



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2025 – 12:16 PM EDT

PDB ID : 4MMX
Title : Integrin AlphaVBeta3 ectodomain bound to the tenth domain of Fibronectin
Authors : van Agthoven, J.; Xiong, J.; Arnaout, M.A.
Deposited on : 2013-09-09
Resolution : 3.32 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

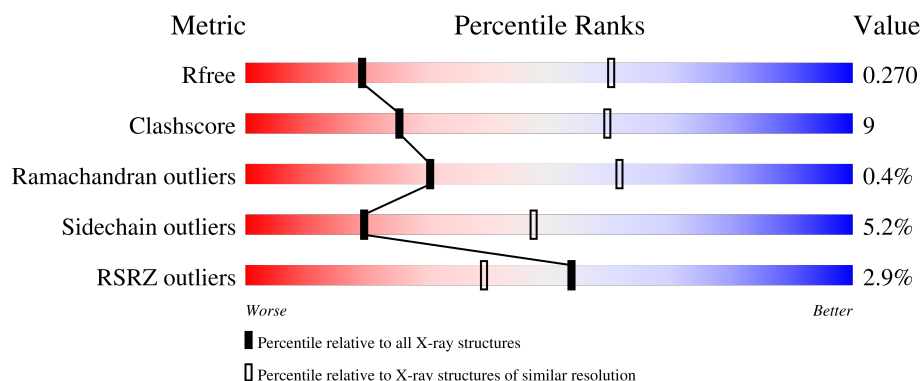
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.32 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




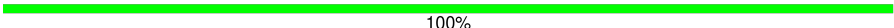


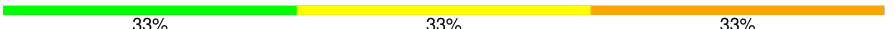


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1066 (3.34-3.30)
Clashscore	180529	1111 (3.34-3.30)
Ramachandran outliers	177936	1109 (3.34-3.30)
Sidechain outliers	177891	1108 (3.34-3.30)
RSRZ outliers	164620	1066 (3.34-3.30)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	959	<div> <div></div> <div>72%</div> <div>23%</div> <div>• •</div> </div>
2	B	692	<div> <div>4%</div> <div>77%</div> <div>21%</div> <div>•</div> </div>
3	C	98	<div> <div>12%</div> <div>53%</div> <div>36%</div> <div>6%</div> <div>5%</div> </div>
4	D	4	<div> <div>50%</div> <div>50%</div> </div>
4	G	4	<div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
5	E	2	 50% 50%
5	H	2	 100%
5	I	2	 50% 50%
5	K	2	 50% 50%
6	F	6	 33% 33% 33%
7	J	3	 67% 33%
7	L	3	 33% 67%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 13626 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 Integrin alpha-V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	924	Total	C	N	O	S	0	0	0
			7196	4556	1221	1384	35			

- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	690	Total	C	N	O	S	0	0	0
			5294	3250	904	1070	70			

- Molecule 3 is a protein called Fibronectin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	93	Total	C	N	O	0	0	0
			694	438	115	141			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1510	GLY	-	expression tag	UNP P02751
C	1511	LYS	-	expression tag	UNP P02751
C	1512	LYS	-	expression tag	UNP P02751
C	1513	GLY	-	expression tag	UNP P02751
C	1514	LYS	-	expression tag	UNP P02751

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



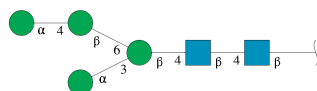
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	4	Total	C	N	O	0	0	0
			50	28	2	20			
4	G	4	Total	C	N	O	0	0	0
			50	28	2	20			

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



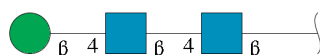
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	K	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



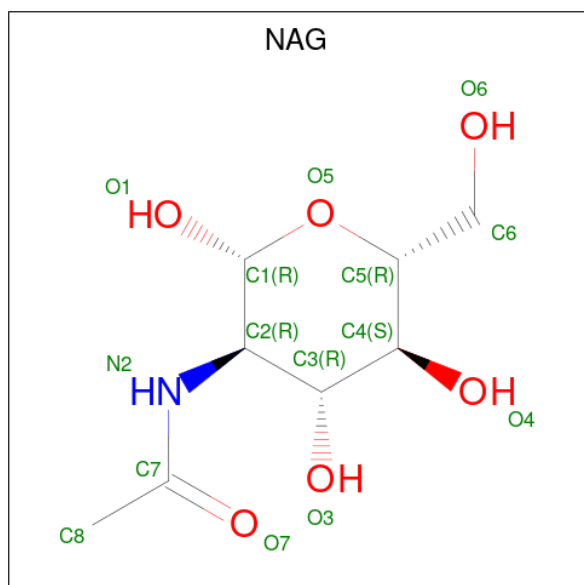
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	F	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 7 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
7	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
7	L	3	Total	C	N	O	0	0	0
			39	22	2	15			

