Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2024 – 06:32 PM JST

PDB ID	:	5JSE
Title	:	Crystal structure of phiAB6 tailspike in complex with three-repeated oligosaccharides of Acinetobacter baumannii surface polysaccharide
Authors	:	Lee, I.M.; Tu, I.F.; Huang, K.F.; Wu, S.H.
Deposited on	:	2016-05-08
Resolution	:	1.89 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:

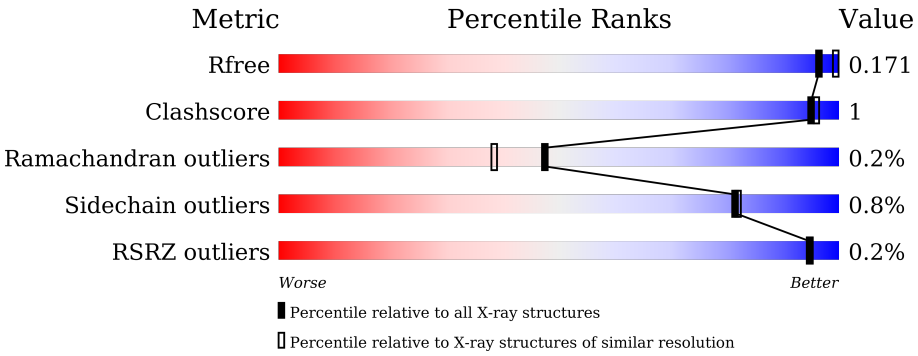
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.89 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 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	719	73% · 24%
1	B	719	73% · 24%
1	C	719	73% · 24%
2	D	8	25% 75%
2	E	8	25% 75%
2	F	8	25% 75%

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	BGC	D	8	-	-	-	X
2	BGC	E	8	-	-	-	X
2	BGC	F	8	-	-	-	X

2 Entry composition (i)

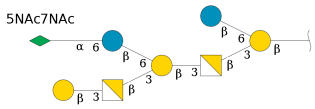
There are 5 unique types of molecules in this entry. The entry contains 15059 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 phiAB6 tailspike.

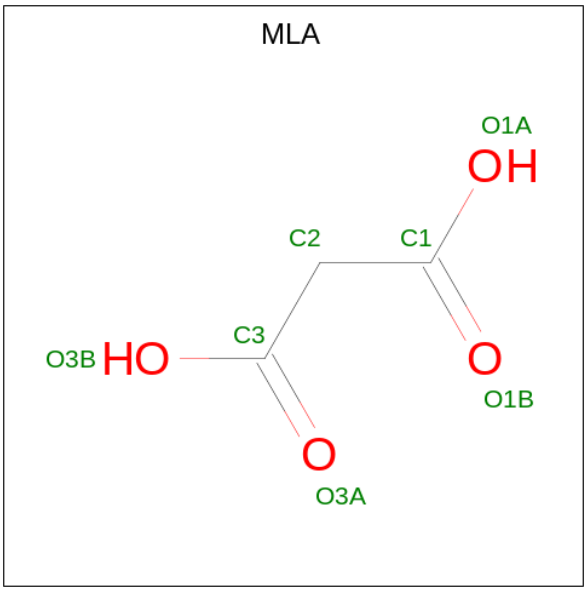
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	548	Total	C	N	O	S	0	0	0
			4188	2637	712	819	20			
1	B	548	Total	C	N	O	S	0	0	0
			4188	2637	712	819	20			
1	C	548	Total	C	N	O	S	0	0	0
			4188	2637	712	819	20			

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[5,7-bisacetamido-3,5,7,9-tetradeoxy-L-glycero-alpha-L-manno-non-2-ulopyranosonic acid-(2-6)-beta-D-glucopyranose-(1-6)]beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[beta-D-glucopyranose-(1-6)]beta-D-galactopyranose.



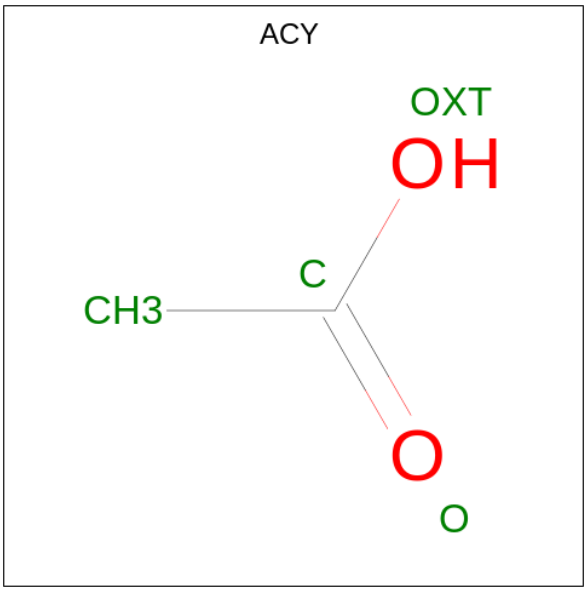
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	8	Total	C	N	O	0	0	0
			100	55	4	41			
2	E	8	Total	C	N	O	0	0	0
			100	55	4	41			
2	F	8	Total	C	N	O	0	0	0
			100	55	4	41			

- Molecule 3 is MALONIC ACID (three-letter code: MLA) (formula: $C_3H_4O_4$).



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

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 3 2 1	0	0
4	A	1	Total C O 3 2 1	0	0
4	B	1	Total C O 3 2 1	0	0
4	B	1	Total C O 3 2 1	0	0
4	C	1	Total C O 3 2 1	0	0
4	C	1	Total C O 3 2 1	0	0

- Molecule 5 is water.

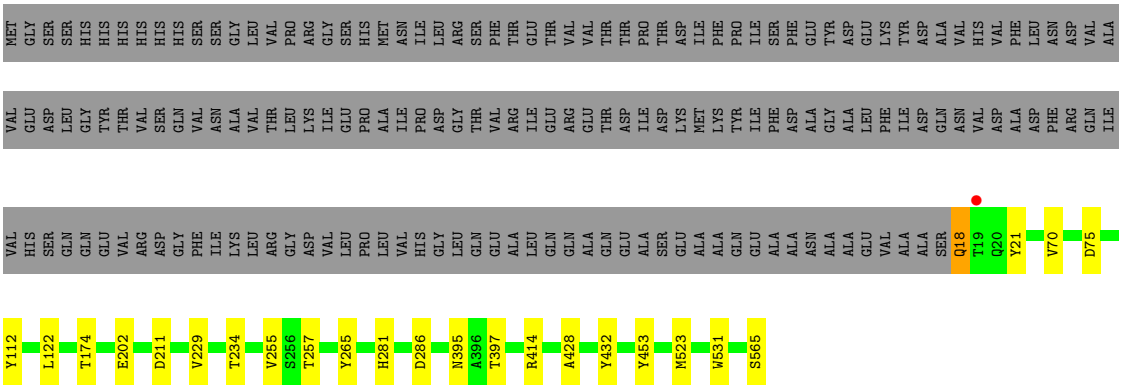
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	737	Total O 737 737	0	0
5	B	699	Total O 699 699	0	0
5	C	699	Total O 699 699	0	0

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.

