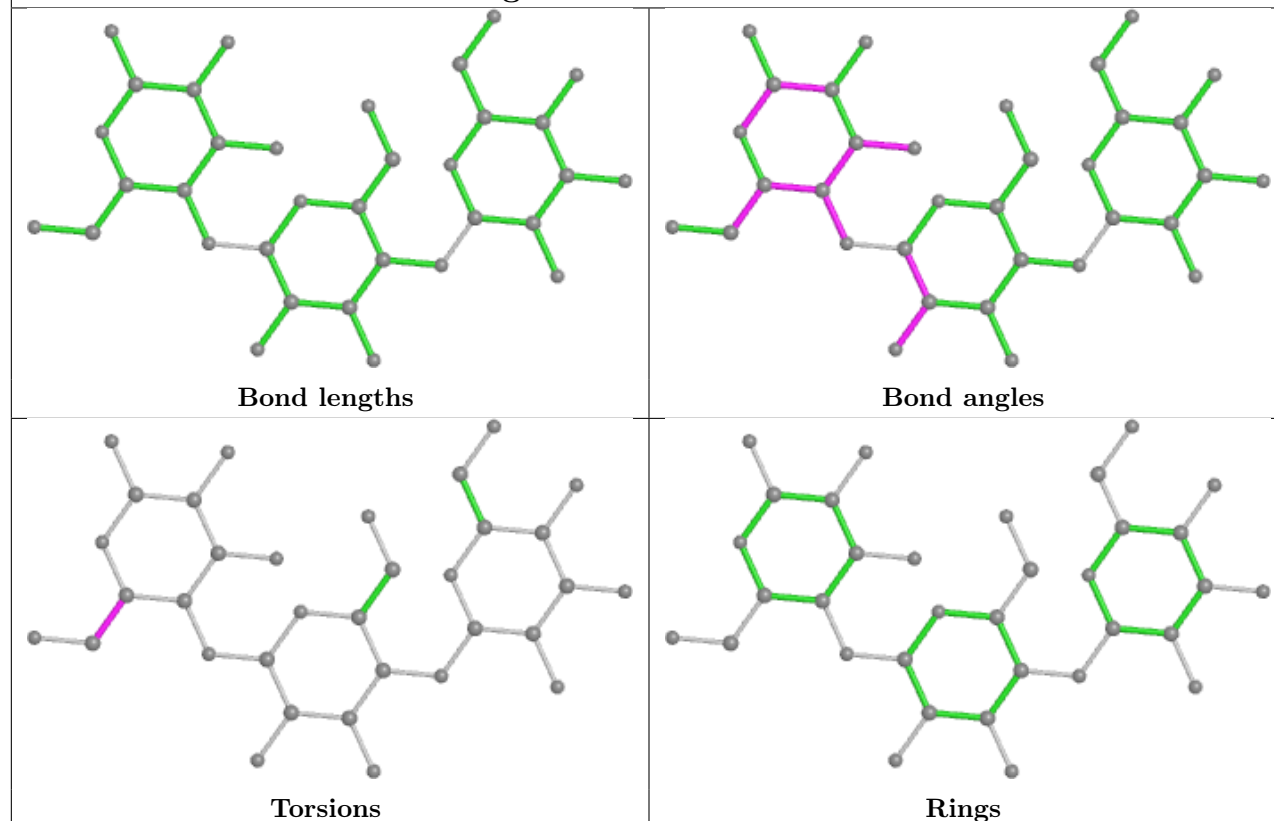
Mol	Chain	Res	Type	Atoms
2	C	1	GLC	C4-C5-C6-O6
2	C	1	GLC	O5-C5-C6-O6

There are no ring outliers.

