



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:00 AM UTC

PDB ID : 5H41 / pdb_00005h41
Title : Crystal Structure of 1,2-beta-oligoglucan phosphorylase from Lachnoclostridium phytofermentans in complex with sophorose, isofagomine, sulfate ion
Authors : Nakajima, M.; Tanaka, N.; Furukawa, N.; Nihira, T.; Kodutsumi, Y.; Takahashi, Y.; Sugimoto, N.; Miyanaga, A.; Fushinobu, S.; Taguchi, H.; Nakai, H.
Deposited on : 2016-10-28
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 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

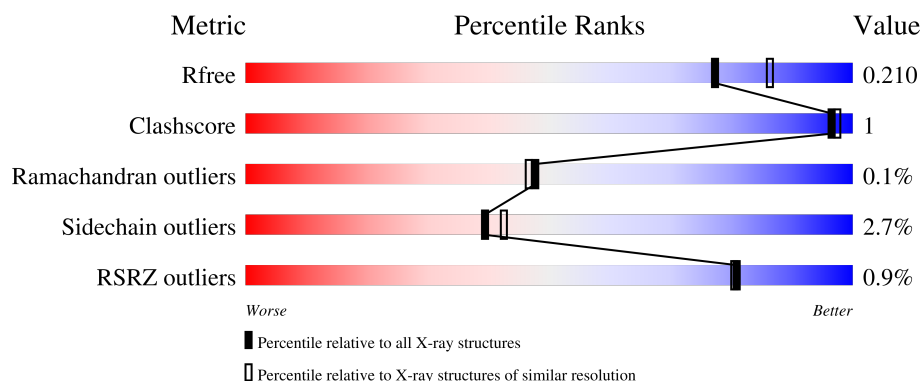
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 of 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	1122	% 94% 5% ..
1	B	1122	% 94% 5% .
2	C	2	50% 50%
2	D	2	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18781 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.

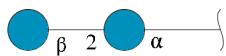
- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1113	Total	C	N	O	S	0	1	0
			8928	5718	1486	1692	32			
1	B	1113	Total	C	N	O	S	0	1	0
			8928	5718	1486	1692	32			

There are 20 discrepancies between the modelled and reference sequences:

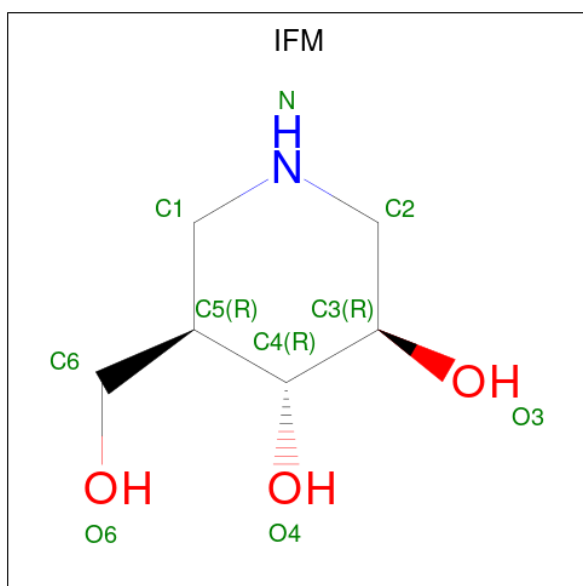
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP A9KJS6
A	1	GLY	-	expression tag	UNP A9KJS6
A	1114	LEU	-	expression tag	UNP A9KJS6
A	1115	GLU	-	expression tag	UNP A9KJS6
A	1116	HIS	-	expression tag	UNP A9KJS6
A	1117	HIS	-	expression tag	UNP A9KJS6
A	1118	HIS	-	expression tag	UNP A9KJS6
A	1119	HIS	-	expression tag	UNP A9KJS6
A	1120	HIS	-	expression tag	UNP A9KJS6
A	1121	HIS	-	expression tag	UNP A9KJS6
B	0	MET	-	expression tag	UNP A9KJS6
B	1	GLY	-	expression tag	UNP A9KJS6
B	1114	LEU	-	expression tag	UNP A9KJS6
B	1115	GLU	-	expression tag	UNP A9KJS6
B	1116	HIS	-	expression tag	UNP A9KJS6
B	1117	HIS	-	expression tag	UNP A9KJS6
B	1118	HIS	-	expression tag	UNP A9KJS6
B	1119	HIS	-	expression tag	UNP A9KJS6
B	1120	HIS	-	expression tag	UNP A9KJS6
B	1121	HIS	-	expression tag	UNP A9KJS6