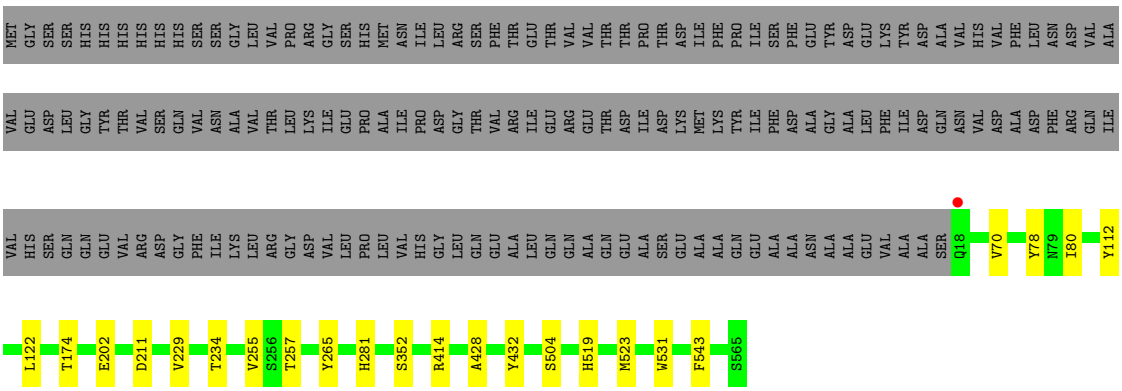
• Molecule 1: phiAB6 tailspike

Chain A:



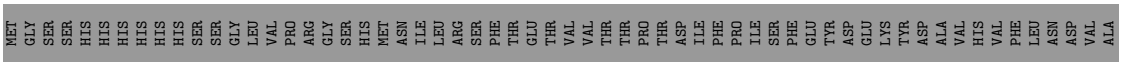
• Molecule 1: phiAB6 tailspike

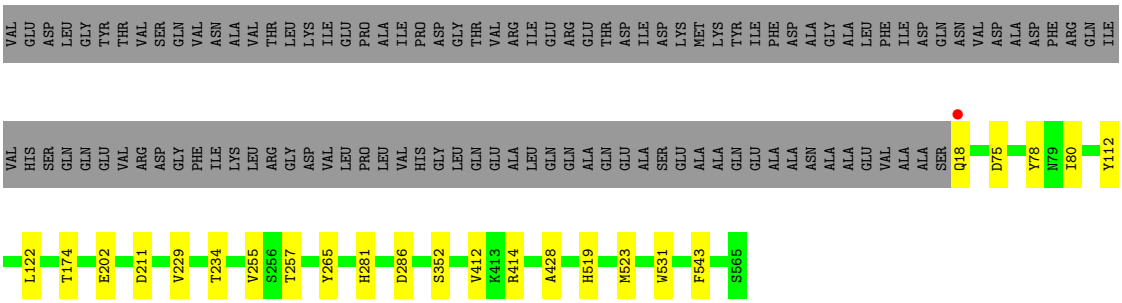
Chain B:



• Molecule 1: phiAB6 tailspike

Chain C:



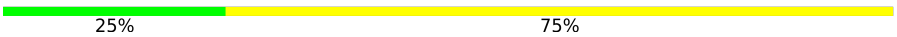


• Molecule 2: beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[5,7-bisacetamido-3,5,7,9-tetradeoxy-L-glycero-alpha-L-manno-non-2-ulopyranosonic acid-(2-6)-beta-D-glucopyranose-(1-6)]beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[beta-D-glucopyranose-(1-6)]beta-D-galactopyranose

Chain D:

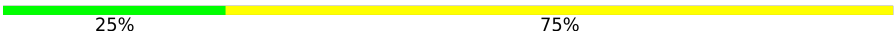
• Molecule 2: beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[5,7-bisacetamido-3,5,7,9-tetradeoxy-L-glycero-alpha-L-manno-non-2-ulopyranosonic acid-(2-6)-beta-D-glucopyranose-(1-6)]beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[beta-D-glucopyranose-(1-6)]beta-D-galactopyranose

Chain E:



• Molecule 2: beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[5,7-bisacetamido-3,5,7,9-tetradeoxy-L-glycero-alpha-L-manno-non-2-ulopyranosonic acid-(2-6)-beta-D-glucopyranose-(1-6)]beta-D-galactopyranose-(1-3)-2-amino-2-deoxy-beta-D-galactopyranose-(1-3)-[beta-D-glucopyranose-(1-6)]beta-D-galactopyranose

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	135.52Å 78.14Å 248.41Å 90.00° 100.47° 90.00°	Depositor
Resolution (Å)	24.86 – 1.89 24.65 – 1.89	Depositor EDS
% Data completeness (in resolution range)	98.1 (24.86-1.89) 98.1 (24.65-1.89)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.79 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.131 , 0.165 0.143 , 0.171	Depositor DCC
R_{free} test set	9852 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	19.7	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 35.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.479 for 1/2*h-3/2*k,-1/2*h-1/2*k,-1/2*h+1/2*k-l 0.478 for 1/2*h+3/2*k,1/2*h-1/2*k,-1/2*h-1/2*k-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	15059	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% 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: BGC, GAL, ACY, MLA, 6PZ, 1GN

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	0.43	0/4281	0.65	1/5814 (0.0%)
1	B	0.43	0/4281	0.65	0/5814
1	C	0.43	0/4281	0.64	1/5814 (0.0%)
All	All	0.43	0/12843	0.64	2/17442 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	286	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	286	ASP	CB-CG-OD1	5.24	123.01	118.30

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	4188	0	4034	11	0
1	B	4188	0	4034	10	0
1	C	4188	0	4034	12	0
2	D	100	0	63	0	0
2	E	100	0	63	0	0
2	F	100	0	63	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	14	0	4	0	0
3	B	14	0	4	0	0
3	C	14	0	4	0	0
4	A	6	0	6	0	0
4	B	6	0	6	0	0
4	C	6	0	6	0	0
5	A	737	0	0	0	0
5	B	699	0	0	1	0
5	C	699	0	0	2	0
All	All	15059	0	12321	30	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 (30) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:174:THR:HG21	1:C:202:GLU:HG3	1.84	0.59
1:A:174:THR:HG21	1:A:202:GLU:HG3	1.87	0.57
1:B:174:THR:HG21	1:B:202:GLU:HG3	1.87	0.57
1:A:257:THR:HA	1:A:281:HIS:O	2.11	0.50
1:C:523:MET:HG3	1:C:531:TRP:CE2	2.47	0.50
1:C:257:THR:HA	1:C:281:HIS:O	2.11	0.50
1:A:18:GLN:HB3	1:A:21:TYR:CE2	2.47	0.50
1:B:523:MET:HG3	1:B:531:TRP:CE2	2.48	0.49
1:C:18:GLN:N	5:C:703:HOH:O	2.46	0.49
1:A:523:MET:HG3	1:A:531:TRP:CE2	2.48	0.49
1:B:257:THR:HA	1:B:281:HIS:O	2.13	0.49
1:A:414:ARG:HA	1:A:428:ALA:O	2.16	0.46
1:B:112:TYR:CE1	1:B:122:LEU:HA	2.52	0.45
1:A:112:TYR:CE1	1:A:122:LEU:HA	2.51	0.45
1:A:75:ASP:HA	1:B:70:VAL:HG22	2.00	0.44
1:A:453:TYR:OH	1:A:565:SER:O	2.22	0.44
1:A:397:THR:HA	1:C:412:VAL:O	2.18	0.43
1:A:70:VAL:HG22	1:C:75:ASP:HA	2.00	0.43
1:C:414:ARG:HA	1:C:428:ALA:O	2.19	0.43
1:C:112:TYR:CE1	1:C:122:LEU:HA	2.53	0.43
1:B:414:ARG:HA	1:B:428:ALA:O	2.18	0.43
1:C:78:TYR:HB2	1:C:80:ILE:HG12	2.00	0.42
1:B:352:SER:HB3	5:B:714:HOH:O	2.20	0.42
1:C:352:SER:HB3	5:C:733:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:ASP:HA	1:A:234:THR:O	2.20	0.41
1:C:211:ASP:HA	1:C:234:THR:O	2.21	0.41
1:B:519:HIS:HA	1:B:543:PHE:O	2.21	0.41
1:B:211:ASP:HA	1:B:234:THR:O	2.21	0.41
1:C:519:HIS:HA	1:C:543:PHE:O	2.21	0.40
1:B:78:TYR:HB2	1:B:80:ILE:HG12	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	546/719 (76%)	528 (97%)	17 (3%)	1 (0%)	47	38
1	B	546/719 (76%)	529 (97%)	16 (3%)	1 (0%)	47	38
1	C	546/719 (76%)	528 (97%)	17 (3%)	1 (0%)	47	38
All	All	1638/2157 (76%)	1585 (97%)	50 (3%)	3 (0%)	47	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	255	VAL
1	B	255	VAL
1	C	255	VAL

