wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2020 – 07:16 PM BST

PDB ID	:	2YPG
Title	:	Haemagglutinin of 1968 Human H3N2 Virus in Complex with Human Receptor Analogue LSTc
Authors	:	Liu, J.; Xiong, X.; Haire, L.F.; Lin, Y.P.; Wharton, S.A.; Martin, S.R.; Coombs, P.J.; Vachieri, S.G.; Christodoulou, E.; Walker, P.A.; Skehel, J.J.; Gamblin, S.J.; Hay, A.J.; Daniels, R.S.; McCauley, J.W.
Deposited on	:	2012-10-30
Resolution	:	2.85 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 following versions of software and data (see references (1)) were used in the production of this report:

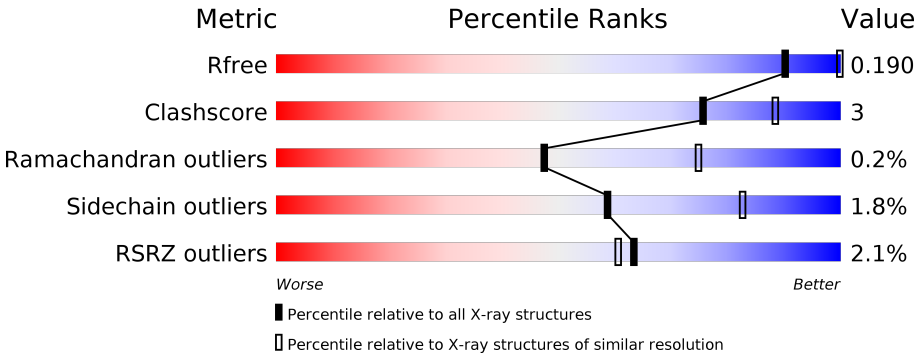
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 <=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	328	2% 88% 9%
1	C	328	3% 89% 8%
1	E	328	% 89% 7%
2	B	175	3% 93% 5%
2	D	175	2% 93%
2	F	175	% 94%

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Mol	Chain	Length	Quality of chain
3	G	3	67% 33%
4	H	3	67% 33%
4	M	3	33% 33% 33%
5	I	2	100%
5	K	2	100%
5	L	2	100%
5	N	2	100%
5	Q	2	50% 50%
6	J	5	40% 60%
6	R	5	40% 60%
7	O	4	50% 50%
8	P	3	33% 67%

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
10	FLC	A	1339	-	-	-	X
10	FLC	B	1176	-	-	-	X
10	FLC	B	1177	-	-	-	X
10	FLC	E	1336	-	-	-	X
10	FLC	E	1337	-	-	-	X
6	GAL	R	2	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 12735 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.

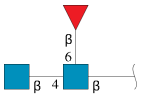
- Molecule 1 is a protein called HEMAGGLUTININ HA1 CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	0
			2446	1532	429	472	13			
1	C	320	Total	C	N	O	S	0	0	0
			2472	1547	435	477	13			
1	E	318	Total	C	N	O	S	0	0	0
			2455	1538	431	473	13			

- Molecule 2 is a protein called HEMAGGLUTININ HA2 CHAIN.

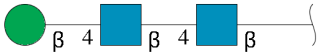
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1407	874	247	280	6			
2	D	172	Total	C	N	O	S	0	0	0
			1399	868	246	279	6			
2	F	173	Total	C	N	O	S	0	0	0
			1407	874	247	280	6			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

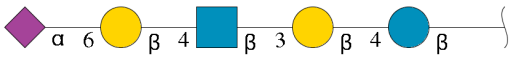


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	H	3	Total C N O 39 22 2 15	0	0	0
4	M	3	Total C N O 39 22 2 15	0	0	0

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	I	2	Total C N O 28 16 2 10	0	0	0
5	K	2	Total C N O 28 16 2 10	0	0	0
5	L	2	Total C N O 28 16 2 10	0	0	0
5	N	2	Total C N O 28 16 2 10	0	0	0
5	Q	2	Total C N O 28 16 2 10	0	0	0

- Molecule 6 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose.

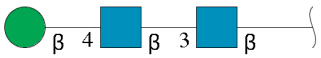


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	J	5	Total C N O 68 37 2 29	0	0	0
6	R	5	Total C N O 68 37 2 29	0	0	0

- Molecule 7 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galacto pyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose.

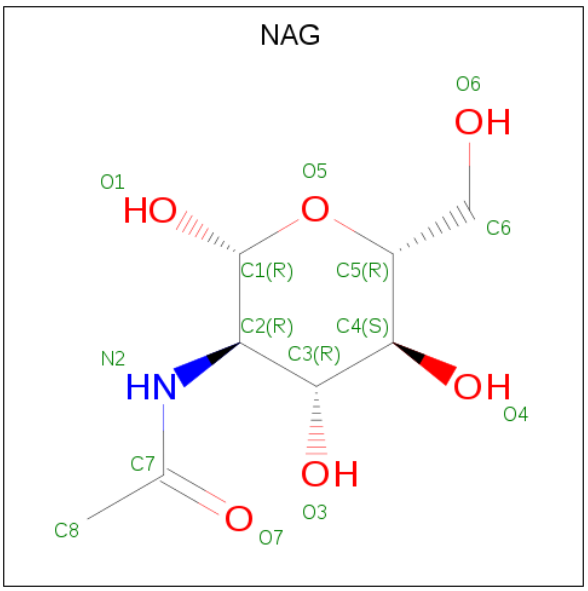
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	O	4	Total	C	N	O	0	0	1
			46	25	2	19			

- Molecule 8 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	P	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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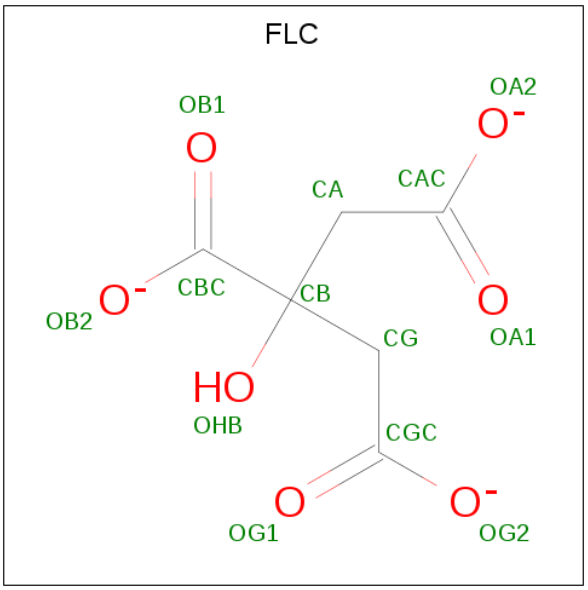
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	C	1	Total C N O 14 8 1 5	0	0
9	D	1	Total C N O 14 8 1 5	0	0
9	E	1	Total C N O 14 8 1 5	0	0
9	F	1	Total C N O 14 8 1 5	0	0

- Molecule 10 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C O 13 6 7	0	0
10	A	1	Total C O 13 6 7	0	0
10	B	1	Total C O 13 6 7	0	0
10	B	1	Total C O 13 6 7	0	0
10	B	1	Total C O 13 6 7	0	0
10	C	1	Total C O 13 6 7	0	0
10	C	1	Total C O 13 6 7	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	C	1	Total C O 13 6 7	0	0
10	D	1	Total C O 13 6 7	0	0
10	E	1	Total C O 13 6 7	0	0
10	E	1	Total C O 13 6 7	0	0
10	E	1	Total C O 13 6 7	0	0
10	F	1	Total C O 13 6 7	0	0

- Molecule 11 is water.

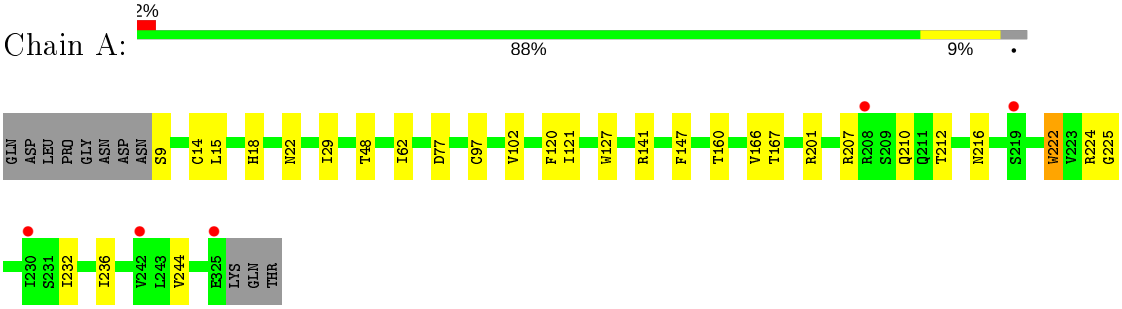
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	96	Total O 96 96	0	0
11	B	61	Total O 61 61	0	0
11	C	83	Total O 83 83	0	0
11	D	61	Total O 61 61	0	0
11	E	93	Total O 93 93	0	0
11	F	39	Total O 39 39	0	0

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.

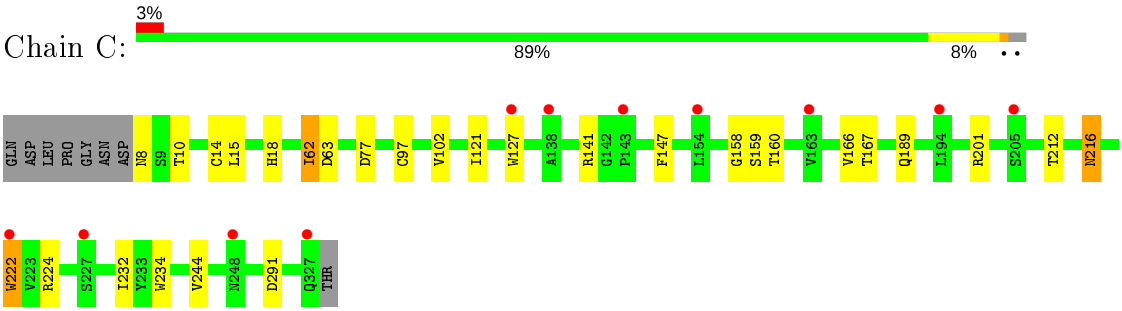
- Molecule 1: HEMAGGLUTININ HA1 CHAIN

Chain A:



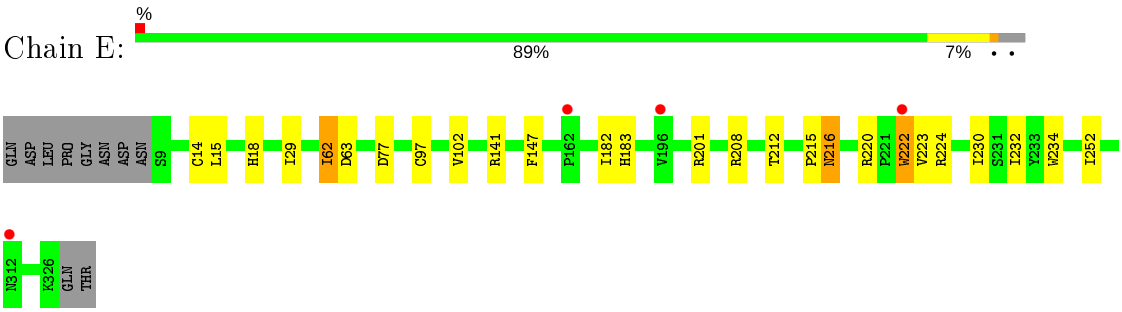
- Molecule 1: HEMAGGLUTININ HA1 CHAIN

Chain C:



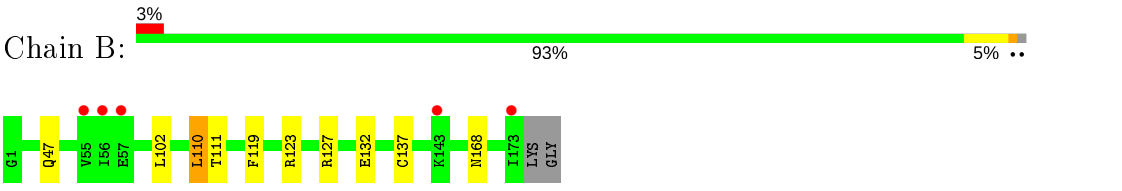
- Molecule 1: HEMAGGLUTININ HA1 CHAIN

Chain E:



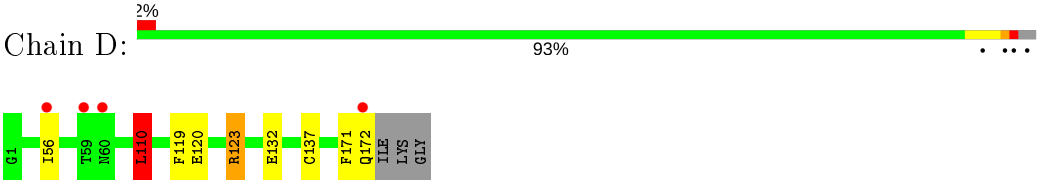
- Molecule 2: HEMAGGLUTININ HA2 CHAIN

Chain B:



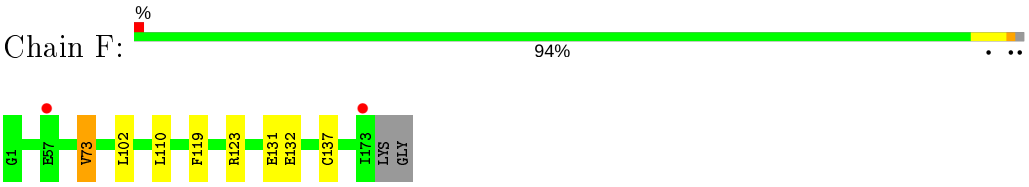
• Molecule 2: HEMAGGLUTININ HA2 CHAIN

Chain D:



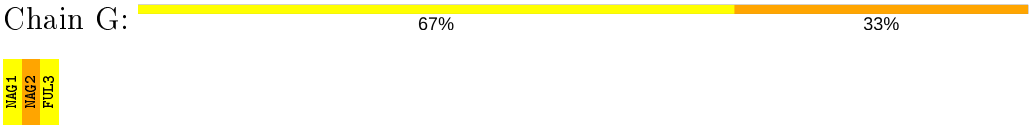
• Molecule 2: HEMAGGLUTININ HA2 CHAIN

Chain F:



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:

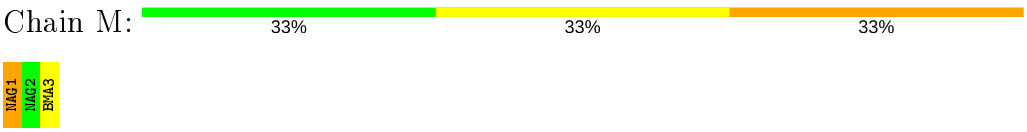


• Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:

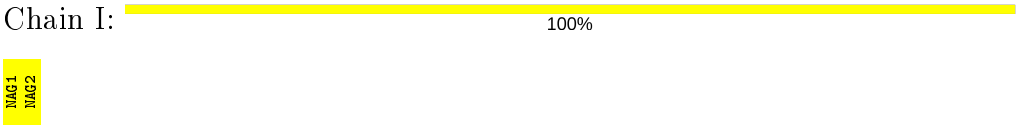
• Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:



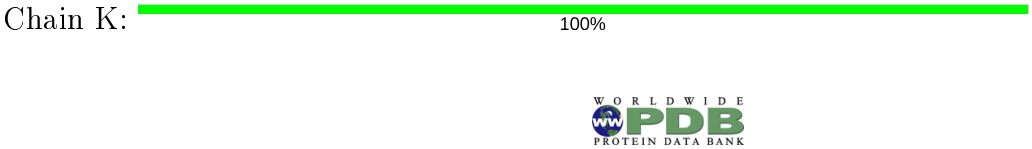
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:



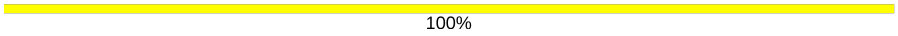
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:



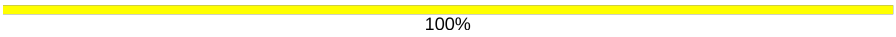
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

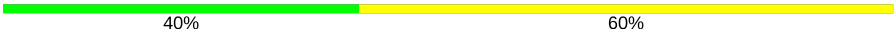
Chain Q:

• Molecule 6: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain J:

• Molecule 6: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain R:



• Molecule 7: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose

Chain O:

• Molecule 8: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α, β, γ	160.77Å 160.77Å 177.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	160.77 – 2.85 160.77 – 2.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (160.77-2.85) 100.0 (160.77-2.85)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.40 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.177 , 0.190 0.177 , 0.190	Depositor DCC
R_{free} test set	5238 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	47.4	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 42.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	12735	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.03% 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, NAG, SIA, GAL, BMA, FLC, FUL

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	0.48	1/2502 (0.0%)	0.57	0/3410
1	C	0.48	2/2528 (0.1%)	0.56	0/3444
1	E	0.48	2/2511 (0.1%)	0.55	0/3421
2	B	0.48	0/1431	0.61	1/1923 (0.1%)
2	D	0.49	0/1423	0.61	2/1912 (0.1%)
2	F	0.50	0/1431	0.60	1/1923 (0.1%)
All	All	0.48	5/11826 (0.0%)	0.57	4/16033 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	222	TRP	CD2-CE2	5.99	1.48	1.41
1	E	222	TRP	CD2-CE2	5.77	1.48	1.41
1	A	222	TRP	CD2-CE2	5.27	1.47	1.41
1	C	234	TRP	CD2-CE2	5.19	1.47	1.41
1	E	234	TRP	CD2-CE2	5.05	1.47	1.41

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	123	ARG	NE-CZ-NH1	6.75	123.68	120.30
2	F	123	ARG	NE-CZ-NH1	6.51	123.56	120.30
2	D	110	LEU	CA-CB-CG	6.19	129.54	115.30
2	D	123	ARG	NE-CZ-NH1	5.15	122.87	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2446	0	2393	29	0
1	C	2472	0	2419	24	0
1	E	2455	0	2406	15	0
2	B	1407	0	1329	6	0
2	D	1399	0	1318	9	0
2	F	1407	0	1329	6	0
3	G	38	0	34	1	0
4	H	39	0	34	2	0
4	M	39	0	34	1	0
5	I	28	0	25	0	0
5	K	28	0	25	0	0
5	L	28	0	25	0	0
5	N	28	0	25	0	0
5	Q	28	0	25	0	0
6	J	68	0	58	0	0
6	R	68	0	58	0	0
7	O	46	0	38	0	0
8	P	39	0	32	2	0
9	A	14	0	13	0	0
9	C	14	0	13	0	0
9	D	14	0	13	0	0
9	E	14	0	13	0	0
9	F	14	0	13	0	0
10	A	26	0	10	0	0
10	B	39	0	15	4	0
10	C	39	0	15	0	0
10	D	13	0	5	0	0
10	E	39	0	15	0	0
10	F	13	0	5	0	0
11	A	96	0	0	2	0
11	B	61	0	0	1	0
11	C	83	0	0	0	0
11	D	61	0	0	0	0
11	E	93	0	0	0	0
11	F	39	0	0	0	0
All	All	12735	0	11737	75	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 3.

The worst 5 of 75 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:216:ASN:ND2	1:C:212:THR:HG21	1.53	1.22
1:C:216:ASN:HB3	1:E:212:THR:HG21	1.46	0.97
1:A:216:ASN:ND2	1:C:212:THR:CG2	2.28	0.95
1:A:216:ASN:HD22	1:C:212:THR:HG21	1.23	0.93
1:C:167:THR:HG22	1:C:244:VAL:HG22	1.54	0.89

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	315/328 (96%)	307 (98%)	7 (2%)	1 (0%)	41	68
1	C	318/328 (97%)	309 (97%)	8 (2%)	1 (0%)	41	68
1	E	316/328 (96%)	309 (98%)	6 (2%)	1 (0%)	41	68
2	B	171/175 (98%)	162 (95%)	9 (5%)	0	100	100
2	D	170/175 (97%)	162 (95%)	8 (5%)	0	100	100
2	F	171/175 (98%)	164 (96%)	7 (4%)	0	100	100
All	All	1461/1509 (97%)	1413 (97%)	45 (3%)	3 (0%)	47	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	ILE
1	C	62	ILE
1	E	62	ILE

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	279/289 (96%)	274 (98%)	5 (2%)	59 82
1	C	282/289 (98%)	276 (98%)	6 (2%)	53 79
1	E	280/289 (97%)	274 (98%)	6 (2%)	53 79
2	B	148/149 (99%)	145 (98%)	3 (2%)	55 80
2	D	147/149 (99%)	146 (99%)	1 (1%)	84 94
2	F	148/149 (99%)	146 (99%)	2 (1%)	67 86
All	All	1284/1314 (98%)	1261 (98%)	23 (2%)	59 82

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	189	GLN
1	C	216	ASN
2	F	73	VAL
1	C	201	ARG
1	C	222	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	197	GLN
2	D	26	HIS
1	E	197	GLN
1	C	171	ASN
1	E	171	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)

Of 36 monosaccharides modelled in this entry, 35 were used 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	NAG	G	1	1,3	14,14,15	0.54	0	17,19,21	1.49	3 (17%)
3	NAG	G	2	3	14,14,15	0.71	0	17,19,21	1.31	2 (11%)
3	FUL	G	3	3	10,10,11	0.70	0	14,14,16	1.45	2 (14%)
4	NAG	H	1	1,4	14,14,15	1.92	1 (7%)	17,19,21	1.38	3 (17%)
4	NAG	H	2	4	14,14,15	0.58	0	17,19,21	1.52	2 (11%)
4	BMA	H	3	4	11,11,12	0.64	0	15,15,17	0.98	2 (13%)
5	NAG	I	1	1,5	14,14,15	0.54	0	17,19,21	1.14	1 (5%)
5	NAG	I	2	5	14,14,15	0.49	0	17,19,21	0.89	1 (5%)
6	BGC	J	1	6	12,12,12	0.46	0	17,17,17	0.59	0
6	GAL	J	2	6	11,11,12	0.33	0	15,15,17	0.72	1 (6%)
6	NAG	J	3	6	14,14,15	0.34	0	17,19,21	1.02	2 (11%)
6	GAL	J	4	6	11,11,12	0.29	0	15,15,17	0.66	0
6	SIA	J	5	6	17,20,21	0.37	0	21,28,31	1.03	1 (4%)
5	NAG	K	1	2,5	14,14,15	0.51	0	17,19,21	0.92	0
5	NAG	K	2	5	14,14,15	0.46	0	17,19,21	1.07	0
5	NAG	L	1	1,5	14,14,15	1.67	1 (7%)	17,19,21	1.80	5 (29%)
5	NAG	L	2	5	14,14,15	0.73	0	17,19,21	1.13	2 (11%)
4	NAG	M	1	1,4	14,14,15	0.68	0	17,19,21	1.75	4 (23%)
4	NAG	M	2	4	14,14,15	0.57	0	17,19,21	0.66	0
4	BMA	M	3	4	11,11,12	0.56	0	15,15,17	0.86	1 (6%)
5	NAG	N	1	1,5	14,14,15	2.04	1 (7%)	17,19,21	1.77	3 (17%)
5	NAG	N	2	5	14,14,15	0.51	0	17,19,21	0.89	2 (11%)
7	NAG	O	2	7	14,14,15	0.39	0	17,19,21	1.19	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	GAL	O	3	7	11,11,12	0.34	0	15,15,17	0.66	0
7	SIA	O	4	7	17,20,21	0.42	0	21,28,31	1.08	2 (9%)
8	NAG	P	1	1,8	14,14,15	0.74	0	17,19,21	2.36	7 (41%)
8	NAG	P	2	8	14,14,15	0.87	1 (7%)	17,19,21	2.41	4 (23%)
8	BMA	P	3	8	11,11,12	0.49	0	15,15,17	1.21	1 (6%)
5	NAG	Q	1	1,5	14,14,15	0.57	0	17,19,21	1.10	1 (5%)
5	NAG	Q	2	5	14,14,15	0.50	0	17,19,21	0.90	0
6	BGC	R	1	6	12,12,12	0.46	0	17,17,17	0.56	0
6	GAL	R	2	6	11,11,12	0.47	0	15,15,17	0.80	1 (6%)
6	NAG	R	3	6	14,14,15	0.46	0	17,19,21	1.30	1 (5%)
6	GAL	R	4	6	11,11,12	0.40	0	15,15,17	0.72	0
6	SIA	R	5	6	17,20,21	0.40	0	21,28,31	1.17	3 (14%)

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	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	4/6/23/26	0/1/1/1
3	FUL	G	3	3	-	-	0/1/1/1
4	NAG	H	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
5	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	2/6/23/26	0/1/1/1
6	BGC	J	1	6	-	0/2/22/22	0/1/1/1
6	GAL	J	2	6	-	2/2/19/22	0/1/1/1
6	NAG	J	3	6	-	0/6/23/26	0/1/1/1
6	GAL	J	4	6	-	0/2/19/22	0/1/1/1
6	SIA	J	5	6	-	0/14/34/38	0/1/1/1
5	NAG	K	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	K	2	5	-	4/6/23/26	0/1/1/1
5	NAG	L	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	L	2	5	-	2/6/23/26	0/1/1/1
4	NAG	M	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	M	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	M	3	4	-	0/2/19/22	0/1/1/1
5	NAG	N	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
7	NAG	O	2	7	-	2/6/23/26	0/1/1/1
7	GAL	O	3	7	-	0/2/19/22	0/1/1/1
7	SIA	O	4	7	-	0/14/34/38	0/1/1/1
8	NAG	P	1	1,8	-	4/6/23/26	0/1/1/1
8	NAG	P	2	8	-	2/6/23/26	0/1/1/1
8	BMA	P	3	8	-	2/2/19/22	0/1/1/1
5	NAG	Q	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	0/6/23/26	0/1/1/1
6	BGC	R	1	6	-	2/2/22/22	0/1/1/1
6	GAL	R	2	6	-	2/2/19/22	0/1/1/1
6	NAG	R	3	6	-	0/6/23/26	0/1/1/1
6	GAL	R	4	6	-	0/2/19/22	0/1/1/1
6	SIA	R	5	6	-	0/14/34/38	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	N	1	NAG	O5-C1	-7.37	1.31	1.43
4	H	1	NAG	O5-C1	-6.77	1.32	1.43
5	L	1	NAG	O5-C1	-5.90	1.34	1.43
8	P	2	NAG	C1-C2	2.36	1.55	1.52

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	P	2	NAG	C1-C2-N2	5.54	119.96	110.49
5	N	1	NAG	C1-O5-C5	-5.27	105.06	112.19
8	P	1	NAG	O5-C1-C2	-5.22	103.05	111.29
8	P	1	NAG	O5-C5-C6	5.03	115.09	107.20
8	P	2	NAG	C1-O5-C5	4.77	118.66	112.19

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	P	1	NAG	C3-C2-N2-C7
4	H	3	BMA	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	I	1	NAG	O5-C5-C6-O6
5	Q	1	NAG	O5-C5-C6-O6
4	H	1	NAG	C4-C5-C6-O6

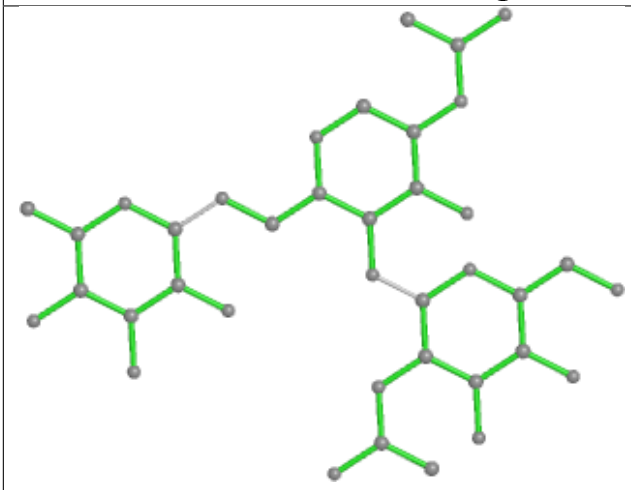
There are no ring outliers.

