wwPDB X-ray Structure Validation Summary Report (i)

Oct 15, 2024 – 08:52 AM JST

PDB ID	:	6JDY
Title	:	Ligand complex structure of GH10 family xylanase XynAF1, soaking for 120 minutes
Authors	:	Li, G.; Miao, Y.; Zhang, R.
Deposited on	:	2019-02-02
Resolution	:	1.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

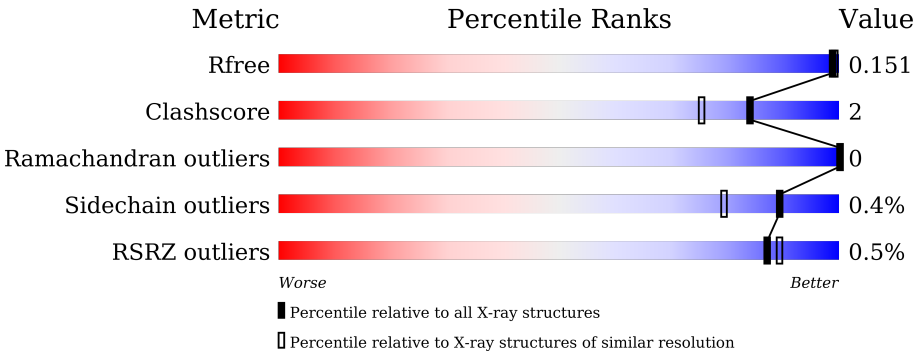
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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}	164625	3717 (1.50-1.50)
Clashscore	180529	4048 (1.50-1.50)
Ramachandran outliers	177936	3970 (1.50-1.50)
Sidechain outliers	177891	3967 (1.50-1.50)
RSRZ outliers	164620	3718 (1.50-1.50)

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 <=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	319	% 91% 9%
1	B	319	95% 5%
2	C	2	50% 50%
2	D	2	50% 50%
2	E	2	50% 50%
2	F	2	100%

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	XYP	D	1	X	-	-	-
2	XYP	F	1	X	-	-	-
4	PEG	A	506	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5708 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.

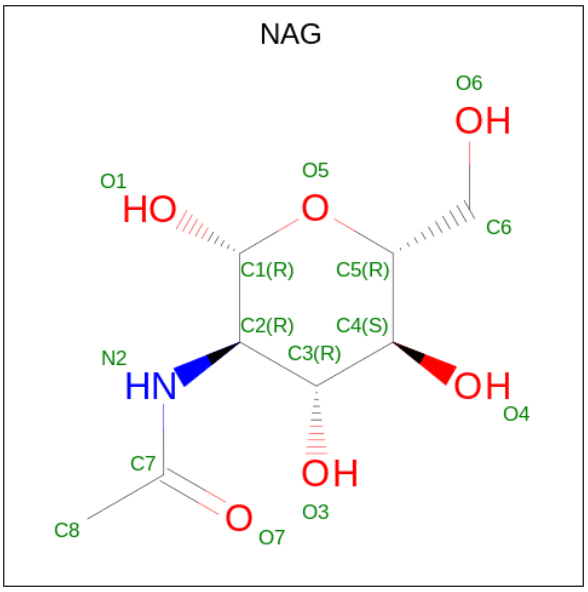
- Molecule 1 is a protein called Beta-xylanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	9	0
			2483	1576	409	488	10			
1	B	319	Total	C	N	O	S	0	10	0
			2493	1583	411	489	10			

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

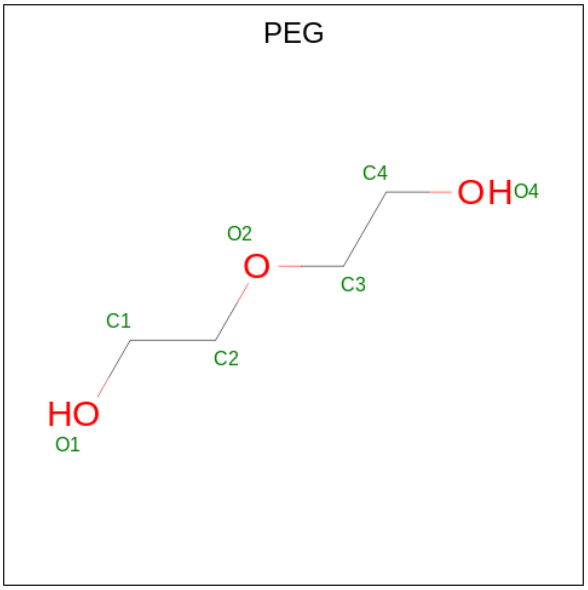
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	O		0	0	0
			19	10	9				
2	D	2	Total	C	O		0	0	0
			19	10	9				
2	E	2	Total	C	O		0	0	0
			19	10	9				
2	F	2	Total	C	O		0	0	0
			19	10	9				