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	0	0	0
			23	12	11			
2	D	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is 5-HYDROXYMETHYL-3,4-DIHYDROXYPIPERIDINE (CCD ID: IFM) (formula: $C_6H_{13}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	6	1	3		
3	B	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

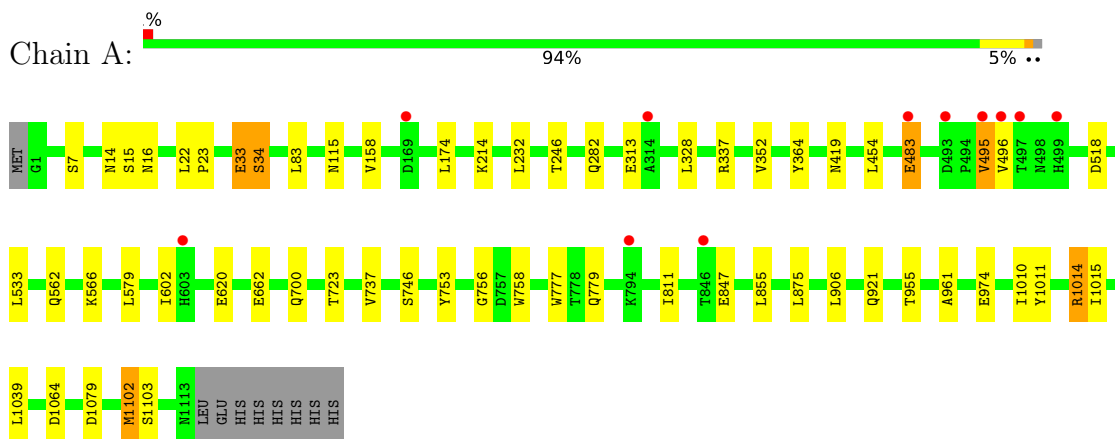
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	383	Total	O	0	0
			383	383		
5	B	456	Total	O	0	0
			456	456		

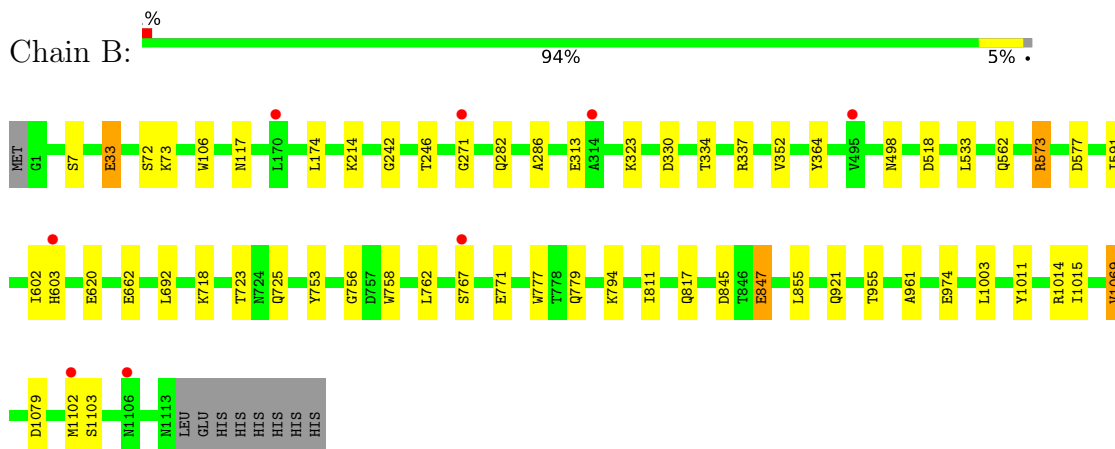
3 Residue-property plots

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: Uncharacterized protein



- Molecule 1: Uncharacterized protein



- Molecule 2: beta-D-glucopyranose-(1-2)-alpha-D-glucopyranose



- Molecule 2: beta-D-glucopyranose-(1-2)-alpha-D-glucopyranose

Chain D:

100%

GLC1
BGC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.69Å 94.88Å 157.36Å 90.00° 100.81° 90.00°	Depositor
Resolution (Å)	48.27 – 2.00 48.27 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.27-2.00) 99.7 (48.27-2.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.168 , 0.204 0.176 , 0.210	Depositor DCC
R_{free} test set	8340 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	24.5	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18781	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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: GLC, BGC, IFM, 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	1.10	2/9154 (0.0%)	1.00	5/12435 (0.0%)
1	B	1.12	2/9154 (0.0%)	1.00	13/12435 (0.1%)
All	All	1.11	4/18308 (0.0%)	1.00	18/24870 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	73	LYS	N-CA	8.24	1.58	1.46
1	A	115	ASN	N-CA	-5.42	1.40	1.46
1	B	498	ASN	N-CA	5.21	1.52	1.46
1	A	737	VAL	N-CA	5.10	1.52	1.46

