wwPDB X-ray Structure Validation Summary Report (i)

Sep 6, 2023 – 09:09 PM EDT

PDB ID	:	4GDI
Title	:	A subtype N10 neuraminidase-like protein of A/little yellow-shouldered bat/ Guatemala/164/2009
Authors	:	Zhu, X.; Wilson, I.A.
Deposited on	:	2012-07-31
Resolution	:	1.95 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 (1)) were used in the production of this report:

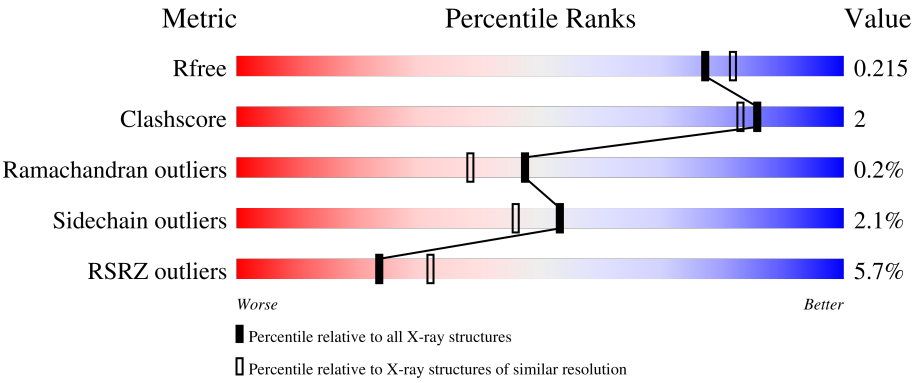
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	373	3% 93% 5% ·
1	B	373	6% 92% 6% ·
1	C	373	10% 87% 11% ··
1	D	373	7% 91% 7% ··
1	E	373	6% 89% 9% ··

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Mol	Chain	Length	Quality of chain
1	F	373	2% 94%
2	G	5	60% 40%
3	H	6	17% 67% 17%
4	I	4	75% 25%
4	K	4	25% 75%
4	M	4	50% 50%
5	J	3	100%
6	L	2	100%
7	N	3	67% 33%

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
3	MAN	H	4	-	-	-	X
7	FUL	N	2	-	-	-	X
7	NAG	N	3	-	-	-	X

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 36150 atoms, of which 16780 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 Neuraminidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	367	Total	C	H	N	O	S	0	0	0
			5654	1816	2778	489	551	20			
1	B	367	Total	C	H	N	O	S	0	0	0
			5654	1816	2778	489	551	20			
1	C	367	Total	C	H	N	O	S	0	0	0
			5654	1816	2778	489	551	20			
1	D	367	Total	C	H	N	O	S	0	0	0
			5654	1816	2778	489	551	20			
1	E	367	Total	C	H	N	O	S	0	0	0
			5654	1816	2778	489	551	20			
1	F	367	Total	C	H	N	O	S	0	0	0
			5654	1816	2778	489	551	20			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	GLY	-	expression tag	UNP H6QM85
A	78	SER	-	expression tag	UNP H6QM85
A	79	PRO	-	expression tag	UNP H6QM85
A	80	SER	-	expression tag	UNP H6QM85
A	81	ARG	-	expression tag	UNP H6QM85
B	77	GLY	-	expression tag	UNP H6QM85
B	78	SER	-	expression tag	UNP H6QM85
B	79	PRO	-	expression tag	UNP H6QM85
B	80	SER	-	expression tag	UNP H6QM85
B	81	ARG	-	expression tag	UNP H6QM85
C	77	GLY	-	expression tag	UNP H6QM85
C	78	SER	-	expression tag	UNP H6QM85
C	79	PRO	-	expression tag	UNP H6QM85
C	80	SER	-	expression tag	UNP H6QM85
C	81	ARG	-	expression tag	UNP H6QM85
D	77	GLY	-	expression tag	UNP H6QM85
D	78	SER	-	expression tag	UNP H6QM85

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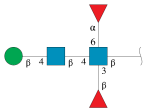
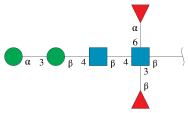
Chain	Residue	Modelled	Actual	Comment	Reference
D	79	PRO	-	expression tag	UNP H6QM85
D	80	SER	-	expression tag	UNP H6QM85
D	81	ARG	-	expression tag	UNP H6QM85
E	77	GLY	-	expression tag	UNP H6QM85
E	78	SER	-	expression tag	UNP H6QM85
E	79	PRO	-	expression tag	UNP H6QM85
E	80	SER	-	expression tag	UNP H6QM85
E	81	ARG	-	expression tag	UNP H6QM85
F	77	GLY	-	expression tag	UNP H6QM85
F	78	SER	-	expression tag	UNP H6QM85
F	79	PRO	-	expression tag	UNP H6QM85
F	80	SER	-	expression tag	UNP H6QM85
F	81	ARG	-	expression tag	UNP H6QM85

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



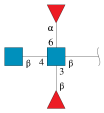
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	G	5	59	34	2	23	0	0	0

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



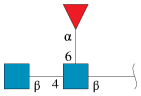
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	H	6	70	40	2	28	0	0	0

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	I	4	Total C N O 48 28 2 18	0	0	0
4	K	4	Total C N O 48 28 2 18	0	0	0
4	M	4	Total C N O 48 28 2 18	0	0	0

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.

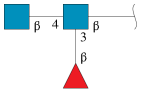


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
5	J	3	Total C N O 38 22 2 14	0	0	0

- Molecule 6 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.

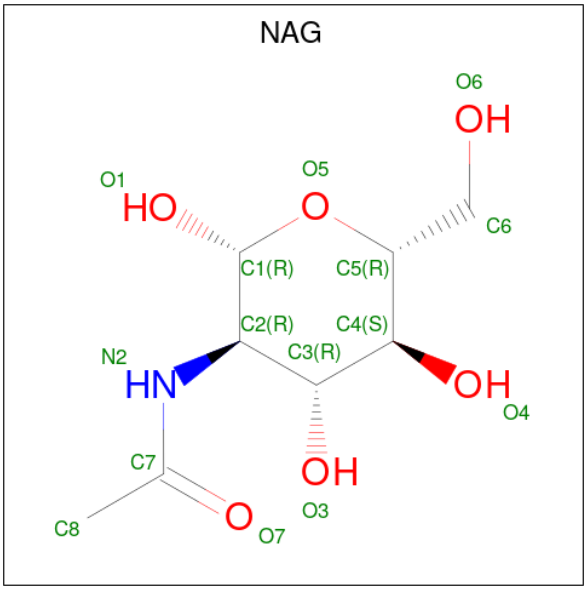
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
6	L	2	Total C N O 24 14 1 9	0	0	0

- Molecule 7 is an oligosaccharide called beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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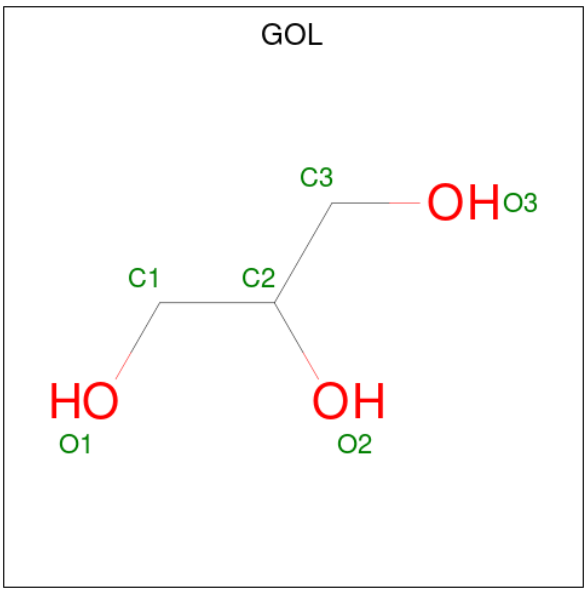
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	E	1	Total C N O 14 8 1 5	0	0
8	F	1	Total C N O 14 8 1 5	0	0
8	F	1	Total C N O 14 8 1 5	0	0

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

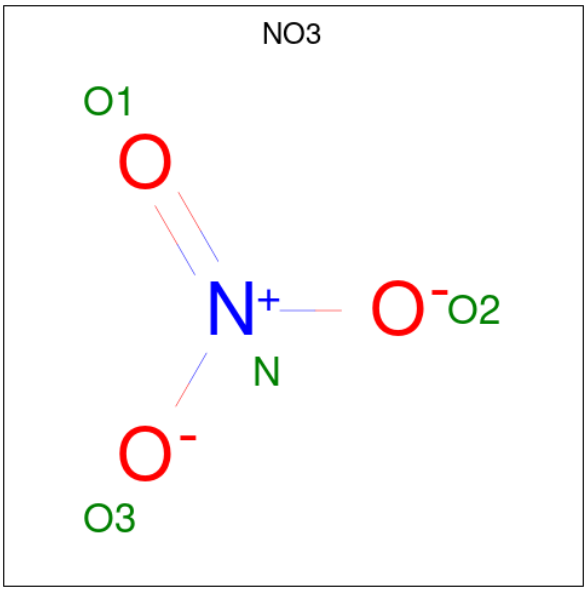
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total Ca 1 1	0	0
9	B	2	Total Ca 2 2	0	0
9	C	2	Total Ca 2 2	0	0
9	D	2	Total Ca 2 2	0	0
9	E	2	Total Ca 2 2	0	0
9	F	2	Total Ca 2 2	0	0

- Molecule 10 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	H	O	0	0
			14	3	8	3		
10	A	1	Total	C	H	O	0	0
			14	3	8	3		
10	A	1	Total	C	H	O	0	0
			14	3	8	3		
10	B	1	Total	C	H	O	0	0
			14	3	8	3		
10	B	1	Total	C	H	O	0	0
			14	3	8	3		
10	C	1	Total	C	H	O	0	0
			14	3	8	3		
10	D	1	Total	C	H	O	0	0
			14	3	8	3		
10	E	1	Total	C	H	O	0	0
			14	3	8	3		
10	E	1	Total	C	H	O	0	0
			14	3	8	3		
10	E	1	Total	C	H	O	0	0
			14	3	8	3		
10	F	1	Total	C	H	O	0	0
			14	3	8	3		
10	F	1	Total	C	H	O	0	0
			14	3	8	3		
10	F	1	Total	C	H	O	0	0
			14	3	8	3		
10	F	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 11 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	1	Total N O 4 1 3	0	0
11	A	1	Total N O 4 1 3	0	0
11	B	1	Total N O 4 1 3	0	0
11	B	1	Total N O 4 1 3	0	0
11	B	1	Total N O 4 1 3	0	0
11	B	1	Total N O 4 1 3	0	0
11	B	1	Total N O 4 1 3	0	0
11	C	1	Total N O 4 1 3	0	0
11	C	1	Total N O 4 1 3	0	0
11	D	1	Total N O 4 1 3	0	0
11	D	1	Total N O 4 1 3	0	0
11	F	1	Total N O 4 1 3	0	0
11	F	1	Total N O 4 1 3	0	0
11	F	1	Total N O 4 1 3	0	0

- Molecule 12 is water.

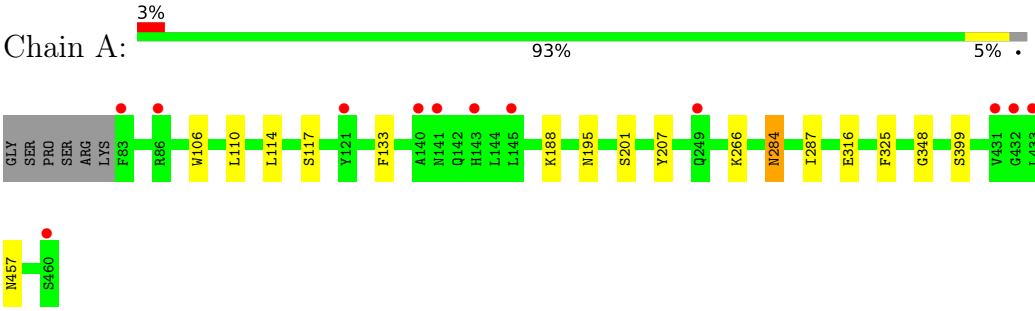
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	247	Total O 247 247	0	0
12	B	246	Total O 246 246	0	0
12	C	176	Total O 176 176	0	0
12	D	213	Total O 213 213	0	0
12	E	207	Total O 207 207	0	0
12	F	319	Total O 319 319	0	0

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.