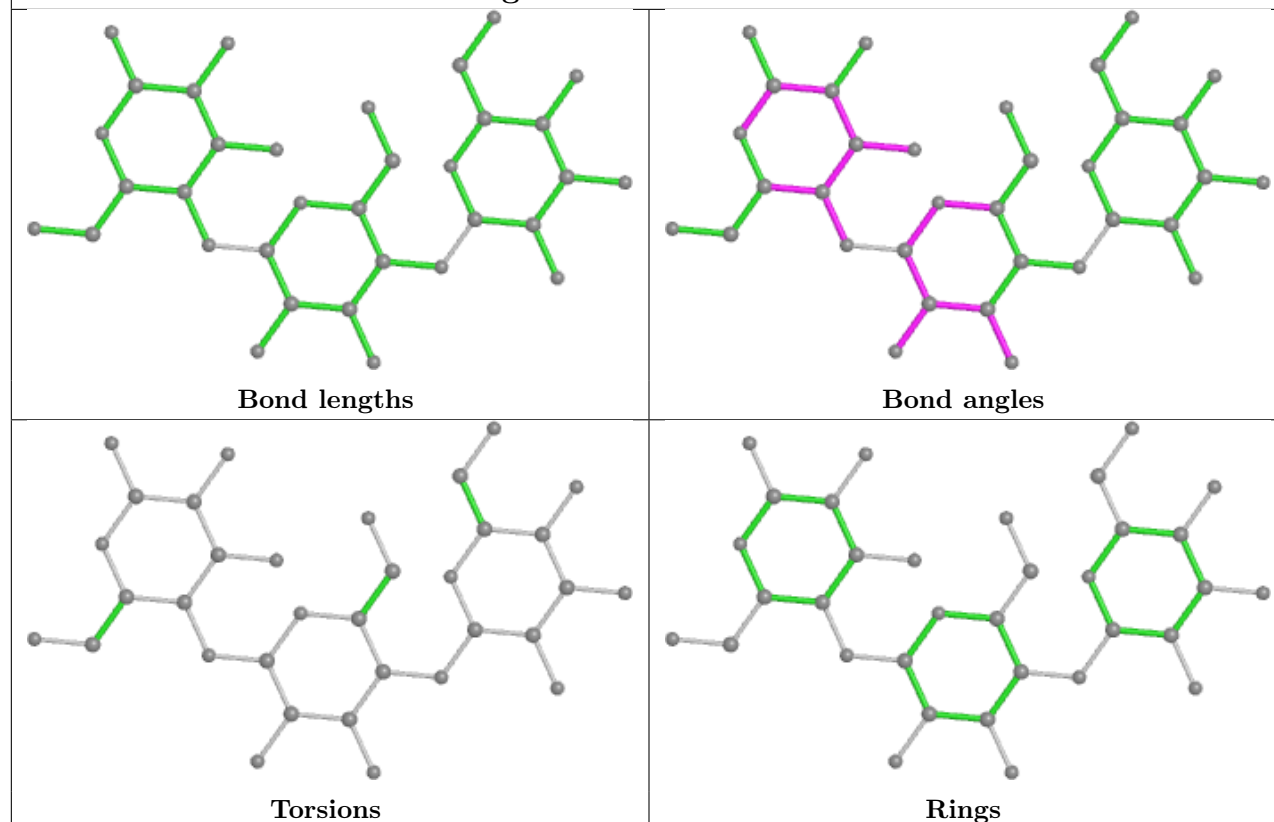
No monomer is involved in short contacts.

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

Oligosaccharide Chain C



Oligosaccharide Chain D



5.6 Ligand geometry

Of 14 ligands modelled in this entry, 5 are monoatomic - leaving 9 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	$\# Z > 2$
8	CO3	A	509	-	0,3,3	0.00	-	0,3,3	0.00	-
7	EDO	A	506	-	3,3,3	0.21	0	2,2,2	0.26	0
6	SO4	A	505	-	4,4,4	0.33	0	6,6,6	0.11	0
7	EDO	A	507	-	3,3,3	0.12	0	2,2,2	0.11	0
5	SO2	A	504	-	2,2,2	0.30	0	1,1,1	0.21	0
8	CO3	A	510	-	0,3,3	0.00	-	0,3,3	0.00	-
8	CO3	A	508	-	0,3,3	0.00	-	0,3,3	0.00	-
6	SO4	B	503	-	4,4,4	0.37	0	6,6,6	0.06	0
7	EDO	B	504	-	3,3,3	0.27	0	2,2,2	0.10	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
7	EDO	B	504	-	-	1/1/1/1	-
7	EDO	A	506	-	-	0/1/1/1	-
7	EDO	A	507	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	504	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	510	CO3	1	0
7	B	504	EDO	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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 ²)	Q<0.9
1	A	417/423 (98%)	-0.43	0 100 100	14, 25, 43, 61	0
1	B	417/423 (98%)	-0.23	12 (2%) 51 50	18, 32, 58, 87	0
All	All	834/846 (98%)	-0.33	12 (1%) 75 74	14, 28, 52, 87	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	200	GLY	6.1
1	B	348	GLN	4.6
1	B	198	ALA	4.3
1	B	343	SER	3.6
1	B	342	TRP	3.1
1	B	201	ARG	3.1
1	B	345	PRO	3.1
1	B	349	GLN	3.0
1	B	199	GLY	2.5
1	B	339	ARG	2.4
1	B	418	HIS	2.3
1	B	107	ARG	2.0