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	352	VAL	CA-C-N	-6.57	113.87	120.31
1	B	352	VAL	C-N-CA	-6.57	113.87	120.31
1	A	352	VAL	CA-C-N	-6.55	113.89	120.31
1	A	352	VAL	C-N-CA	-6.55	113.89	120.31
1	A	33	GLU	CA-C-N	-6.36	115.19	126.45
1	A	33	GLU	C-N-CA	-6.36	115.19	126.45
1	B	33	GLU	CA-C-N	-6.25	112.72	122.67
1	B	33	GLU	C-N-CA	-6.25	112.72	122.67
1	B	72	SER	CA-C-N	-5.61	114.26	122.40
1	B	72	SER	C-N-CA	-5.61	114.26	122.40
1	B	573	ARG	CB-CG-CD	5.45	123.84	111.30
1	B	817	GLN	N-CA-C	5.42	117.26	111.36
1	A	495	VAL	N-CA-CB	5.40	117.66	111.39
1	B	591	ILE	CA-C-N	-5.26	114.34	119.76
1	B	591	ILE	C-N-CA	-5.26	114.34	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1069	VAL	CB-CA-C	5.20	118.33	110.63
1	B	286	ALA	CA-C-N	-5.17	114.91	120.03
1	B	286	ALA	C-N-CA	-5.17	114.91	120.03

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	8928	0	8681	16	0
1	B	8928	0	8681	18	0
2	C	23	0	21	1	0
2	D	23	0	20	0	0
3	A	10	0	13	1	0
3	B	10	0	13	0	0
4	A	10	0	0	0	0
4	B	10	0	0	0	0
5	A	383	0	0	0	0
5	B	456	0	0	0	0
All	All	18781	0	17429	35	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 1.

All (35) 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:483:GLU:O	1:A:483:GLU:HG2	1.97	0.65
1:B:518:ASP:HA	1:B:533:LEU:O	2.06	0.56
1:A:518:ASP:HA	1:A:533:LEU:O	2.08	0.53
1:B:753:TYR:CZ	1:B:756:GLY:HA2	2.44	0.53
1:B:662:GLU:OE2	1:B:725:GLN:NE2	2.43	0.52
1:B:33:GLU:HB2	1:B:246:THR:HG21	1.93	0.51
1:B:845:ASP:OD1	1:B:847:GLU:OE1	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:TYR:CZ	1:A:756:GLY:HA2	2.47	0.49
1:A:1102:MET:HE2	1:A:1102:MET:HA	1.95	0.49
1:A:33:GLU:HB2	1:A:246:THR:HG21	1.94	0.49
1:B:1102:MET:HA	1:B:1102:MET:HE2	1.95	0.49
1:A:662:GLU:HB2	1:A:723:THR:HG21	1.95	0.48
1:A:779:GLN:NE2	1:A:811:ILE:HG23	2.29	0.47
1:B:662:GLU:HB2	1:B:723:THR:HG21	1.97	0.47
1:A:955:THR:HG22	1:A:961:ALA:O	2.16	0.46
1:A:33:GLU:O	1:A:34:SER:CB	2.63	0.46
1:B:779:GLN:NE2	1:B:811:ILE:HG23	2.30	0.46
1:A:758:TRP:HB2	1:A:777:TRP:CH2	2.51	0.46
1:B:767:SER:O	1:B:771:GLU:HG3	2.15	0.45
1:B:758:TRP:HB2	1:B:777:TRP:CH2	2.52	0.45
1:B:955:THR:HG22	1:B:961:ALA:O	2.17	0.45
1:A:16:ASN:HB3	1:A:33:GLU:HG2	1.99	0.44
1:B:323:LYS:HB3	1:B:603[B]:HIS:CE1	2.53	0.44
1:B:573:ARG:NH2	1:B:577:ASP:OD2	2.50	0.43
1:B:330:ASP:O	1:B:334:THR:HG23	2.19	0.43
1:B:337:ARG:HD3	1:B:620:GLU:OE2	2.18	0.43
1:A:1011:TYR:CE2	1:A:1015:ILE:HD11	2.55	0.42
1:A:337:ARG:HD3	1:A:620:GLU:OE2	2.19	0.42
1:B:106:TRP:CZ2	1:B:242:GLY:HA3	2.55	0.41
1:A:14:ASN:O	1:A:15:SER:C	2.64	0.41
3:A:1203:IFM:H1C2	2:C:2:BGC:O2	2.21	0.41
1:B:1003:LEU:C	1:B:1003:LEU:HD23	2.46	0.41
1:A:22:LEU:HB3	1:A:23:PRO:HD2	2.02	0.41
1:B:1011:TYR:CE2	1:B:1015:ILE:HD11	2.56	0.40
1:A:1010:ILE:O	1:A:1014:ARG:HD2	2.22	0.40

There are no symmetry-related clashes.