5 monomers are involved in 6 short contacts:

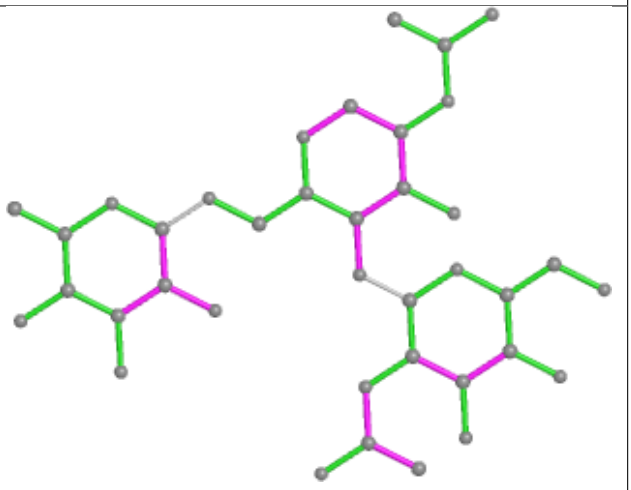
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	1	NAG	1	0
3	G	2	NAG	1	0
8	P	1	NAG	2	0
8	P	2	NAG	2	0
4	H	1	NAG	2	0

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

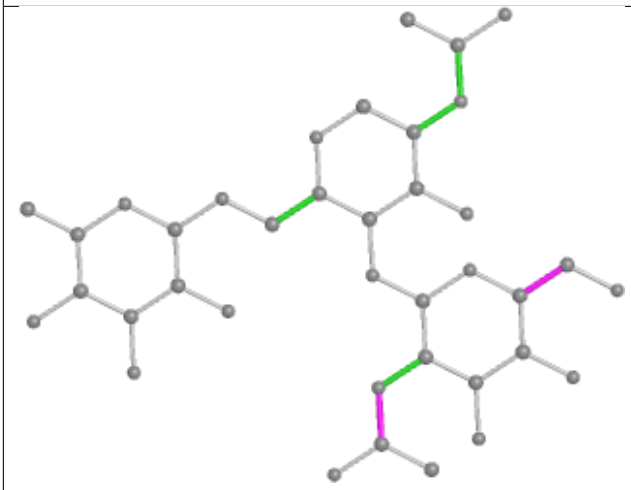
Oligosaccharide Chain G



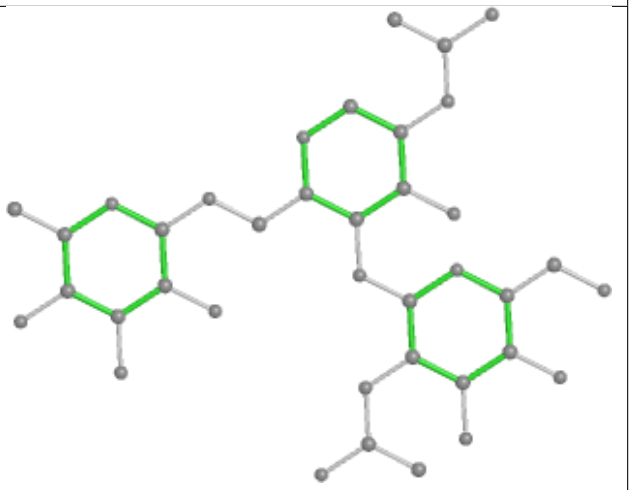
Bond lengths



Bond angles

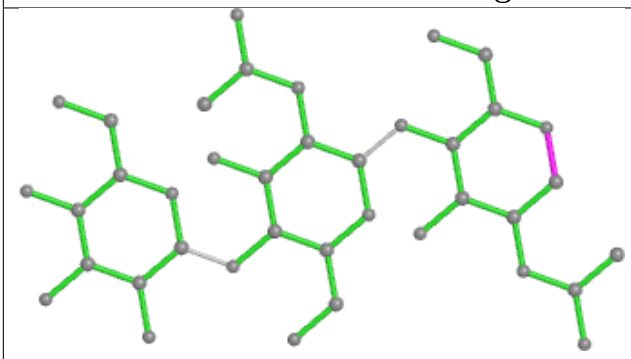


Torsions

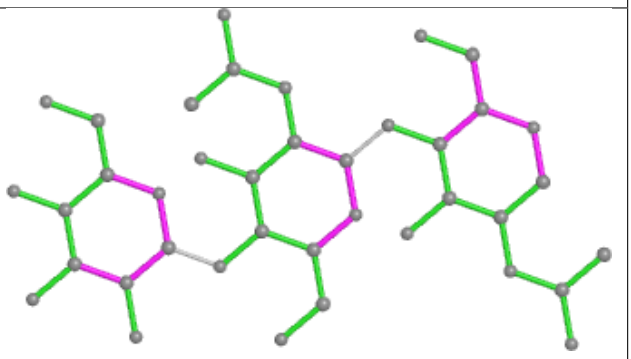


Rings

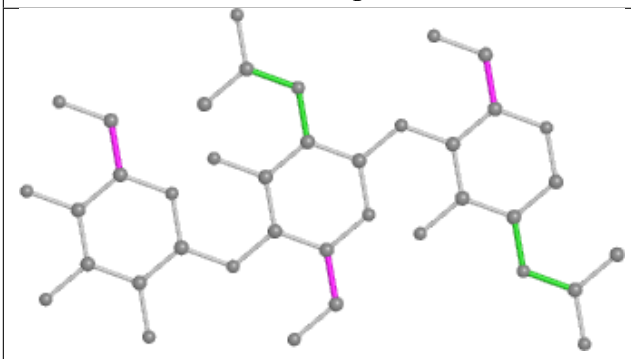
Oligosaccharide Chain H



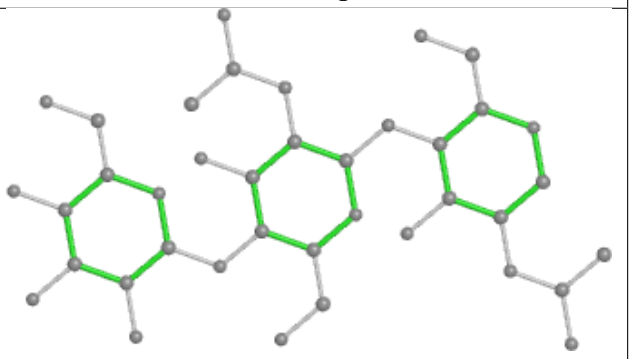
Bond lengths



Bond angles

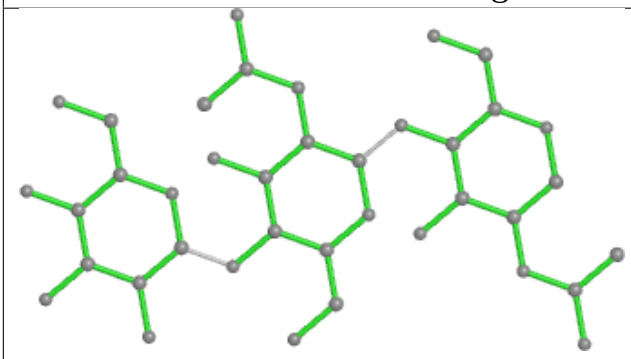


Torsions

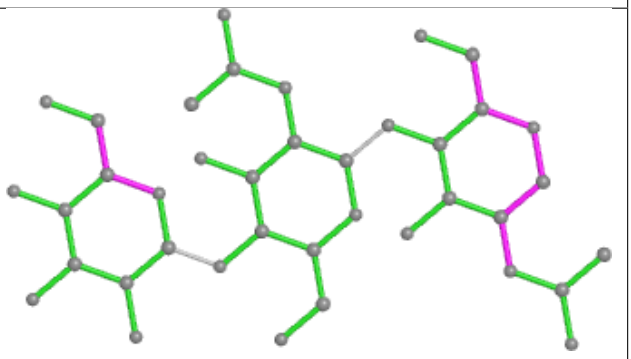


Rings

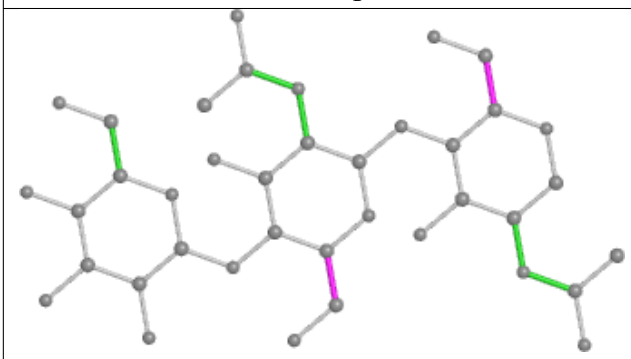
Oligosaccharide Chain M



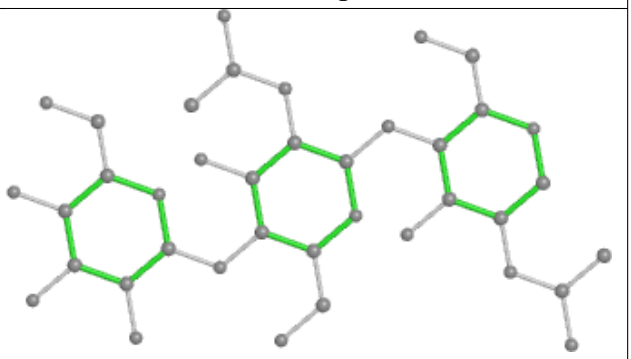
Bond lengths



Bond angles

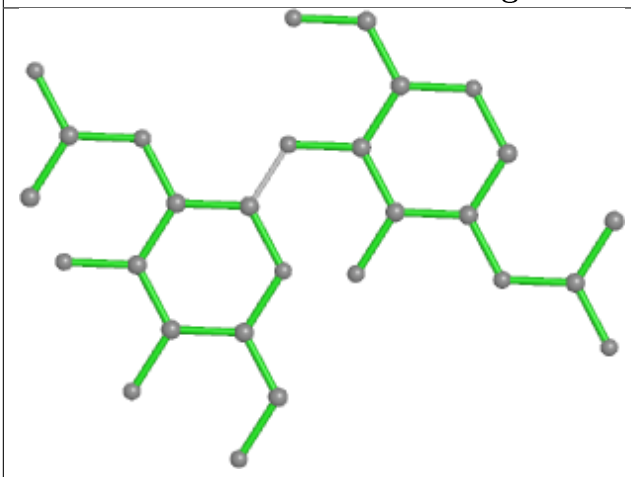


Torsions

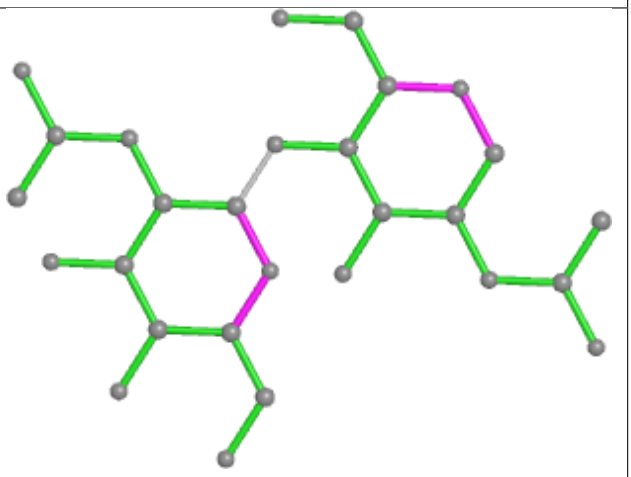