- 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	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	5	Total	Mn	0	0
			5	5		
9	B	3	Total	Mn	0	0
			3	3		

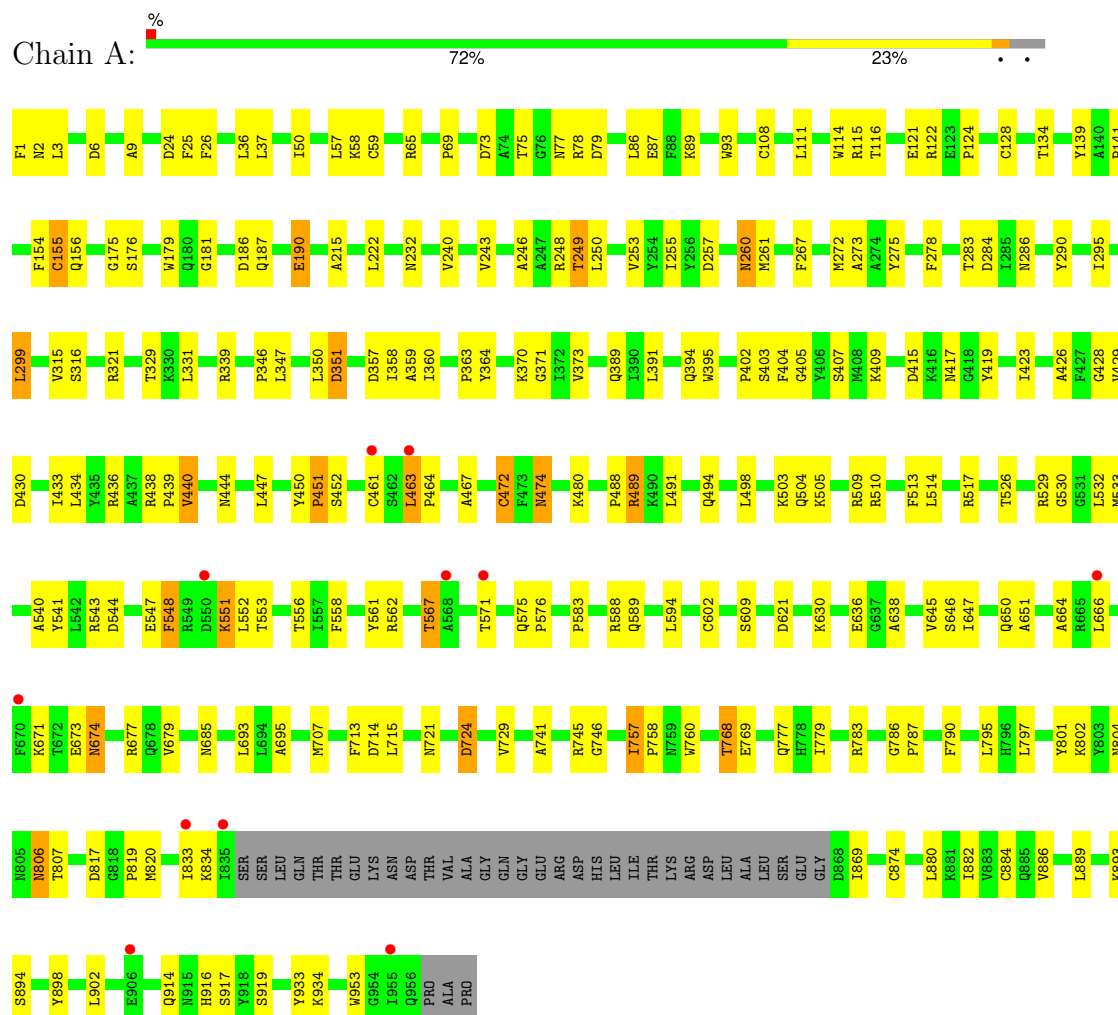
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	2	Total	O	0	0
			2	2		