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	1112/1122 (99%)	1063 (96%)	47 (4%)	2 (0%)	43	42
1	B	1112/1122 (99%)	1068 (96%)	43 (4%)	1 (0%)	48	46
All	All	2224/2244 (99%)	2131 (96%)	90 (4%)	3 (0%)	48	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	496	VAL
1	B	271	GLY
1	A	906	LEU

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	A	976/984 (99%)	944 (97%)	32 (3%)	33	34
1	B	976/984 (99%)	955 (98%)	21 (2%)	45	50
All	All	1952/1968 (99%)	1899 (97%)	53 (3%)	39	42

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	SER
1	A	34	SER
1	A	83	LEU
1	A	158	VAL
1	A	174	LEU
1	A	214	LYS
1	A	232	LEU
1	A	282	GLN
1	A	313	GLU
1	A	328	LEU
1	A	364	TYR
1	A	419	ASN
1	A	454	LEU

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Mol	Chain	Res	Type
1	A	483	GLU
1	A	495	VAL
1	A	562	GLN
1	A	566	LYS
1	A	579	LEU
1	A	602	ILE
1	A	700	GLN
1	A	746	SER
1	A	847	GLU
1	A	855	LEU
1	A	875	LEU
1	A	921	GLN
1	A	974	GLU
1	A	1014	ARG
1	A	1039	LEU
1	A	1064	ASP
1	A	1079	ASP
1	A	1102	MET
1	A	1103	SER
1	B	7	SER
1	B	117	ASN
1	B	174	LEU
1	B	214	LYS
1	B	282	GLN
1	B	313	GLU
1	B	364	TYR
1	B	562	GLN
1	B	602	ILE
1	B	692	LEU
1	B	718	LYS
1	B	762	LEU
1	B	794	LYS
1	B	847	GLU
1	B	855	LEU
1	B	921	GLN
1	B	974	GLU
1	B	1014	ARG
1	B	1069	VAL
1	B	1079	ASP
1	B	1103	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	ASN
1	A	175	GLN
1	A	215	ASN
1	A	268	HIS
1	A	282	GLN
1	A	397	GLN
1	A	524	HIS
1	A	582	ASN
1	A	809	ASN
1	A	1080	ASN
1	B	136	ASN
1	B	175	GLN
1	B	215	ASN
1	B	397	GLN
1	B	472	ASN
1	B	582	ASN
1	B	1080	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](#)

4 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	2.35	4 (33%)	17,17,17	1.79	5 (29%)
2	BGC	C	2	2	11,11,12	1.22	2 (18%)	15,15,17	0.89	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	D	1	2	12,12,12	1.94	3 (25%)	17,17,17	1.73	2 (11%)
2	BGC	D	2	2	11,11,12	0.90	0	15,15,17	1.12	1 (6%)

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	-	0/2/22/22	0/1/1/1
2	BGC	C	2	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

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	GLC	O2-C2	5.15	1.55	1.43
2	D	1	GLC	O2-C2	4.59	1.54	1.43
2	C	1	GLC	O1-C1	3.52	1.50	1.39
2	C	1	GLC	O5-C5	3.17	1.52	1.44
2	D	1	GLC	O3-C3	3.11	1.50	1.43
2	C	2	BGC	C4-C5	2.46	1.58	1.53
2	C	2	BGC	O2-C2	-2.24	1.38	1.43
2	D	1	GLC	O1-C1	2.21	1.46	1.39
2	C	1	GLC	O4-C4	-2.19	1.37	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	GLC	O2-C2-C3	4.55	121.09	110.38
2	D	1	GLC	C1-C2-C3	4.53	119.60	110.36
2	C	1	GLC	C1-C2-C3	4.03	118.57	110.36
2	C	1	GLC	O2-C2-C1	3.01	116.18	109.25
2	C	1	GLC	C1-O5-C5	-2.97	107.91	113.65
2	D	2	BGC	C1-O5-C5	-2.87	108.34	112.19
2	C	1	GLC	O3-C3-C4	2.81	117.01	110.38
2	C	1	GLC	O1-C1-O5	2.25	117.09	110.41

There are no chirality outliers.

