



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 01:04 AM BST

PDB ID : 5YSF
Title : Crystal structure of beta-1,2-glucooligosaccharide binding protein in complex with sophoropentaose
Authors : Abe, K.; Nakajima, M.; Taguchi, H.; Arakawa, T.; Fushinobu, S.
Deposited on : 2017-11-14
Resolution : 1.90 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 : 2.13.1
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) : 2.13.1

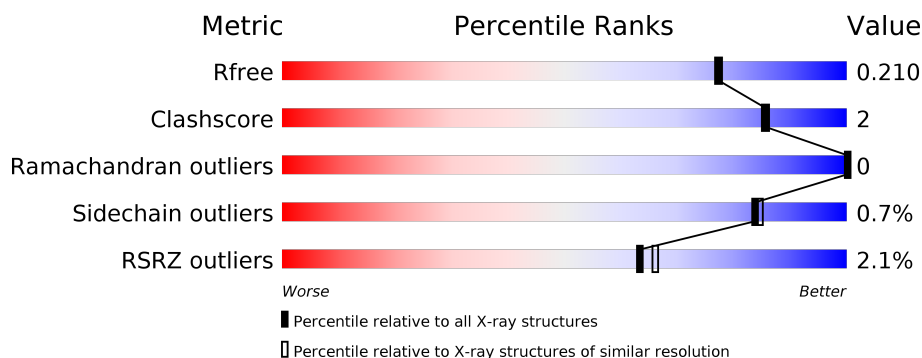
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	397	<div> <div>2%</div> <div>88%</div> <div>9%</div> <div>.</div> </div>
1	B	397	<div> <div>3%</div> <div>92%</div> <div>6%</div> <div>.</div> </div>
2	C	5	<div> <div>40%</div> <div>60%</div> </div>
2	D	5	<div> <div>20%</div> <div>80%</div> </div>

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
3	MPD	A	501	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6765 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.

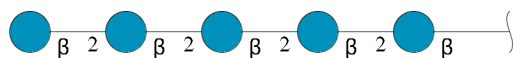
- Molecule 1 is a protein called Lin1841 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	3	0
			3094	1975	506	597	16			
1	B	389	Total	C	N	O	S	0	1	0
			3087	1971	504	596	16			

There are 18 discrepancies between the modelled and reference sequences:

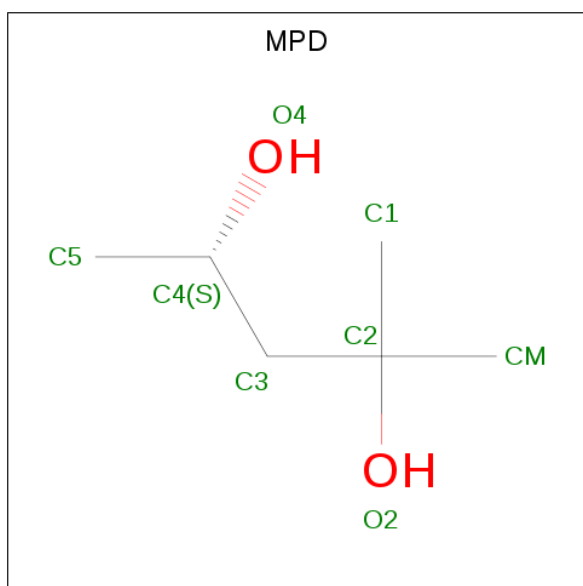
Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	expression tag	UNP Q92AS8
A	415	LEU	-	expression tag	UNP Q92AS8
A	416	GLU	-	expression tag	UNP Q92AS8
A	417	HIS	-	expression tag	UNP Q92AS8
A	418	HIS	-	expression tag	UNP Q92AS8
A	419	HIS	-	expression tag	UNP Q92AS8
A	420	HIS	-	expression tag	UNP Q92AS8
A	421	HIS	-	expression tag	UNP Q92AS8
A	422	HIS	-	expression tag	UNP Q92AS8
B	26	MET	-	expression tag	UNP Q92AS8
B	415	LEU	-	expression tag	UNP Q92AS8
B	416	GLU	-	expression tag	UNP Q92AS8
B	417	HIS	-	expression tag	UNP Q92AS8
B	418	HIS	-	expression tag	UNP Q92AS8
B	419	HIS	-	expression tag	UNP Q92AS8
B	420	HIS	-	expression tag	UNP Q92AS8
B	421	HIS	-	expression tag	UNP Q92AS8
B	422	HIS	-	expression tag	UNP Q92AS8