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

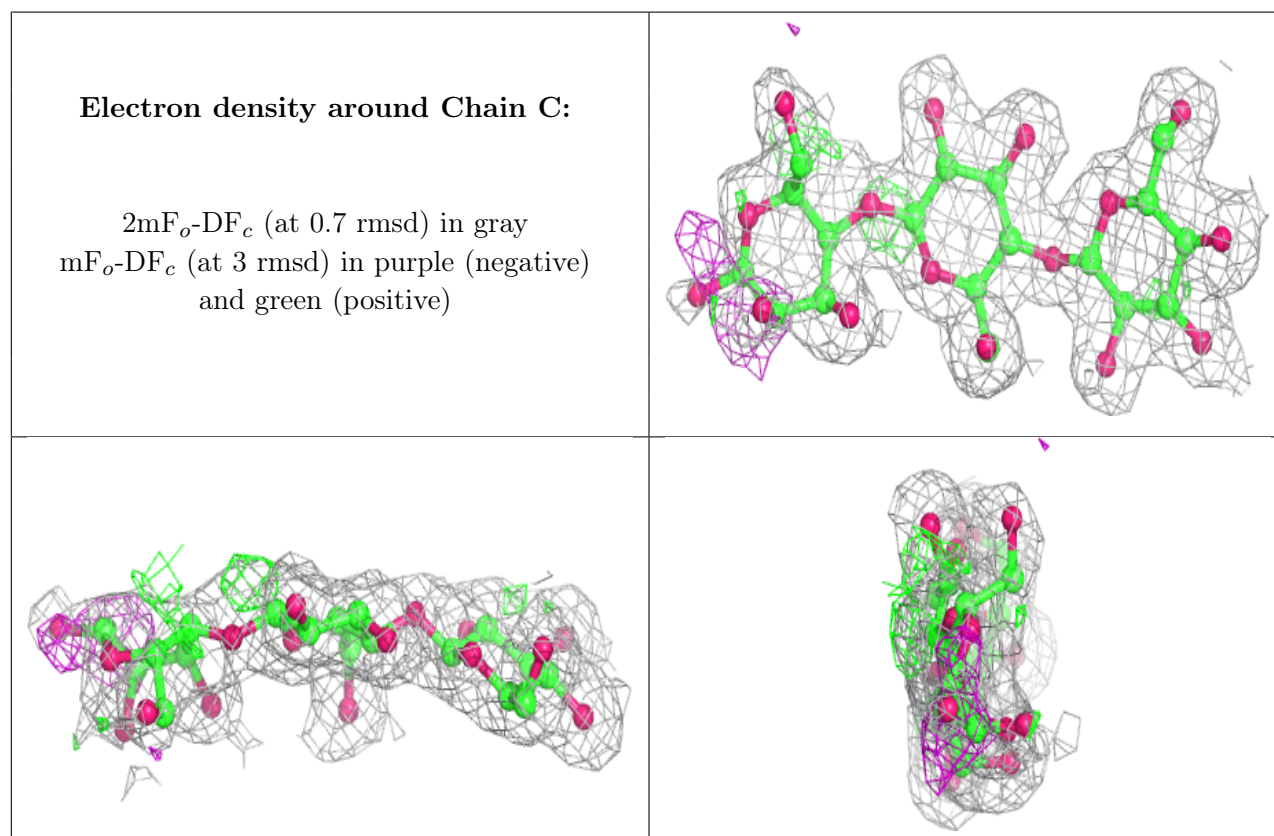
There are no non-standard protein/DNA/RNA residues in this entry.