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0

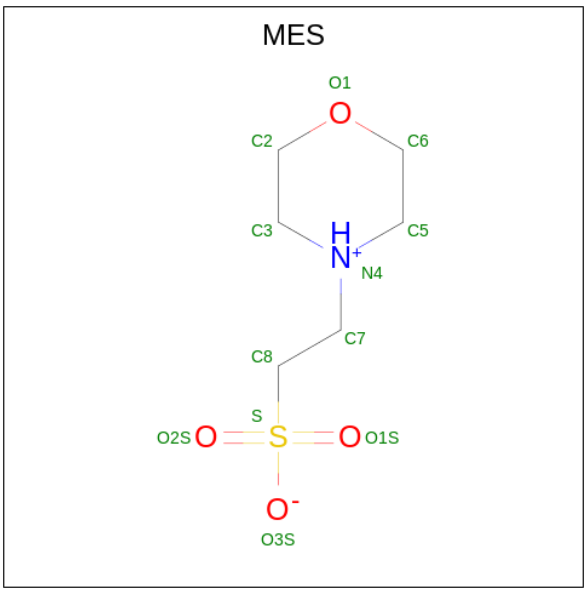
- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES)

(formula: $C_6H_{13}NO_4S$).



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

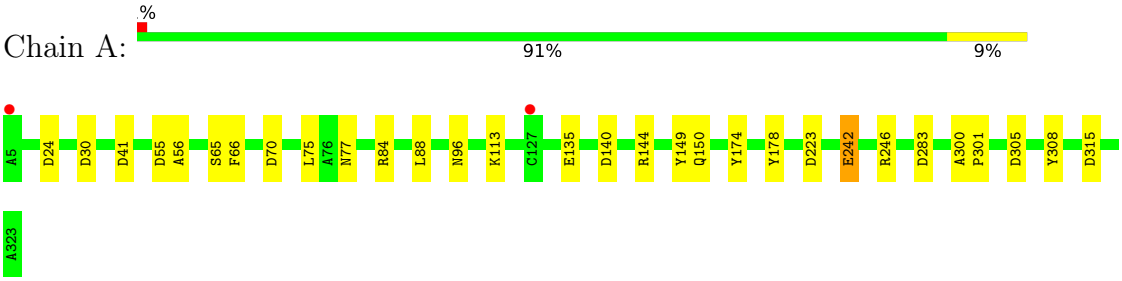
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	315	Total	O	0	0
			315	315		
6	B	294	Total	O	0	0
			294	294		

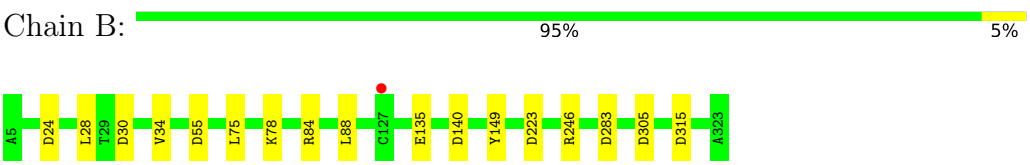
3 Residue-property plots (i)

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: Beta-xylanase



• Molecule 1: Beta-xylanase



• Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

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• Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose

Chain F:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	44.33Å 57.11Å 64.73Å 74.19° 80.96° 68.87°	Depositor
Resolution (Å)	62.15 – 1.50 62.15 – 1.50	Depositor EDS
% Data completeness (in resolution range)	92.2 (62.15-1.50) 92.2 (62.15-1.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	14.56 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.121 , 0.151 0.122 , 0.151	Depositor DCC
R_{free} test set	4535 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	11.3	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 42.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	5708	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.17% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG, XYP, PEG, MES

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	1.24	3/2546 (0.1%)	1.23	19/3478 (0.5%)
1	B	1.26	3/2556 (0.1%)	1.20	10/3491 (0.3%)
All	All	1.25	6/5102 (0.1%)	1.21	29/6969 (0.4%)

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
1	B	0	1
All	All	0	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	242	GLU	CD-OE2	7.04	1.33	1.25
1	B	223	ASP	CB-CG	6.39	1.65	1.51
1	B	223	ASP	CG-OD2	5.96	1.39	1.25
1	A	96	ASN	CG-ND2	-5.64	1.18	1.32
1	A	149	TYR	CZ-OH	5.48	1.47	1.37

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	24	ASP	CB-CG-OD2	-8.66	110.51	118.30
1	A	24	ASP	CB-CG-OD2	-8.62	110.54	118.30
1	A	315	ASP	CB-CG-OD2	-8.49	110.66	118.30
1	A	84	ARG	NE-CZ-NH1	8.07	124.33	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	24	ASP	CB-CG-OD1	8.04	125.54	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	88	LEU	Mainchain
1	B	88	LEU	Mainchain

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	2483	0	2367	12	0
1	B	2493	0	2380	3	0
2	C	19	0	0	3	0
2	D	19	0	0	3	0
2	E	19	0	0	1	0
2	F	19	0	0	4	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
4	A	7	0	10	5	0
5	B	12	0	13	0	0
6	A	315	0	0	3	1
6	B	294	0	0	1	1
All	All	5708	0	4796	21	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 2.