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	5	Total	C	O	0	0	0
			56	30	26			
2	D	5	Total	C	O	0	0	0
			56	30	26			

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

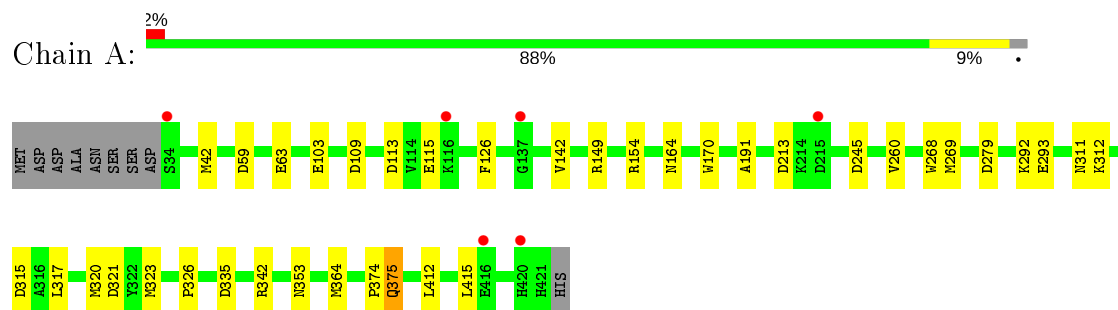
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	274	Total 274	O 274	0	0
5	B	181	Total 181	O 181	0	0

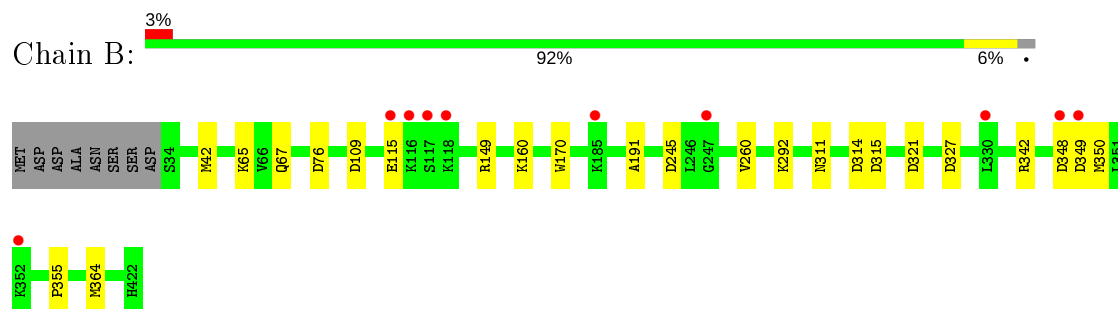
3 Residue-property plots [i](#)

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.

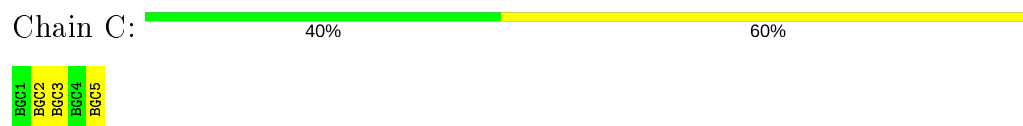
- Molecule 1: Lin1841 protein



- Molecule 1: Lin1841 protein



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	36.22Å 125.99Å 91.04Å 90.00° 100.45° 90.00°	Depositor
Resolution (Å)	44.76 – 1.90 34.05 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (44.76-1.90) 97.5 (34.05-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0158, Coot	Depositor
R, R_{free}	0.166 , 0.203 0.177 , 0.210	Depositor DCC
R_{free} test set	3100 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	22.9	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6765	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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: MG, BGC, MPD