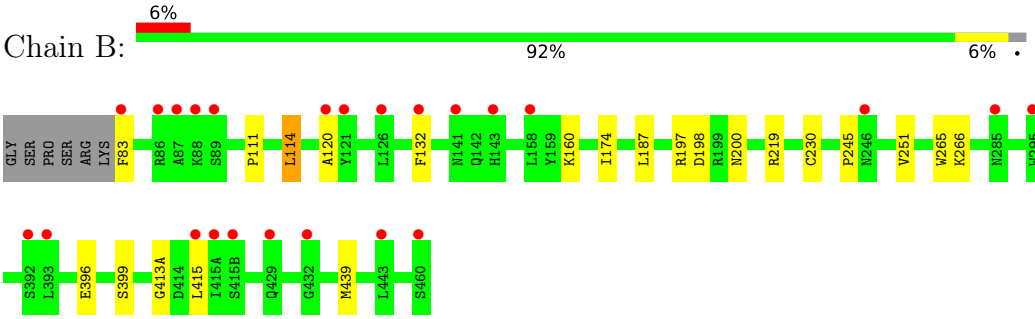
- Molecule 1: Neuraminidase

Chain A:



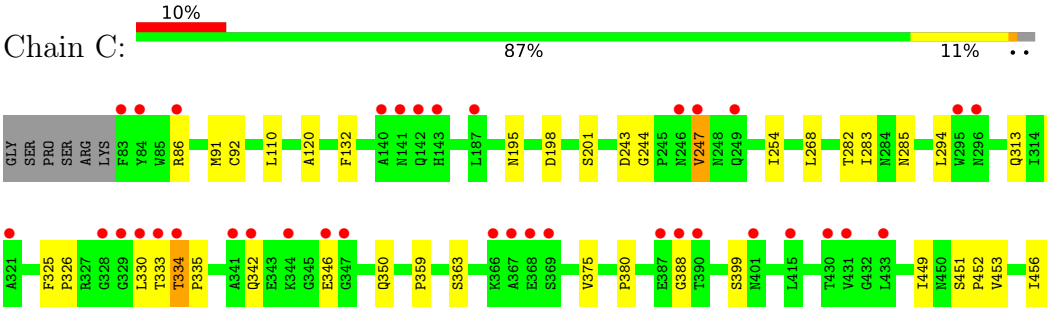
- Molecule 1: Neuraminidase

Chain B:



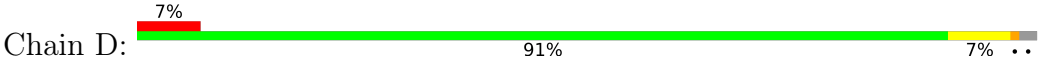
- Molecule 1: Neuraminidase

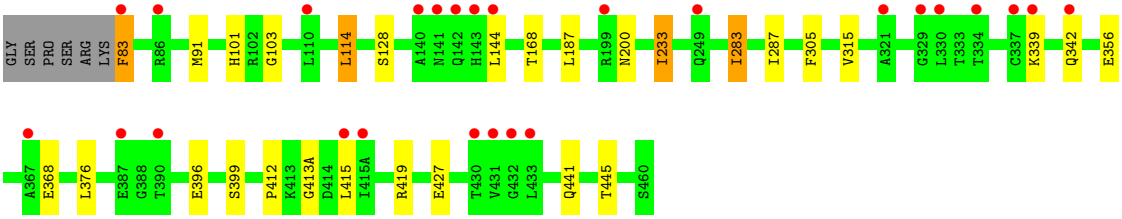
Chain C:



- Molecule 1: Neuraminidase

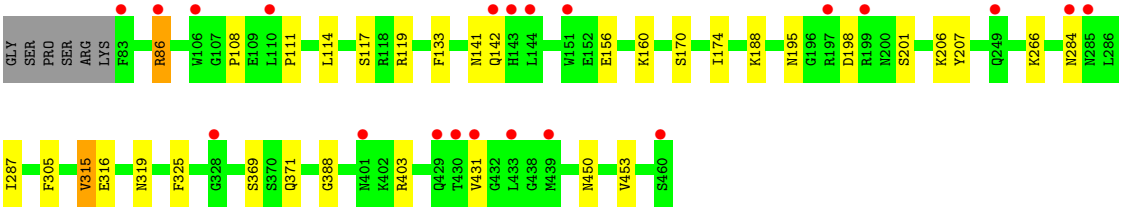
Chain D:





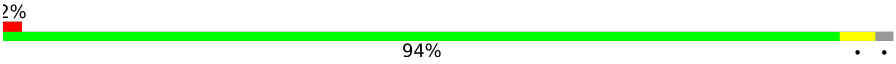
• Molecule 1: Neuraminidase

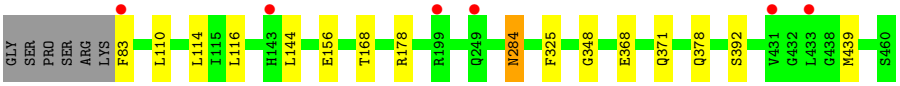
Chain E:



• Molecule 1: Neuraminidase

Chain F:



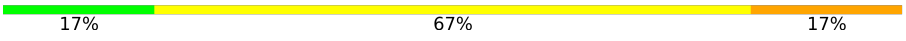


• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:

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

Chain H:

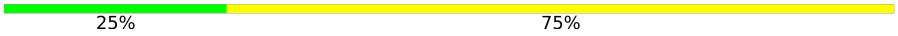


• Molecule 4: beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:

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

Chain K:



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

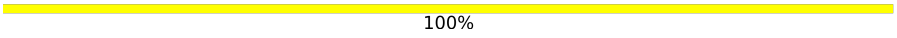
Chain M:

• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:

• Molecule 6: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:



• Molecule 7: beta-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α, β, γ	176.32Å 176.32Å 193.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.11 – 1.95 40.11 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.6 (40.11-1.95) 98.6 (40.11-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	1.70 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.180 , 0.223 0.172 , 0.215	Depositor DCC
R_{free} test set	10567 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	31.8	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 52.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -h,k,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	36150	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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: FUL, NAG, BMA, MAN, FUC, GOL, CA, NO3

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	0.39	0/2945	0.58	0/3990
1	B	0.40	0/2945	0.58	0/3990
1	C	0.35	0/2945	0.55	0/3990
1	D	0.37	0/2945	0.55	0/3990
1	E	0.37	0/2945	0.56	0/3990
1	F	0.42	0/2945	0.59	0/3990
All	All	0.39	0/17670	0.57	0/23940

There are no bond length outliers.

There are no bond angle outliers.

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	2876	2778	2775	9	0
1	B	2876	2778	2776	12	0
1	C	2876	2778	2776	19	0
1	D	2876	2778	2776	15	0
1	E	2876	2778	2775	14	0
1	F	2876	2778	2775	8	0
2	G	59	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	70	0	61	1	0
4	I	48	0	43	0	0
4	K	48	0	43	0	0
4	M	48	0	43	0	0
5	J	38	0	34	0	0
6	L	24	0	22	0	0
7	N	38	0	34	0	0
8	A	42	0	39	0	0
8	B	28	0	26	0	0
8	C	28	0	26	0	0
8	D	28	0	26	0	0
8	E	28	0	26	1	0
8	F	28	0	26	0	0
9	A	1	0	0	0	0
9	B	2	0	0	0	0
9	C	2	0	0	0	0
9	D	2	0	0	0	0
9	E	2	0	0	0	0
9	F	2	0	0	0	0
10	A	18	24	24	2	0
10	B	12	16	16	0	0
10	C	6	8	8	0	0
10	D	6	8	8	1	0
10	E	18	24	24	1	0
10	F	24	32	32	0	0
11	A	8	0	0	1	0
11	B	20	0	0	1	0
11	C	8	0	0	1	0
11	D	8	0	0	0	0
11	F	12	0	0	0	0
12	A	247	0	0	0	0
12	B	246	0	0	1	0
12	C	176	0	0	0	0
12	D	213	0	0	1	0
12	E	207	0	0	1	0
12	F	319	0	0	1	0
All	All	19370	16780	17266	78	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 78 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:451:SER:HB2	1:C:452:PRO:CD	2.29	0.63
1:E:108:PRO:HB2	1:E:431:VAL:HG13	1.82	0.60
1:D:91:MET:HE1	1:D:356:GLU:HG3	1.84	0.59
1:B:396:GLU:OE2	1:B:399:SER:OG	2.19	0.58
1:D:103:GLY:O	10:D:508:GOL:O3	2.21	0.57

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	365/373 (98%)	354 (97%)	10 (3%)	1 (0%)	41 30
1	B	365/373 (98%)	353 (97%)	12 (3%)	0	100 100
1	C	365/373 (98%)	349 (96%)	13 (4%)	3 (1%)	19 9
1	D	365/373 (98%)	353 (97%)	12 (3%)	0	100 100
1	E	365/373 (98%)	351 (96%)	13 (4%)	1 (0%)	41 30
1	F	365/373 (98%)	352 (96%)	13 (4%)	0	100 100
All	All	2190/2238 (98%)	2112 (96%)	73 (3%)	5 (0%)	47 38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	ASN
1	C	198	ASP
1	C	285	ASN
1	E	198	ASP
1	C	335	PRO

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	320/325 (98%)	316 (99%)	4 (1%)	69	65
1	B	320/325 (98%)	314 (98%)	6 (2%)	57	50
1	C	320/325 (98%)	313 (98%)	7 (2%)	52	44
1	D	320/325 (98%)	310 (97%)	10 (3%)	40	28
1	E	320/325 (98%)	311 (97%)	9 (3%)	43	33
1	F	320/325 (98%)	316 (99%)	4 (1%)	69	65
All	All	1920/1950 (98%)	1880 (98%)	40 (2%)	53	46

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	170	SER
1	E	453	VAL
1	E	206	LYS
1	E	315	VAL
1	F	110	LEU

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

Mol	Chain	Res	Type
1	C	143	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)

31 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	NAG	G	1	2,1	14,14,15	0.55	0	17,19,21	1.29	3 (17%)
2	NAG	G	2	2	14,14,15	0.45	0	17,19,21	0.70	0
2	BMA	G	3	2	11,11,12	0.62	0	15,15,17	0.68	0
2	FUL	G	4	2	10,10,11	0.75	0	14,14,16	2.14	4 (28%)
2	FUC	G	5	2	10,10,11	0.67	0	14,14,16	0.82	0
3	NAG	H	1	3,1	14,14,15	0.62	0	17,19,21	1.56	3 (17%)
3	NAG	H	2	3	14,14,15	0.47	0	17,19,21	0.59	0
3	BMA	H	3	3	11,11,12	0.66	0	15,15,17	0.65	0
3	MAN	H	4	3	11,11,12	0.56	0	15,15,17	1.03	1 (6%)
3	FUL	H	5	3	10,10,11	0.82	0	14,14,16	2.68	5 (35%)
3	FUC	H	6	3	10,10,11	0.68	0	14,14,16	1.05	1 (7%)
4	NAG	I	1	4,1	14,14,15	0.65	0	17,19,21	1.24	3 (17%)
4	FUL	I	2	4	10,10,11	0.69	0	14,14,16	0.62	0
4	NAG	I	3	4	14,14,15	0.44	0	17,19,21	0.92	0
4	FUC	I	4	4	10,10,11	0.62	0	14,14,16	0.86	0
5	NAG	J	1	1,5	14,14,15	0.61	0	17,19,21	1.07	0
5	NAG	J	2	5	14,14,15	0.44	0	17,19,21	0.80	0
5	FUC	J	3	5	10,10,11	0.60	0	14,14,16	0.69	0
4	NAG	K	1	4,1	14,14,15	0.56	0	17,19,21	1.07	2 (11%)
4	FUL	K	2	4	10,10,11	0.73	0	14,14,16	2.29	4 (28%)
4	NAG	K	3	4	14,14,15	0.49	0	17,19,21	0.70	0
4	FUC	K	4	4	10,10,11	0.65	0	14,14,16	0.89	1 (7%)
6	NAG	L	1	6,1	14,14,15	0.53	0	17,19,21	1.10	2 (11%)
6	FUC	L	2	6	10,10,11	0.79	0	14,14,16	1.16	1 (7%)
4	NAG	M	1	4,1	14,14,15	0.50	0	17,19,21	1.23	1 (5%)
4	FUL	M	2	4	10,10,11	0.71	0	14,14,16	1.88	3 (21%)
4	NAG	M	3	4	14,14,15	0.52	0	17,19,21	0.90	0
4	FUC	M	4	4	10,10,11	0.70	0	14,14,16	1.04	0
7	NAG	N	1	1,7	14,14,15	0.60	0	17,19,21	1.30	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	FUL	N	2	7	10,10,11	0.70	0	14,14,16	0.56	0
7	NAG	N	3	7	14,14,15	0.49	0	17,19,21	0.85	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
2	NAG	G	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	1/2/19/22	0/1/1/1
2	FUL	G	4	2	-	-	0/1/1/1
2	FUC	G	5	2	-	-	0/1/1/1
3	NAG	H	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	BMA	H	3	3	-	0/2/19/22	1/1/1/1
3	MAN	H	4	3	-	1/2/19/22	1/1/1/1
3	FUL	H	5	3	-	-	0/1/1/1
3	FUC	H	6	3	-	-	0/1/1/1
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	FUL	I	2	4	-	-	0/1/1/1
4	NAG	I	3	4	-	1/6/23/26	0/1/1/1
4	FUC	I	4	4	-	-	0/1/1/1
5	NAG	J	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	J	2	5	-	0/6/23/26	0/1/1/1
5	FUC	J	3	5	-	-	0/1/1/1
4	NAG	K	1	4,1	-	0/6/23/26	0/1/1/1
4	FUL	K	2	4	-	-	0/1/1/1
4	NAG	K	3	4	-	0/6/23/26	0/1/1/1
4	FUC	K	4	4	-	-	0/1/1/1
6	NAG	L	1	6,1	-	2/6/23/26	0/1/1/1
6	FUC	L	2	6	-	-	0/1/1/1
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	FUL	M	2	4	-	-	0/1/1/1
4	NAG	M	3	4	-	0/6/23/26	0/1/1/1
4	FUC	M	4	4	-	-	0/1/1/1
7	NAG	N	1	1,7	-	2/6/23/26	0/1/1/1
7	FUL	N	2	7	-	-	0/1/1/1
7	NAG	N	3	7	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	H	5	FUL	C1-C2-C3	-7.21	100.80	109.67
4	K	2	FUL	C1-C2-C3	-6.17	102.09	109.67
2	G	4	FUL	C1-C2-C3	-5.52	102.88	109.67
4	M	2	FUL	C1-C2-C3	-4.58	104.03	109.67
4	K	2	FUL	O5-C1-C2	-3.76	104.96	110.77