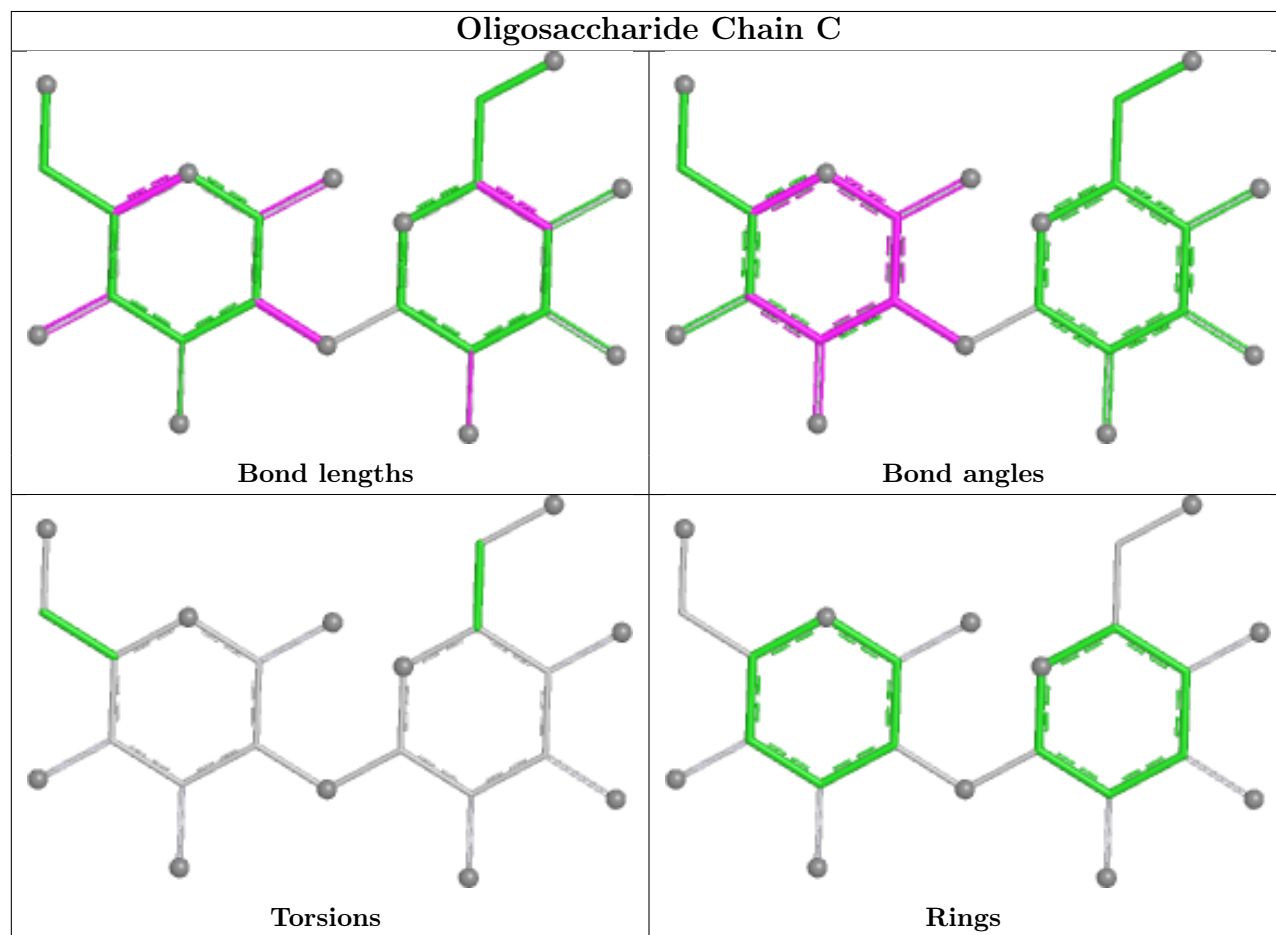
There are no torsion outliers.