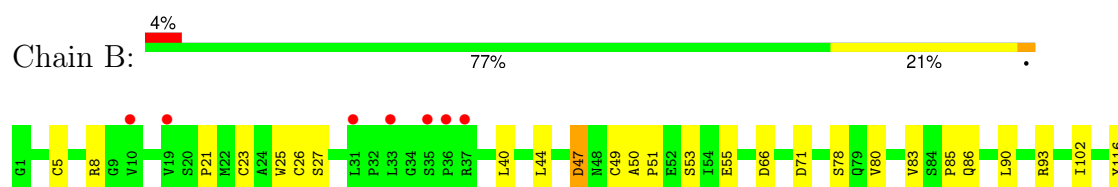
3 Residue-property plots

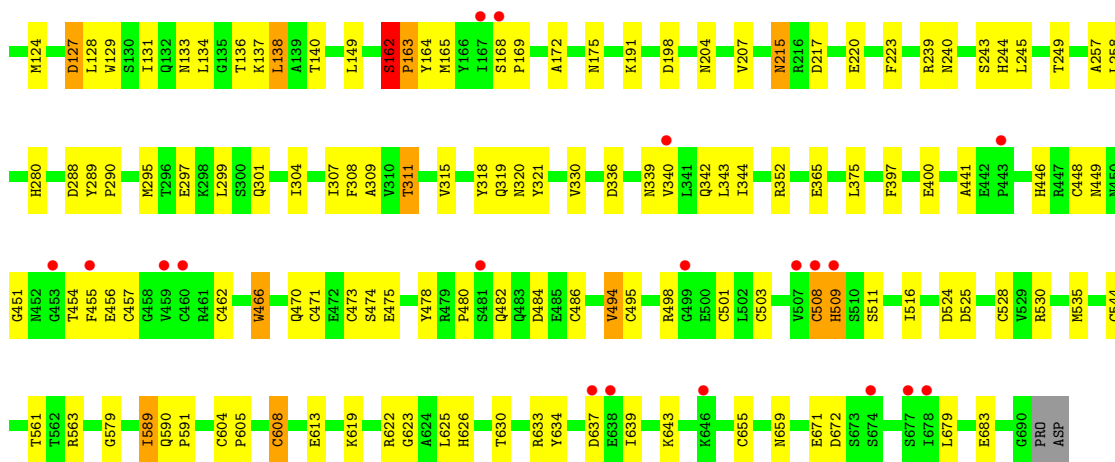
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Integrin alpha-V

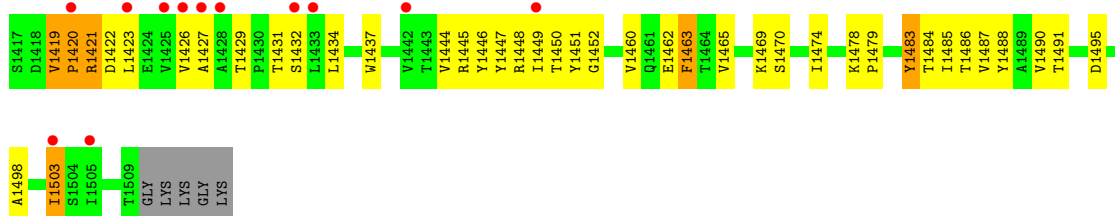


• Molecule 2: Integrin beta-3





• Molecule 3: Fibronectin



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



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



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



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

Chain H:  100%

MAG1
MAG2

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

Chain I:  50% 50%

MAG1
MAG2

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

Chain K:  50% 50%

MAG1
MAG2

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

Chain F:  33% 33% 33%

MAG1
MAG2
BMA3
BMA4
MAN5
MAN6

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  67% 33%

MAG1
MAG2
BMA3

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  33% 67%

MAG1
MAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	129.86Å 129.86Å 305.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.51 – 3.32 42.51 – 3.32	Depositor EDS
% Data completeness (in resolution range)	88.0 (42.51-3.32) 87.9 (42.51-3.32)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 3.32Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.220 , 0.269 0.220 , 0.270	Depositor DCC
R_{free} test set	1943 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	86.7	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 61.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13626	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA, MN, MAN