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	1	NAG	C4-C5-C6-O6
6	L	1	NAG	O5-C5-C6-O6
7	N	1	NAG	C8-C7-N2-C2
7	N	3	NAG	C4-C5-C6-O6
2	G	3	BMA	O5-C5-C6-O6

All (2) ring outliers are listed below:

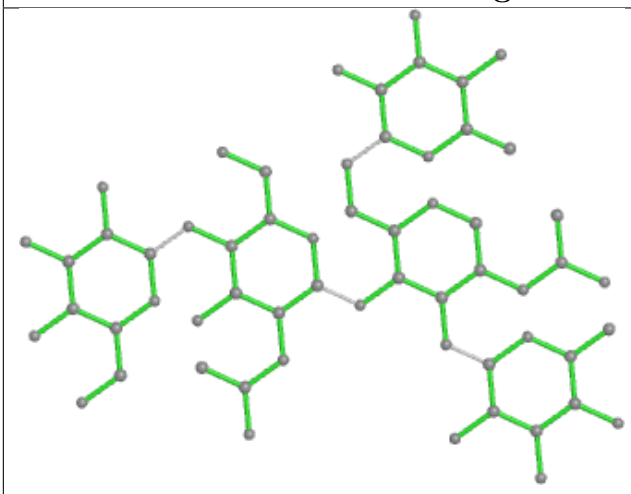
Mol	Chain	Res	Type	Atoms
3	H	3	BMA	C1-C2-C3-C4-C5-O5
3	H	4	MAN	C1-C2-C3-C4-C5-O5

2 monomers are involved in 1 short contact:

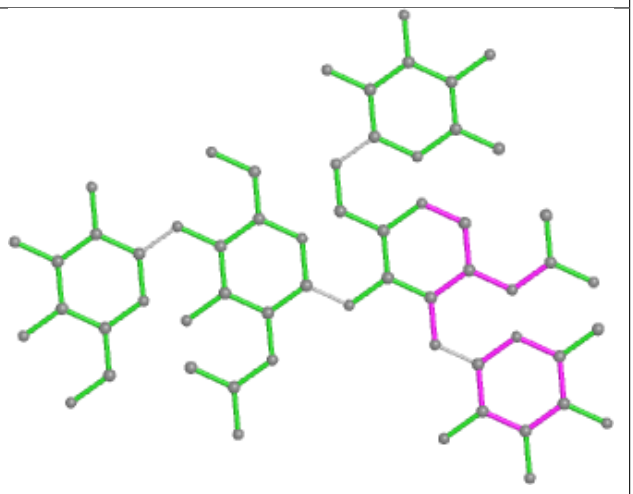
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	4	MAN	1	0
3	H	3	BMA	1	0