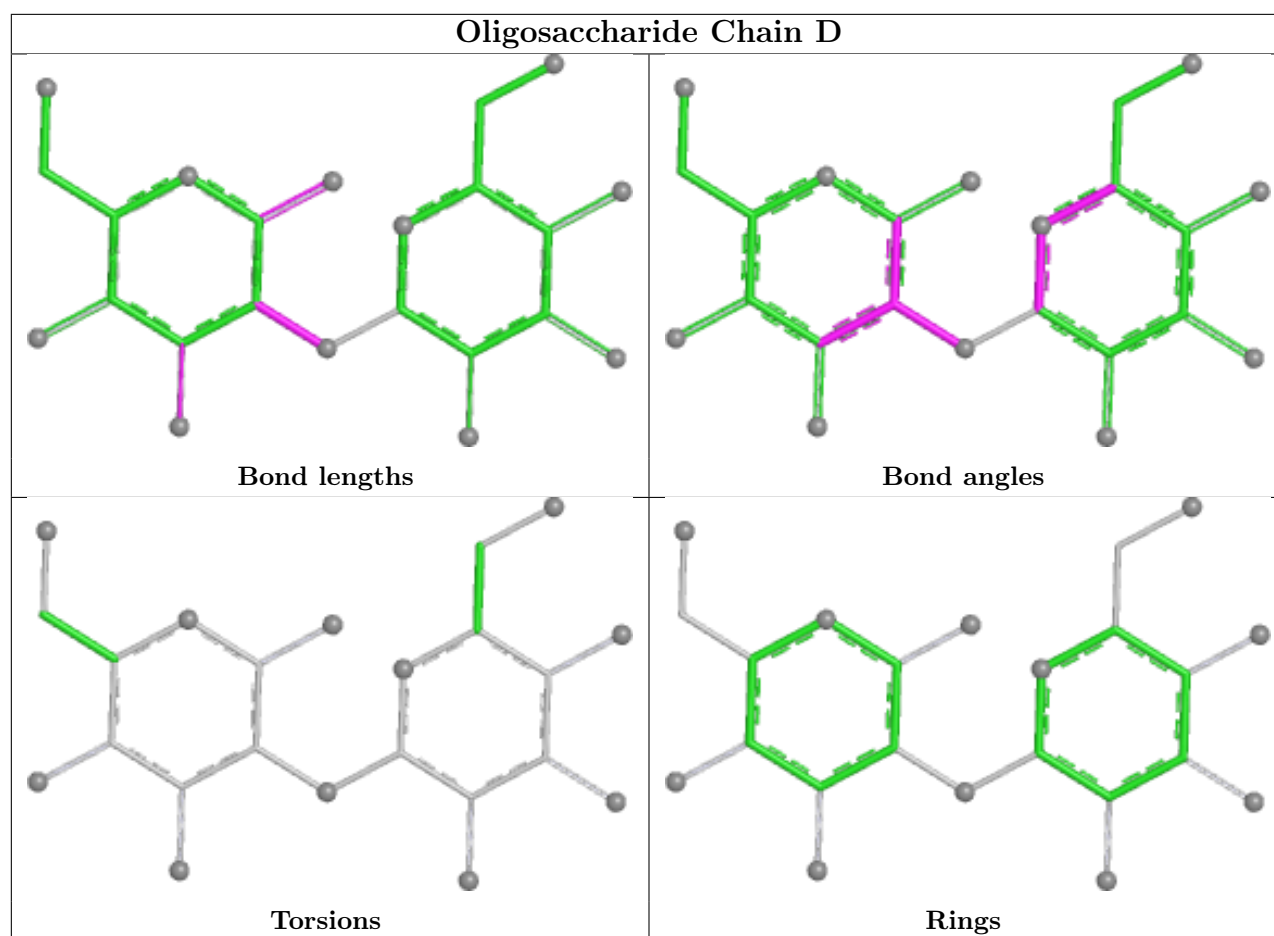
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	BGC	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](#)

6 ligands 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	$\# Z > 2$
3	IFM	A	1203	-	10,10,10	1.02	0	9,13,13	1.13	1 (11%)
4	SO4	A	1205	-	4,4,4	0.71	0	6,6,6	0.39	0
4	SO4	B	1205	-	4,4,4	0.35	0	6,6,6	0.83	0
4	SO4	B	1204	-	4,4,4	1.00	0	6,6,6	0.58	0
3	IFM	B	1203	-	10,10,10	1.22	1 (10%)	9,13,13	1.60	2 (22%)
4	SO4	A	1204	-	4,4,4	0.94	0	6,6,6	0.48	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
3	IFM	A	1203	-	-	0/2/16/16	0/1/1/1
3	IFM	B	1203	-	-	0/2/16/16	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1203	IFM	C5-C4	2.04	1.59	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1203	IFM	C1-N-C2	3.16	115.44	111.78
3	A	1203	IFM	O3-C3-C2	-2.56	104.70	109.65
3	B	1203	IFM	O3-C3-C2	-2.08	105.62	109.65