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	0.98	3/3172 (0.1%)	0.98	15/4295 (0.3%)
1	B	0.88	0/3166	0.95	15/4284 (0.4%)
All	All	0.93	3/6338 (0.0%)	0.96	30/8579 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	293	GLU	CD-OE2	5.80	1.32	1.25
1	A	63	GLU	CD-OE2	5.27	1.31	1.25
1	A	268	TRP	CE3-CZ3	5.09	1.47	1.38

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	342	ARG	NE-CZ-NH1	8.27	124.43	120.30
1	B	342	ARG	NE-CZ-NH2	-7.95	116.33	120.30
1	A	342	ARG	NE-CZ-NH2	-7.92	116.34	120.30
1	A	109	ASP	CB-CG-OD1	7.84	125.35	118.30
1	A	321	ASP	CB-CG-OD1	7.50	125.05	118.30
1	B	349	ASP	CB-CG-OD1	7.39	124.95	118.30
1	B	321	ASP	CB-CG-OD1	7.38	124.95	118.30
1	B	109	ASP	CB-CG-OD1	7.03	124.63	118.30
1	A	315	ASP	CB-CG-OD2	-6.44	112.50	118.30
1	B	315	ASP	CB-CG-OD2	-6.43	112.51	118.30
1	A	269	MET	CG-SD-CE	-6.26	90.18	100.20
1	A	213	ASP	CB-CG-OD2	-6.22	112.70	118.30
1	B	149	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	A	279	ASP	CB-CG-OD1	5.88	123.60	118.30
1	A	154	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	245	ASP	CB-CG-OD1	5.73	123.46	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	59	ASP	CB-CG-OD1	5.70	123.43	118.30
1	A	342	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	B	350	MET	CG-SD-CE	5.54	109.07	100.20
1	B	348	ASP	CB-CG-OD1	5.53	123.27	118.30
1	B	327	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	335	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	323	MET	CG-SD-CE	5.36	108.77	100.20
1	A	149	ARG	NE-CZ-NH1	5.31	122.96	120.30
1	B	245	ASP	CB-CG-OD2	-5.30	113.53	118.30
1	A	335	ASP	CB-CG-OD2	-5.26	113.56	118.30
1	B	149	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	B	76	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	160	LYS	CA-CB-CG	5.02	124.44	113.40
1	B	311	ASN	CB-CA-C	-5.00	100.40	110.40

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	3094	0	3012	19	0
1	B	3087	0	3003	6	0
2	C	56	0	48	0	0
2	D	56	0	48	0	0
3	A	16	0	28	6	0
4	A	1	0	0	0	0
5	A	274	0	0	2	0
5	B	181	0	0	1	0
All	All	6765	0	6139	27	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 2.

All (27) 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:375[A]:GLN:NE2	1:A:375[A]:GLN:H	1.94	0.65
1:A:374:PRO:HG2	1:A:375[A]:GLN:OE1	1.97	0.64
1:A:113:ASP:HB3	1:A:317:LEU:HD21	1.84	0.58
1:A:375[A]:GLN:CD	1:A:375[A]:GLN:N	2.57	0.57
3:A:502:MPD:H52	3:A:502:MPD:H12	1.87	0.55
1:A:115:GLU:HA	1:A:115:GLU:OE1	2.08	0.54
1:B:65:LYS:HE3	1:B:67:GLN:OE1	2.10	0.52
1:A:375[A]:GLN:CD	1:A:375[A]:GLN:H	2.14	0.51
3:A:502:MPD:H53	5:A:751:HOH:O	2.11	0.51
1:B:115:GLU:HA	1:B:115:GLU:OE1	2.12	0.49
1:A:311:ASN:OD1	1:A:312:LYS:HG3	2.13	0.48
1:A:353:ASN:ND2	5:A:603:HOH:O	2.45	0.47
1:A:164:ASN:H	3:A:501:MPD:H12	1.79	0.47
1:A:126:PHE:CD2	1:A:364:MET:CE	2.98	0.46
1:B:191:ALA:HB2	1:B:260:VAL:HG11	1.98	0.46
1:A:164:ASN:H	3:A:501:MPD:C1	2.28	0.45
1:A:191:ALA:HB2	1:A:260:VAL:HG11	1.98	0.45
1:A:126:PHE:CD2	1:A:364:MET:HE2	2.52	0.45
1:B:170:TRP:CE2	1:B:292:LYS:HB2	2.52	0.45
1:A:170:TRP:CE2	1:A:292:LYS:HB2	2.52	0.43
1:A:164:ASN:HB2	3:A:501:MPD:H13	2.01	0.42
1:B:364:MET:HE3	1:B:364:MET:HB3	1.91	0.42
1:A:375[A]:GLN:OE1	1:A:415:LEU:HD22	2.20	0.42
1:B:314:ASP:HB2	5:B:701:HOH:O	2.20	0.42
1:A:375[B]:GLN:OE1	1:A:412:LEU:HD23	2.20	0.41
1:A:326:PRO:HB2	3:A:502:MPD:H51	2.01	0.41
1:A:142[A]:VAL:HG12	1:A:320:MET:HE3	2.02	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	389/397 (98%)	383 (98%)	6 (2%)	0	100	100
1	B	388/397 (98%)	380 (98%)	8 (2%)	0	100	100
All	All	777/794 (98%)	763 (98%)	14 (2%)	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	A	336/341 (98%)	332 (99%)	4 (1%)	71	70
1	B	335/341 (98%)	333 (99%)	2 (1%)	86	87
All	All	671/682 (98%)	665 (99%)	6 (1%)	84	79