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

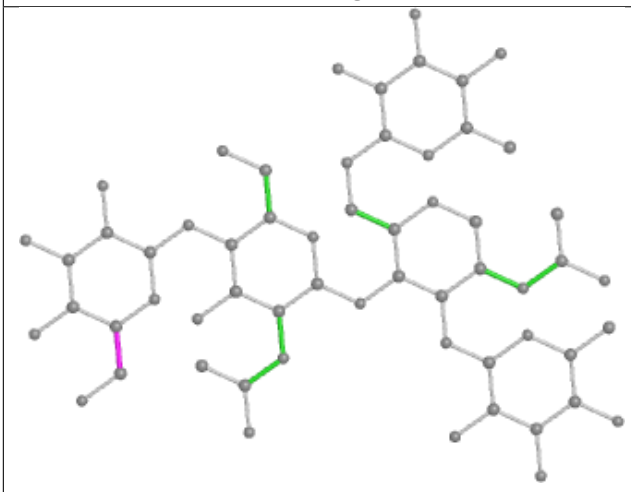
Oligosaccharide Chain G



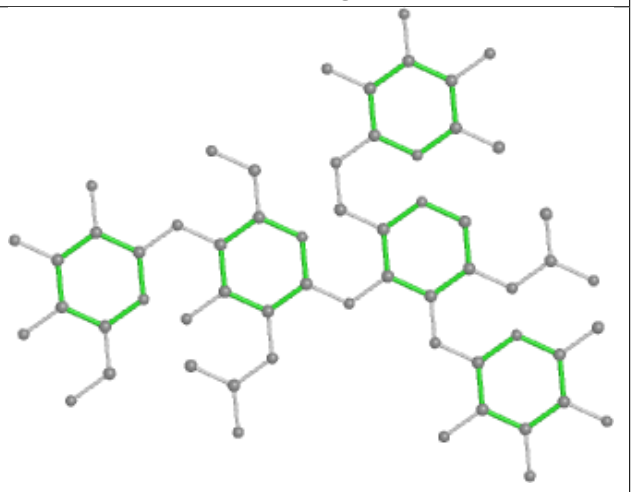
Bond lengths



Bond angles

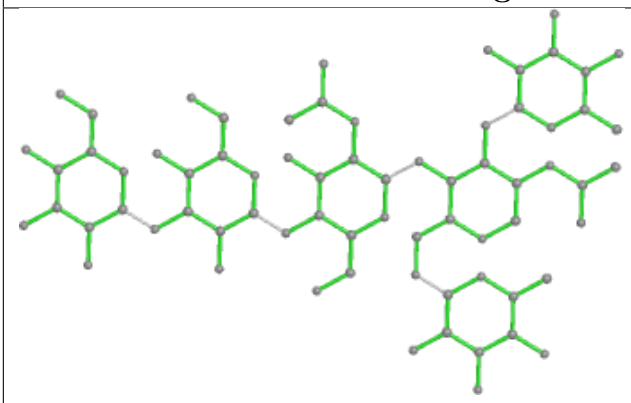


Torsions

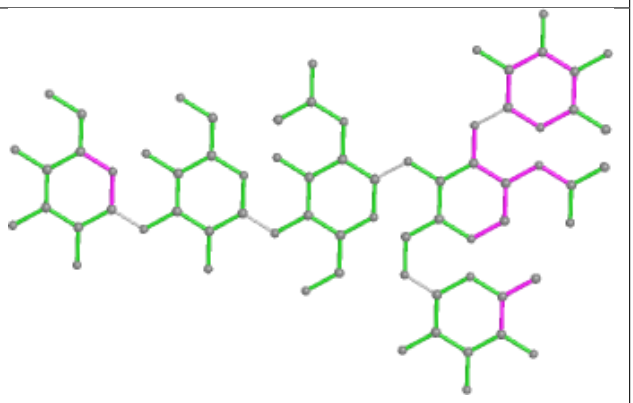


Rings

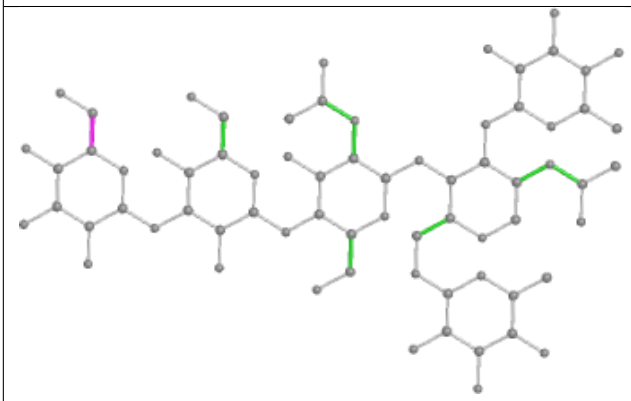
Oligosaccharide Chain H



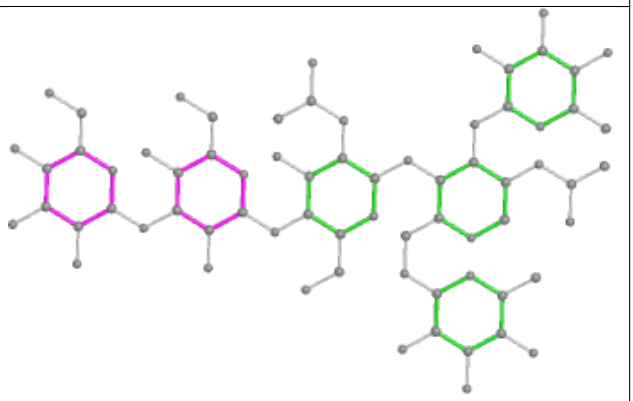
Bond lengths



Bond angles

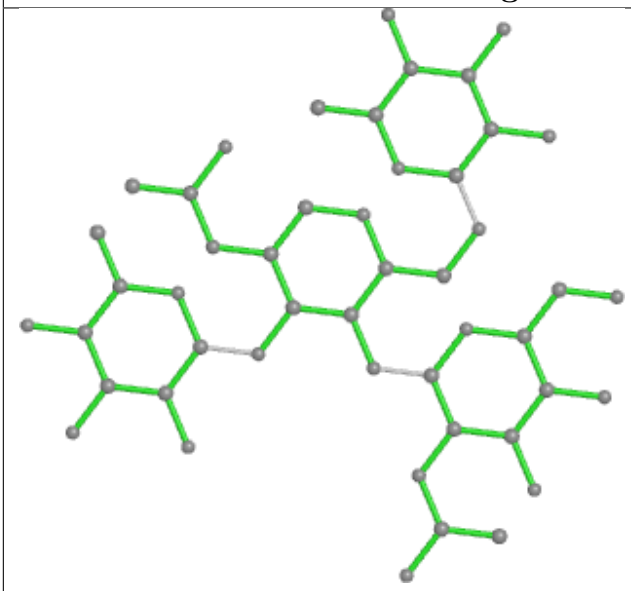


Torsions

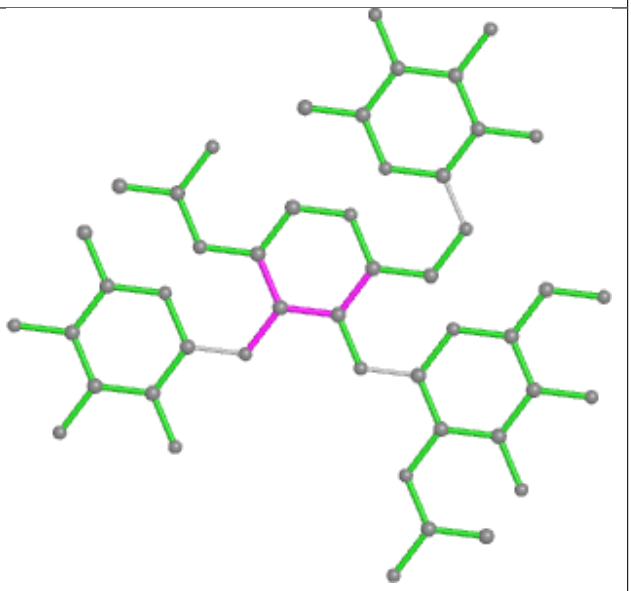


Rings

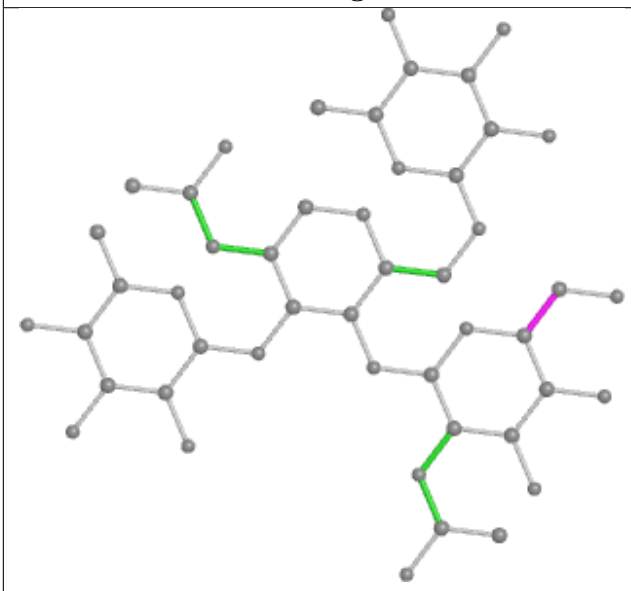
Oligosaccharide Chain I



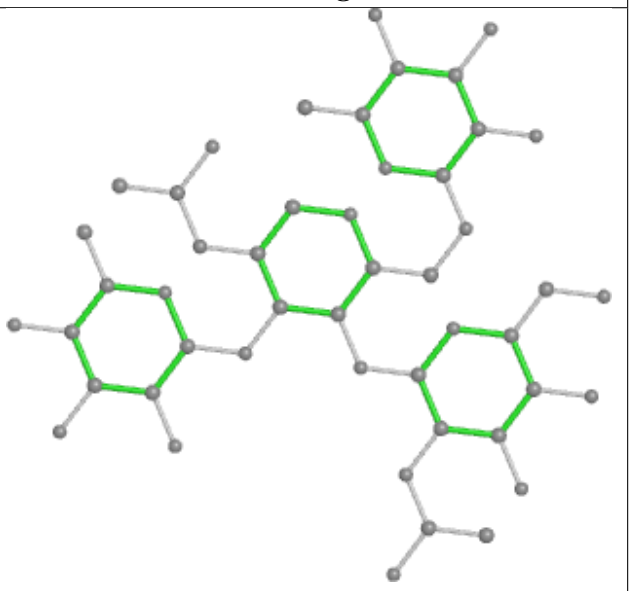
Bond lengths



Bond angles

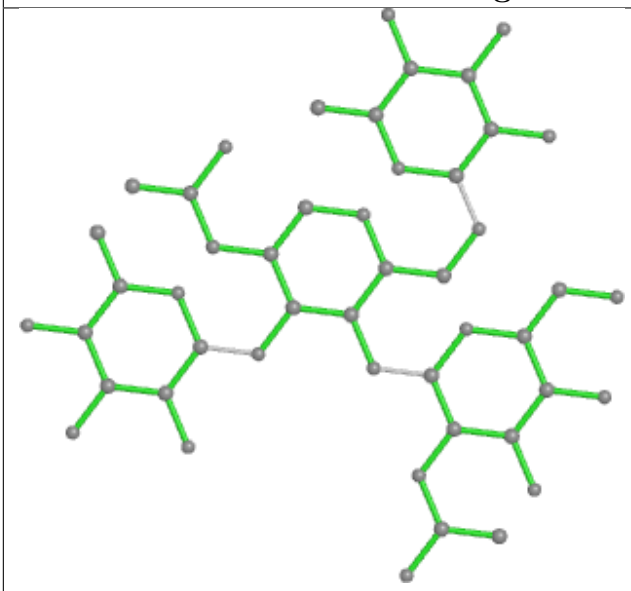


Torsions

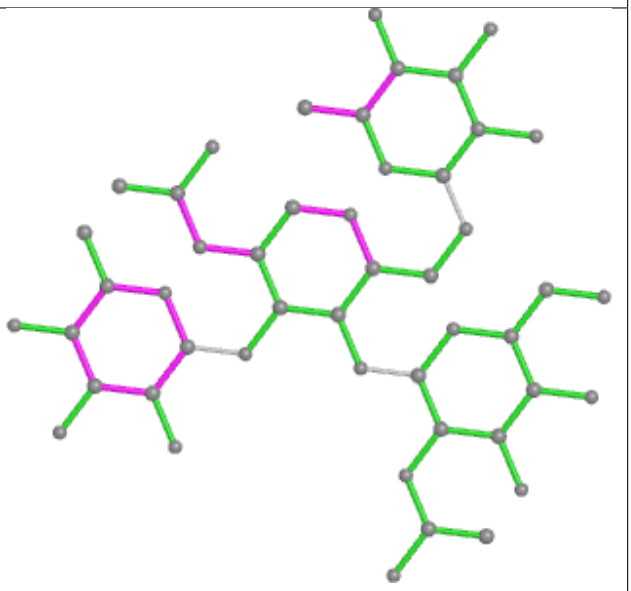


Rings

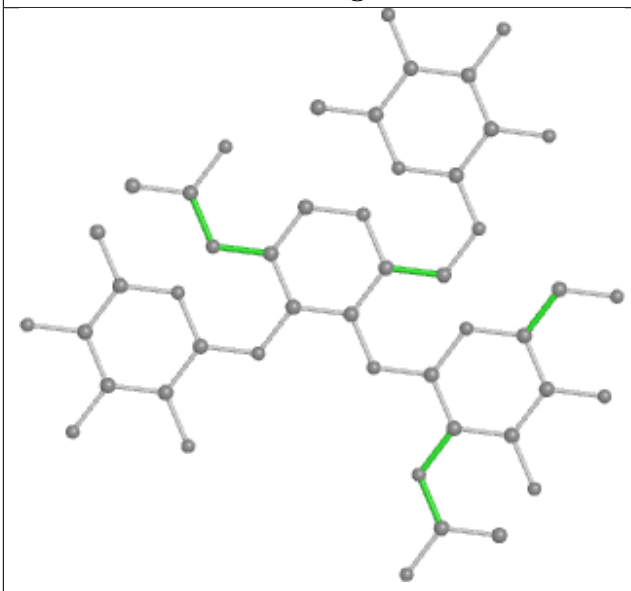
Oligosaccharide Chain K



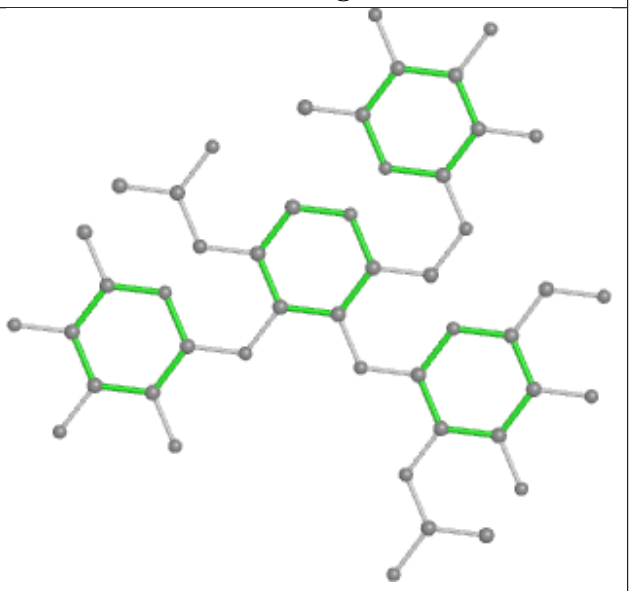
Bond lengths



Bond angles

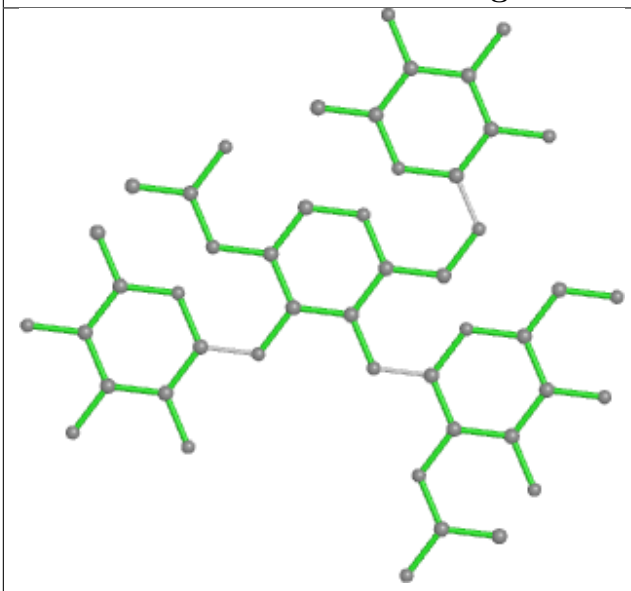


Torsions

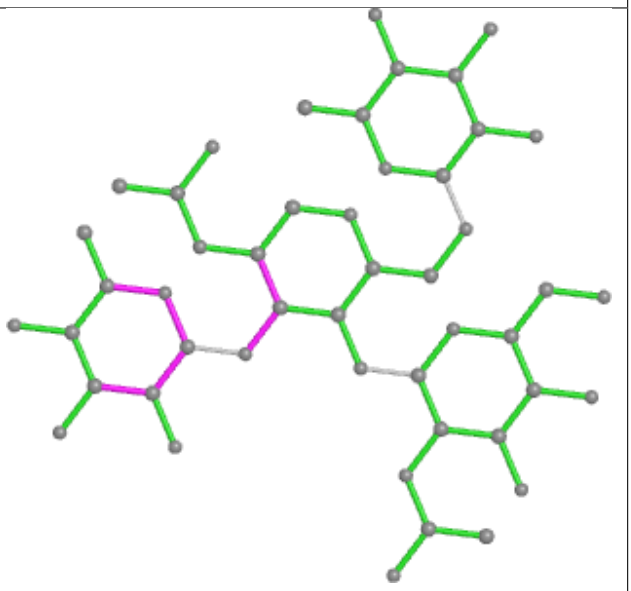


Rings

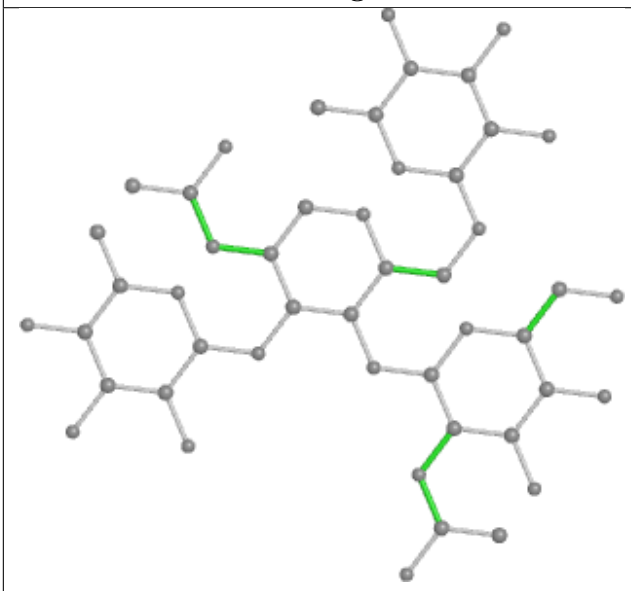
Oligosaccharide Chain M



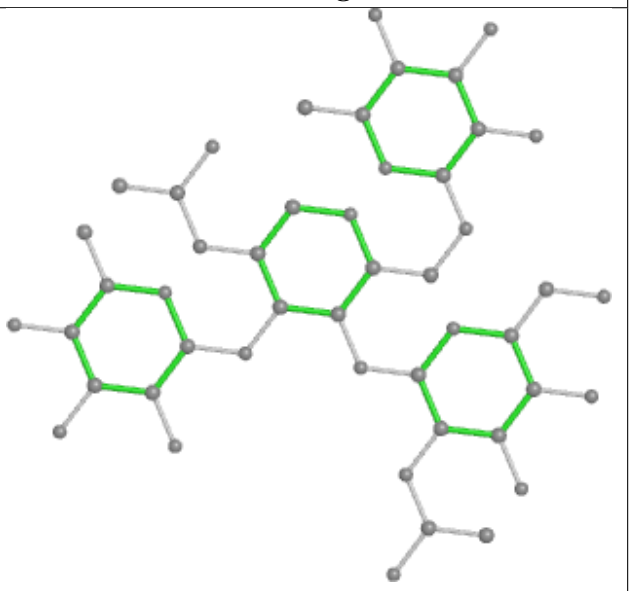
Bond lengths



Bond angles

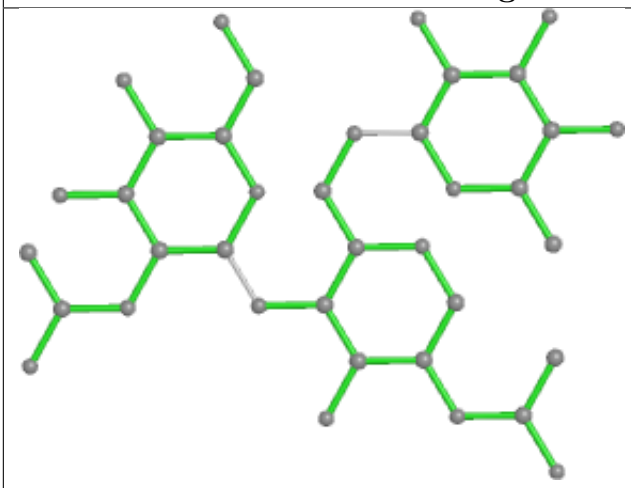


Torsions

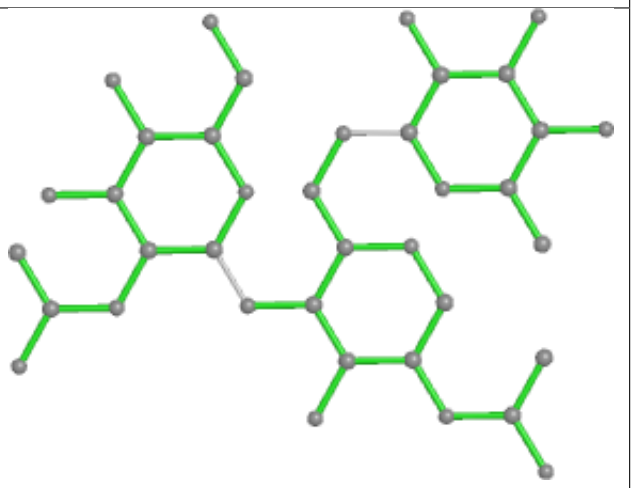


Rings

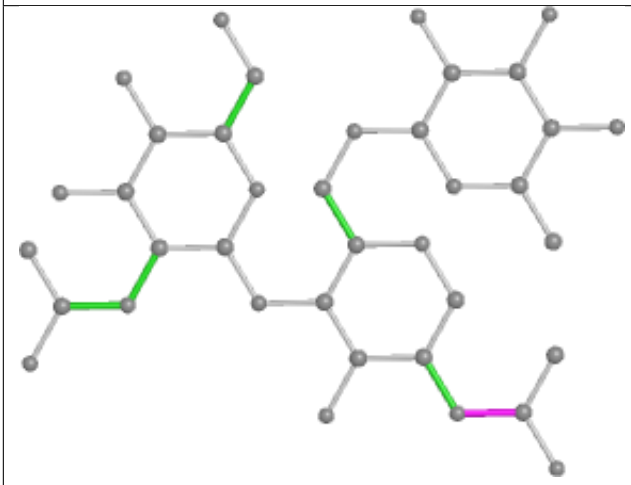
Oligosaccharide Chain J



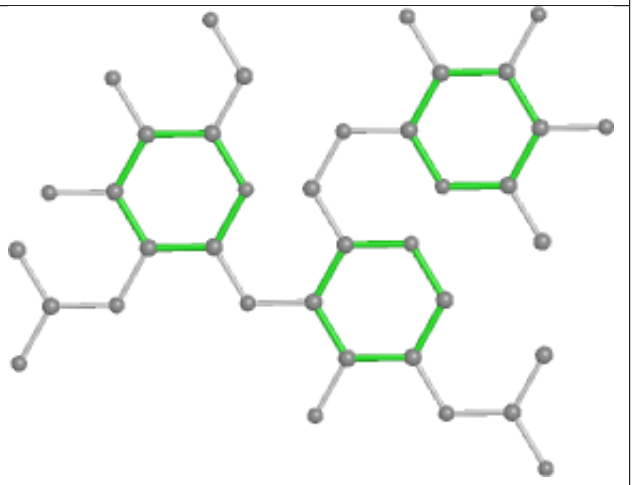
Bond lengths



Bond angles

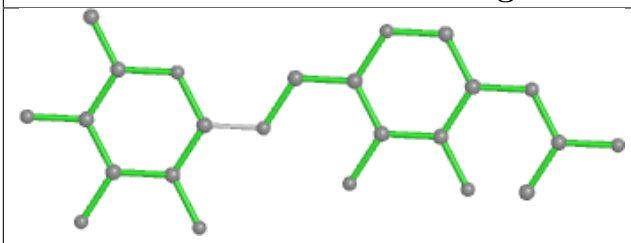


Torsions

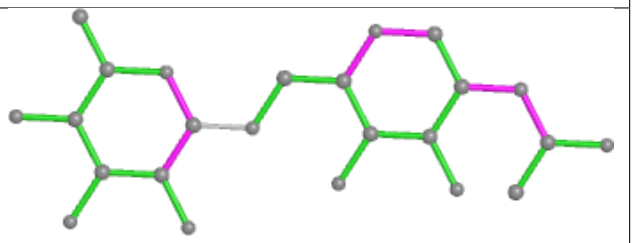


Rings

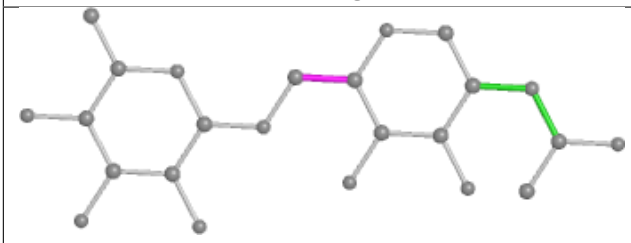
Oligosaccharide Chain L



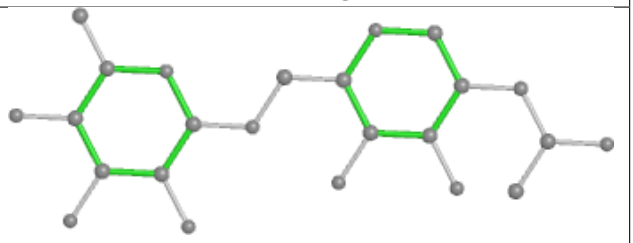
Bond lengths



Bond angles

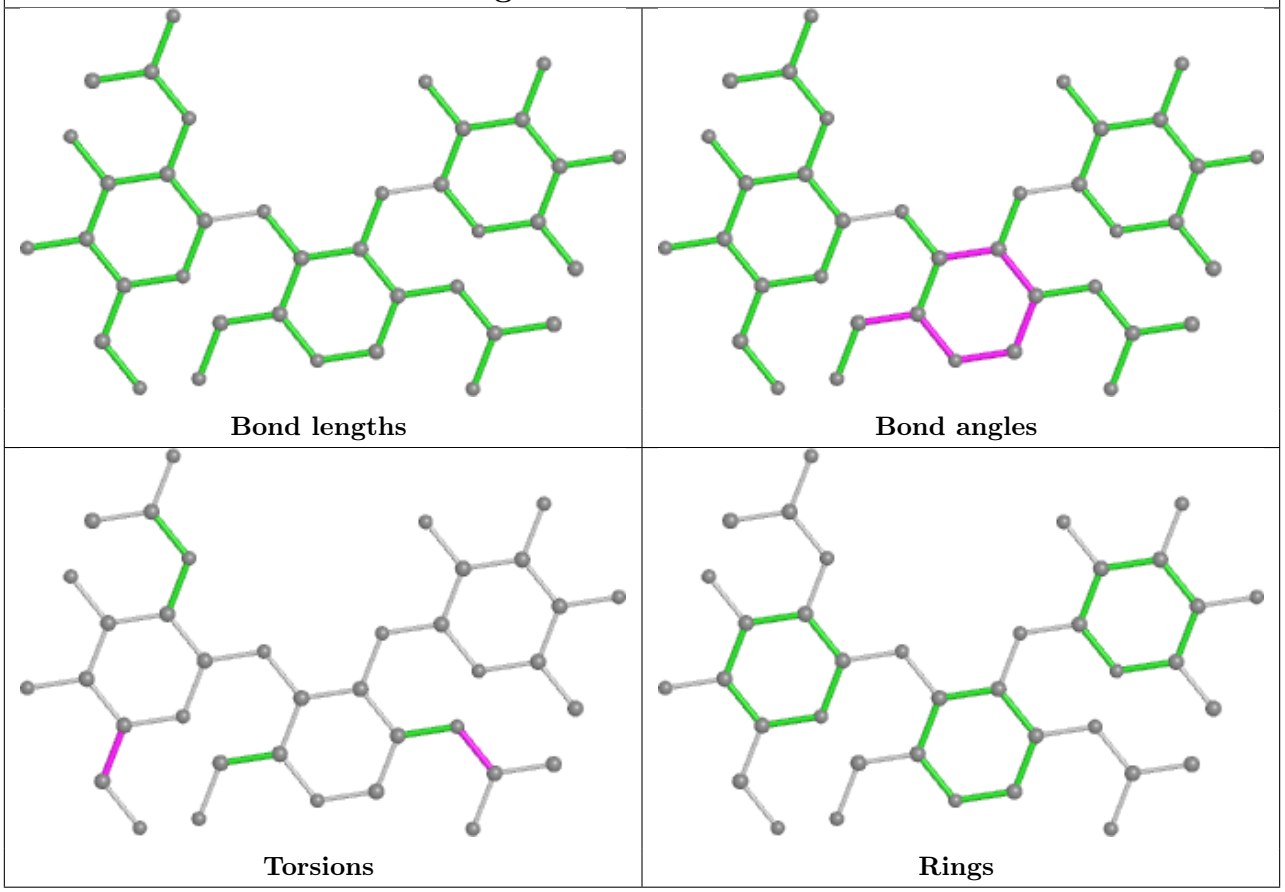


Torsions



Rings

Oligosaccharide Chain N



5.6 Ligand geometry (i)

Of 52 ligands modelled in this entry, 11 are monoatomic - leaving 41 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	$\#\|Z\| > 2$