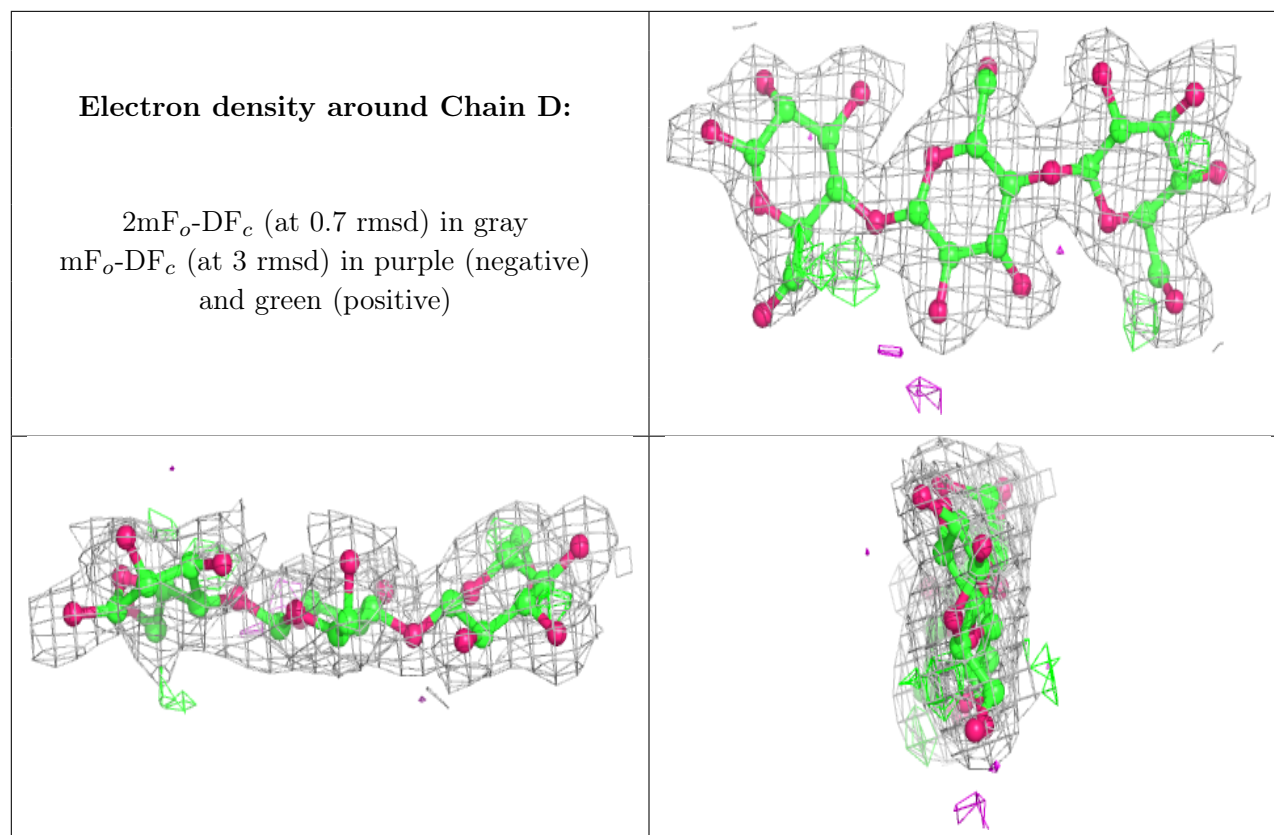
6.3 Carbohydrates [i](#)

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, 95th 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(\AA^2)	Q<0.9
2	GLC	C	1	12/12	0.82	0.21	26,47,52,54	0
2	GLC	D	1	12/12	0.89	0.17	28,42,48,52	0
2	BGC	C	2	11/12	0.96	0.10	14,17,18,20	0
2	BGC	D	3	11/12	0.96	0.10	17,18,19,20	0
2	BGC	D	2	11/12	0.97	0.08	17,18,20,21	0
2	BGC	C	3	11/12	0.98	0.10	14,16,19,19	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.





6.4 Ligands ⓘ

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, 95th 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(\AA^2)	Q<0.9
7	EDO	A	507	4/4	0.83	0.18	45,48,51,53	0
7	EDO	B	504	4/4	0.88	0.14	43,45,52,53	0
8	CO3	A	508	4/4	0.88	0.14	46,47,49,49	0
8	CO3	A	510	4/4	0.89	0.15	43,45,47,47	0
7	EDO	A	506	4/4	0.95	0.15	34,41,42,42	0
4	NA	A	503	1/1	0.96	0.14	33,33,33,33	0
5	SO2	A	504	3/3	0.96	0.07	55,55,58,63	0
8	CO3	A	509	4/4	0.96	0.14	54,55,58,58	0
6	SO4	A	505	5/5	0.97	0.12	55,56,59,59	0
3	CL	A	502	1/1	0.97	0.07	39,39,39,39	0
4	NA	B	502	1/1	0.98	0.19	33,33,33,33	0
6	SO4	B	503	5/5	0.98	0.18	53,55,61,62	0
3	CL	B	501	1/1	0.99	0.04	29,29,29,29	0
3	CL	A	501	1/1	0.99	0.06	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.