The worst 5 of 21 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)
4:A:506:PEG:O1	6:A:601:HOH:O	1.77	1.00
1:A:77:ASN:HB2	6:A:752:HOH:O	1.63	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1:XYP:O1	2:D:2:XYP:O4	1.94	0.86
1:A:135:GLU:OE2	2:D:2:XYP:O4	1.97	0.82
1:A:113:LYS:HZ2	4:A:506:PEG:H42	1.48	0.76

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)
6:A:733:HOH:O	6:B:617:HOH:O[1_654]	2.16	0.04

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	326/319 (102%)	319 (98%)	7 (2%)	0	100	100
1	B	327/319 (102%)	320 (98%)	7 (2%)	0	100	100
All	All	653/638 (102%)	639 (98%)	14 (2%)	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	260/251 (104%)	259 (100%)	1 (0%)	89	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	261/251 (104%)	260 (100%)	1 (0%)	89 79
All	All	521/502 (104%)	519 (100%)	2 (0%)	89 79

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	150	GLN
1	B	283	ASP

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

Mol	Chain	Res	Type
1	A	96	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)

8 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	XYP	C	1	2	10,10,10	1.65	2 (20%)	14,14,14	1.97	4 (28%)
2	XYP	C	2	2	9,9,10	0.95	0	10,12,14	1.80	4 (40%)
2	XYP	D	1	2	10,10,10	1.64	2 (20%)	14,14,14	3.36	7 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	XYP	D	2	2	9,9,10	1.26	1 (11%)	10,12,14	4.95	6 (60%)
2	XYP	E	1	2	10,10,10	1.86	2 (20%)	14,14,14	1.82	3 (21%)
2	XYP	E	2	2	9,9,10	1.91	2 (22%)	10,12,14	2.01	3 (30%)
2	XYP	F	1	2	10,10,10	1.47	1 (10%)	14,14,14	2.88	8 (57%)
2	XYP	F	2	2	9,9,10	1.10	1 (11%)	10,12,14	3.44	6 (60%)

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	XYP	C	1	2	-	-	0/1/1/1
2	XYP	C	2	2	-	-	0/1/1/1
2	XYP	D	1	2	1/1/4/4	-	0/1/1/1
2	XYP	D	2	2	-	-	0/1/1/1
2	XYP	E	1	2	-	-	0/1/1/1
2	XYP	E	2	2	-	-	0/1/1/1
2	XYP	F	1	2	1/1/4/4	-	0/1/1/1
2	XYP	F	2	2	-	-	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2	XYP	O4-C4	3.87	1.51	1.43
2	E	2	XYP	C5-C4	-3.38	1.44	1.52
2	E	1	XYP	C1-C2	3.37	1.60	1.52
2	F	1	XYP	O5-C1	-3.32	1.38	1.43
2	E	1	XYP	O5-C1	3.12	1.47	1.43

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	2	XYP	O3-C3-C2	9.27	127.74	109.99
2	D	2	XYP	O3-C3-C4	-8.12	94.45	109.99
2	D	2	XYP	C5-C4-C3	6.99	118.25	109.67
2	F	2	XYP	C5-C4-C3	6.80	118.02	109.67
2	F	1	XYP	O1-C1-O5	6.19	125.86	109.72