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
3	A	1203	IFM	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	1113/1122 (99%)	-0.17	11 (0%) 79 79	13, 26, 47, 77	1 (0%)
1	B	1113/1122 (99%)	-0.30	8 (0%) 84 84	13, 24, 43, 72	1 (0%)
All	All	2226/2244 (99%)	-0.24	19 (0%) 81 80	13, 25, 45, 77	2 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	495	VAL	4.8
1	B	271	GLY	3.9
1	A	496	VAL	3.1
1	B	170	LEU	2.7
1	A	846	THR	2.6
1	A	314	ALA	2.4
1	B	495	VAL	2.4
1	B	767	SER	2.4
1	B	1102	MET	2.3
1	B	603[A]	HIS	2.2
1	A	483	GLU	2.2
1	B	314	ALA	2.2
1	A	169	ASP	2.2
1	A	499	HIS	2.1
1	A	603[A]	HIS	2.1
1	A	493	ASP	2.1
1	A	497	THR	2.1
1	B	1106	ASN	2.0
1	A	794	LYS	2.0

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

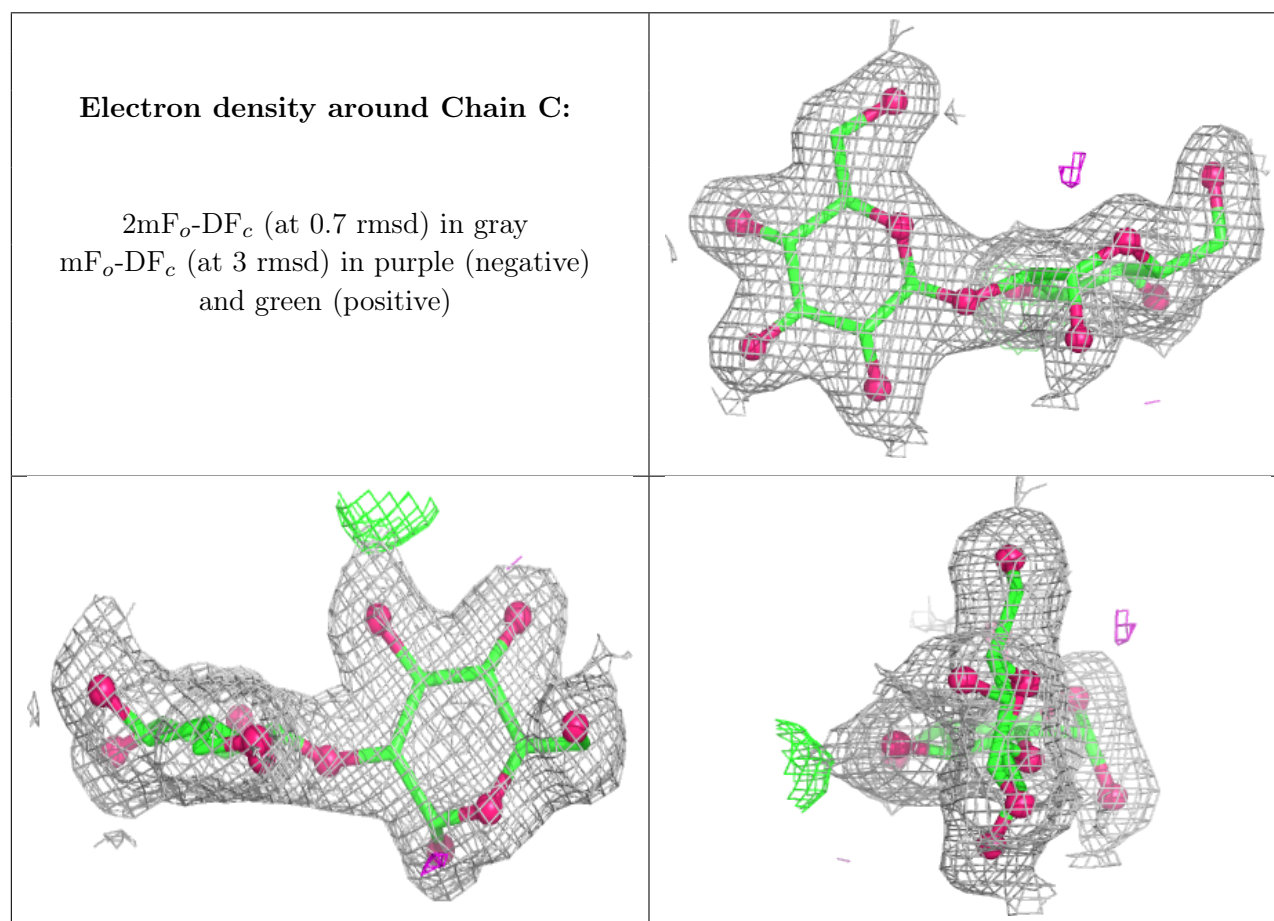
There are no non-standard protein/DNA/RNA residues in this entry.