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	0.27	0/7352	0.52	0/9967
2	B	0.27	0/5390	0.52	0/7289
3	C	0.25	0/710	0.58	0/975
All	All	0.27	0/13452	0.53	0/18231

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	162	SER	Peptide
2	B	475	GLU	Peptide
2	B	78	SER	Peptide

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	7196	0	7013	145	0
2	B	5294	0	5024	89	0
3	C	694	0	688	28	0
4	D	50	0	43	0	0
4	G	50	0	43	0	0
5	E	28	0	25	0	0
5	H	28	0	25	0	0
5	I	28	0	25	0	0
5	K	28	0	25	1	0
6	F	72	0	61	2	0
7	J	39	0	34	0	0
7	L	39	0	34	0	0
8	A	42	0	39	1	0
8	B	28	0	26	2	0
9	A	5	0	0	0	0
9	B	3	0	0	0	0
10	B	2	0	0	0	0
All	All	13626	0	13105	253	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 9.

The worst 5 of 253 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)
3:C:1421:ARG:HG2	3:C:1422:ASP:H	1.38	0.87
1:A:488:PRO:HG2	1:A:567:THR:HG22	1.60	0.82
2:B:134:LEU:O	2:B:138:LEU:N	2.13	0.76
1:A:551:LYS:HB3	1:A:553:THR:H	1.49	0.76
1:A:504:GLN:HG2	1:A:509:ARG:HG3	1.67	0.75

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	920/959 (96%)	862 (94%)	56 (6%)	2 (0%)	44	72
2	B	688/692 (99%)	607 (88%)	78 (11%)	3 (0%)	30	61
3	C	91/98 (93%)	80 (88%)	9 (10%)	2 (2%)	5	28
All	All	1699/1749 (97%)	1549 (91%)	143 (8%)	7 (0%)	30	61

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	451	PRO
3	C	1421	ARG
2	B	162	SER
2	B	163	PRO
2	B	49	CYS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	784/813 (96%)	745 (95%)	39 (5%)	20	49
2	B	612/614 (100%)	583 (95%)	29 (5%)	22	51
3	C	78/81 (96%)	70 (90%)	8 (10%)	6	22
All	All	1474/1508 (98%)	1398 (95%)	76 (5%)	19	47

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	344	ILE
3	C	1469	LYS
2	B	466	TRP
2	B	589	ILE
3	C	1503	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
2	B	509	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