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	1	XYP	C1
2	F	1	XYP	C1

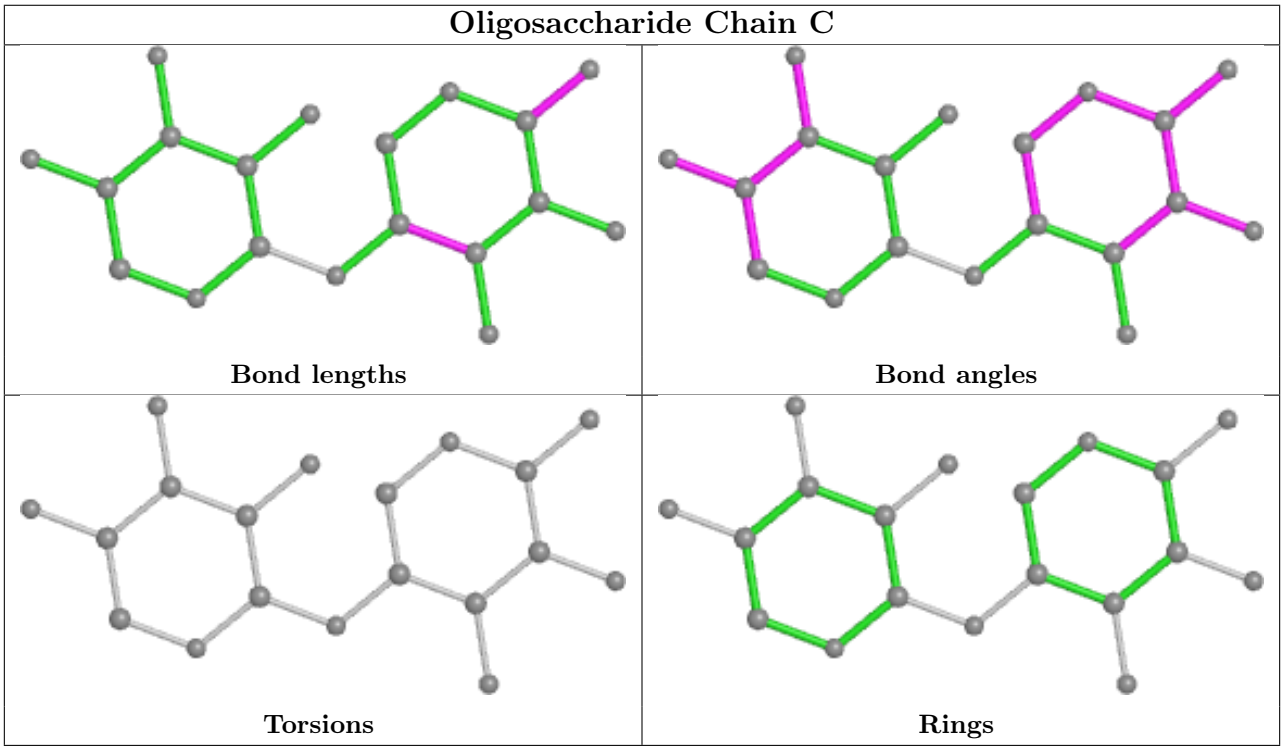
There are no torsion outliers.

There are no ring outliers.

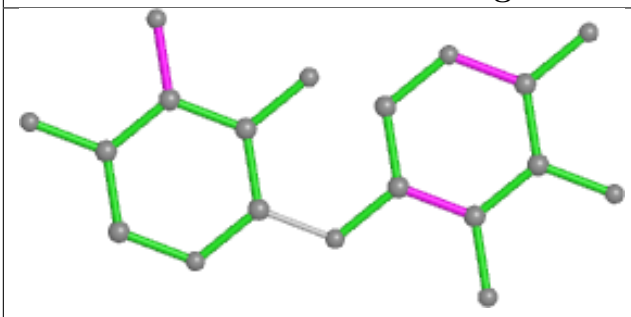
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	XYP	3	0
2	E	1	XYP	1	0
2	C	1	XYP	3	0
2	D	2	XYP	3	0
2	F	1	XYP	2	0

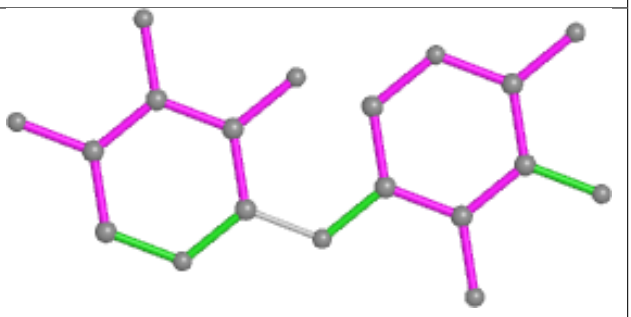
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