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	MET
1	A	103	GLU
1	A	375[A]	GLN
1	A	375[B]	GLN
1	B	42	MET
1	B	355	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

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	BGC	C	1	2	12,12,12	0.88	0	17,17,17	1.02	0
2	BGC	C	2	2	11,11,12	0.52	0	15,15,17	1.39	3 (20%)
2	BGC	C	3	2	11,11,12	0.50	0	15,15,17	1.45	1 (6%)
2	BGC	C	4	2	11,11,12	0.59	0	15,15,17	1.01	0
2	BGC	C	5	2	11,11,12	0.91	1 (9%)	15,15,17	1.04	1 (6%)
2	BGC	D	1	2	12,12,12	0.84	0	17,17,17	0.74	0
2	BGC	D	2	2	11,11,12	0.73	0	15,15,17	1.18	1 (6%)
2	BGC	D	3	2	11,11,12	0.60	0	15,15,17	1.55	2 (13%)
2	BGC	D	4	2	11,11,12	0.82	0	15,15,17	1.09	1 (6%)
2	BGC	D	5	2	11,11,12	0.41	0	15,15,17	0.71	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	BGC	C	1	2	-	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	BGC	C	4	2	-	0/2/19/22	0/1/1/1
2	BGC	C	5	2	-	0/2/19/22	0/1/1/1
2	BGC	D	1	2	-	2/2/22/22	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
2	BGC	D	4	2	-	0/2/19/22	0/1/1/1
2	BGC	D	5	2	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	5	BGC	O5-C1	-2.43	1.39	1.43

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3	BGC	C1-C2-C3	-3.42	105.46	109.67
2	D	3	BGC	O5-C5-C6	3.40	112.53	107.20
2	C	3	BGC	O5-C5-C6	2.70	111.43	107.20
2	D	2	BGC	O5-C5-C6	2.45	111.05	107.20
2	D	4	BGC	O3-C3-C2	2.37	114.52	109.99
2	C	2	BGC	C1-O5-C5	2.31	115.33	112.19
2	C	2	BGC	O5-C1-C2	-2.28	107.26	110.77
2	C	5	BGC	O3-C3-C4	2.25	115.54	110.35
2	C	2	BGC	O4-C4-C5	-2.05	104.20	109.30
2	D	5	BGC	C1-O5-C5	2.02	114.93	112.19

There are no chirality outliers.