11	NO3	F	517	-	1,3,3	3.74	1 (100%)	0,3,3	-	-
10	GOL	A	511	-	5,5,5	0.45	0	5,5,5	0.20	0
10	GOL	F	514	-	5,5,5	0.34	0	5,5,5	0.31	0
8	NAG	A	507	1	14,14,15	0.42	0	17,19,21	1.31	3 (17%)
10	GOL	D	508	-	5,5,5	0.37	0	5,5,5	0.37	0
11	NO3	F	516	-	1,3,3	3.53	1 (100%)	0,3,3	-	-
8	NAG	B	507	1	14,14,15	0.64	0	17,19,21	0.96	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
8	NAG	F	506	1	14,14,15	0.52	0	17,19,21	0.92	1 (5%)
11	NO3	F	518	-	1,3,3	3.45	1 (100%)	0,3,3	-	-
10	GOL	A	512	-	5,5,5	0.43	0	5,5,5	0.18	0
10	GOL	B	512	-	5,5,5	0.31	0	5,5,5	0.30	0
11	NO3	C	510	-	1,3,3	3.34	1 (100%)	0,3,3	-	-
8	NAG	A	508	1	14,14,15	0.57	0	17,19,21	1.04	1 (5%)
8	NAG	E	508	1	14,14,15	0.68	0	17,19,21	1.23	2 (11%)
8	NAG	F	505	1	14,14,15	0.58	0	17,19,21	0.85	1 (5%)
8	NAG	A	506	1	14,14,15	0.52	0	17,19,21	1.10	1 (5%)
11	NO3	B	513	-	1,3,3	3.65	1 (100%)	0,3,3	-	-
11	NO3	D	510	-	1,3,3	3.55	1 (100%)	0,3,3	-	-
11	NO3	A	513	-	1,3,3	3.49	1 (100%)	0,3,3	-	-
10	GOL	E	511	-	5,5,5	0.33	0	5,5,5	0.43	0
8	NAG	D	505	1	14,14,15	0.59	0	17,19,21	1.18	2 (11%)
8	NAG	C	505	1	14,14,15	0.57	0	17,19,21	0.85	0
10	GOL	F	513	-	5,5,5	0.34	0	5,5,5	0.48	0
11	NO3	B	516	-	1,3,3	3.29	1 (100%)	0,3,3	-	-
8	NAG	C	506	1	14,14,15	0.66	0	17,19,21	1.15	1 (5%)
8	NAG	E	505	1	14,14,15	0.63	0	17,19,21	0.86	0
10	GOL	E	512	-	5,5,5	0.47	0	5,5,5	0.25	0
11	NO3	B	517	-	1,3,3	3.53	1 (100%)	0,3,3	-	-
10	GOL	C	509	-	5,5,5	0.34	0	5,5,5	0.50	0
11	NO3	B	515	-	1,3,3	3.70	1 (100%)	0,3,3	-	-
11	NO3	D	509	-	1,3,3	3.41	1 (100%)	0,3,3	-	-
10	GOL	E	513	-	5,5,5	0.35	0	5,5,5	0.26	0
8	NAG	B	508	1	14,14,15	0.54	0	17,19,21	0.84	0
10	GOL	B	511	-	5,5,5	0.31	0	5,5,5	0.40	0
11	NO3	B	514	-	1,3,3	3.44	1 (100%)	0,3,3	-	-
8	NAG	D	504	1	14,14,15	0.54	0	17,19,21	1.39	1 (5%)
10	GOL	F	515	-	5,5,5	0.34	0	5,5,5	0.49	0
10	GOL	A	510	-	5,5,5	0.31	0	5,5,5	0.44	0
10	GOL	F	512	-	5,5,5	0.54	0	5,5,5	0.60	0
11	NO3	A	514	-	1,3,3	3.61	1 (100%)	0,3,3	-	-
11	NO3	C	511	-	1,3,3	3.46	1 (100%)	0,3,3	-	-