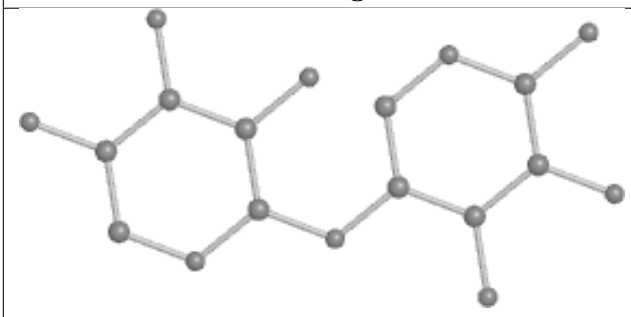
Oligosaccharide Chain D



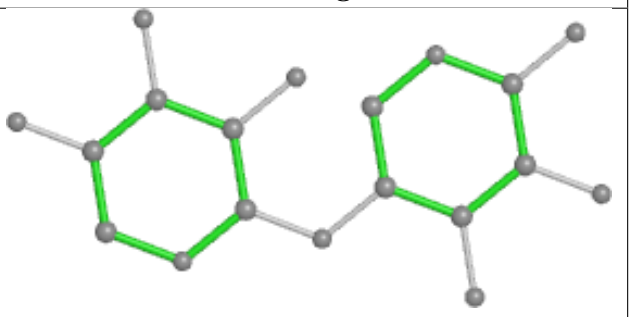
Bond lengths



Bond angles

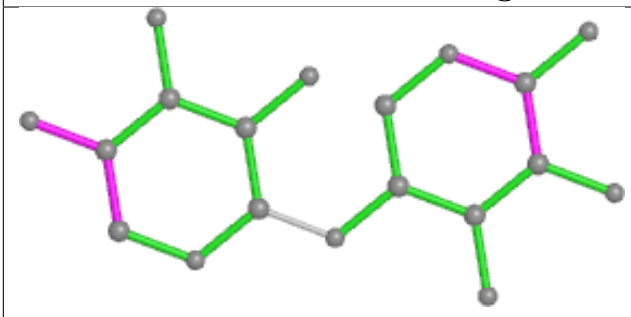


Torsions

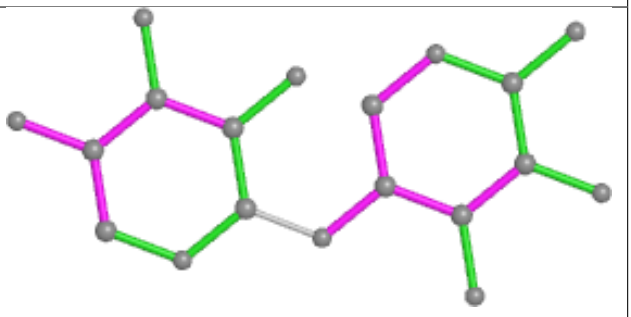


Rings

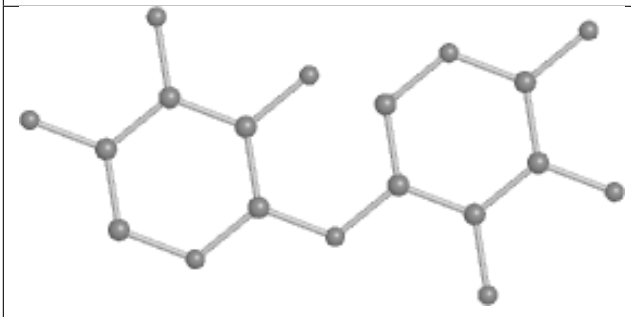
Oligosaccharide Chain E



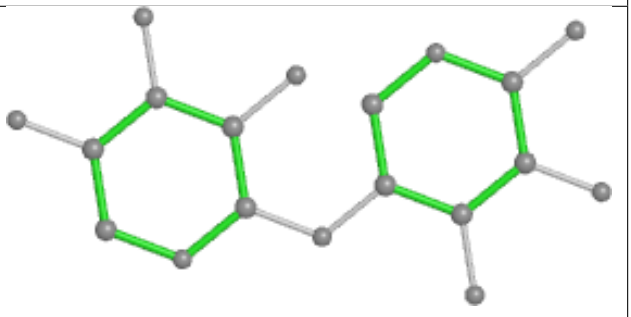
Bond lengths



Bond angles

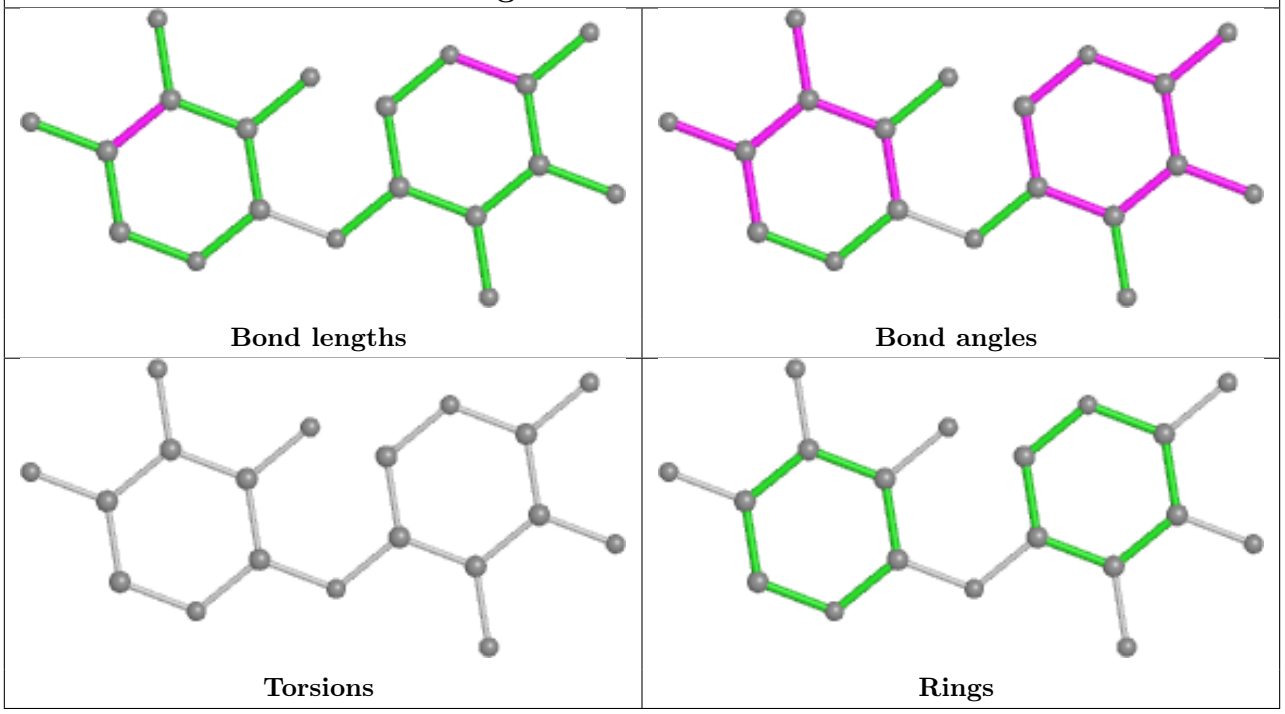


Torsions



Rings

Oligosaccharide Chain F



5.6 Ligand geometry (i)

4 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	$\#\|Z\| > 2$
4	PEG	A	506	-	6,6,6	0.52	0	5,5,5	1.32	1 (20%)
5	MES	B	506	-	12,12,12	3.03	6 (50%)	14,16,16	5.12	6 (42%)
3	NAG	A	505	1	14,14,15	2.26	7 (50%)	17,19,21	2.69	9 (52%)
3	NAG	B	505	1	14,14,15	1.97	2 (14%)	17,19,21	2.47	7 (41%)

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
4	PEG	A	506	-	-	1/4/4/4	-
5	MES	B	506	-	-	4/6/14/14	0/1/1/1
3	NAG	A	505	1	-	0/6/23/26	0/1/1/1
3	NAG	B	505	1	-	0/6/23/26	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	506	MES	C8-S	-6.68	1.68	1.77
3	B	505	NAG	O5-C1	-5.58	1.34	1.43
3	A	505	NAG	O5-C1	-4.93	1.35	1.43
5	B	506	MES	O2S-S	4.61	1.58	1.45
5	B	506	MES	O1S-S	3.18	1.54	1.45

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	506	MES	O2S-S-C8	16.33	126.58	106.92