Rings

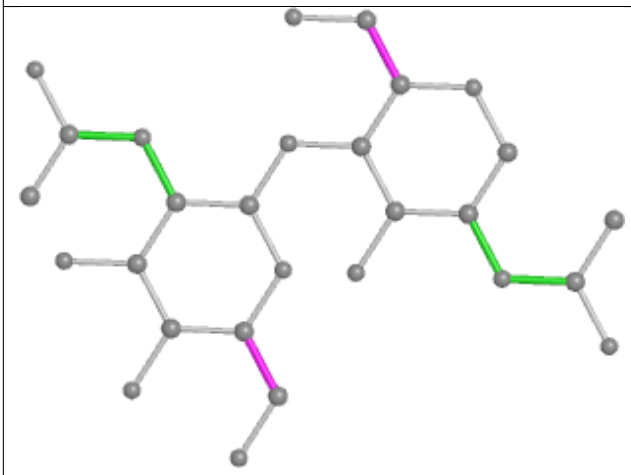
Oligosaccharide Chain I



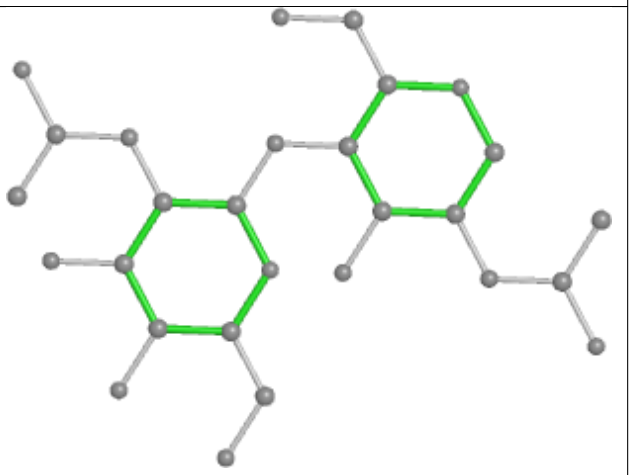
Bond lengths



Bond angles

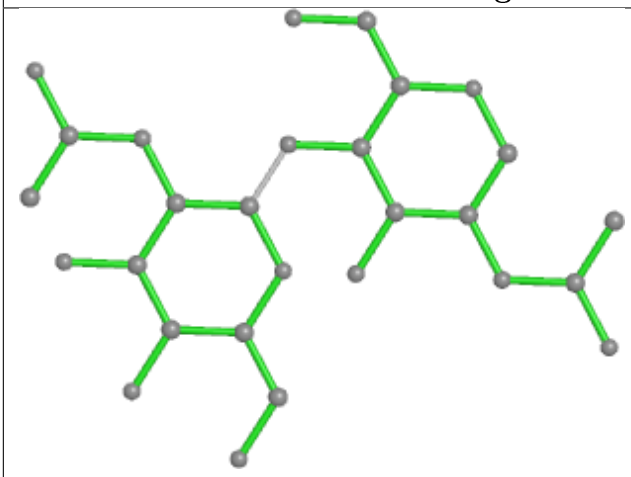


Torsions

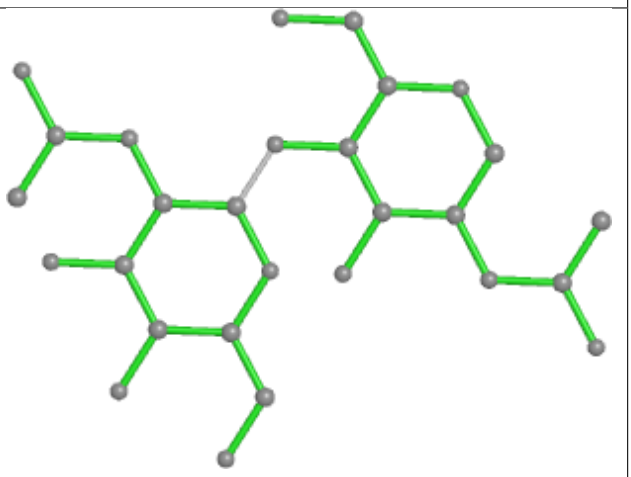


Rings

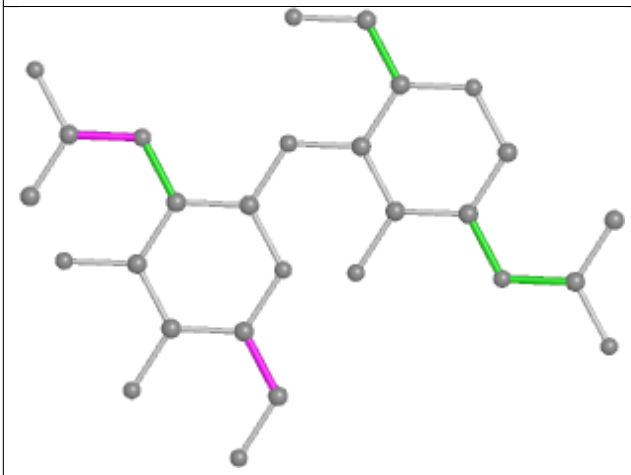
Oligosaccharide Chain K



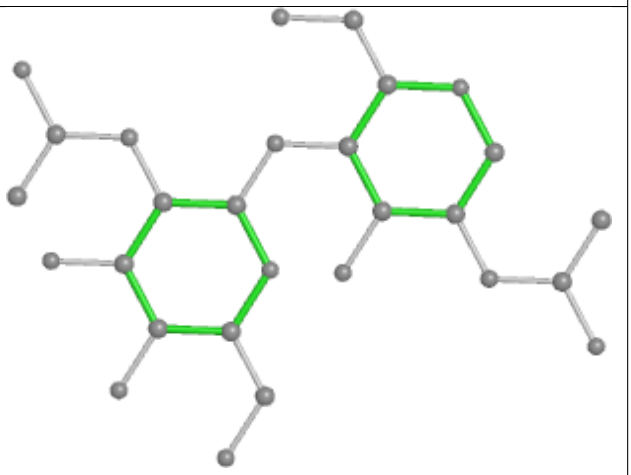
Bond lengths



Bond angles

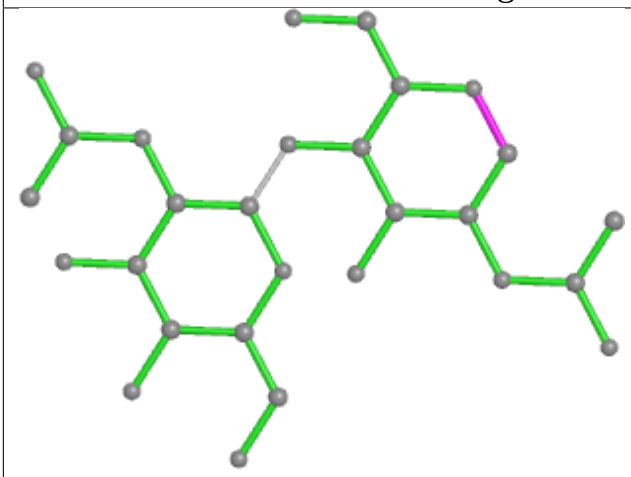


Torsions

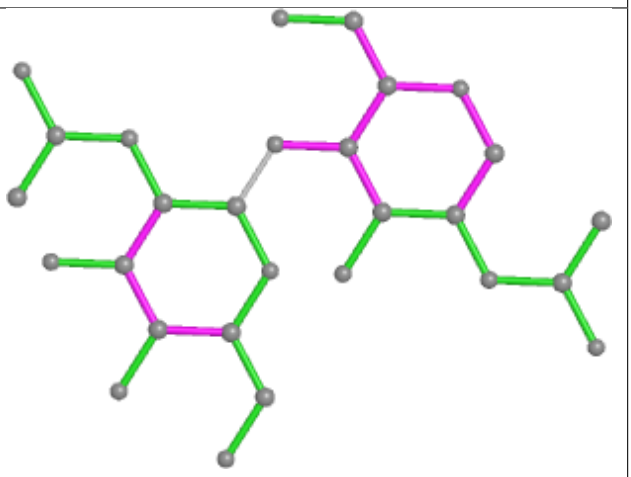


Rings

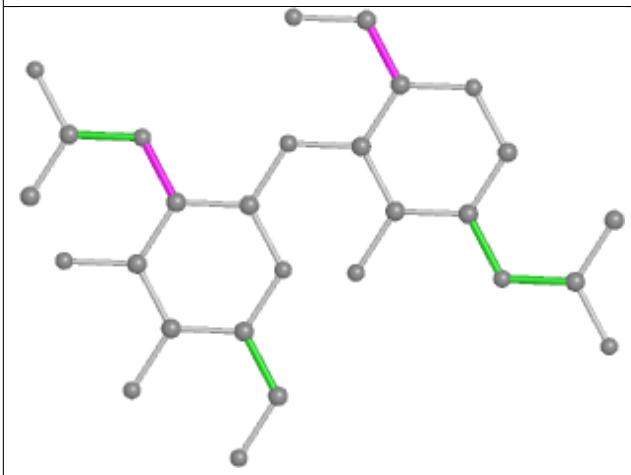
Oligosaccharide Chain L



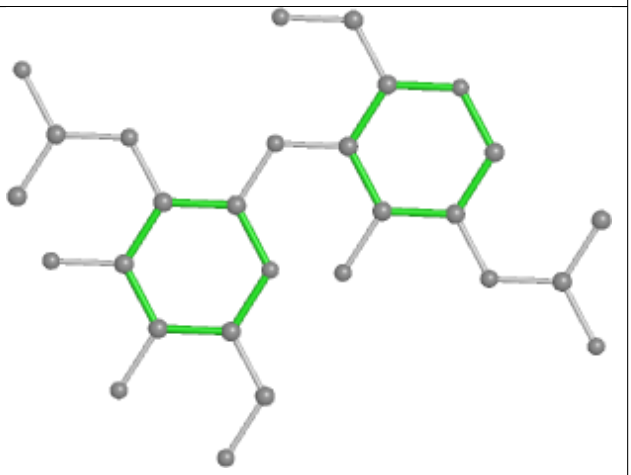
Bond lengths



Bond angles

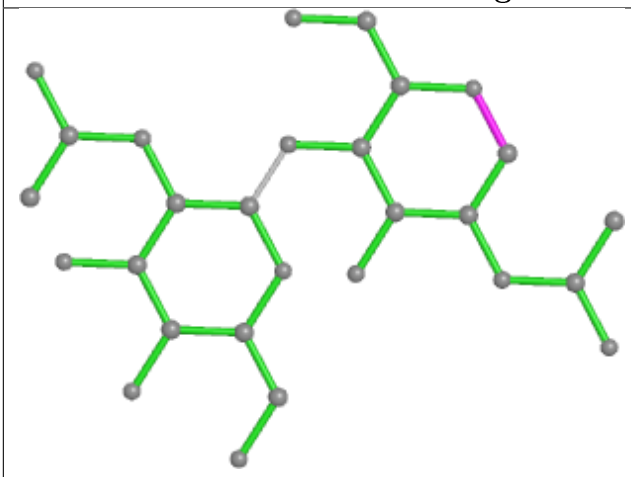


Torsions

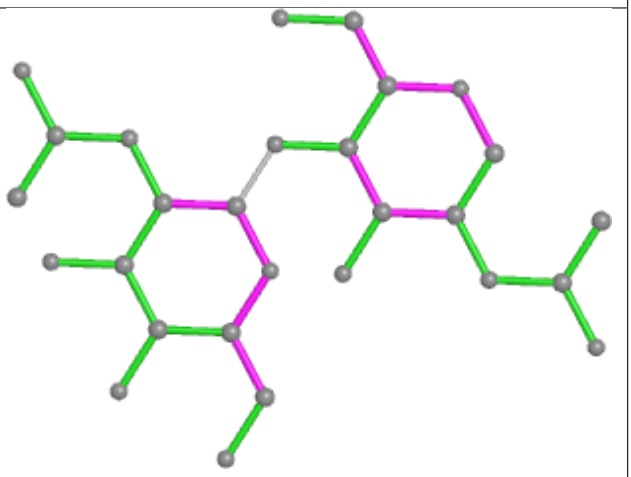


Rings

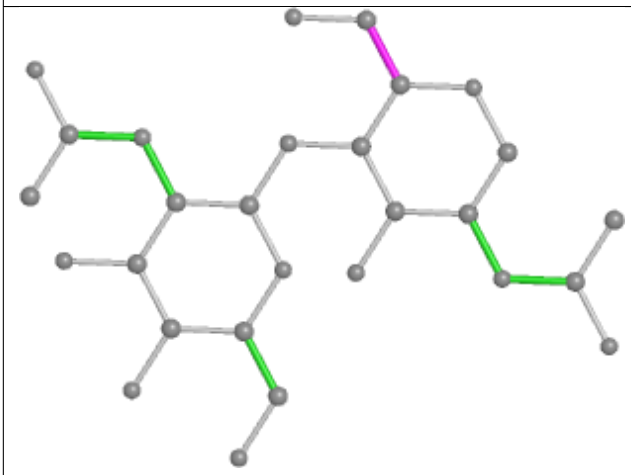
Oligosaccharide Chain N



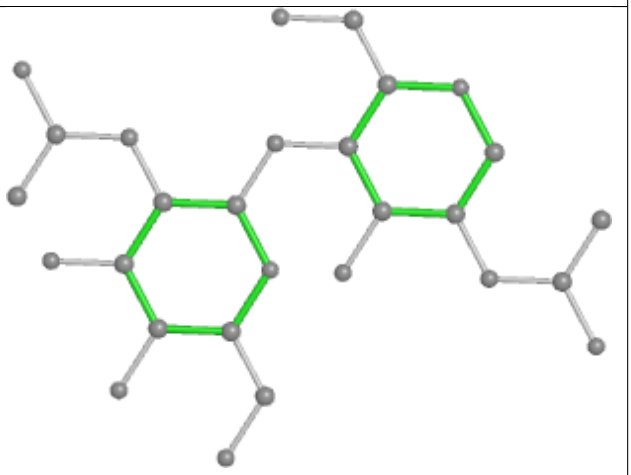
Bond lengths



Bond angles

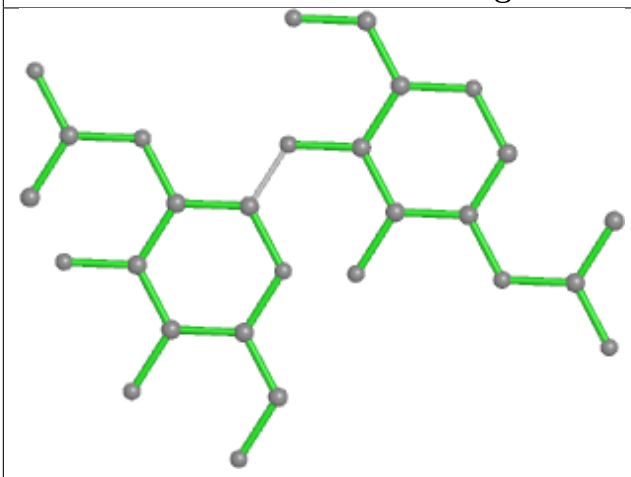


Torsions

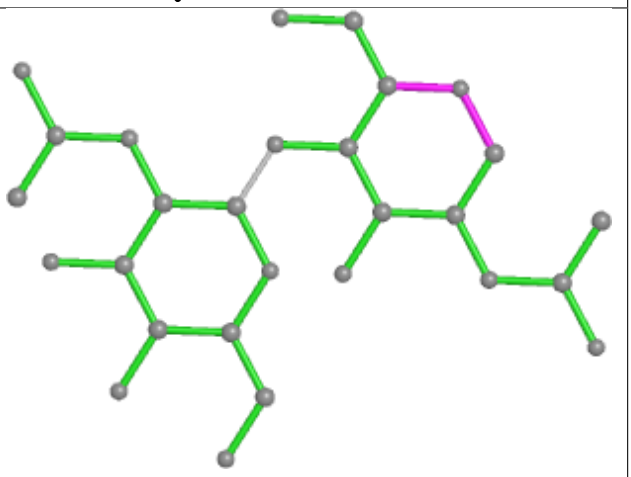