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	453/597 (76%)	448 (99%)	5 (1%)	73	73
1	B	453/597 (76%)	449 (99%)	4 (1%)	78	79
1	C	453/597 (76%)	451 (100%)	2 (0%)	91	91
All	All	1359/1791 (76%)	1348 (99%)	11 (1%)	81	82

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	229	VAL
1	A	265	TYR
1	A	395	ASN
1	A	432	TYR
1	B	229	VAL
1	B	265	TYR
1	B	432	TYR
1	B	504	SER
1	C	229	VAL
1	C	265	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	20	GLN
1	A	232	ASN
1	A	314	ASN
1	A	395	ASN
1	A	519	HIS
1	B	52	ASN
1	B	232	ASN
1	B	314	ASN
1	B	462	GLN
1	B	519	HIS
1	C	52	ASN
1	C	184	GLN
1	C	232	ASN
1	C	314	ASN
1	C	519	HIS

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)

24 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	GAL	D	1	2	12,12,12	0.84	1 (8%)	17,17,17	1.70	2 (11%)
2	1GN	D	2	4,2	11,11,12	0.32	0	12,15,17	1.16	1 (8%)
2	GAL	D	3	2	11,11,12	0.29	0	15,15,17	0.72	0
2	1GN	D	4	4,2	11,11,12	0.50	0	12,15,17	1.06	1 (8%)
2	GAL	D	5	2	11,11,12	0.53	0	15,15,17	1.53	1 (6%)
2	BGC	D	6	2	11,11,12	0.46	0	15,15,17	0.90	0
2	6PZ	D	7	2	21,22,23	1.22	1 (4%)	25,31,34	1.80	8 (32%)
2	BGC	D	8	2	11,11,12	0.46	0	15,15,17	0.95	1 (6%)
2	GAL	E	1	2	12,12,12	0.81	0	17,17,17	1.49	3 (17%)
2	1GN	E	2	4,2	11,11,12	0.37	0	12,15,17	1.07	1 (8%)
2	GAL	E	3	2	11,11,12	0.41	0	15,15,17	0.64	0
2	1GN	E	4	4,2	11,11,12	0.55	0	12,15,17	1.22	1 (8%)
2	GAL	E	5	2	11,11,12	0.51	0	15,15,17	1.61	1 (6%)
2	BGC	E	6	2	11,11,12	0.47	0	15,15,17	0.98	0
2	6PZ	E	7	2	21,22,23	1.20	2 (9%)	25,31,34	1.88	10 (40%)
2	BGC	E	8	2	11,11,12	0.73	0	15,15,17	1.46	2 (13%)
2	GAL	F	1	2	12,12,12	0.81	0	17,17,17	1.46	3 (17%)
2	1GN	F	2	4,2	11,11,12	0.37	0	12,15,17	0.78	0
2	GAL	F	3	2	11,11,12	0.38	0	15,15,17	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	1GN	F	4	4,2	11,11,12	0.56	0	12,15,17	1.48	2 (16%)
2	GAL	F	5	2	11,11,12	0.51	0	15,15,17	1.59	1 (6%)
2	BGC	F	6	2	11,11,12	0.49	0	15,15,17	1.08	2 (13%)
2	6PZ	F	7	2	21,22,23	1.18	2 (9%)	25,31,34	1.86	7 (28%)
2	BGC	F	8	2	11,11,12	0.71	0	15,15,17	1.29	3 (20%)

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	GAL	D	1	2	-	2/2/22/22	0/1/1/1
2	1GN	D	2	4,2	-	0/2/19/22	0/1/1/1
2	GAL	D	3	2	-	0/2/19/22	0/1/1/1
2	1GN	D	4	4,2	-	0/2/19/22	0/1/1/1
2	GAL	D	5	2	-	1/2/19/22	0/1/1/1
2	BGC	D	6	2	-	0/2/19/22	0/1/1/1
2	6PZ	D	7	2	-	0/20/36/40	0/1/1/1
2	BGC	D	8	2	-	2/2/19/22	0/1/1/1
2	GAL	E	1	2	-	1/2/22/22	0/1/1/1
2	1GN	E	2	4,2	-	0/2/19/22	0/1/1/1
2	GAL	E	3	2	-	0/2/19/22	0/1/1/1
2	1GN	E	4	4,2	-	0/2/19/22	0/1/1/1
2	GAL	E	5	2	-	1/2/19/22	0/1/1/1
2	BGC	E	6	2	-	0/2/19/22	0/1/1/1
2	6PZ	E	7	2	-	0/20/36/40	0/1/1/1
2	BGC	E	8	2	-	1/2/19/22	0/1/1/1
2	GAL	F	1	2	-	0/2/22/22	0/1/1/1
2	1GN	F	2	4,2	-	0/2/19/22	0/1/1/1
2	GAL	F	3	2	-	0/2/19/22	0/1/1/1
2	1GN	F	4	4,2	-	1/2/19/22	0/1/1/1
2	GAL	F	5	2	-	1/2/19/22	0/1/1/1
2	BGC	F	6	2	-	0/2/19/22	0/1/1/1
2	6PZ	F	7	2	-	0/20/36/40	0/1/1/1
2	BGC	F	8	2	-	1/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	7	6PZ	C5-N5	2.33	1.49	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	7	6PZ	C5-N5	2.32	1.49	1.45
2	D	7	6PZ	C5-N5	2.20	1.49	1.45
2	F	7	6PZ	C7-N1	2.19	1.49	1.45
2	D	1	GAL	O1-C1	2.16	1.46	1.39
2	E	7	6PZ	C7-N1	2.10	1.49	1.45