28 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	$\# Z > 2$
4	NAG	D	1	4,1	14,14,15	0.39	0	17,19,21	0.45	0
4	NAG	D	2	4	14,14,15	0.23	0	17,19,21	0.49	0
4	BMA	D	3	4	11,11,12	0.90	0	15,15,17	1.04	1 (6%)
4	MAN	D	4	4	11,11,12	0.68	0	15,15,17	1.03	2 (13%)
5	NAG	E	1	5,1	14,14,15	1.22	1 (7%)	17,19,21	1.75	4 (23%)
5	NAG	E	2	5	14,14,15	0.21	0	17,19,21	0.39	0
6	NAG	F	1	6,1	14,14,15	0.35	0	17,19,21	0.42	0
6	NAG	F	2	6	14,14,15	0.23	0	17,19,21	0.49	0
6	BMA	F	3	6	11,11,12	0.66	0	15,15,17	0.74	0
6	BMA	F	4	6	11,11,12	1.19	2 (18%)	15,15,17	1.07	1 (6%)
6	MAN	F	5	6	11,11,12	1.01	1 (9%)	15,15,17	1.49	4 (26%)
6	MAN	F	6	6	11,11,12	0.78	0	15,15,17	0.94	2 (13%)
4	NAG	G	1	4,1	14,14,15	0.24	0	17,19,21	0.47	0
4	NAG	G	2	4	14,14,15	0.27	0	17,19,21	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BMA	G	3	4	11,11,12	0.72	0	15,15,17	0.86	1 (6%)
4	MAN	G	4	4	11,11,12	0.58	0	15,15,17	1.01	2 (13%)
5	NAG	H	1	5,1	14,14,15	0.30	0	17,19,21	0.36	0
5	NAG	H	2	5	14,14,15	0.26	0	17,19,21	0.40	0
5	NAG	I	1	5,1	14,14,15	0.39	0	17,19,21	0.37	0
5	NAG	I	2	5	14,14,15	0.65	0	17,19,21	0.90	1 (5%)
7	NAG	J	1	7,1	14,14,15	0.27	0	17,19,21	0.47	0
7	NAG	J	2	7	14,14,15	0.42	0	17,19,21	0.49	0
7	BMA	J	3	7	11,11,12	0.95	1 (9%)	15,15,17	1.30	2 (13%)
5	NAG	K	1	2,5	14,14,15	0.48	0	17,19,21	0.96	1 (5%)
5	NAG	K	2	5	14,14,15	0.38	0	17,19,21	1.08	2 (11%)
7	NAG	L	1	7,2	14,14,15	0.23	0	17,19,21	0.42	0
7	NAG	L	2	7	14,14,15	0.78	1 (7%)	17,19,21	1.22	1 (5%)
7	BMA	L	3	7	11,11,12	0.83	0	15,15,17	1.12	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	4/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	MAN	D	4	4	-	0/2/19/22	0/1/1/1
5	NAG	E	1	5,1	-	6/6/23/26	0/1/1/1
5	NAG	E	2	5	-	4/6/23/26	0/1/1/1
6	NAG	F	1	6,1	-	0/6/23/26	0/1/1/1
6	NAG	F	2	6	-	0/6/23/26	0/1/1/1
6	BMA	F	3	6	-	1/2/19/22	0/1/1/1
6	BMA	F	4	6	-	1/2/19/22	0/1/1/1
6	MAN	F	5	6	-	0/2/19/22	0/1/1/1
6	MAN	F	6	6	-	0/2/19/22	0/1/1/1
4	NAG	G	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	BMA	G	3	4	-	1/2/19/22	0/1/1/1
4	MAN	G	4	4	-	0/2/19/22	0/1/1/1
5	NAG	H	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	H	2	5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	I	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	I	2	5	-	2/6/23/26	0/1/1/1
7	NAG	J	1	7,1	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	0/6/23/26	0/1/1/1
7	BMA	J	3	7	-	0/2/19/22	0/1/1/1
5	NAG	K	1	2,5	-	2/6/23/26	0/1/1/1
5	NAG	K	2	5	-	2/6/23/26	0/1/1/1
7	NAG	L	1	7,2	-	2/6/23/26	0/1/1/1
7	NAG	L	2	7	-	1/6/23/26	0/1/1/1
7	BMA	L	3	7	-	1/2/19/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	1	NAG	O5-C1	-4.36	1.36	1.43
6	F	5	MAN	C1-C2	2.77	1.58	1.52
7	L	2	NAG	O5-C1	2.73	1.48	1.43
7	J	3	BMA	C1-C2	2.39	1.57	1.52
6	F	4	BMA	C4-C5	2.34	1.58	1.53

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1	NAG	C2-N2-C7	4.77	129.29	122.90
7	L	2	NAG	C1-O5-C5	4.71	118.50	112.19
5	E	1	NAG	C3-C4-C5	3.54	116.66	110.23
5	K	2	NAG	C1-O5-C5	3.46	116.82	112.19
5	I	2	NAG	C1-O5-C5	3.45	116.81	112.19