5	B	506	MES	O2S-S-O1S	-6.50	91.46	113.95
3	A	505	NAG	C1-O5-C5	6.31	120.74	112.19
5	B	506	MES	O3S-S-O1S	5.48	124.66	111.27
3	B	505	NAG	O7-C7-N2	-5.12	112.55	121.95

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	506	MES	N4-C7-C8-S
5	B	506	MES	C7-C8-S-O1S
5	B	506	MES	C7-C8-S-O2S
5	B	506	MES	C7-C8-S-O3S
4	A	506	PEG	C4-C3-O2-C2

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	506	PEG	5	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^{th} 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	319/319 (100%)	-0.37	2 (0%)	85	88	5, 11, 18, 34	9 (2%)
1	B	319/319 (100%)	-0.21	1 (0%)	90	92	6, 12, 21, 32	10 (3%)
All	All	638/638 (100%)	-0.29	3 (0%)	87	89	5, 12, 20, 34	19 (2%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	5	ALA	2.8
1	A	127	CYS	2.2
1	B	127	CYS	2.2

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

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, 95^{th} 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	XYP	F	2	9/10	0.87	0.12	24,31,51,54	0
2	XYP	F	1	10/10	0.89	0.13	30,32,40,43	0
2	XYP	D	1	10/10	0.91	0.10	25,29,33,35	0
2	XYP	D	2	9/10	0.91	0.11	14,31,40,43	0
2	XYP	E	2	9/10	0.95	0.07	12,13,16,19	0
2	XYP	E	1	10/10	0.96	0.08	11,15,25,27	0