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	7	6PZ	O6-C2-C3	-5.97	102.25	110.46
2	E	5	GAL	O5-C5-C6	5.71	116.16	107.20
2	F	5	GAL	O5-C5-C6	5.68	116.11	107.20
2	D	5	GAL	O5-C5-C6	5.27	115.47	107.20
2	D	7	6PZ	O6-C2-C3	-5.09	103.45	110.46
2	D	1	GAL	O1-C1-C2	4.58	121.94	109.03
2	D	1	GAL	O5-C1-C2	4.10	117.60	110.28
2	E	7	6PZ	O6-C2-C3	-3.91	105.08	110.46
2	E	1	GAL	O5-C1-C2	-3.76	103.57	110.28
2	F	1	GAL	O5-C1-C2	-3.69	103.70	110.28
2	F	4	1GN	O5-C5-C6	3.46	112.63	107.20
2	E	7	6PZ	O6-C2-C1	-3.40	101.02	107.70
2	F	8	BGC	O5-C5-C6	3.30	112.37	107.20
2	E	8	BGC	C3-C4-C5	3.06	115.70	110.24
2	E	7	6PZ	C7-N1-C10A	3.05	130.59	123.18
2	F	1	GAL	O1-C1-C2	-3.03	100.51	109.03
2	E	1	GAL	O1-C1-C2	-3.01	100.55	109.03
2	D	2	1GN	O5-C5-C6	2.97	111.86	107.20
2	D	7	6PZ	C6-O6-C2	2.97	117.69	111.34
2	E	7	6PZ	C11A-C10A-N1	2.94	121.07	116.10
2	D	7	6PZ	C7-N1-C10A	2.90	130.24	123.18
2	E	7	6PZ	O1B-C1-C2	2.87	121.22	113.03
2	E	7	6PZ	C6-O6-C2	2.84	117.41	111.34
2	F	7	6PZ	C6-O6-C2	2.81	117.35	111.34
2	D	8	BGC	O5-C5-C6	2.74	111.49	107.20
2	E	1	GAL	C1-O5-C5	2.65	118.66	113.66
2	E	8	BGC	O5-C1-C2	-2.53	106.86	110.77
2	E	7	6PZ	C11-C10-N5	2.52	120.36	116.10
2	F	7	6PZ	O1B-C1-C2	2.52	120.21	113.03
2	D	7	6PZ	O6-C2-C1	-2.48	102.84	107.70
2	F	7	6PZ	C11-C10-N5	2.46	120.27	116.10
2	F	6	BGC	C1-C2-C3	2.42	112.64	109.67
2	E	4	1GN	O3-C3-C4	2.42	115.94	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	7	6PZ	O1B-C1-C2	2.39	119.86	113.03
2	F	8	BGC	C1-O5-C5	2.36	115.39	112.19
2	F	7	6PZ	O10-C10-C11	-2.31	117.77	122.06
2	D	7	6PZ	C11A-C10A-N1	2.28	119.96	116.10
2	F	1	GAL	C1-O5-C5	2.28	117.96	113.66
2	E	2	1GN	O5-C5-C6	2.26	110.74	107.20
2	E	7	6PZ	O10-C10-C11	-2.23	117.91	122.06
2	F	4	1GN	O3-C3-C4	2.19	115.42	110.35
2	D	7	6PZ	C11-C10-N5	2.16	119.76	116.10
2	F	7	6PZ	O6-C2-C1	-2.16	103.47	107.70
2	F	8	BGC	C1-C2-C3	2.07	112.21	109.67
2	F	6	BGC	O5-C5-C6	2.04	110.40	107.20
2	D	4	1GN	O3-C3-C4	2.03	115.05	110.35
2	E	7	6PZ	O1B-C1-O1A	-2.03	119.48	124.09
2	F	7	6PZ	C11A-C10A-N1	2.03	119.53	116.10
2	D	7	6PZ	O1B-C1-O1A	-2.02	119.50	124.09
2	E	7	6PZ	O10A-C10A-C11A	-2.01	118.32	122.06

There are no chirality outliers.

All (11) torsion outliers are listed below:

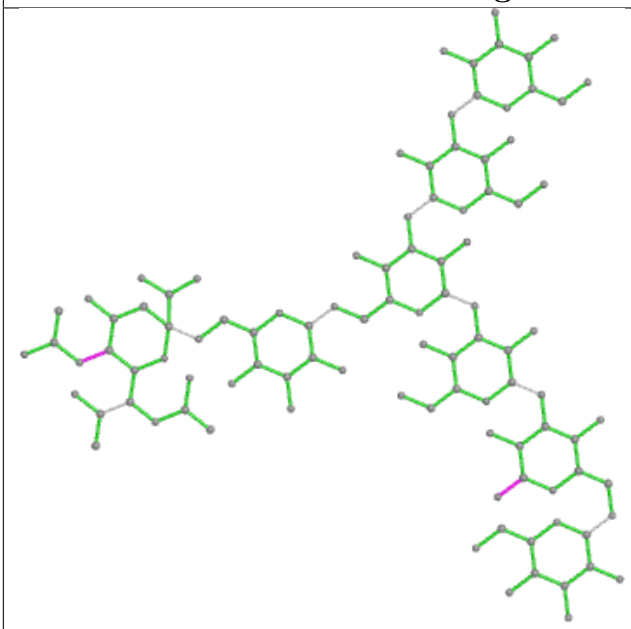
Mol	Chain	Res	Type	Atoms
2	D	8	BGC	O5-C5-C6-O6
2	D	8	BGC	C4-C5-C6-O6
2	D	1	GAL	O5-C5-C6-O6
2	D	5	GAL	O5-C5-C6-O6
2	D	1	GAL	C4-C5-C6-O6
2	E	8	BGC	O5-C5-C6-O6
2	E	5	GAL	O5-C5-C6-O6
2	F	5	GAL	O5-C5-C6-O6
2	F	4	1GN	O5-C5-C6-O6
2	F	8	BGC	O5-C5-C6-O6
2	E	1	GAL	C4-C5-C6-O6

There are no ring outliers.

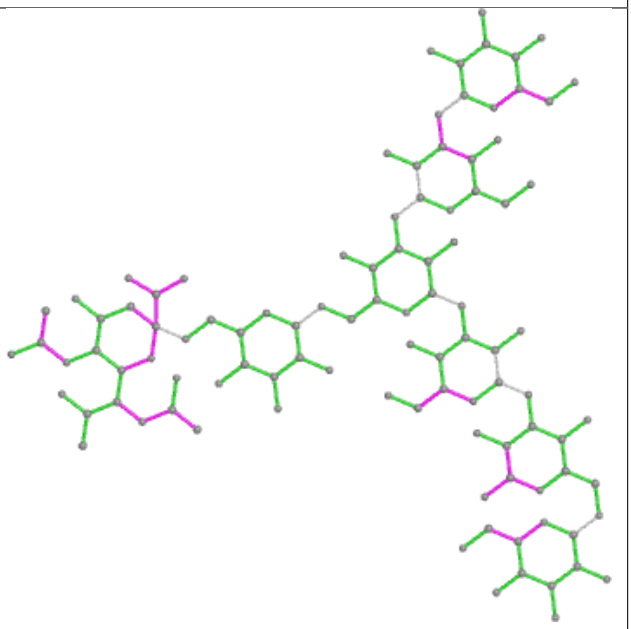
No monomer is involved in short contacts.