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

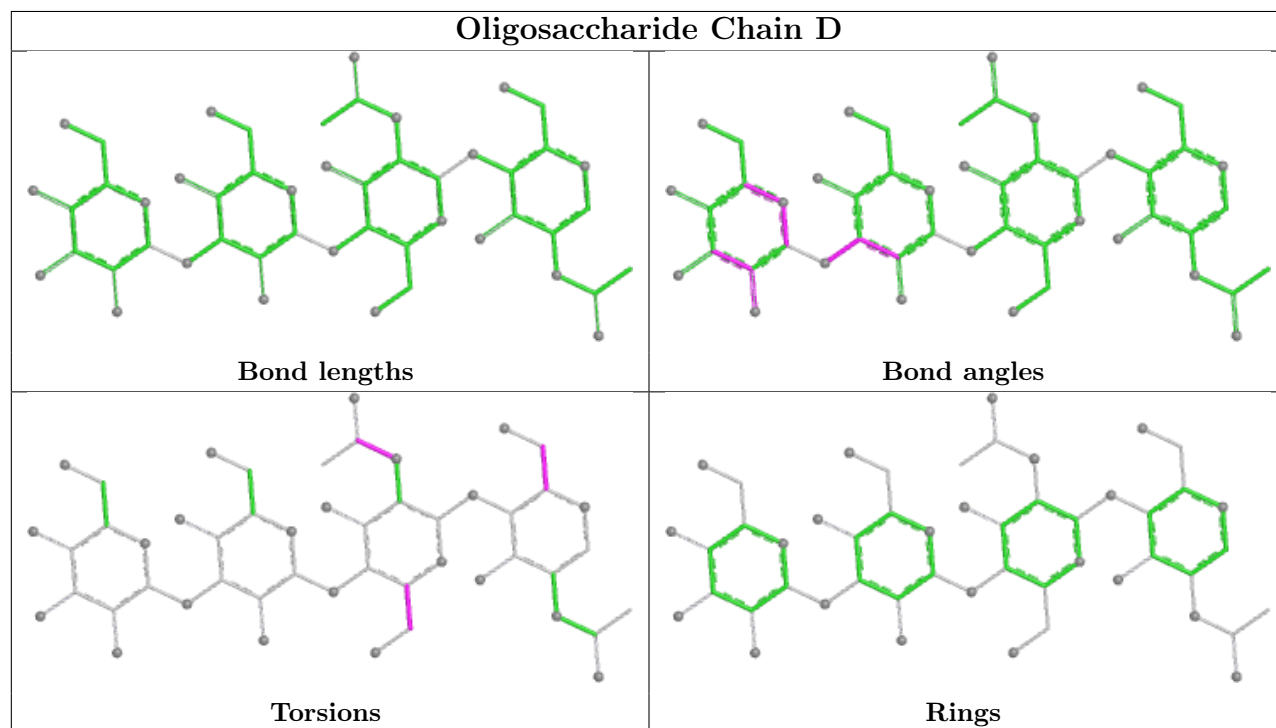
Mol	Chain	Res	Type	Atoms
4	D	1	NAG	O5-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6
5	H	1	NAG	O5-C5-C6-O6
5	E	1	NAG	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6

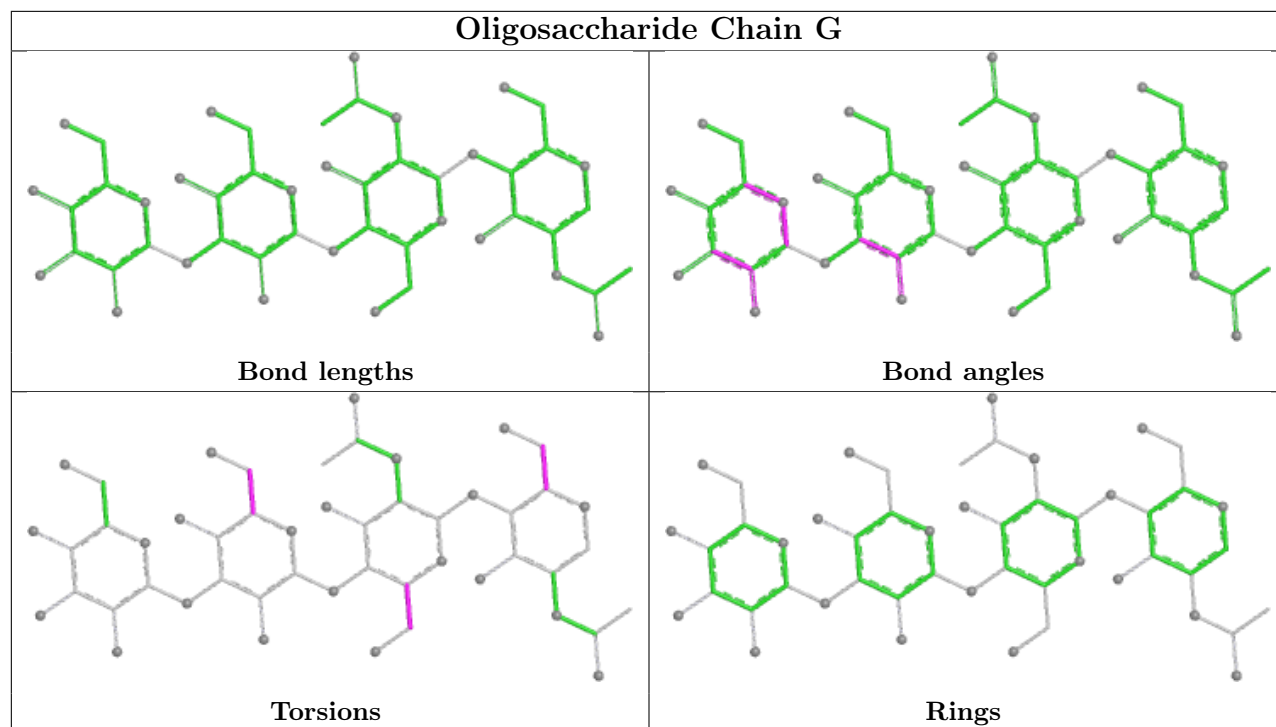
There are no ring outliers.