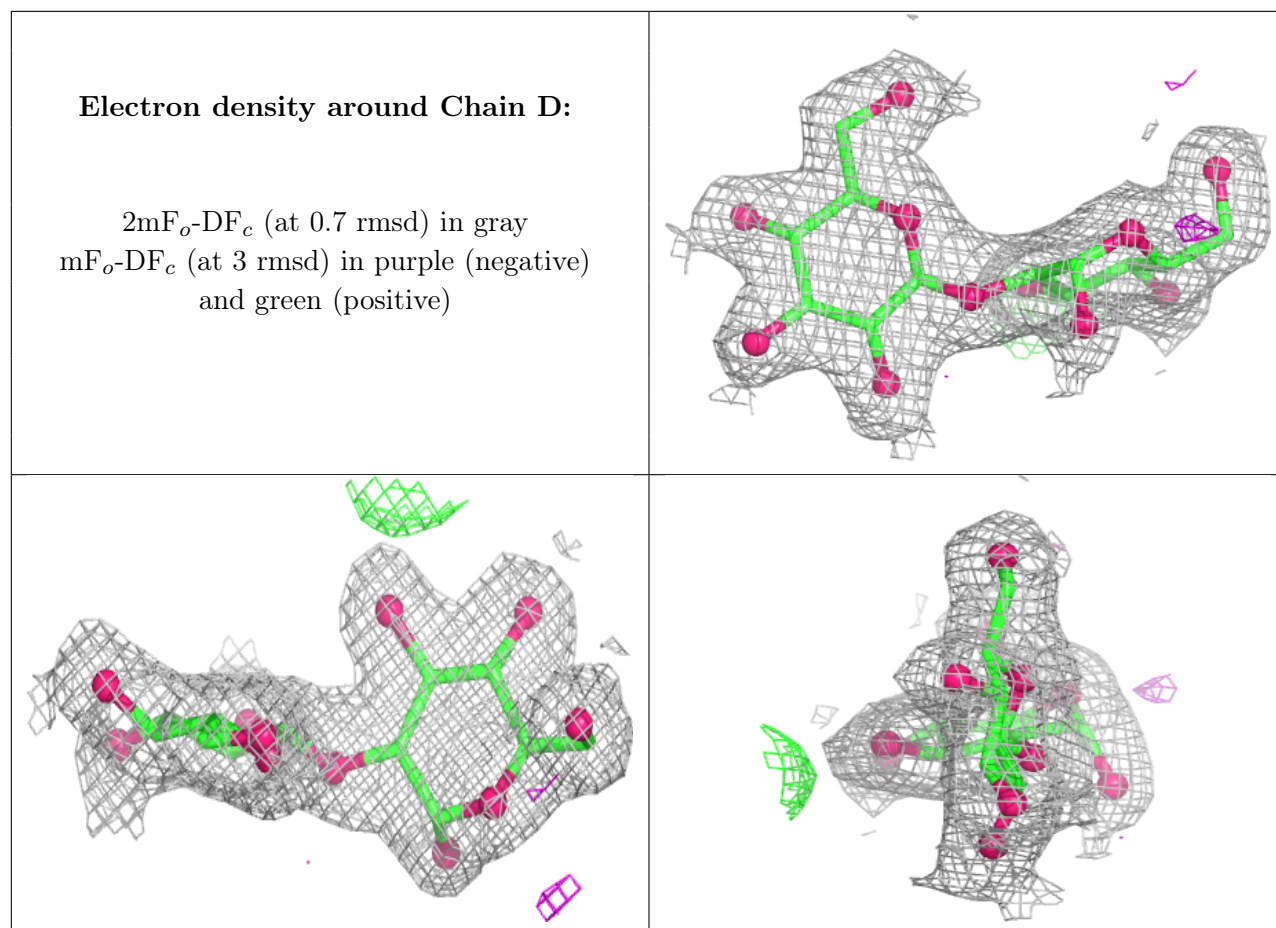
6.3 Carbohydrates ⓘ

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($\text{\AA}^2$)	Q<0.9
2	GLC	C	1	12/12	0.95	0.07	23,26,29,33	0
2	BGC	C	2	11/12	0.96	0.05	24,26,28,28	0
2	GLC	D	1	12/12	0.96	0.05	24,26,28,30	0
2	BGC	D	2	11/12	0.97	0.05	25,25,26,27	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 [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($\text{\AA}^2$)	Q<0.9
3	IFM	B	1203	10/10	0.96	0.06	20,23,24,25	0
3	IFM	A	1203	10/10	0.97	0.06	20,22,23,23	0
4	SO4	A	1205	5/5	0.98	0.06	27,27,30,31	0
4	SO4	B	1204	5/5	0.98	0.09	22,22,24,27	0
4	SO4	B	1205	5/5	0.98	0.06	27,30,31,33	0
4	SO4	A	1204	5/5	0.99	0.07	22,22,24,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.