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

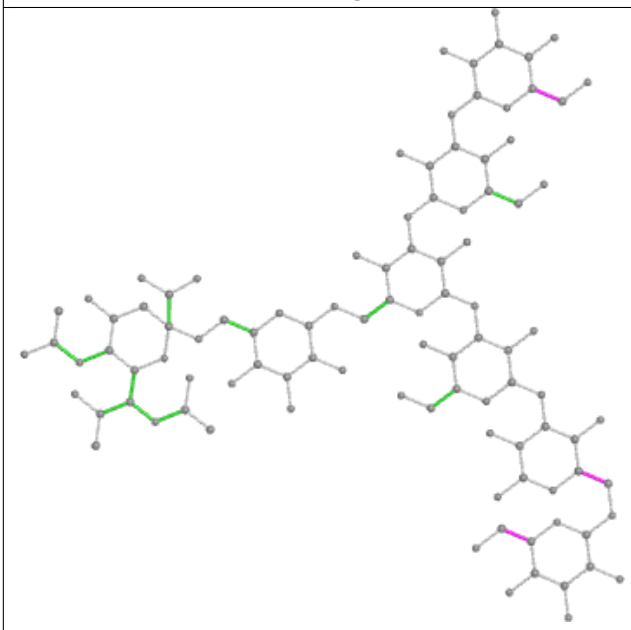
Oligosaccharide Chain D



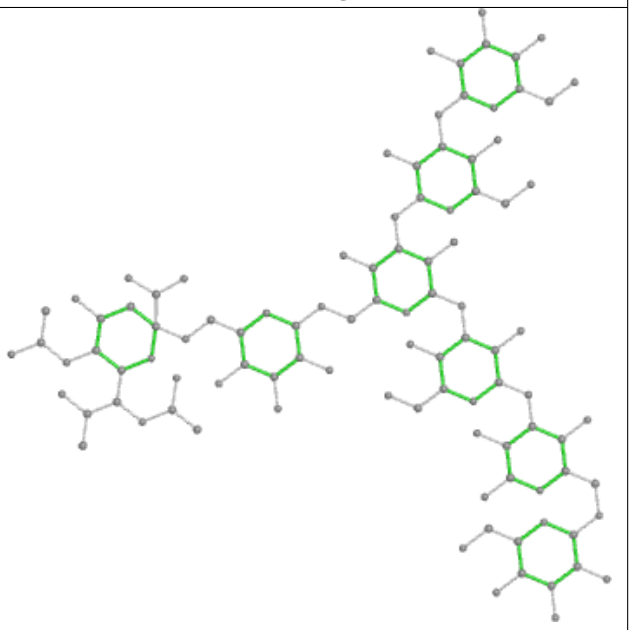
Bond lengths



Bond angles

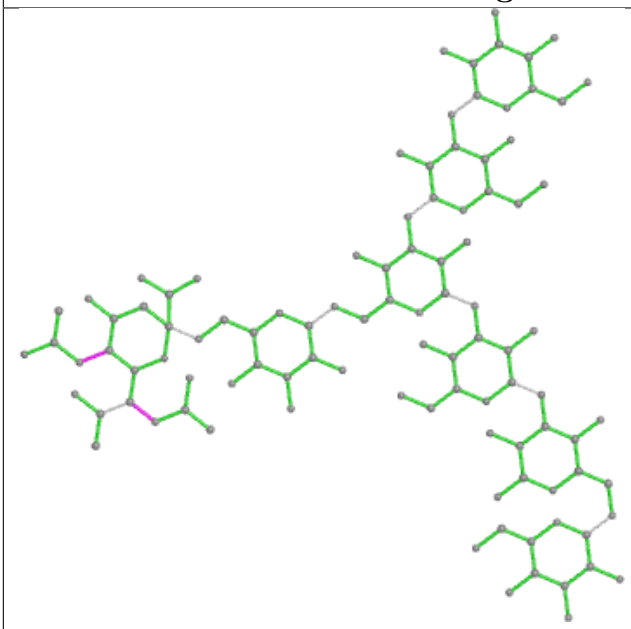


Torsions

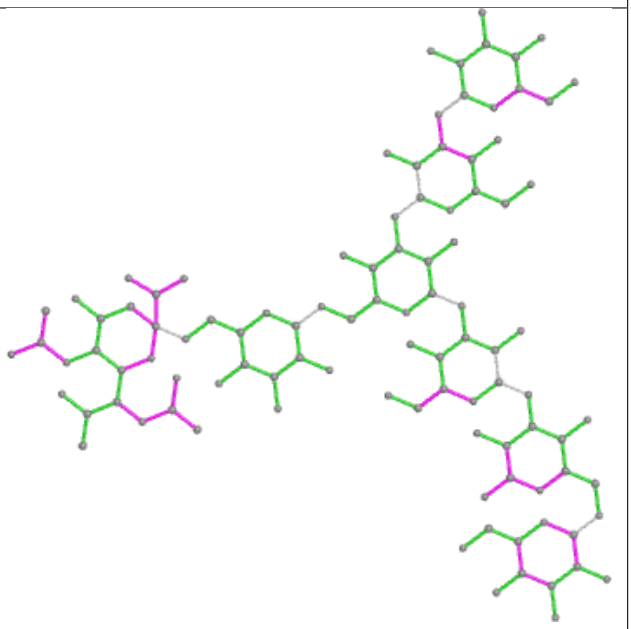


Rings

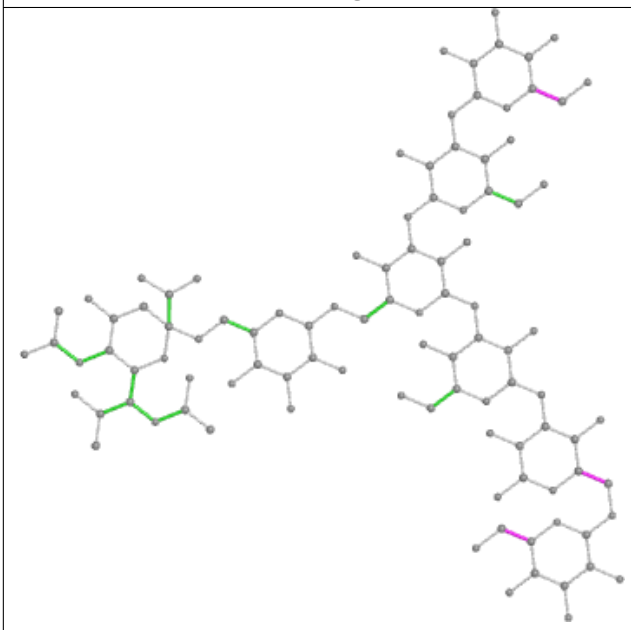
Oligosaccharide Chain E



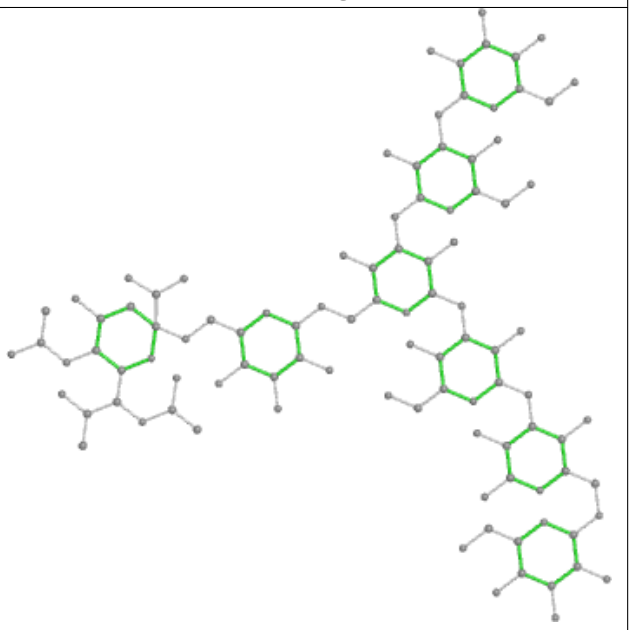
Bond lengths



Bond angles

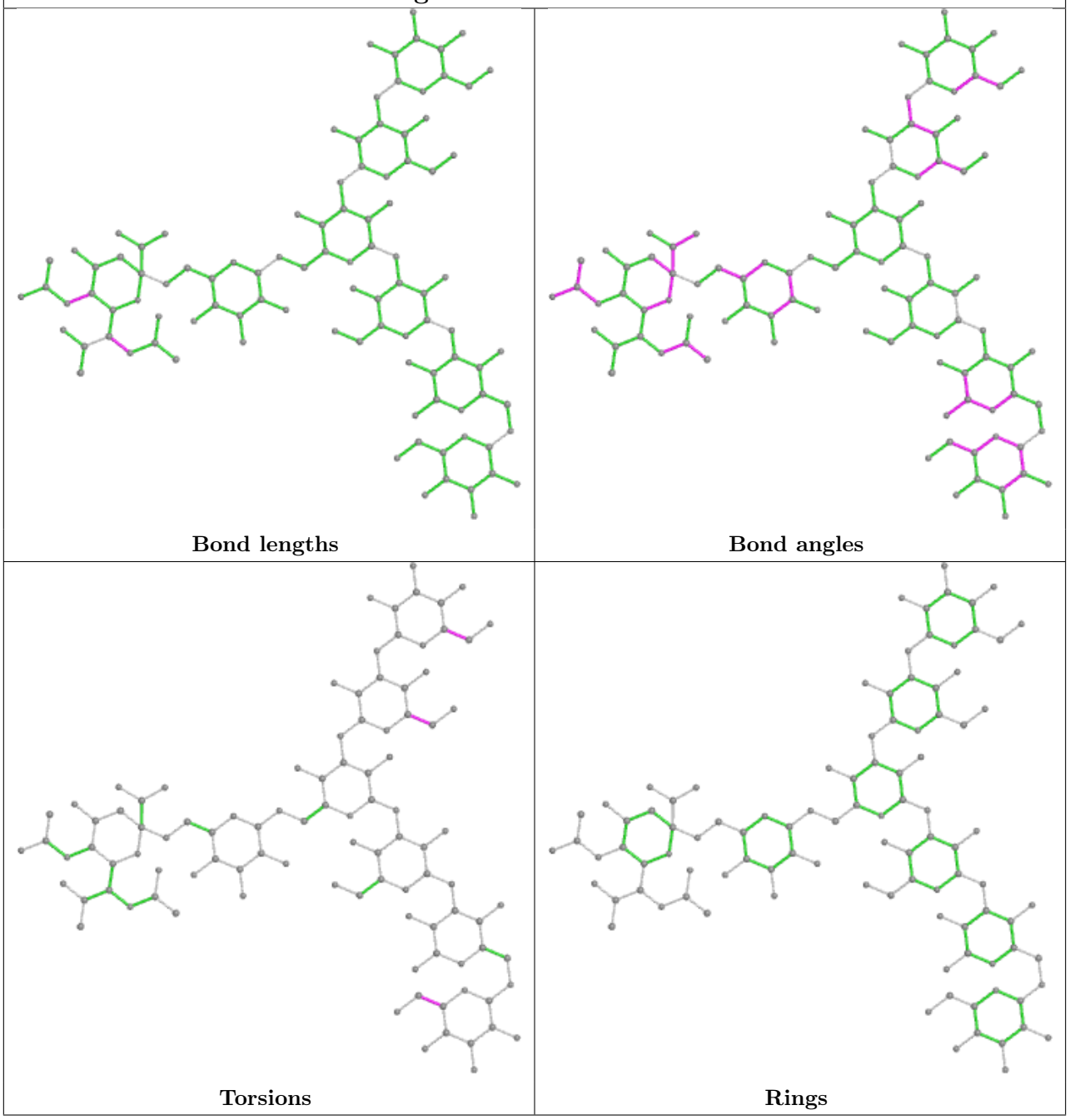


Torsions



Rings

Oligosaccharide Chain F



5.6 Ligand geometry (i)

12 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	MLA	B	601	-	6,6,6	1.07	0	7,7,7	1.31	0
4	ACY	A	612	2	1,2,3	1.43	0	1,1,3	0.78	0
3	MLA	A	601	-	6,6,6	1.18	0	7,7,7	1.29	1 (14%)
3	MLA	A	602	-	6,6,6	1.52	0	7,7,7	0.47	0
4	ACY	C	612	2	1,2,3	1.42	0	1,1,3	1.07	0
3	MLA	C	601	-	6,6,6	1.13	0	7,7,7	1.38	1 (14%)
4	ACY	B	603	2	1,2,3	1.48	0	1,1,3	0.70	0
4	ACY	A	611	2	1,2,3	1.46	0	1,1,3	0.99	0