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	GOL	A	511	-	-	0/4/4/4	-
10	GOL	F	514	-	-	3/4/4/4	-
8	NAG	A	507	1	-	2/6/23/26	0/1/1/1
10	GOL	D	508	-	-	2/4/4/4	-
8	NAG	B	507	1	-	0/6/23/26	0/1/1/1
8	NAG	F	506	1	-	0/6/23/26	0/1/1/1
10	GOL	A	512	-	-	1/4/4/4	-
10	GOL	B	512	-	-	2/4/4/4	-
8	NAG	A	508	1	-	2/6/23/26	0/1/1/1
8	NAG	E	508	1	-	2/6/23/26	0/1/1/1
8	NAG	F	505	1	-	0/6/23/26	0/1/1/1
8	NAG	A	506	1	-	4/6/23/26	0/1/1/1
10	GOL	E	511	-	-	4/4/4/4	-
8	NAG	D	505	1	-	0/6/23/26	0/1/1/1
8	NAG	C	505	1	-	0/6/23/26	0/1/1/1
10	GOL	F	513	-	-	2/4/4/4	-
8	NAG	C	506	1	-	0/6/23/26	0/1/1/1
8	NAG	E	505	1	-	0/6/23/26	0/1/1/1
10	GOL	E	512	-	-	4/4/4/4	-
10	GOL	C	509	-	-	2/4/4/4	-
10	GOL	E	513	-	-	4/4/4/4	-
8	NAG	B	508	1	-	0/6/23/26	0/1/1/1
10	GOL	B	511	-	-	0/4/4/4	-
8	NAG	D	504	1	-	0/6/23/26	0/1/1/1
10	GOL	F	515	-	-	3/4/4/4	-
10	GOL	A	510	-	-	2/4/4/4	-
10	GOL	F	512	-	-	2/4/4/4	-

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	F	517	NO3	O1-N	3.74	1.41	1.24
11	B	515	NO3	O1-N	3.70	1.41	1.24
11	B	513	NO3	O1-N	3.65	1.40	1.24
11	A	514	NO3	O1-N	3.61	1.40	1.24
11	D	510	NO3	O1-N	3.55	1.40	1.24

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	D	504	NAG	C1-O5-C5	4.47	118.25	112.19
8	A	506	NAG	O5-C1-C2	-3.18	106.27	111.29
8	D	505	NAG	C4-C3-C2	3.09	115.55	111.02
8	A	507	NAG	C4-C3-C2	-3.06	106.53	111.02
8	E	508	NAG	C2-N2-C7	-3.03	118.59	122.90

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	507	NAG	O7-C7-N2-C2
10	C	509	GOL	O1-C1-C2-C3
10	D	508	GOL	O1-C1-C2-C3
10	E	511	GOL	O1-C1-C2-C3
10	E	513	GOL	O1-C1-C2-O2

There are no ring outliers.

8 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	511	GOL	1	0
10	D	508	GOL	1	0
10	A	512	GOL	1	0
11	C	510	NO3	1	0
11	A	513	NO3	1	0
10	E	511	GOL	1	0
8	E	505	NAG	1	0
11	B	517	NO3	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	367/373 (98%)	0.32	12 (3%) 46 56	19, 30, 52, 77	0
1	B	367/373 (98%)	0.41	24 (6%) 18 27	20, 32, 61, 93	0
1	C	367/373 (98%)	0.57	37 (10%) 7 11	23, 39, 66, 85	0
1	D	367/373 (98%)	0.47	26 (7%) 16 24	23, 36, 62, 88	0
1	E	367/373 (98%)	0.43	21 (5%) 23 32	22, 36, 60, 92	0
1	F	367/373 (98%)	0.19	6 (1%) 72 79	18, 28, 49, 76	0
All	All	2202/2238 (98%)	0.40	126 (5%) 23 32	18, 33, 60, 93	0

The worst 5 of 126 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	83	PHE	7.4
1	C	83	PHE	6.9
1	E	83	PHE	6.4
1	F	83	PHE	6.2
1	A	83	PHE	6.1

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

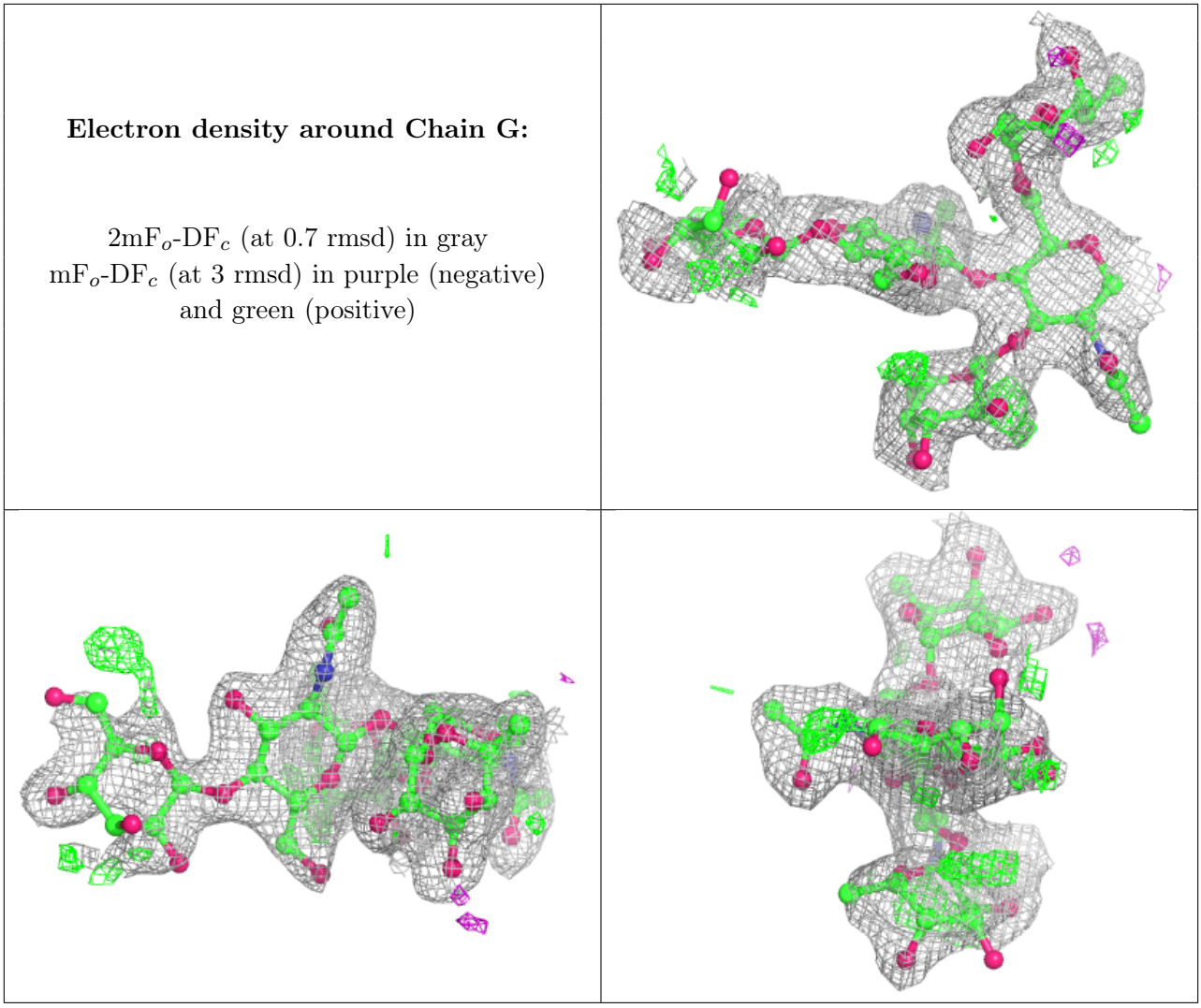
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	MAN	H	4	11/12	0.54	0.46	106,118,121,124	0
2	BMA	G	3	11/12	0.66	0.28	102,115,122,126	0
7	FUL	N	2	10/11	0.68	0.45	103,113,123,131	0
7	NAG	N	3	14/15	0.69	0.43	90,105,113,114	0
4	FUL	I	2	10/11	0.75	0.30	100,113,123,132	0
4	FUL	K	2	10/11	0.75	0.30	73,80,87,88	0
3	BMA	H	3	11/12	0.77	0.38	98,112,119,120	0
4	NAG	I	3	14/15	0.78	0.28	72,83,94,98	0
3	FUL	H	5	10/11	0.78	0.30	63,76,83,83	0
7	NAG	N	1	14/15	0.79	0.25	53,72,95,97	0
2	FUL	G	4	10/11	0.79	0.23	59,70,83,96	0
5	NAG	J	1	14/15	0.79	0.23	50,64,73,92	0
4	FUL	M	2	10/11	0.82	0.19	66,72,76,90	0
5	NAG	J	2	14/15	0.83	0.37	71,78,90,96	0
4	NAG	I	1	14/15	0.84	0.19	64,72,87,101	0
4	FUC	I	4	10/11	0.87	0.16	47,64,80,86	0
6	NAG	L	1	14/15	0.87	0.19	48,55,72,75	0
6	FUC	L	2	10/11	0.87	0.24	87,96,100,100	0
4	NAG	K	1	14/15	0.89	0.16	39,45,68,70	0
3	NAG	H	2	14/15	0.89	0.17	46,54,72,83	0
2	FUC	G	5	10/11	0.90	0.15	23,39,45,49	0
4	NAG	M	3	14/15	0.91	0.18	41,58,67,89	0
5	FUC	J	3	10/11	0.92	0.21	49,55,64,70	0
3	NAG	H	1	14/15	0.92	0.13	40,43,55,59	0
2	NAG	G	1	14/15	0.93	0.16	38,47,53,63	0
2	NAG	G	2	14/15	0.93	0.14	48,62,76,87	0
4	NAG	K	3	14/15	0.93	0.23	53,64,80,89	0
4	FUC	K	4	10/11	0.93	0.16	35,41,50,56	0
4	NAG	M	1	14/15	0.93	0.10	28,35,51,57	0
3	FUC	H	6	10/11	0.94	0.10	30,45,49,51	0
4	FUC	M	4	10/11	0.96	0.10	27,35,40,47	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.