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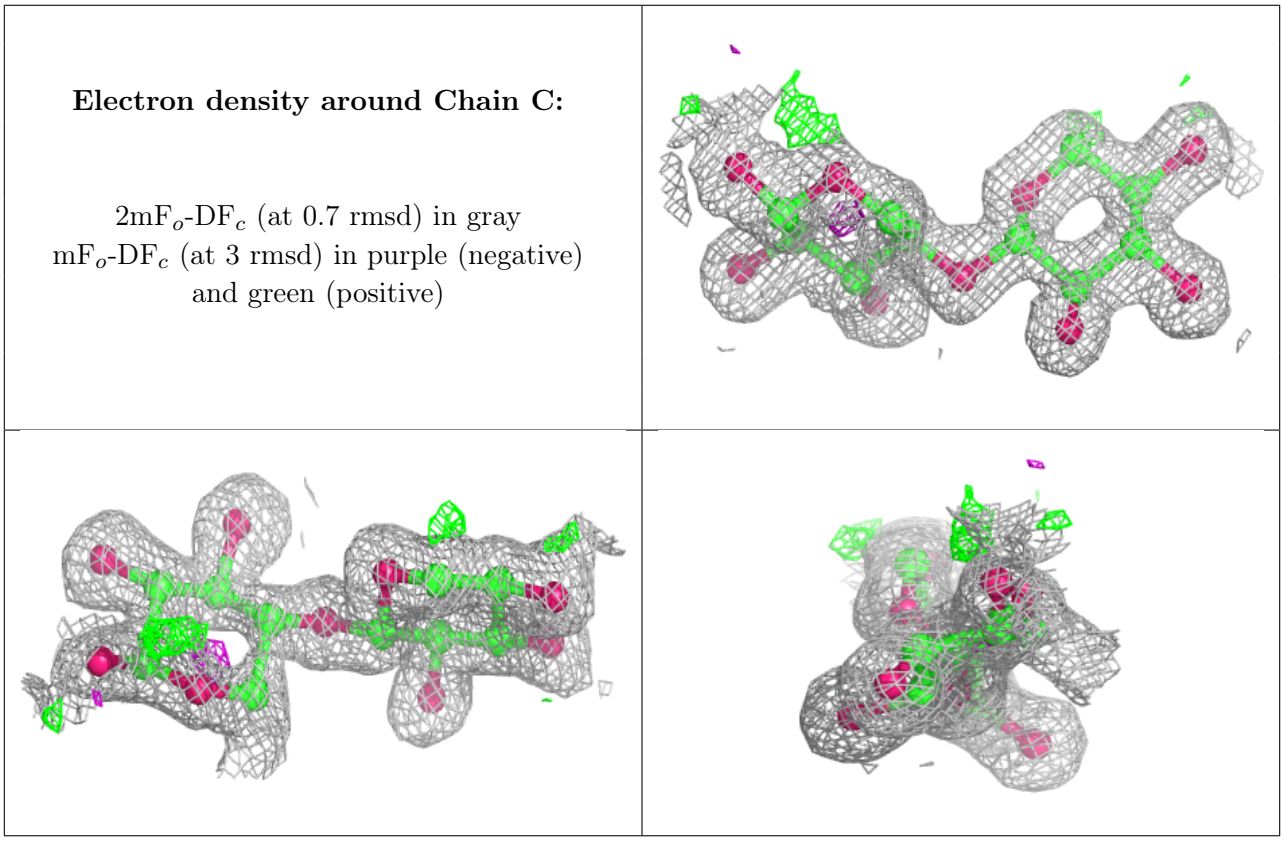
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	XYP	C	1	10/10	0.97	0.07	11,14,25,26	0
2	XYP	C	2	9/10	0.97	0.05	13,14,16,18	0

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.

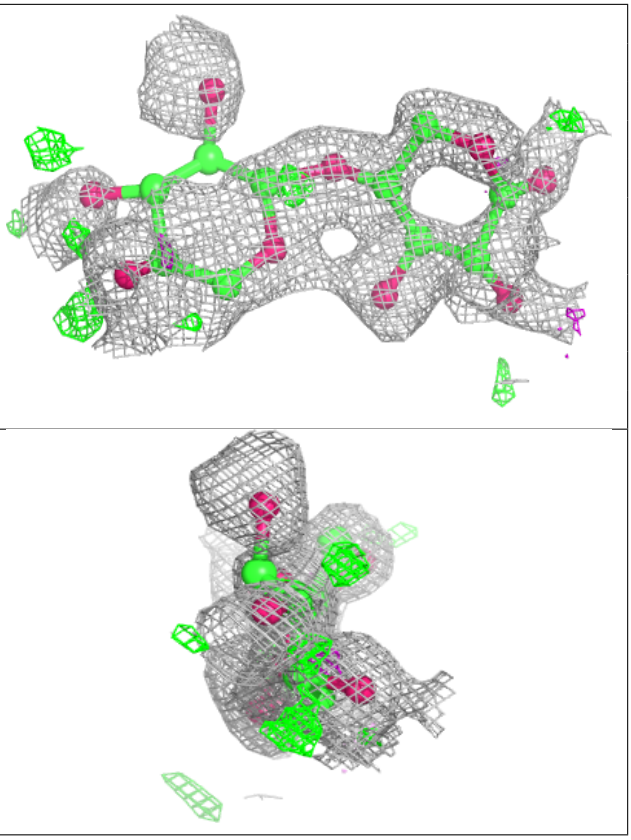
Electron density around Chain C:

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



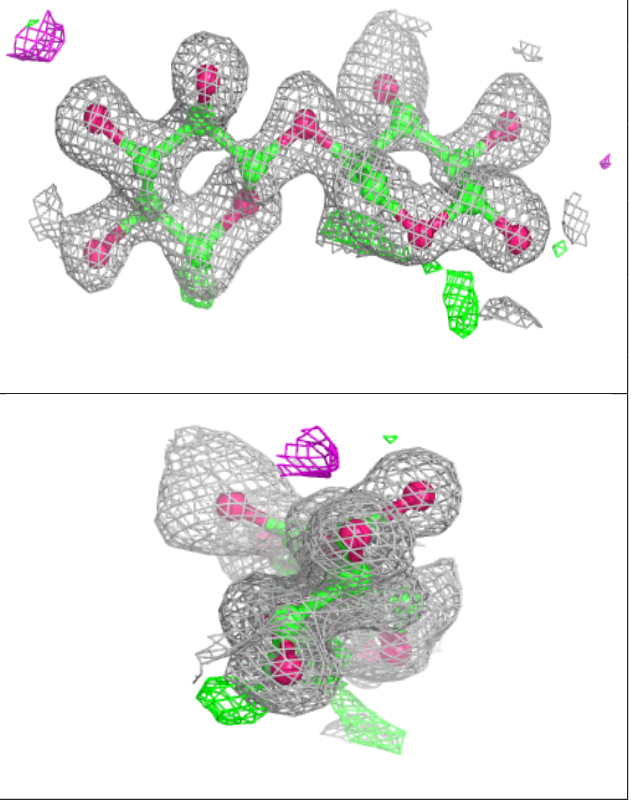
Electron density around Chain D:

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



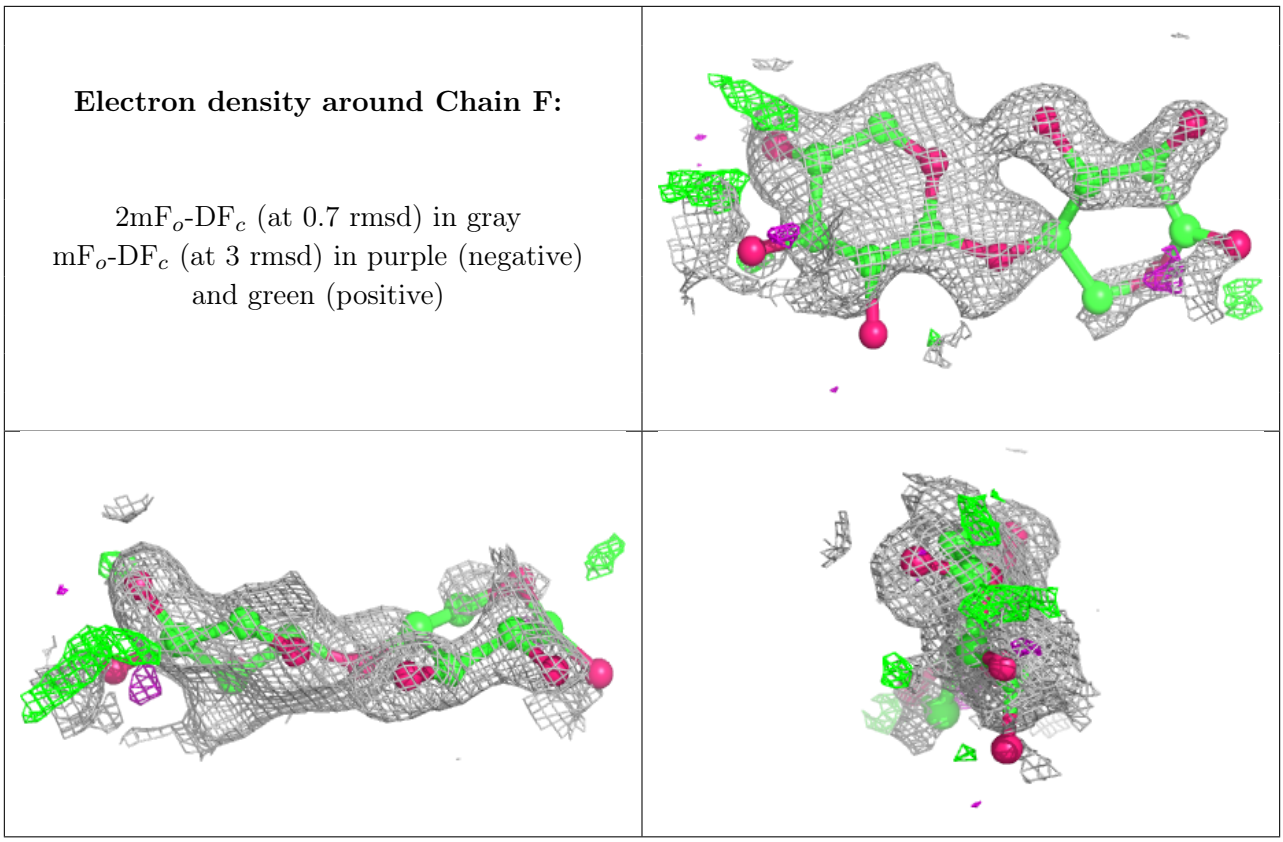
Electron density around Chain E:

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



Electron density around Chain F:

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



6.4 Ligands

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^{th} 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
5	MES	B	506	12/12	0.74	0.15	24,30,35,43	0
4	PEG	A	506	7/7	0.89	0.11	22,25,32,34	0
3	NAG	B	505	14/15	0.93	0.10	18,23,31,33	0
3	NAG	A	505	14/15	0.94	0.09	12,17,26,29	0

6.5 Other polymers

There are no such residues in this entry.