3	MLA	B	602	-	6,6,6	1.15	0	7,7,7	1.42	0
3	MLA	C	602	-	6,6,6	1.13	0	7,7,7	1.17	0
4	ACY	C	603	2	1,2,3	1.41	0	1,1,3	0.85	0
4	ACY	B	612	2	1,2,3	1.41	0	1,1,3	1.09	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	MLA	B	601	-	-	4/4/4/4	-
3	MLA	A	601	-	-	2/4/4/4	-
3	MLA	A	602	-	-	0/4/4/4	-
3	MLA	C	601	-	-	0/4/4/4	-
3	MLA	B	602	-	-	2/4/4/4	-
3	MLA	C	602	-	-	3/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	601	MLA	O1A-C1-C2	2.18	121.51	114.54
3	A	601	MLA	O3B-C3-C2	2.06	121.13	114.54

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	602	MLA	O1A-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
3	C	602	MLA	O1B-C1-C2-C3
3	B	602	MLA	C1-C2-C3-O3B
3	B	602	MLA	C1-C2-C3-O3A
3	B	601	MLA	C1-C2-C3-O3A
3	B	601	MLA	C1-C2-C3-O3B
3	A	601	MLA	O1A-C1-C2-C3
3	B	601	MLA	O1B-C1-C2-C3
3	A	601	MLA	O1B-C1-C2-C3
3	B	601	MLA	O1A-C1-C2-C3
3	C	602	MLA	C1-C2-C3-O3B

There are no ring outliers.

No monomer is involved in short contacts.