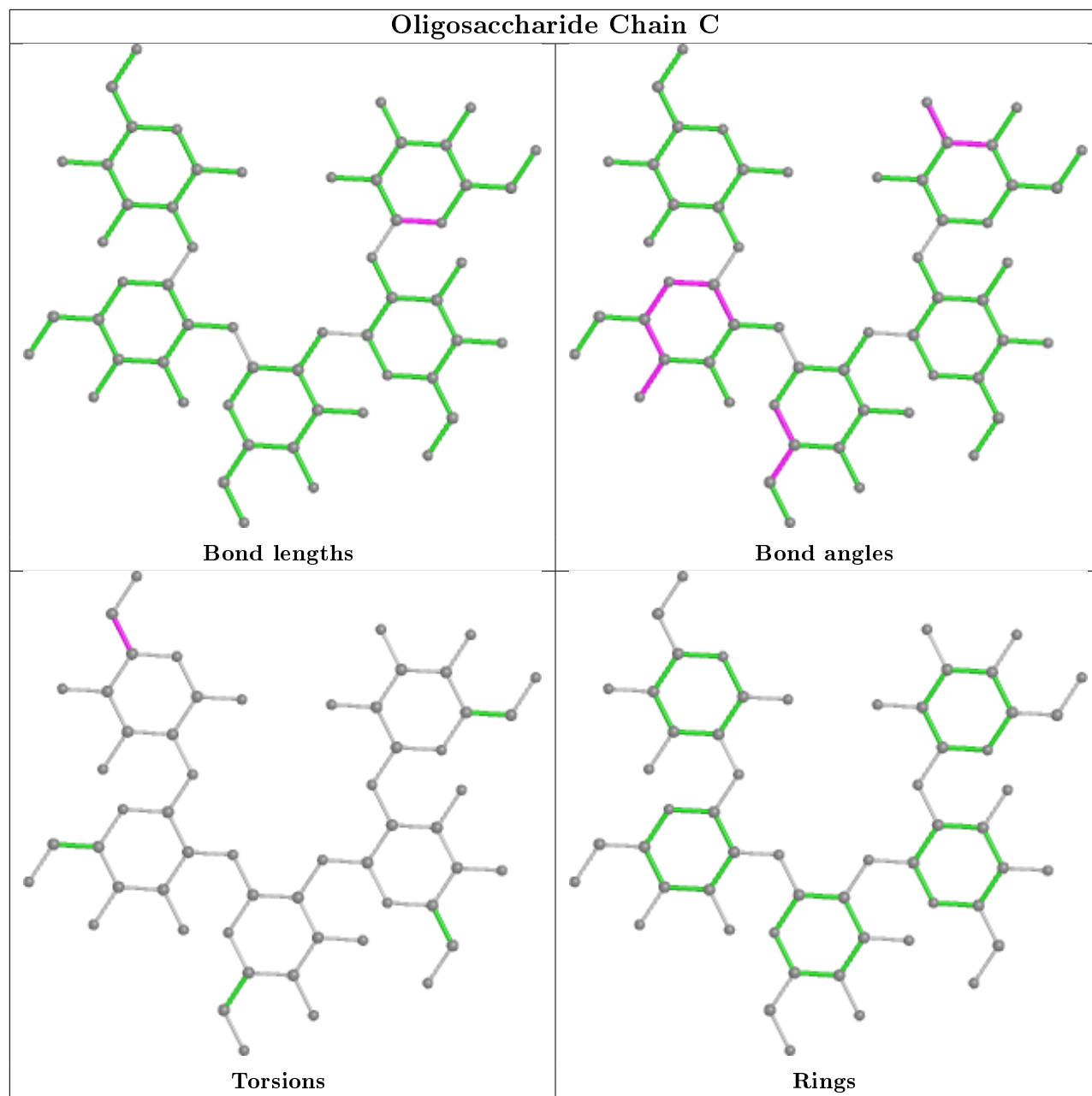
All (4) torsion outliers are listed below:

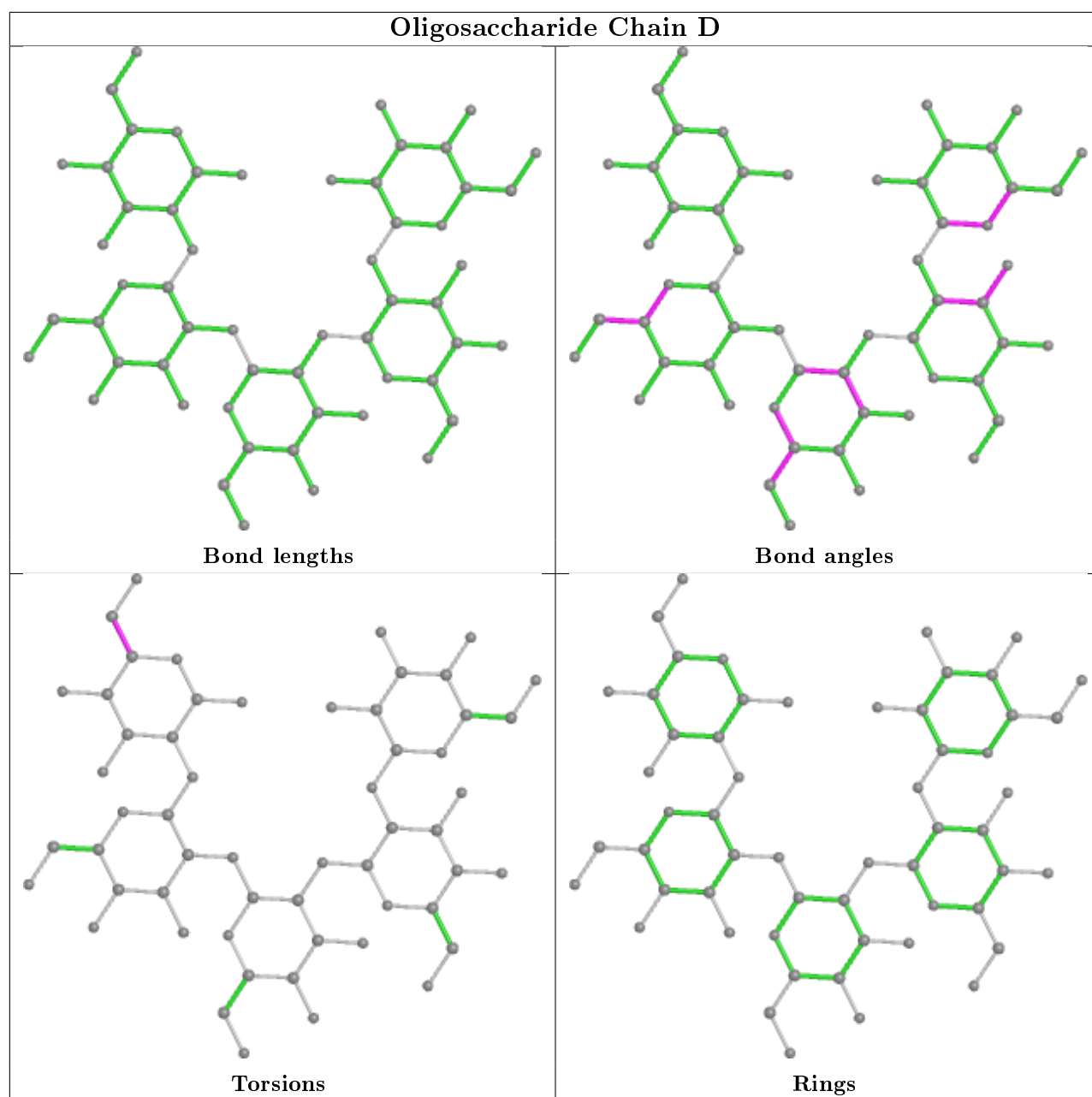
Mol	Chain	Res	Type	Atoms
2	C	1	BGC	C4-C5-C6-O6
2	C	1	BGC	O5-C5-C6-O6
2	D	1	BGC	C4-C5-C6-O6
2	D	1	BGC	O5-C5-C6-O6

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.





5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - 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
3	MPD	A	502	-	7,7,7	0.29	0	9,10,10	0.89	0
3	MPD	A	501	-	7,7,7	0.87	1 (14%)	9,10,10	2.42	6 (66%)

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	MPD	A	502	-	-	1/5/5/5	-
3	MPD	A	501	-	-	3/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	MPD	C3-C2	2.07	1.59	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	MPD	O2-C2-C1	3.52	119.37	108.08
3	A	501	MPD	CM-C2-C3	3.47	126.09	109.96
3	A	501	MPD	O2-C2-C3	-3.10	98.15	109.80
3	A	501	MPD	CM-C2-C1	-2.73	104.89	110.57
3	A	501	MPD	O2-C2-CM	-2.33	100.61	108.08
3	A	501	MPD	O4-C4-C5	-2.22	99.78	109.38