Rings

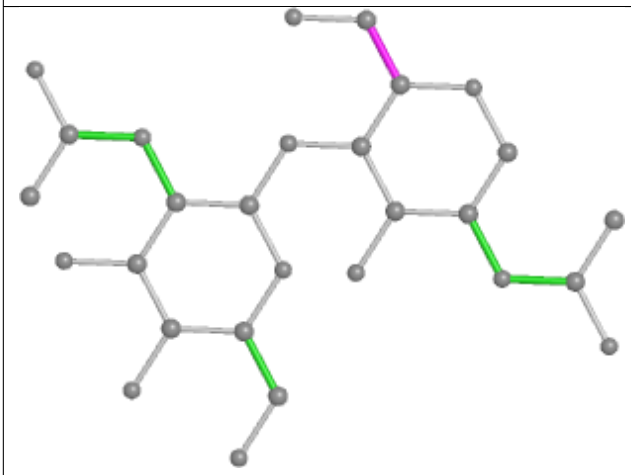
Oligosaccharide Chain Q



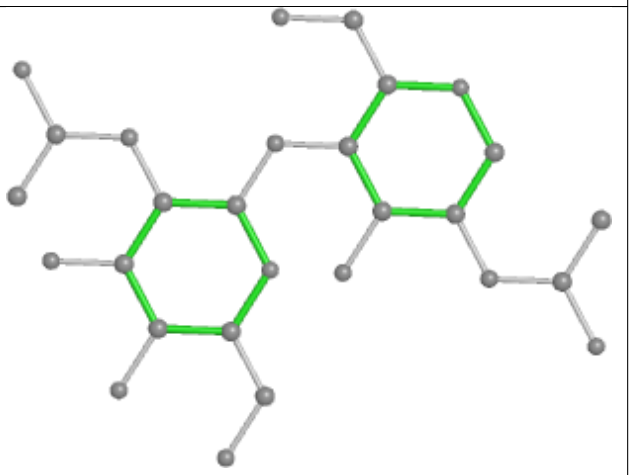
Bond lengths



Bond angles

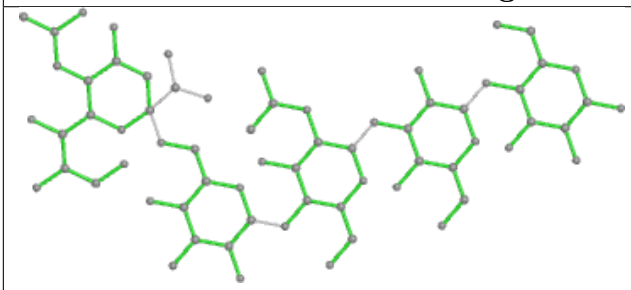


Torsions

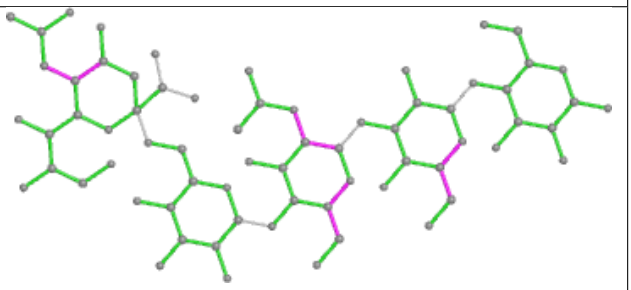


Rings

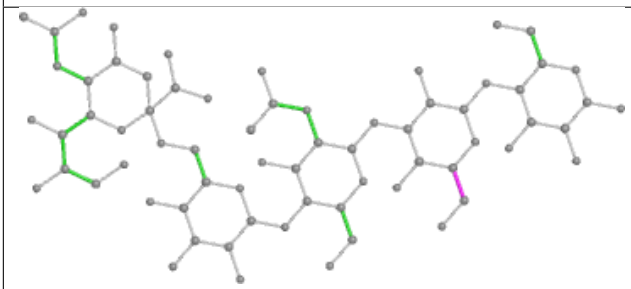
Oligosaccharide Chain J



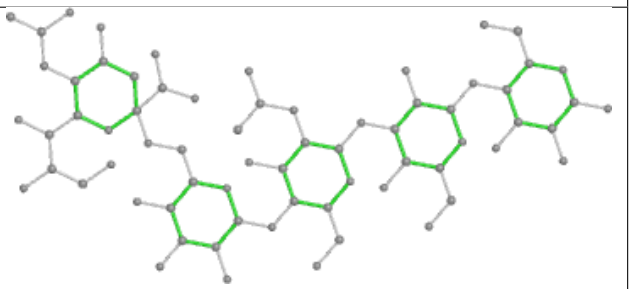
Bond lengths



Bond angles

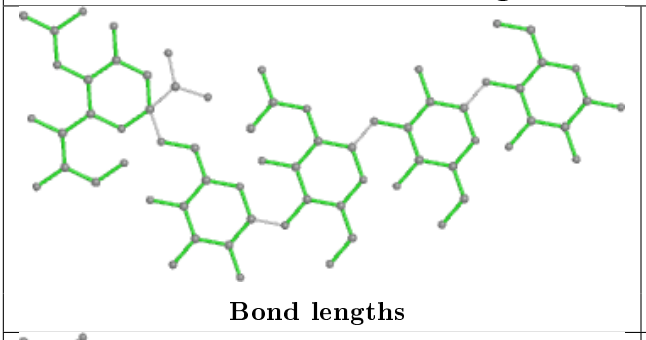


Torsions

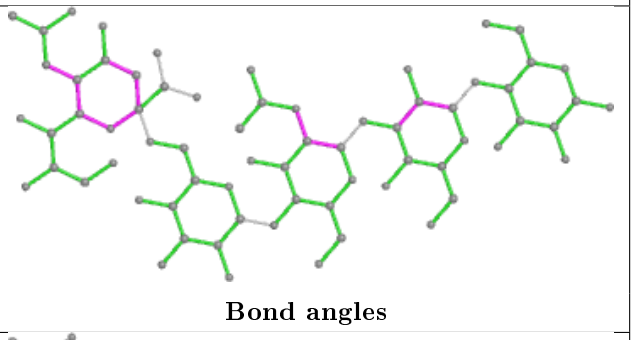


Rings

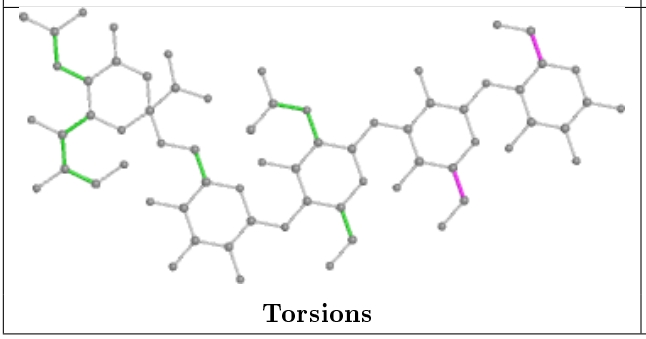
Oligosaccharide Chain R



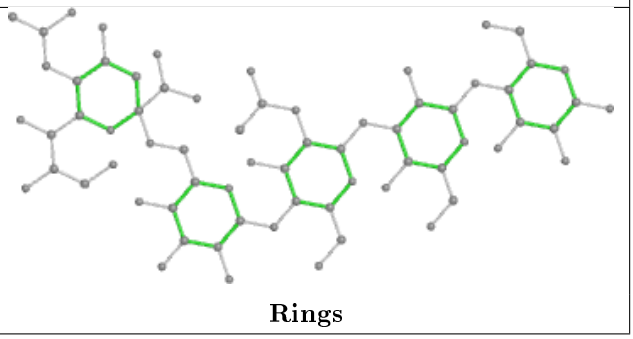
Bond lengths



Bond angles

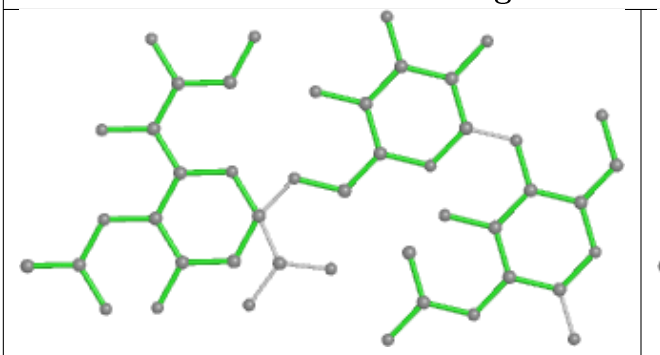


Torsions

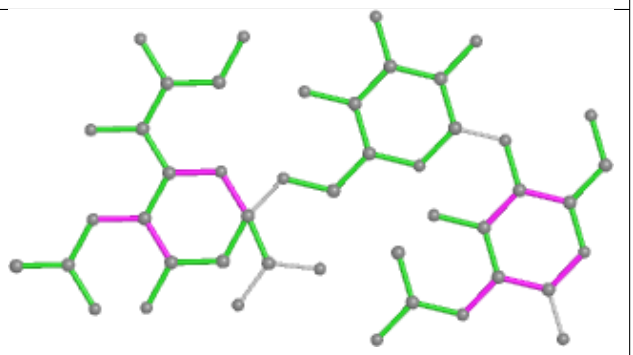


Rings

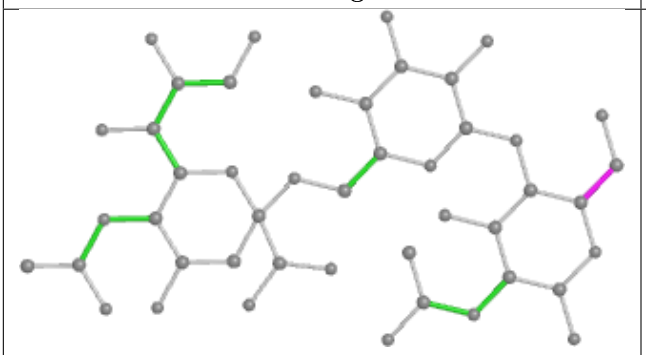
Oligosaccharide Chain O



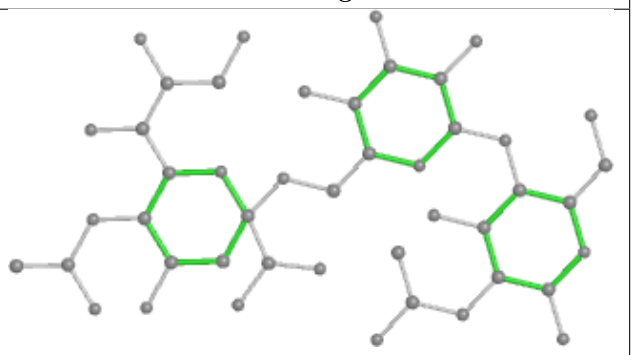
Bond lengths



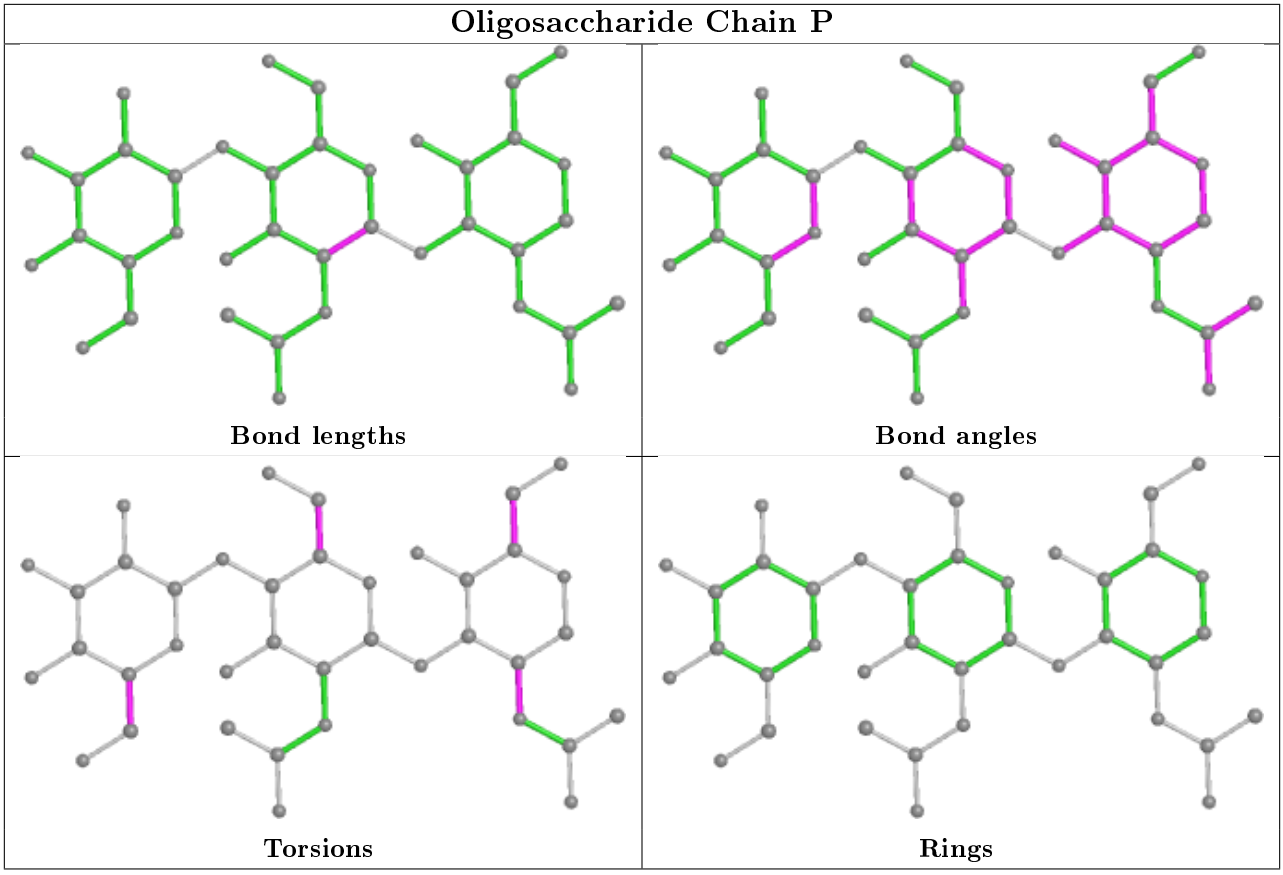
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