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	548/719 (76%)	-0.53	1 (0%)	95	95	12, 19, 30, 68	0
1	B	548/719 (76%)	-0.52	1 (0%)	95	95	12, 19, 30, 77	0
1	C	548/719 (76%)	-0.52	1 (0%)	95	95	12, 20, 30, 83	0
All	All	1644/2157 (76%)	-0.52	3 (0%)	95	95	12, 19, 30, 83	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	18	GLN	6.2
1	C	18	GLN	4.3
1	A	19	THR	2.0

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	BGC	E	8	11/12	0.41	0.63	79,94,101,102	0
2	BGC	F	8	11/12	0.46	0.49	78,86,92,93	0
2	BGC	D	8	11/12	0.72	0.47	82,93,100,101	0
2	GAL	D	1	12/12	0.81	0.26	43,52,64,71	0
2	GAL	F	1	12/12	0.84	0.25	41,53,59,63	0

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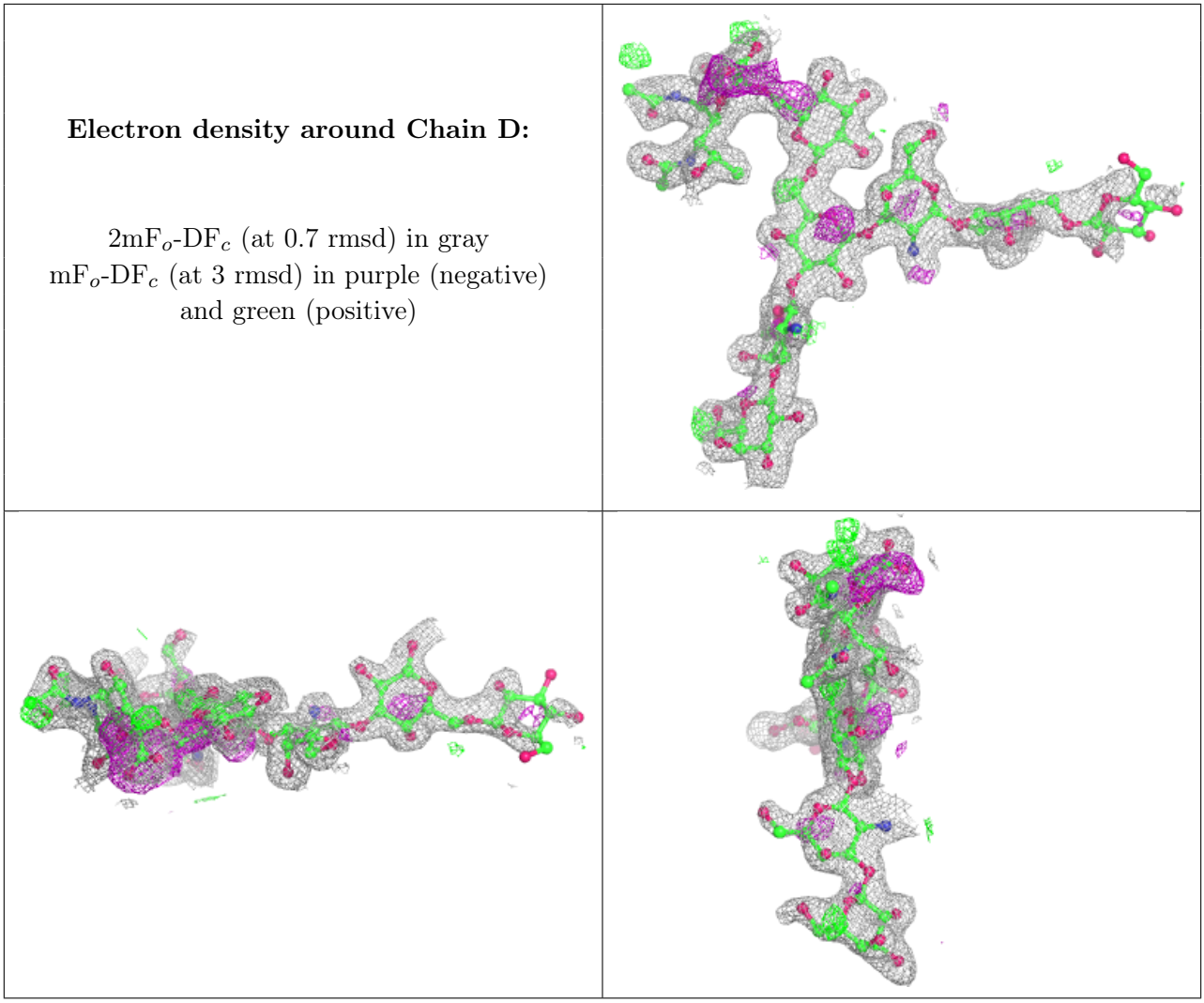
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GAL	F	5	11/12	0.85	0.18	40,49,58,62	0
2	GAL	D	3	11/12	0.86	0.10	41,48,55,57	0
2	GAL	E	5	11/12	0.86	0.20	43,50,56,61	0
2	GAL	E	3	11/12	0.88	0.11	41,48,55,57	0
2	6PZ	F	7	22/23	0.88	0.20	35,38,47,50	0
2	GAL	E	1	12/12	0.88	0.21	39,49,59,61	0
2	GAL	F	3	11/12	0.89	0.11	41,50,55,58	0
2	1GN	E	4	11/12	0.90	0.24	46,48,55,64	0
2	GAL	D	5	11/12	0.90	0.20	41,48,58,63	0
2	1GN	F	4	11/12	0.91	0.22	45,47,52,54	0
2	6PZ	E	7	22/23	0.91	0.19	34,39,46,48	0
2	1GN	D	4	11/12	0.92	0.25	46,47,53,54	0
2	BGC	E	6	11/12	0.92	0.14	27,31,35,36	0
2	1GN	F	2	11/12	0.92	0.15	29,36,40,40	0
2	6PZ	D	7	22/23	0.92	0.19	36,39,48,50	0
2	1GN	E	2	11/12	0.93	0.16	27,38,40,41	0
2	BGC	D	6	11/12	0.93	0.17	27,32,34,36	0
2	1GN	D	2	11/12	0.94	0.18	31,38,40,41	0
2	BGC	F	6	11/12	0.95	0.14	28,32,35,37	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.