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	MPD	C2-C3-C4-O4
3	A	501	MPD	C2-C3-C4-O4
3	A	501	MPD	C2-C3-C4-C5
3	A	501	MPD	O2-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	MPD	3	0
3	A	501	MPD	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 [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	388/397 (97%)	-0.30	6 (1%) 73 76	15, 26, 53, 73	0
1	B	389/397 (97%)	-0.02	10 (2%) 56 58	17, 35, 57, 70	0
All	All	777/794 (97%)	-0.16	16 (2%) 63 66	15, 30, 57, 73	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	116	LYS	3.9
1	B	115	GLU	3.6
1	B	118	LYS	3.6
1	B	247	GLY	3.5
1	B	349	ASP	3.5
1	A	215	ASP	2.9
1	A	34	SER	2.4
1	A	137	GLY	2.3
1	B	185	LYS	2.3
1	A	420	HIS	2.3
1	B	348	ASP	2.3
1	B	330	LEU	2.3
1	B	117	SER	2.3
1	B	116	LYS	2.2
1	B	352	LYS	2.1
1	A	416	GLU	2.1

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 ⓘ

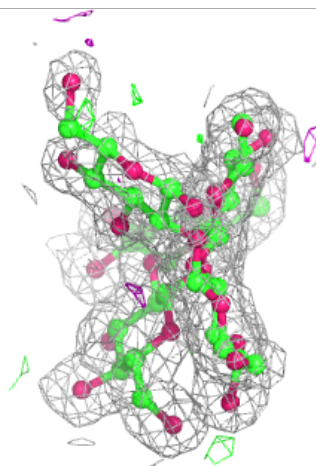
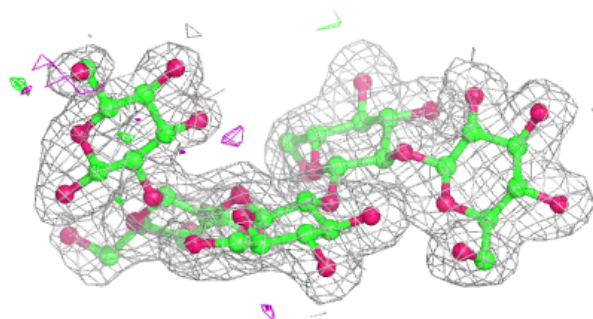
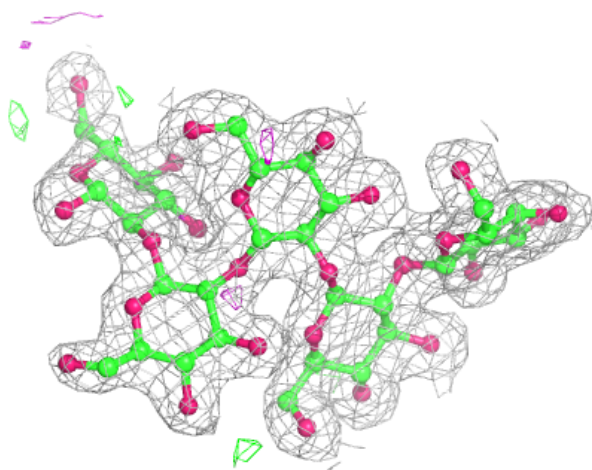
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