18 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	$\#\|Z\| > 2$
10	FLC	B	1176	-	3,12,12	0.77	0	3,17,17	2.26	2 (66%)
10	FLC	F	1175	-	3,12,12	0.69	0	3,17,17	1.41	1 (33%)
9	NAG	A	1326	1	14,14,15	0.66	0	17,19,21	1.41	3 (17%)
9	NAG	C	1328	1	14,14,15	0.56	0	17,19,21	1.39	1 (5%)
10	FLC	E	1337	-	3,12,12	0.23	0	3,17,17	0.94	0
10	FLC	A	1339	-	3,12,12	0.80	0	3,17,17	2.75	1 (33%)
10	FLC	E	1336	-	3,12,12	0.58	0	3,17,17	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
10	FLC	C	1340	-	3,12,12	0.79	0	3,17,17	1.62	1 (33%)
10	FLC	B	1177	-	3,12,12	0.58	0	3,17,17	1.28	1 (33%)
10	FLC	C	1339	-	3,12,12	0.15	0	3,17,17	0.75	0
10	FLC	B	1178	-	3,12,12	0.82	0	3,17,17	1.36	1 (33%)
9	NAG	E	1327	1	14,14,15	0.46	0	17,19,21	1.79	2 (11%)
10	FLC	C	1338	-	3,12,12	0.59	0	3,17,17	1.13	0
10	FLC	A	1338	-	3,12,12	0.74	0	3,17,17	1.31	0
10	FLC	D	1174	-	3,12,12	0.38	0	3,17,17	1.21	1 (33%)
9	NAG	F	1174	2	14,14,15	0.51	0	17,19,21	0.92	1 (5%)
9	NAG	D	1173	2	14,14,15	0.50	0	17,19,21	0.95	1 (5%)
10	FLC	E	1335	-	3,12,12	0.42	0	3,17,17	1.13	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
10	FLC	B	1176	-	-	3/6/16/16	-
10	FLC	F	1175	-	-	0/6/16/16	-
9	NAG	A	1326	1	-	0/6/23/26	0/1/1/1
9	NAG	C	1328	1	-	0/6/23/26	0/1/1/1
10	FLC	E	1337	-	-	3/6/16/16	-
10	FLC	A	1339	-	-	5/6/16/16	-
10	FLC	E	1336	-	-	1/6/16/16	-
10	FLC	C	1340	-	-	1/6/16/16	-
10	FLC	B	1177	-	-	0/6/16/16	-
10	FLC	C	1339	-	-	3/6/16/16	-
10	FLC	B	1178	-	-	3/6/16/16	-
9	NAG	E	1327	1	-	2/6/23/26	0/1/1/1
10	FLC	C	1338	-	-	0/6/16/16	-
10	FLC	A	1338	-	-	5/6/16/16	-
10	FLC	D	1174	-	-	0/6/16/16	-
9	NAG	F	1174	2	-	0/6/23/26	0/1/1/1
9	NAG	D	1173	2	-	0/6/23/26	0/1/1/1
10	FLC	E	1335	-	-	4/6/16/16	-

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	E	1327	NAG	C1-O5-C5	6.58	121.10	112.19
9	C	1328	NAG	C1-O5-C5	4.67	118.53	112.19
10	A	1339	FLC	CG-CB-CA	4.21	120.58	109.33
9	A	1326	NAG	C4-C3-C2	3.10	115.56	111.02
10	B	1176	FLC	CB-CG-CGC	-3.04	110.11	114.98

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	1176	FLC	CAC-CA-CB-CBC
10	B	1176	FLC	CAC-CA-CB-CG
10	B	1176	FLC	CAC-CA-CB-OHB
10	E	1337	FLC	CAC-CA-CB-CBC
10	E	1337	FLC	CAC-CA-CB-OHB

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	1176	FLC	1	0
10	B	1177	FLC	2	0
10	B	1178	FLC	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

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	317/328 (96%)	0.73	5 (1%)	72 70	27, 42, 67, 88	0
1	C	320/328 (97%)	0.81	11 (3%)	45 39	27, 47, 76, 95	0
1	E	318/328 (96%)	0.71	4 (1%)	77 76	27, 40, 61, 90	0
2	B	173/175 (98%)	0.67	5 (2%)	51 47	26, 42, 74, 104	0
2	D	172/175 (98%)	0.59	4 (2%)	60 57	24, 38, 62, 150	0
2	F	173/175 (98%)	0.65	2 (1%)	79 78	23, 40, 62, 104	0
All	All	1473/1509 (97%)	0.71	31 (2%)	63 60	23, 42, 71, 150	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	173	ILE	4.1
2	F	173	ILE	3.2
1	E	222	TRP	3.2
2	F	57	GLU	3.1
1	C	248	ASN	2.9

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

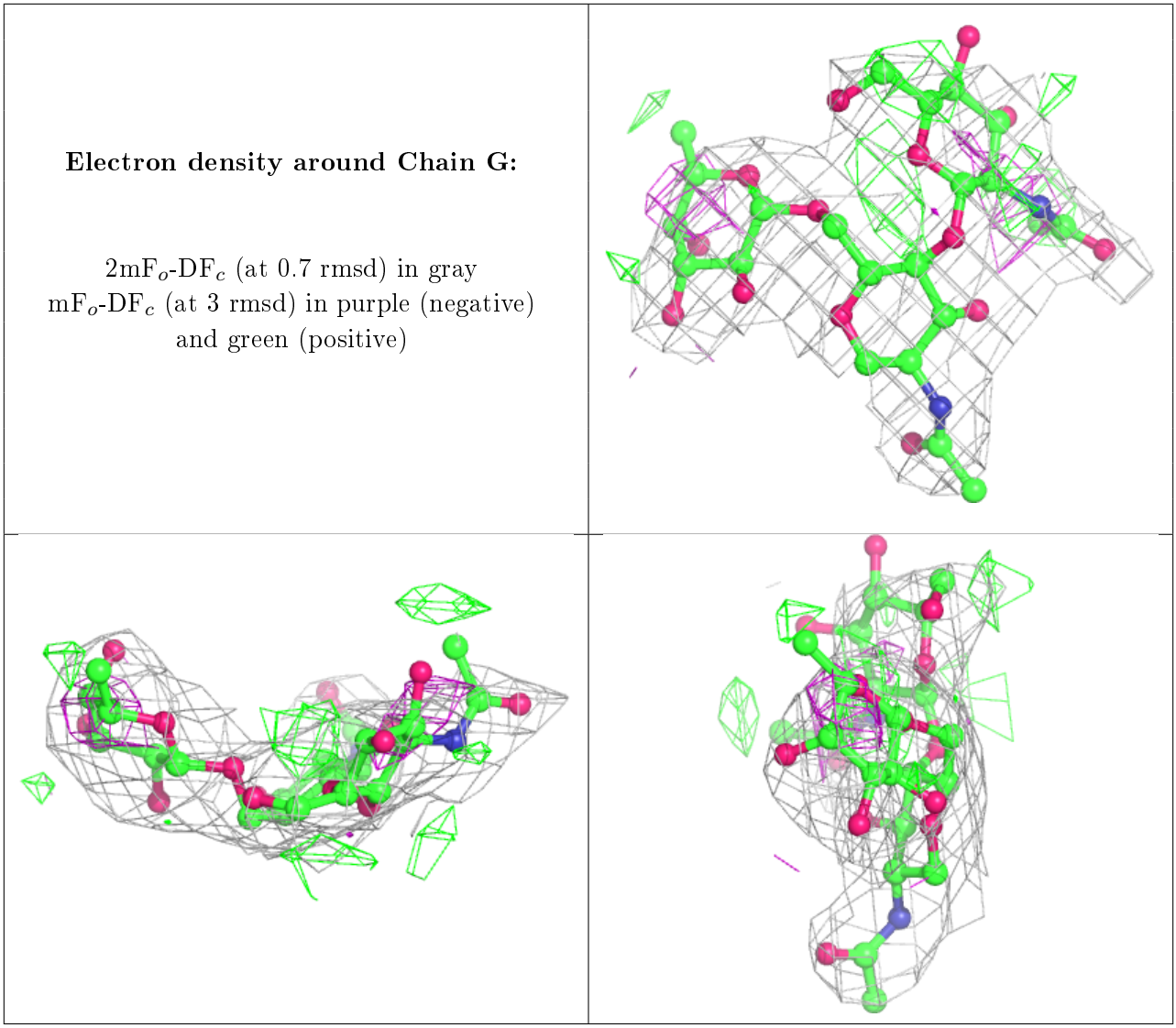
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
8	BMA	P	3	11/12	0.71	0.20	92,102,107,111	0
6	BGC	R	1	12/12	0.74	0.34	142,152,158,159	0
3	NAG	G	2	14/15	0.75	0.33	92,104,114,116	0
5	NAG	L	2	14/15	0.75	0.35	109,116,121,122	0
6	GAL	R	2	11/12	0.79	0.40	134,143,152,152	0
7	NAG	O	2	14/15	0.81	0.54	139,149,153,153	0
6	GAL	J	2	11/12	0.81	0.44	124,133,137,139	0
5	NAG	I	2	14/15	0.81	0.39	78,98,104,105	0
6	BGC	J	1	12/12	0.81	0.39	122,130,135,137	0
5	NAG	Q	2	14/15	0.82	0.34	82,94,102,103	0
7	GAL	O	1	1/12	0.82	0.67	144,144,144,144	0
6	NAG	R	3	14/15	0.85	0.37	98,108,117,122	0
8	NAG	P	1	14/15	0.85	0.28	47,58,67,71	0
5	NAG	N	2	14/15	0.86	0.26	75,85,92,92	0
4	BMA	H	3	11/12	0.87	0.13	75,78,80,80	0
5	NAG	L	1	14/15	0.88	0.21	64,71,82,99	0
3	FUL	G	3	10/11	0.88	0.26	73,82,87,89	0
5	NAG	K	2	14/15	0.89	0.29	85,98,101,101	0
7	GAL	O	3	11/12	0.90	0.28	101,130,138,141	0
4	BMA	M	3	11/12	0.91	0.16	81,85,88,89	0
6	NAG	J	3	14/15	0.92	0.27	96,104,111,113	0
5	NAG	K	1	14/15	0.93	0.19	68,75,85,95	0
8	NAG	P	2	14/15	0.94	0.22	60,73,80,90	0
7	SIA	O	4	20/21	0.94	0.32	68,86,90,91	0
5	NAG	N	1	14/15	0.94	0.22	50,57,62,72	0
3	NAG	G	1	14/15	0.94	0.23	50,61,77,86	0
6	GAL	R	4	11/12	0.94	0.21	61,83,91,92	0
5	NAG	Q	1	14/15	0.94	0.29	55,63,74,84	0
5	NAG	I	1	14/15	0.95	0.23	52,58,69,80	0
4	NAG	H	2	14/15	0.95	0.26	52,57,60,69	0
4	NAG	M	1	14/15	0.96	0.28	47,53,63,69	0
4	NAG	M	2	14/15	0.96	0.31	58,61,70,74	0
6	GAL	J	4	11/12	0.96	0.20	64,81,87,88	0
4	NAG	H	1	14/15	0.96	0.23	50,51,59,61	0
6	SIA	R	5	20/21	0.97	0.23	44,50,55,55	0
6	SIA	J	5	20/21	0.98	0.25	48,56,59,60	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.

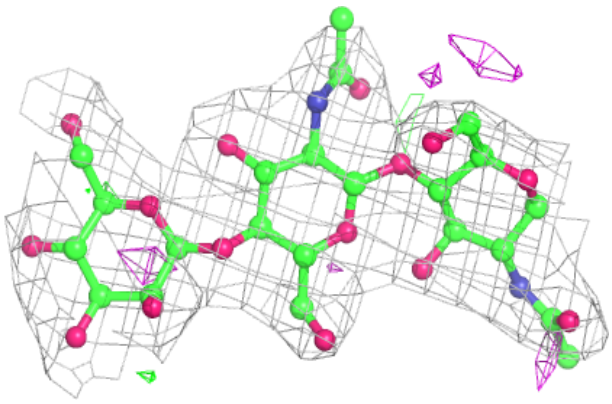
Electron density around Chain G:

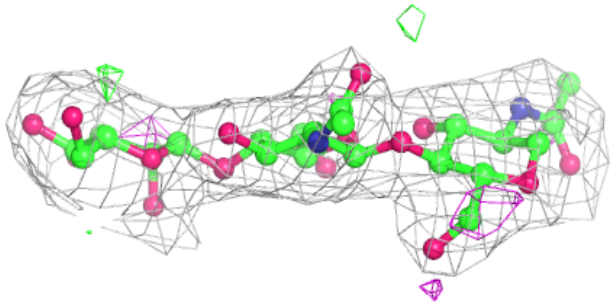
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

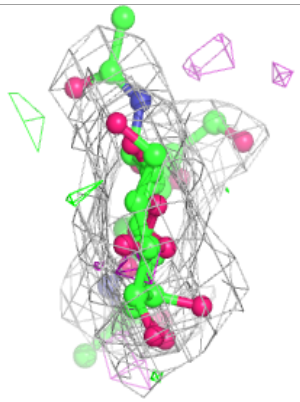


Electron density around Chain H:

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

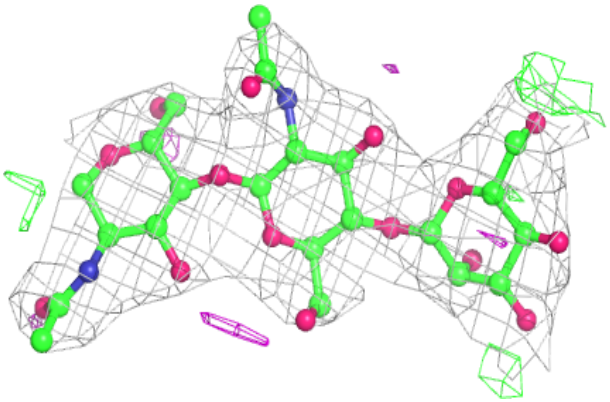


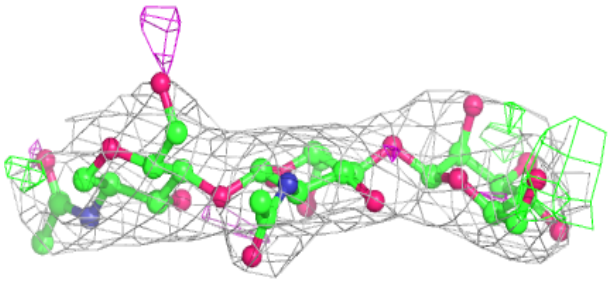


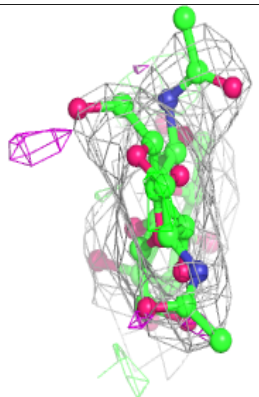


Electron density around Chain M:

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

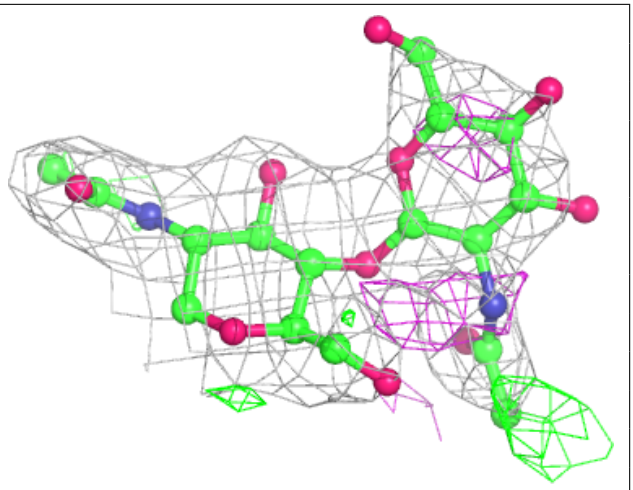


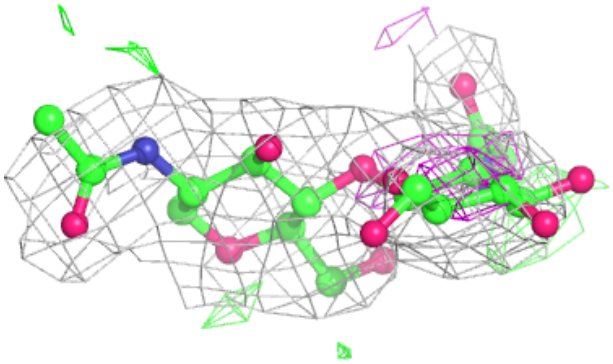


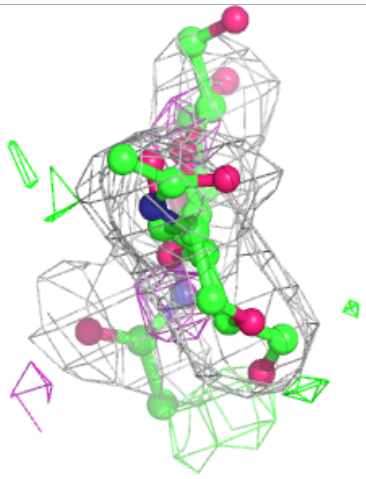


Electron density around Chain I:

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

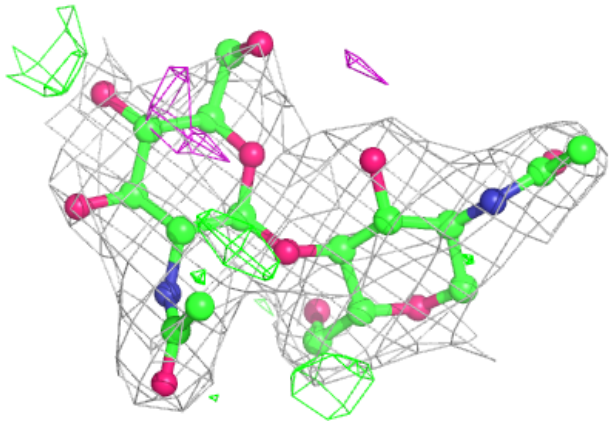


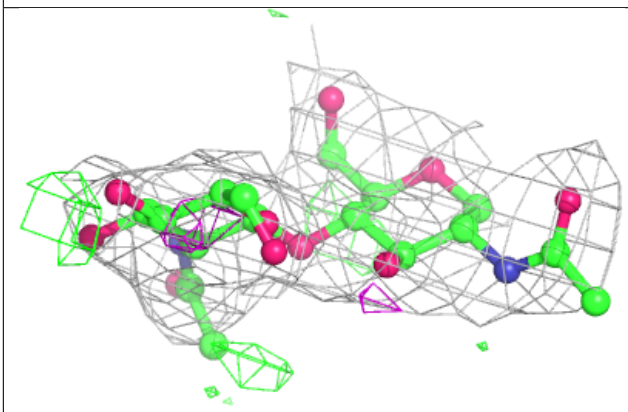




Electron density around Chain K:

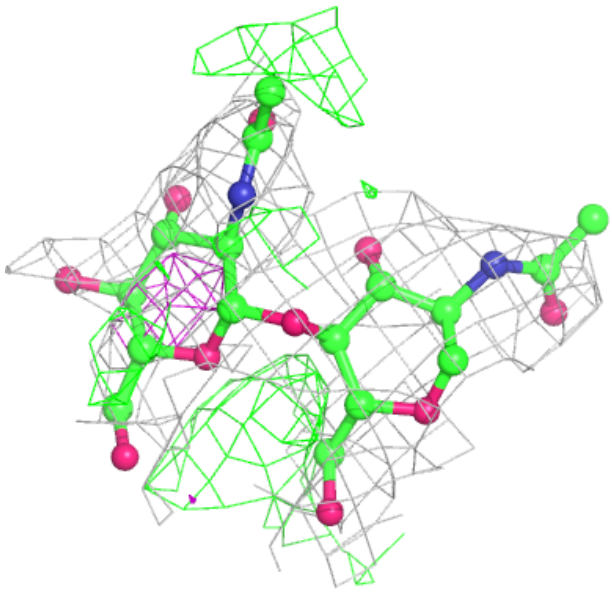
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

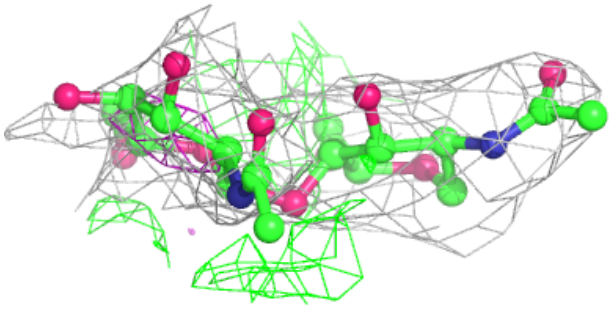




Electron density around Chain L:

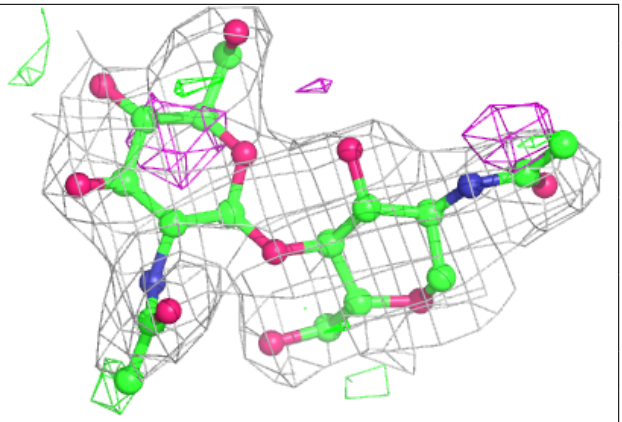
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

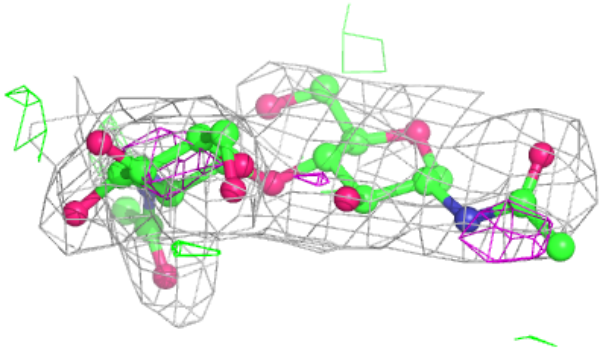


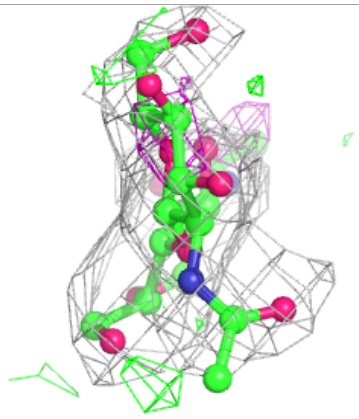


Electron density around Chain N:

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

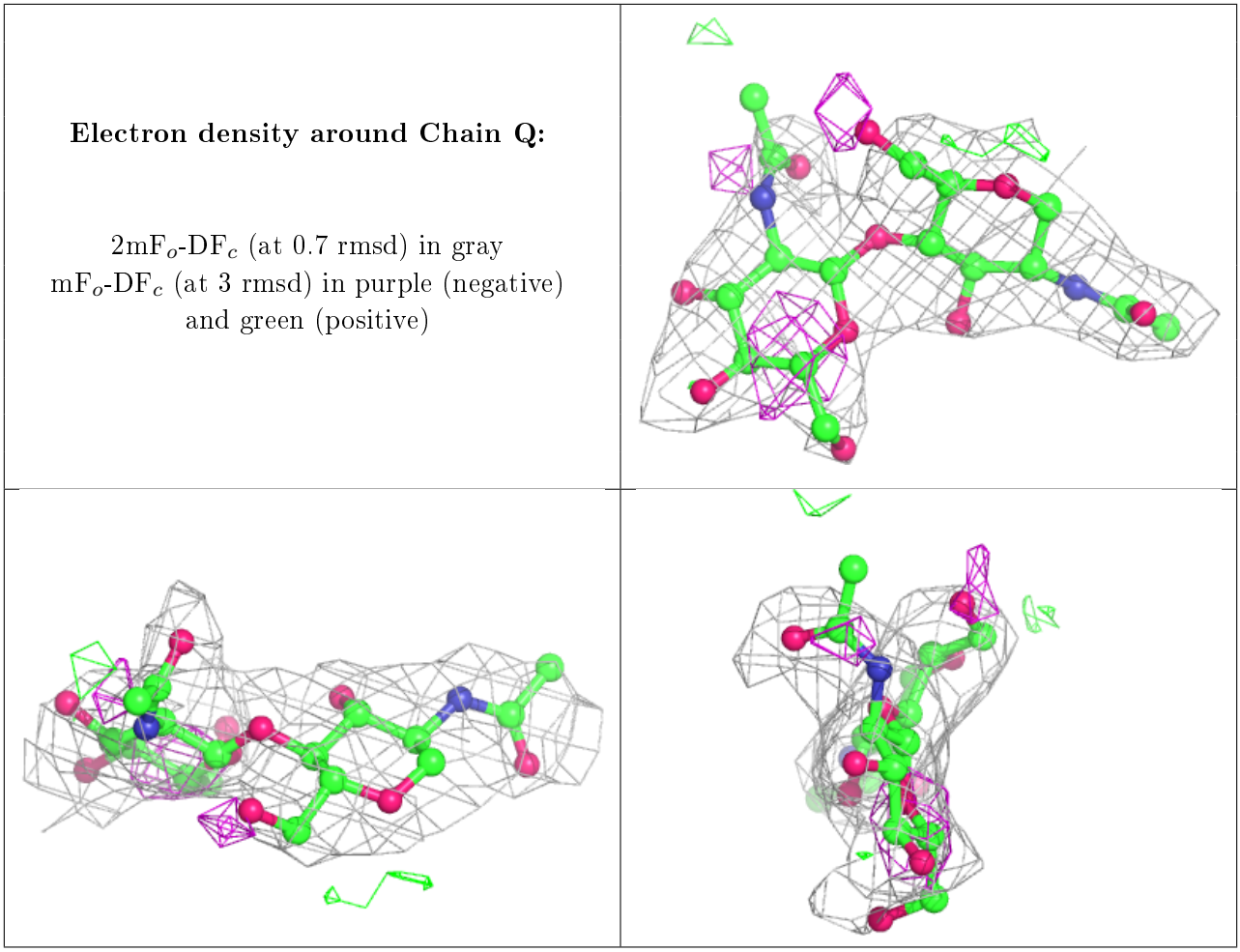






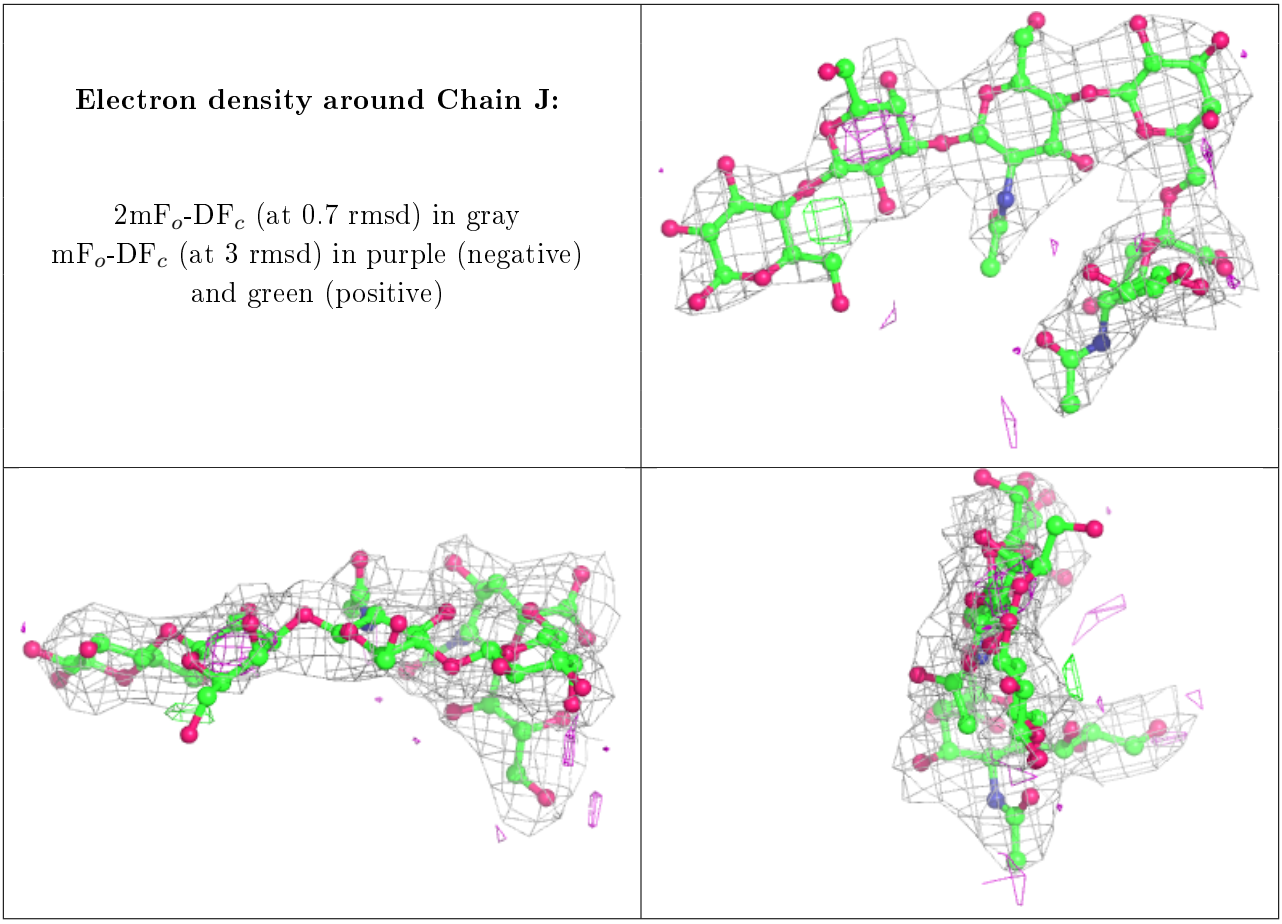
Electron density around Chain Q:

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



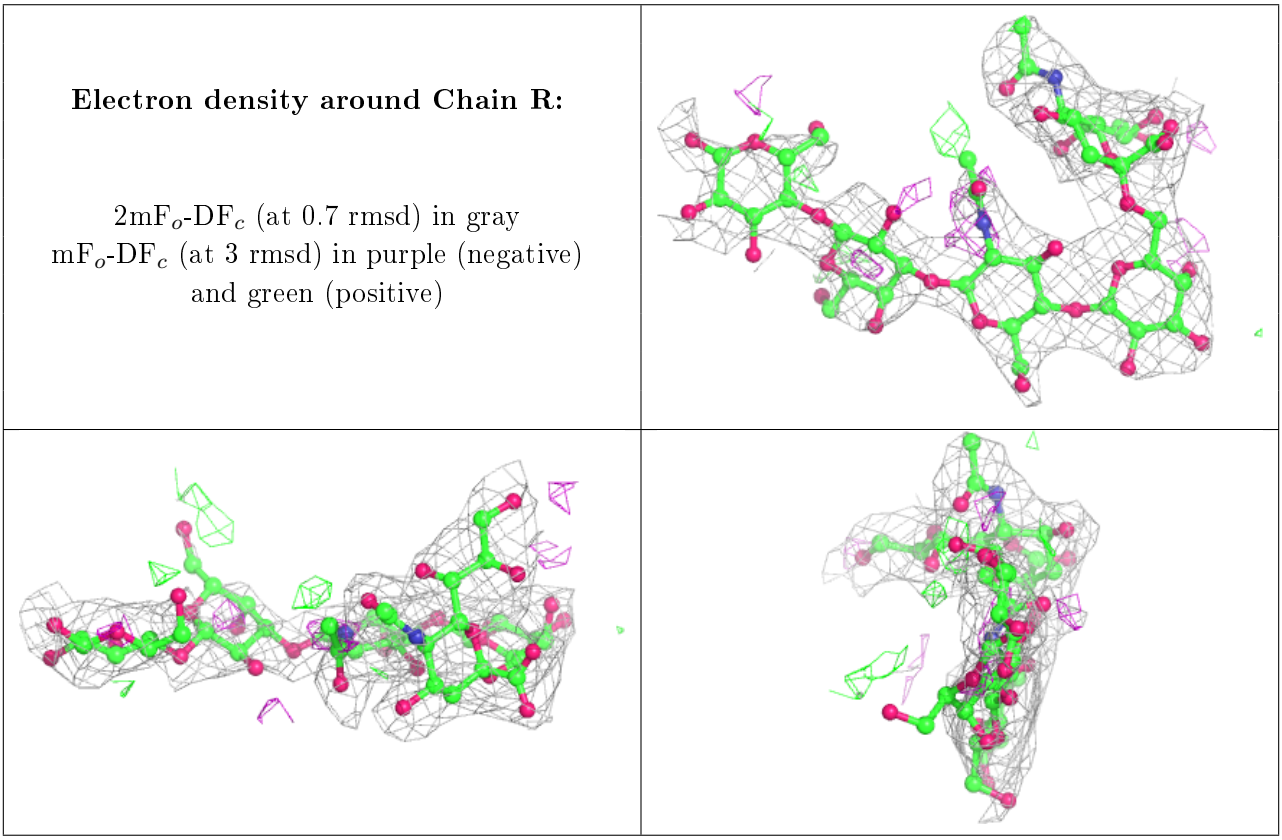
Electron density around Chain J:

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



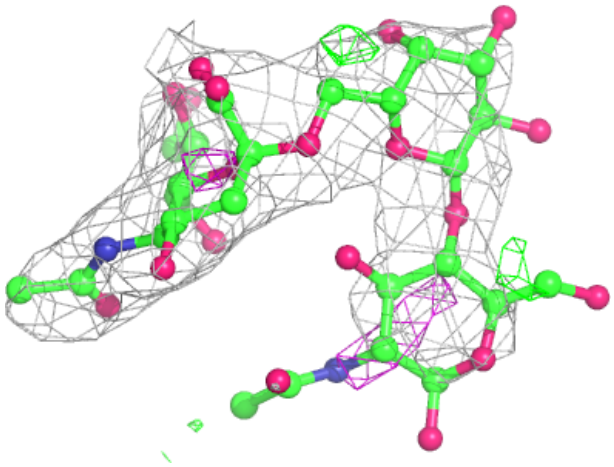
Electron density around Chain R:

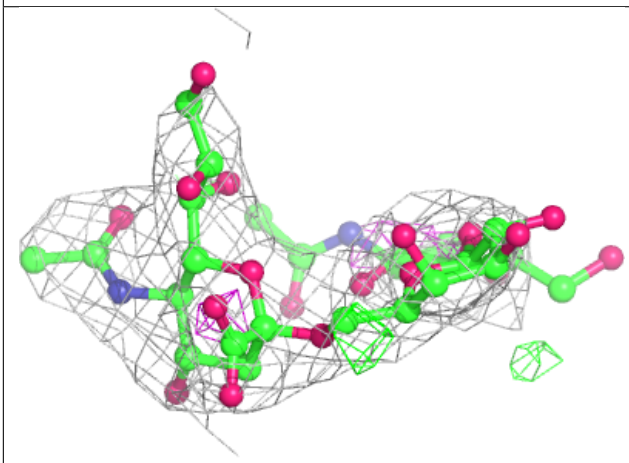
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

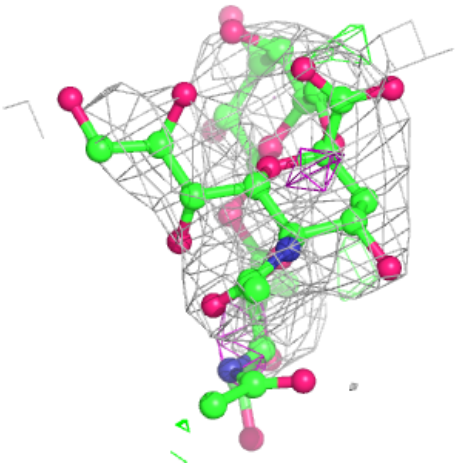


Electron density around Chain O:

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

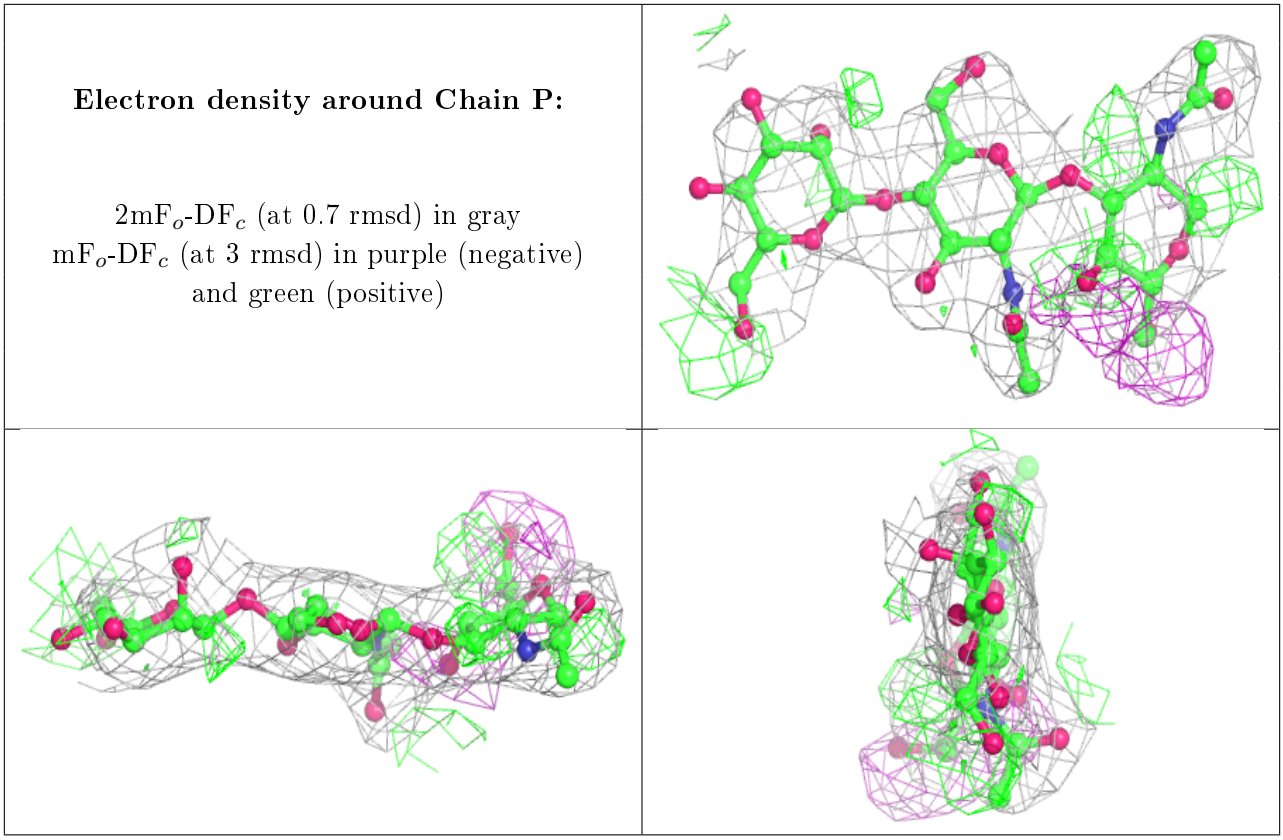






Electron density around Chain P:

$2mF_o$-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
10	FLC	A	1339	13/13	0.56	0.54	101,112,118,126	0
10	FLC	E	1336	13/13	0.66	0.50	82,96,107,108	0
9	NAG	A	1326	14/15	0.71	0.31	70,84,89,91	0
10	FLC	B	1177	13/13	0.77	0.45	60,68,74,75	0
10	FLC	E	1337	13/13	0.79	0.52	94,100,104,110	0
10	FLC	B	1176	13/13	0.79	0.45	48,60,69,70	0
10	FLC	E	1335	13/13	0.80	0.25	71,100,107,107	0
10	FLC	B	1178	13/13	0.81	0.52	71,82,92,94	0
9	NAG	C	1328	14/15	0.81	0.30	68,75,80,82	0
10	FLC	A	1338	13/13	0.82	0.34	75,99,105,105	0
10	FLC	C	1339	13/13	0.82	0.45	60,76,83,84	0
10	FLC	C	1340	13/13	0.84	0.44	84,91,96,99	0
10	FLC	D	1174	13/13	0.86	0.48	53,58,67,68	0
9	NAG	F	1174	14/15	0.87	0.29	58,65,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
10	FLC	C	1338	13/13	0.90	0.26	60,76,88,90	0
9	NAG	E	1327	14/15	0.91	0.15	46,53,56,56	0
10	FLC	F	1175	13/13	0.93	0.28	77,81,83,83	0
9	NAG	D	1173	14/15	0.94	0.25	71,84,87,89	0

6.5 Other polymers (i)

There are no such residues in this entry.