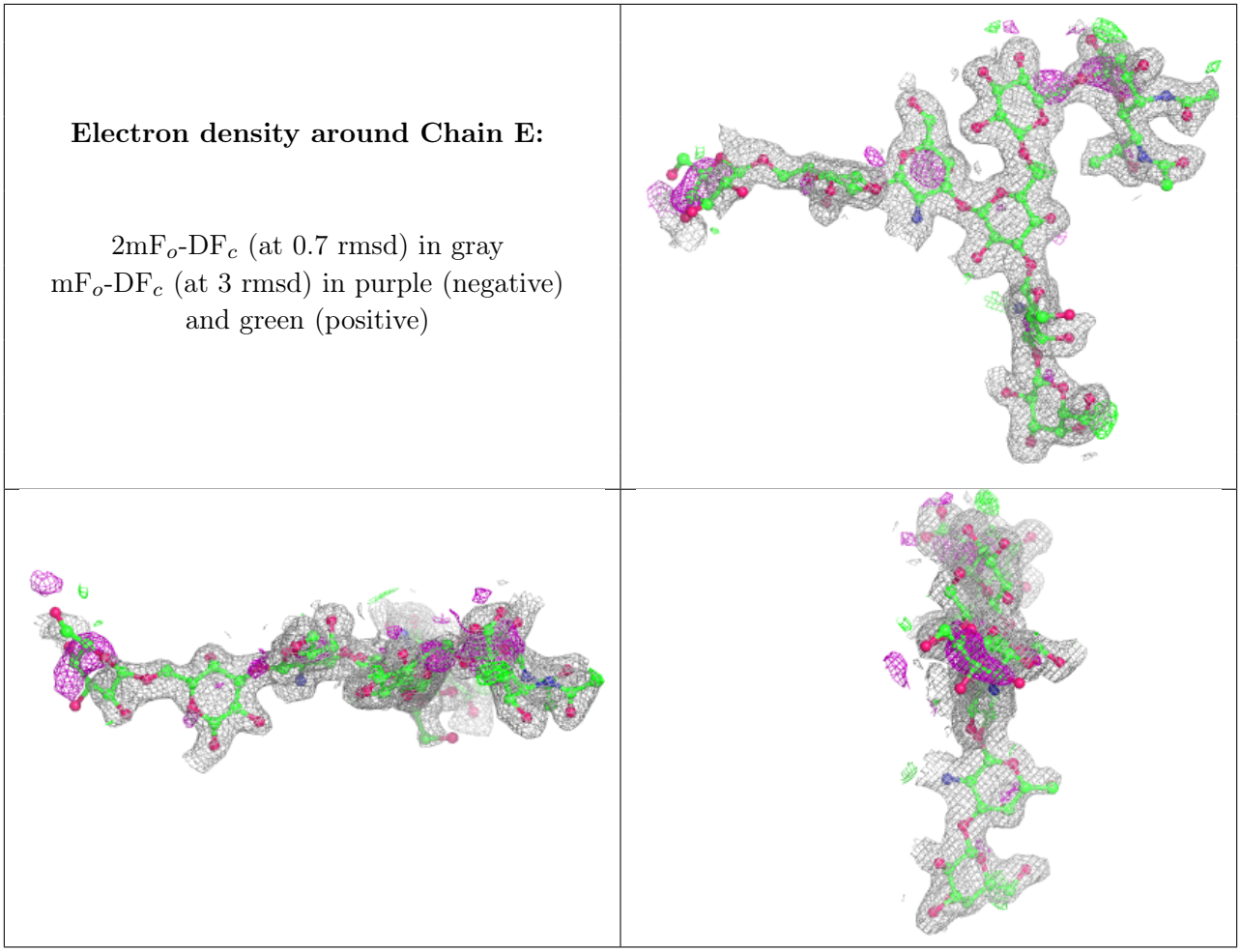
Electron density around Chain D:

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



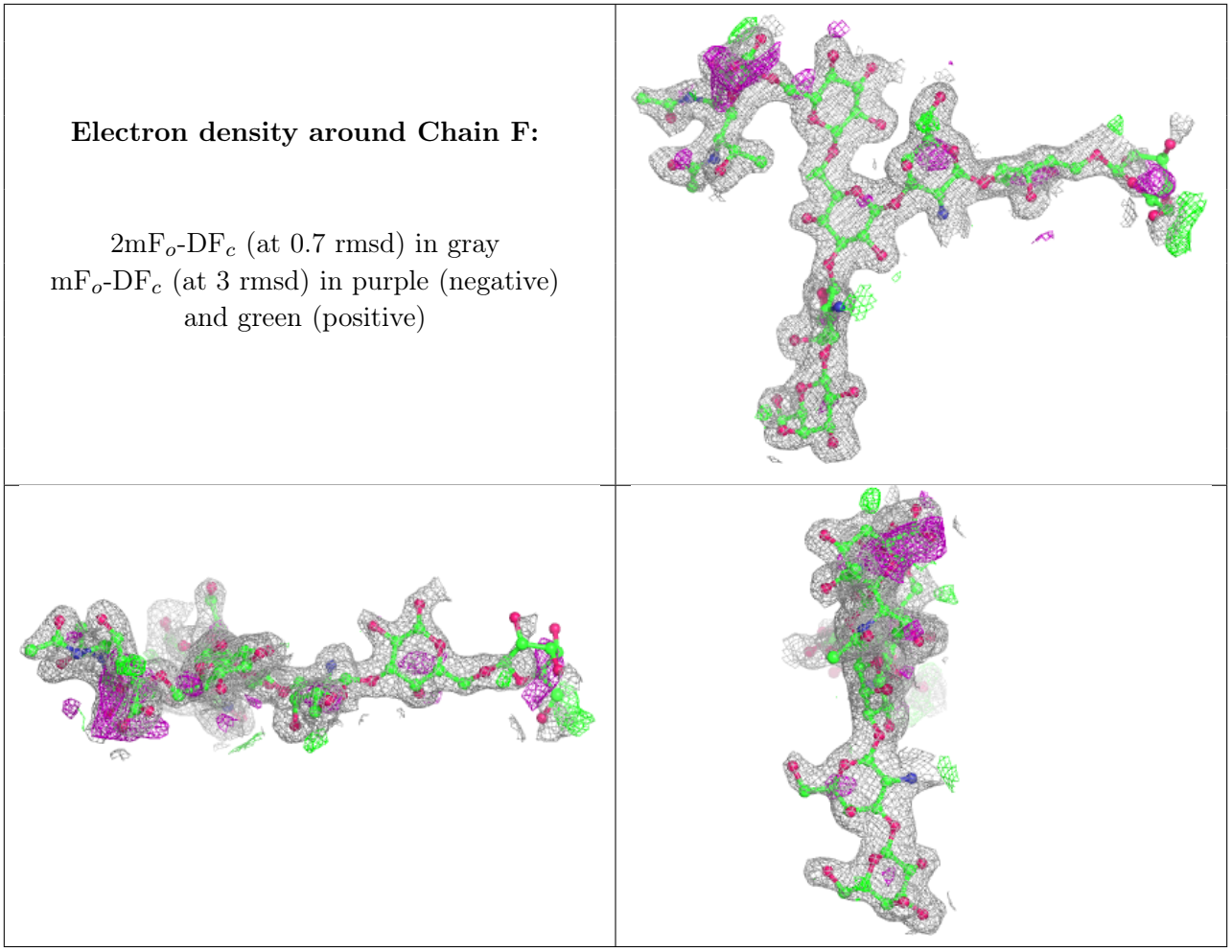
Electron density around Chain E:

$2mF_o$-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
3	MLA	B	602	7/7	0.84	0.23	28,41,50,54	0
3	MLA	C	602	7/7	0.85	0.25	32,45,57,57	0
3	MLA	A	602	7/7	0.87	0.20	28,36,44,51	0
4	ACY	A	612	3/4	0.87	0.14	38,38,43,45	0
4	ACY	B	603	3/4	0.89	0.11	40,40,45,45	0
3	MLA	A	601	7/7	0.91	0.23	34,39,52,57	0
3	MLA	B	601	7/7	0.92	0.21	35,37,50,55	0
4	ACY	A	611	3/4	0.92	0.25	40,40,44,46	0
4	ACY	C	603	3/4	0.93	0.12	40,40,44,46	0
3	MLA	C	601	7/7	0.94	0.27	37,40,50,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	ACY	B	612	3/4	0.95	0.19	40,40,43,46	0
4	ACY	C	612	3/4	0.96	0.24	44,44,45,46	0

6.5 Other polymers (i)

There are no such residues in this entry.