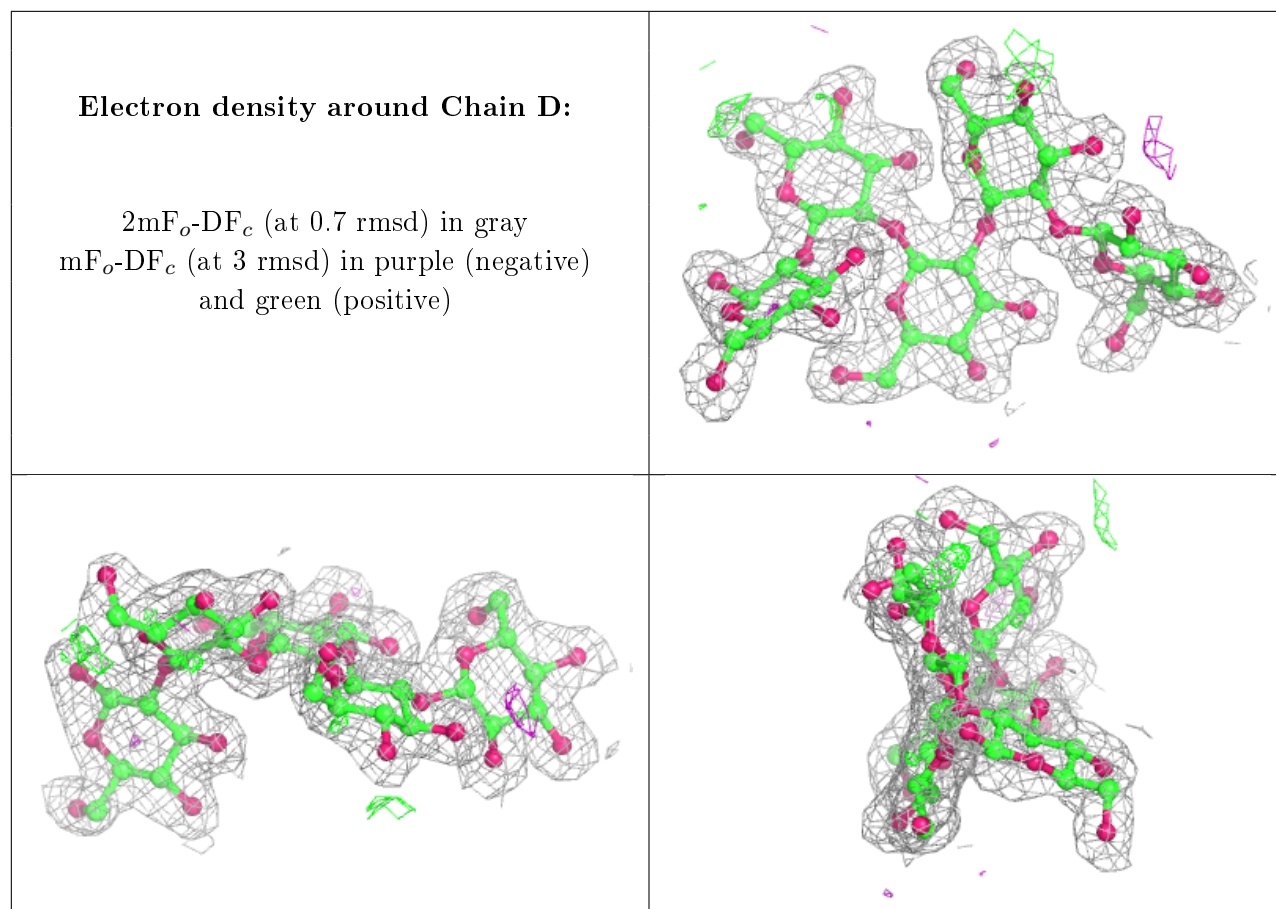
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BGC	D	1	12/12	0.90	0.11	33,38,41,42	0
2	BGC	C	1	12/12	0.91	0.12	29,40,45,46	0
2	BGC	D	2	11/12	0.92	0.10	26,31,39,41	0
2	BGC	D	4	11/12	0.96	0.14	24,26,28,28	0
2	BGC	C	2	11/12	0.96	0.09	18,24,30,38	0
2	BGC	C	4	11/12	0.97	0.12	15,16,17,18	0
2	BGC	D	3	11/12	0.98	0.10	24,25,26,27	0
2	BGC	D	5	11/12	0.98	0.15	21,22,24,24	0
2	BGC	C	5	11/12	0.98	0.13	16,17,20,21	0
2	BGC	C	3	11/12	0.98	0.13	17,18,21,22	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 C:

$2mF_o-DF_c$ (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, 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
3	MPD	A	502	8/8	0.85	0.21	42,51,56,57	0
3	MPD	A	501	8/8	0.86	0.16	26,33,48,51	0
4	MG	A	503	1/1	0.96	0.08	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.