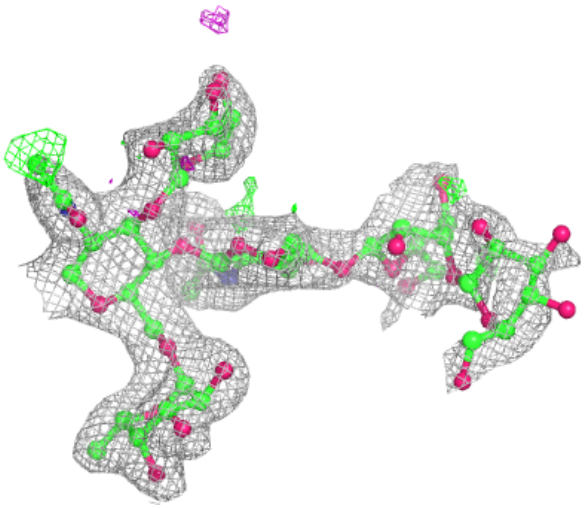
Electron density around Chain G:

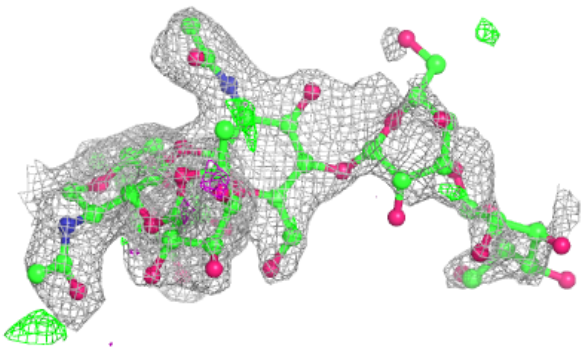
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

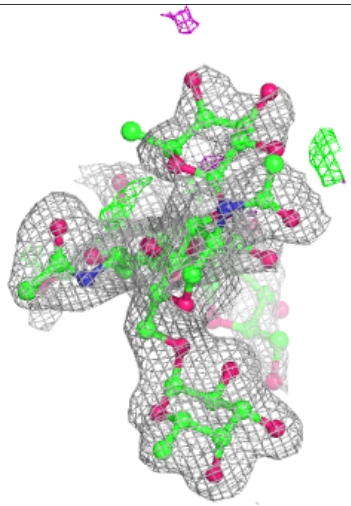


Electron density around Chain H:

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

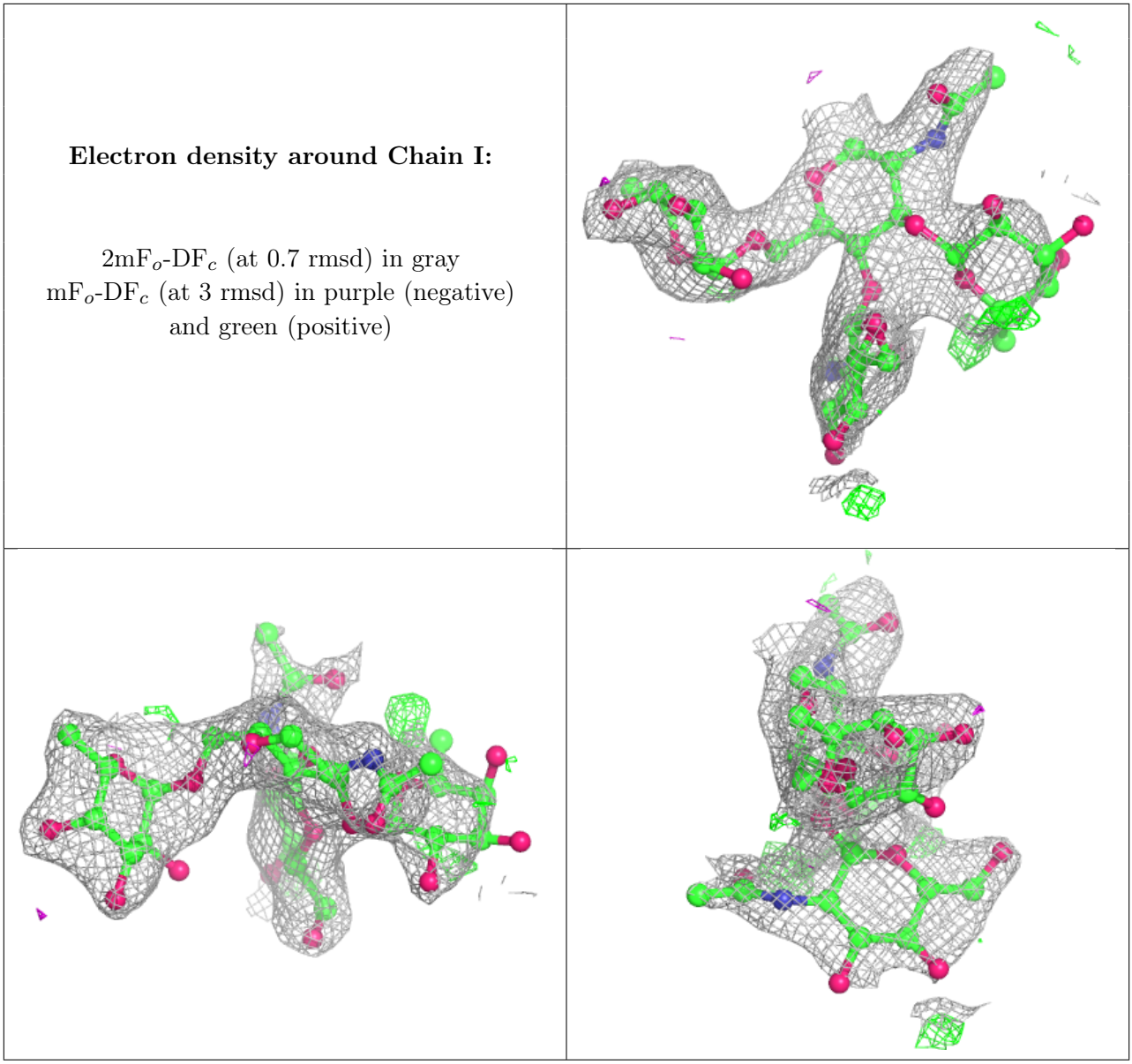






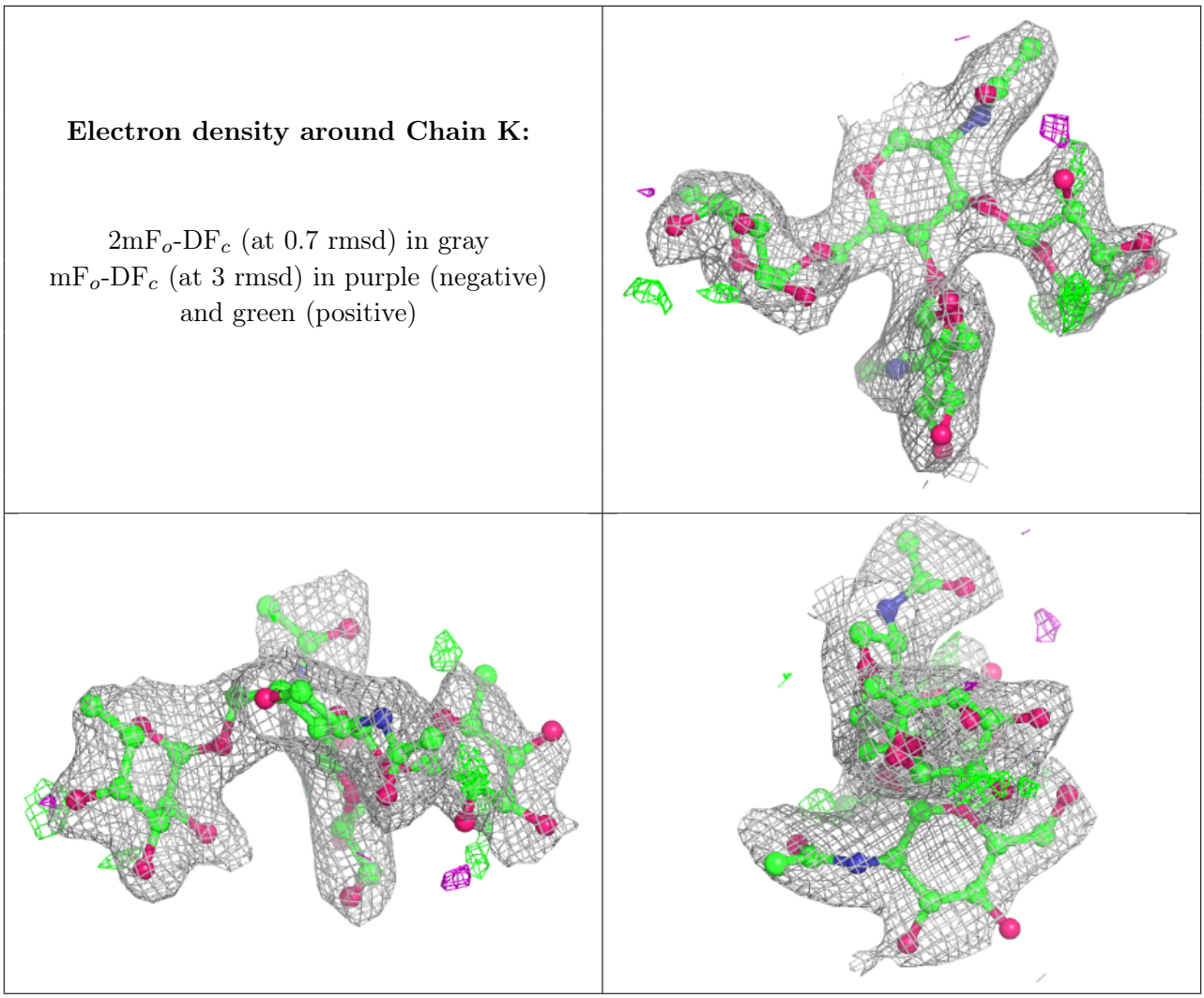
Electron density around Chain I:

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



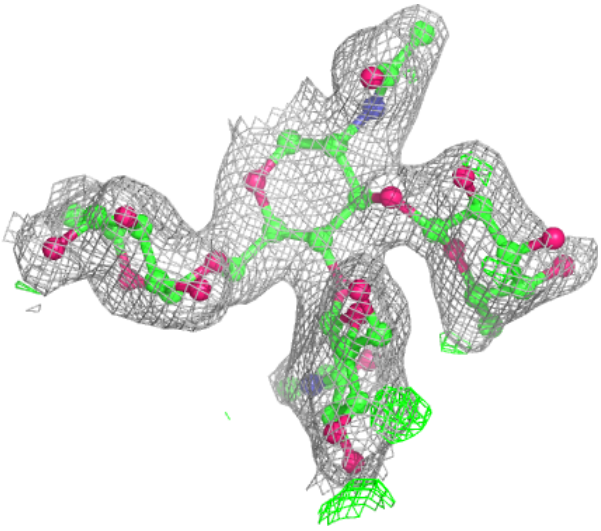
Electron density around Chain K:

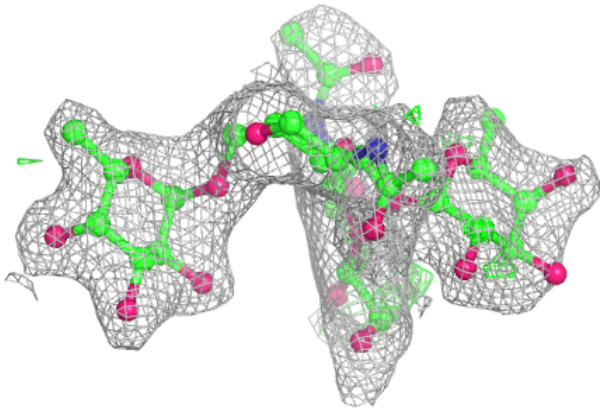
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

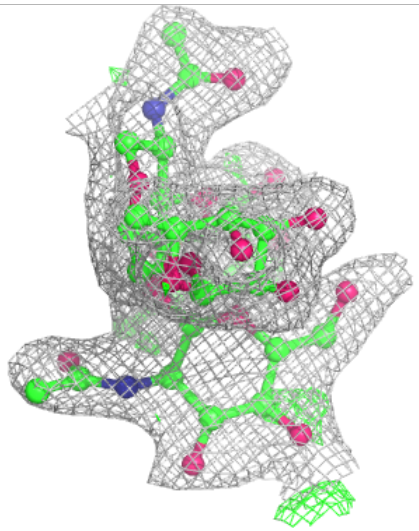


Electron density around Chain M:

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

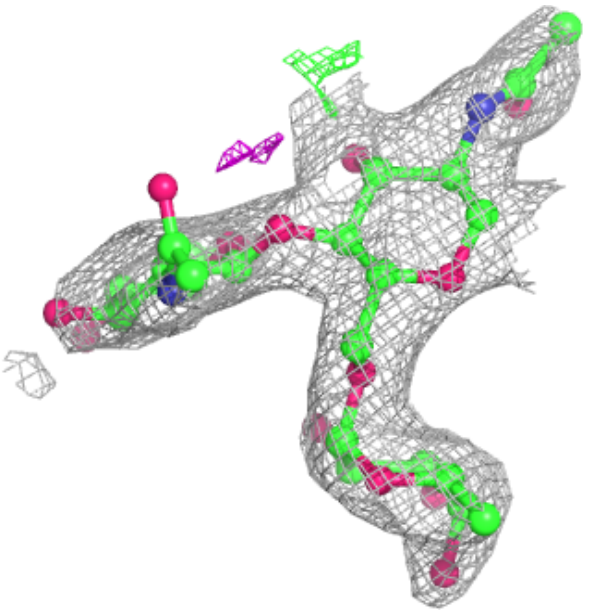


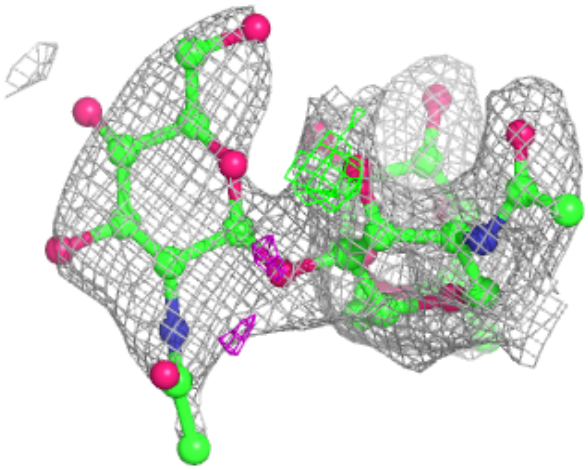


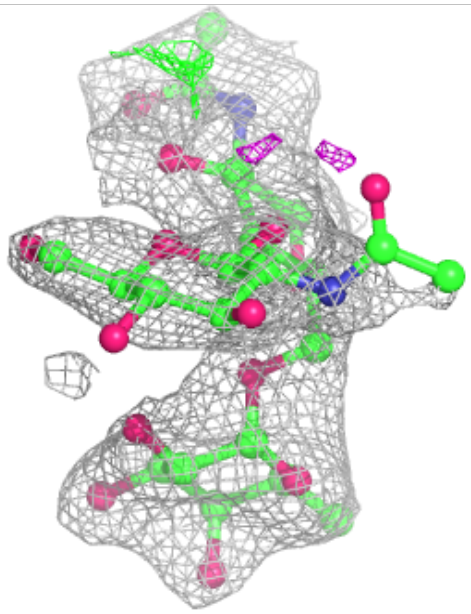


Electron density around Chain J:

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

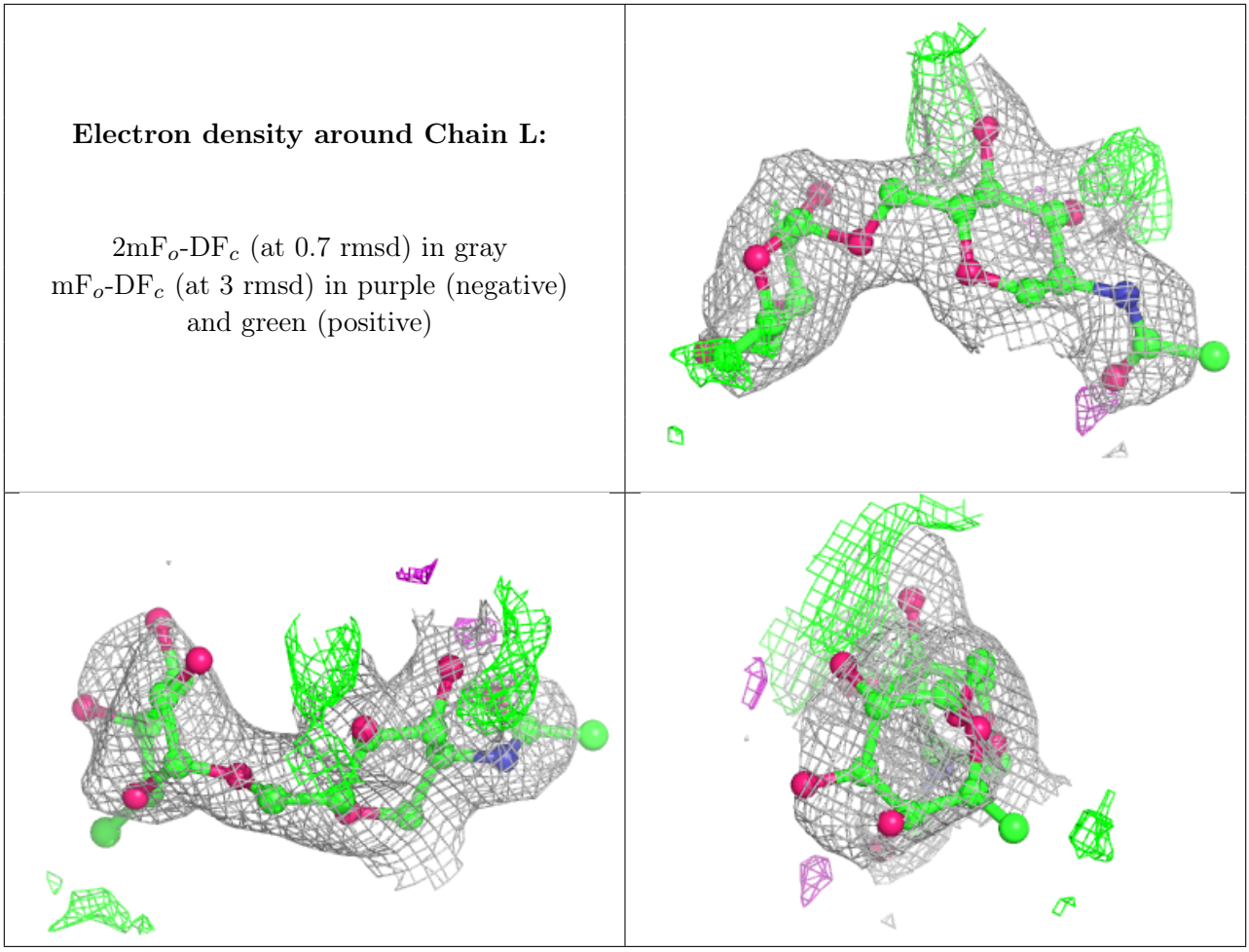






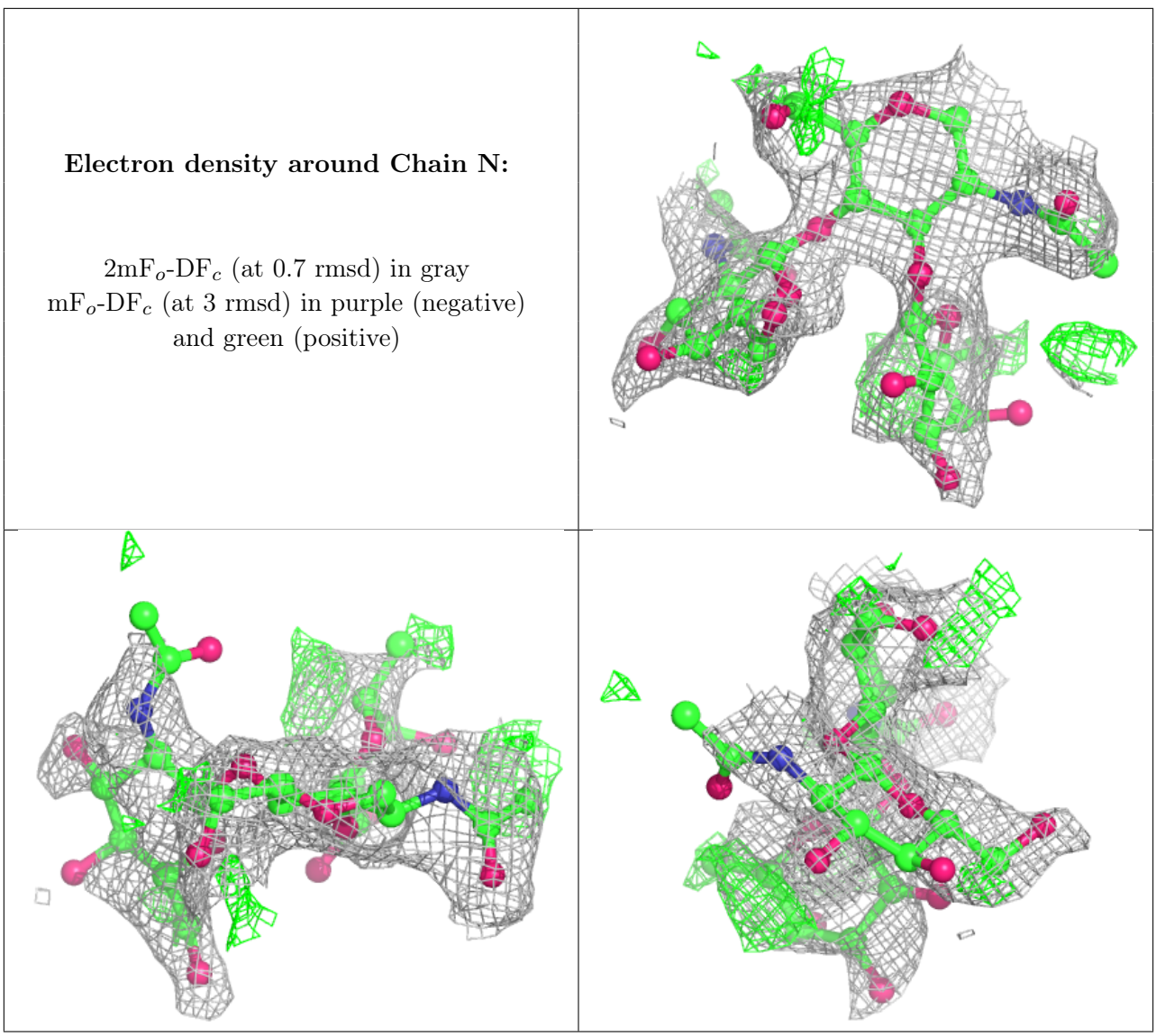
Electron density around Chain L:

$2mF_o$-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)



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	GOL	B	511	6/6	0.54	0.22	37,64,76,77	0
10	GOL	E	511	6/6	0.67	0.26	62,74,80,87	0
8	NAG	D	505	14/15	0.68	0.33	56,75,86,92	0
8	NAG	E	508	14/15	0.68	0.29	68,87,102,114	0
8	NAG	A	508	14/15	0.73	0.27	65,82,93,98	0
8	NAG	C	505	14/15	0.73	0.29	62,73,80,87	0
8	NAG	A	506	14/15	0.73	0.29	47,82,97,105	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	NAG	C	506	14/15	0.74	0.31	65,74,98,101	0
8	NAG	F	506	14/15	0.74	0.36	66,80,88,95	0
10	GOL	D	508	6/6	0.76	0.20	54,73,85,87	0
9	CA	C	508	1/1	0.76	0.06	75,75,75,75	0
8	NAG	B	508	14/15	0.77	0.32	68,73,90,92	0
8	NAG	A	507	14/15	0.81	0.26	67,79,88,89	0
10	GOL	E	513	6/6	0.81	0.16	73,88,97,97	0
11	NO3	F	517	4/4	0.81	0.16	62,66,73,74	0
8	NAG	B	507	14/15	0.84	0.22	65,86,92,100	0
8	NAG	F	505	14/15	0.85	0.22	50,67,74,92	0
8	NAG	E	505	14/15	0.85	0.20	35,55,63,68	0
8	NAG	D	504	14/15	0.86	0.18	37,54,69,73	0
10	GOL	B	512	6/6	0.86	0.18	43,60,74,75	0
10	GOL	F	512	6/6	0.88	0.25	33,58,76,92	0
10	GOL	F	515	6/6	0.89	0.16	47,56,58,58	0
9	CA	D	507	1/1	0.89	0.05	55,55,55,55	0
11	NO3	A	514	4/4	0.90	0.25	26,46,53,69	0
9	CA	E	510	1/1	0.91	0.10	69,69,69,69	0
10	GOL	F	513	6/6	0.92	0.12	31,52,68,70	0
11	NO3	B	517	4/4	0.92	0.22	53,57,58,72	0
11	NO3	C	510	4/4	0.92	0.21	37,54,59,70	0
11	NO3	D	509	4/4	0.92	0.19	46,48,54,61	0
10	GOL	E	512	6/6	0.92	0.15	33,43,74,88	0
11	NO3	A	513	4/4	0.93	0.18	37,46,49,50	0
10	GOL	F	514	6/6	0.93	0.11	28,40,70,84	0
10	GOL	A	512	6/6	0.93	0.23	42,58,69,69	0
9	CA	B	510	1/1	0.94	0.04	59,59,59,59	0
11	NO3	F	516	4/4	0.94	0.12	55,66,66,76	0
9	CA	C	507	1/1	0.94	0.07	48,48,48,48	0
10	GOL	C	509	6/6	0.95	0.13	36,49,58,66	0
10	GOL	A	511	6/6	0.96	0.16	32,61,82,89	0
10	GOL	A	510	6/6	0.96	0.12	26,39,55,66	0
9	CA	F	511	1/1	0.97	0.05	45,45,45,45	0
11	NO3	C	511	4/4	0.97	0.15	42,45,49,52	0
11	NO3	B	513	4/4	0.97	0.15	27,50,51,69	0
11	NO3	D	510	4/4	0.97	0.19	50,57,61,64	0
11	NO3	B	515	4/4	0.97	0.19	37,38,43,61	0
9	CA	E	509	1/1	0.97	0.07	32,32,32,32	0
11	NO3	F	518	4/4	0.97	0.20	36,48,50,62	0
11	NO3	B	516	4/4	0.98	0.15	32,35,37,42	0
11	NO3	B	514	4/4	0.98	0.16	36,41,47,50	0
9	CA	D	506	1/1	0.98	0.06	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
9	CA	F	510	1/1	0.99	0.09	22,22,22,22	0
9	CA	B	509	1/1	0.99	0.08	25,25,25,25	0
9	CA	A	509	1/1	1.00	0.10	25,25,25,25	0

6.5 Other polymers (i)

There are no such residues in this entry.