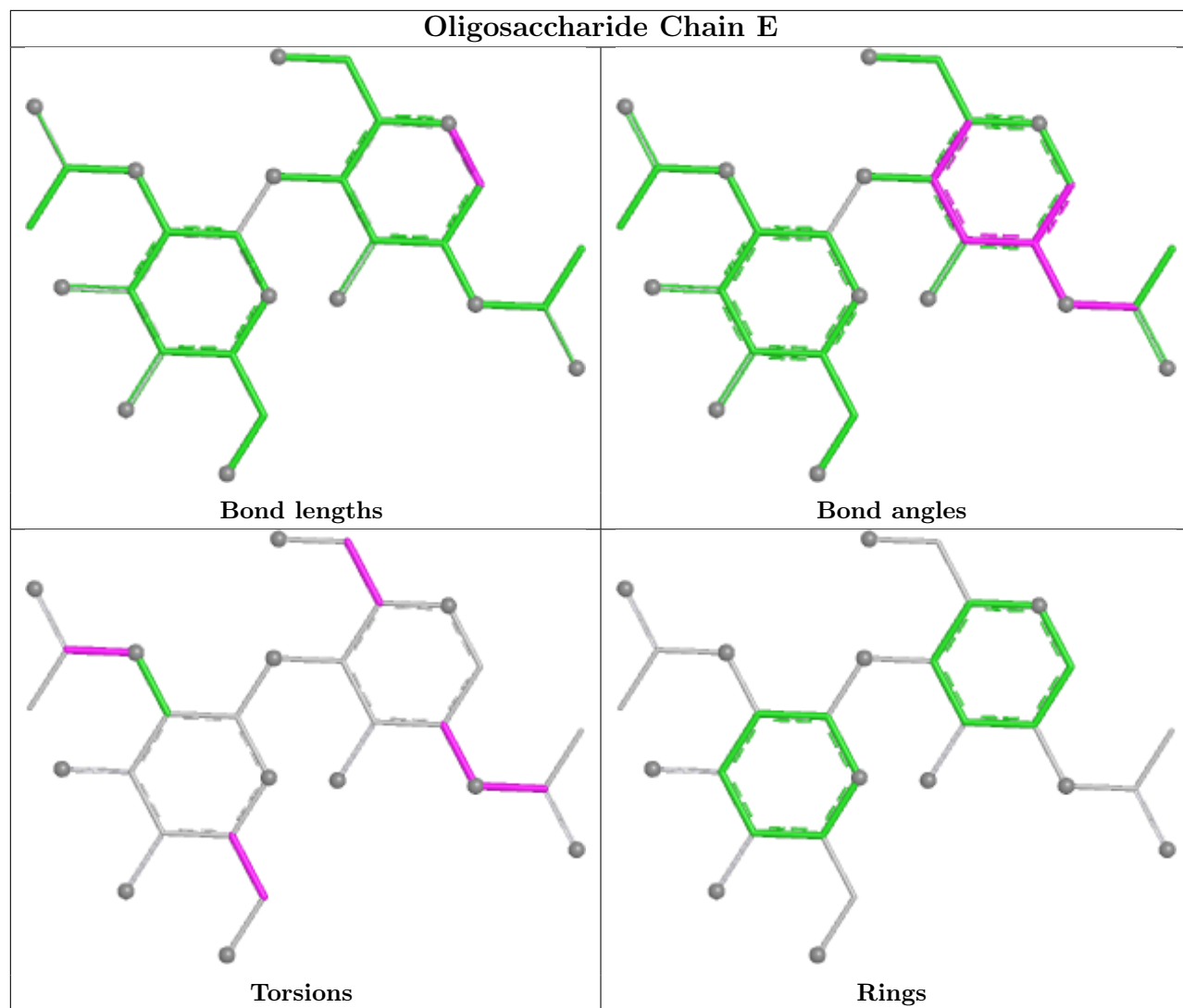
4 monomers are involved in 3 short contacts:

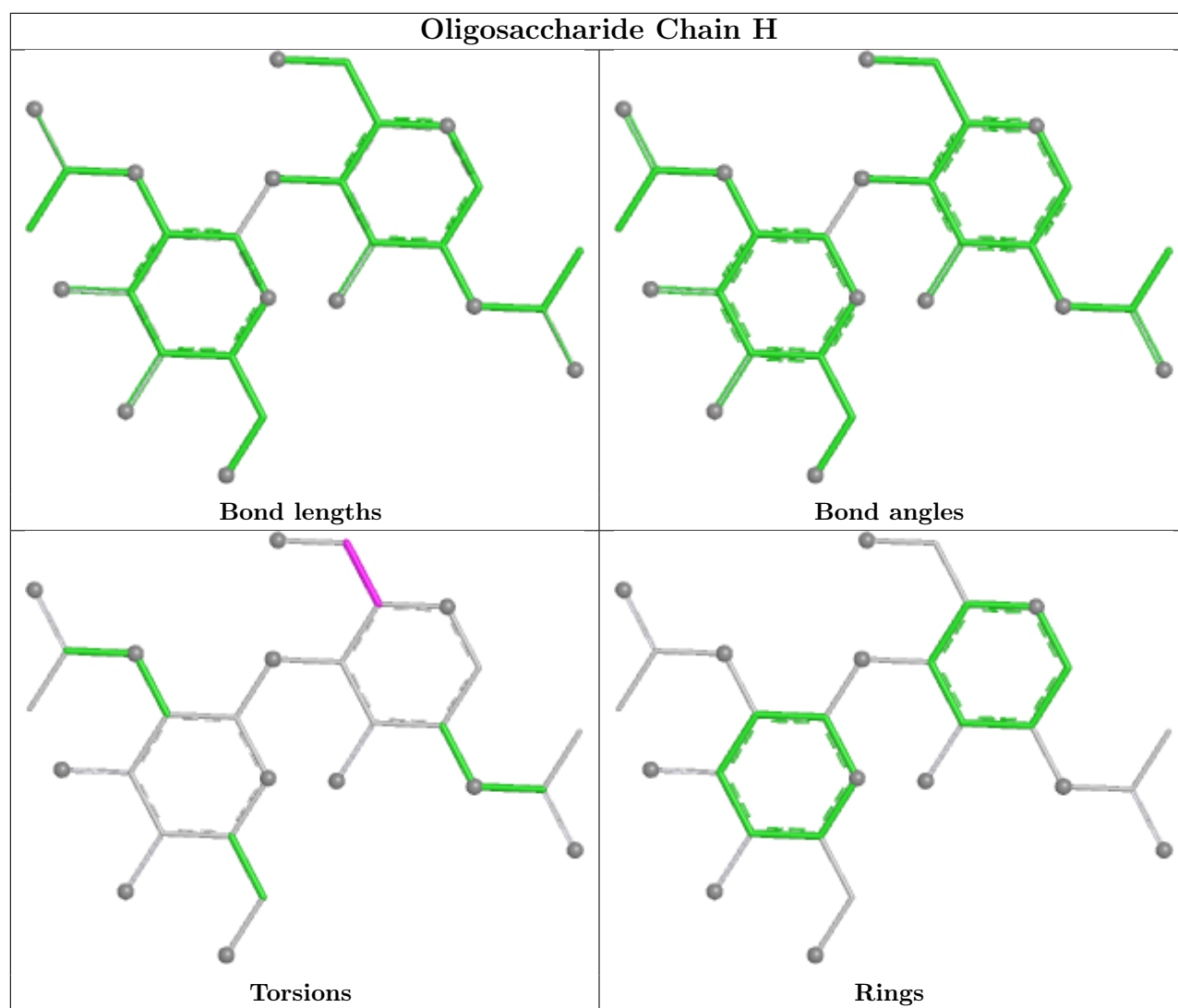
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	3	BMA	1	0
6	F	5	MAN	1	0
6	F	4	BMA	2	0
5	K	1	NAG	1	0

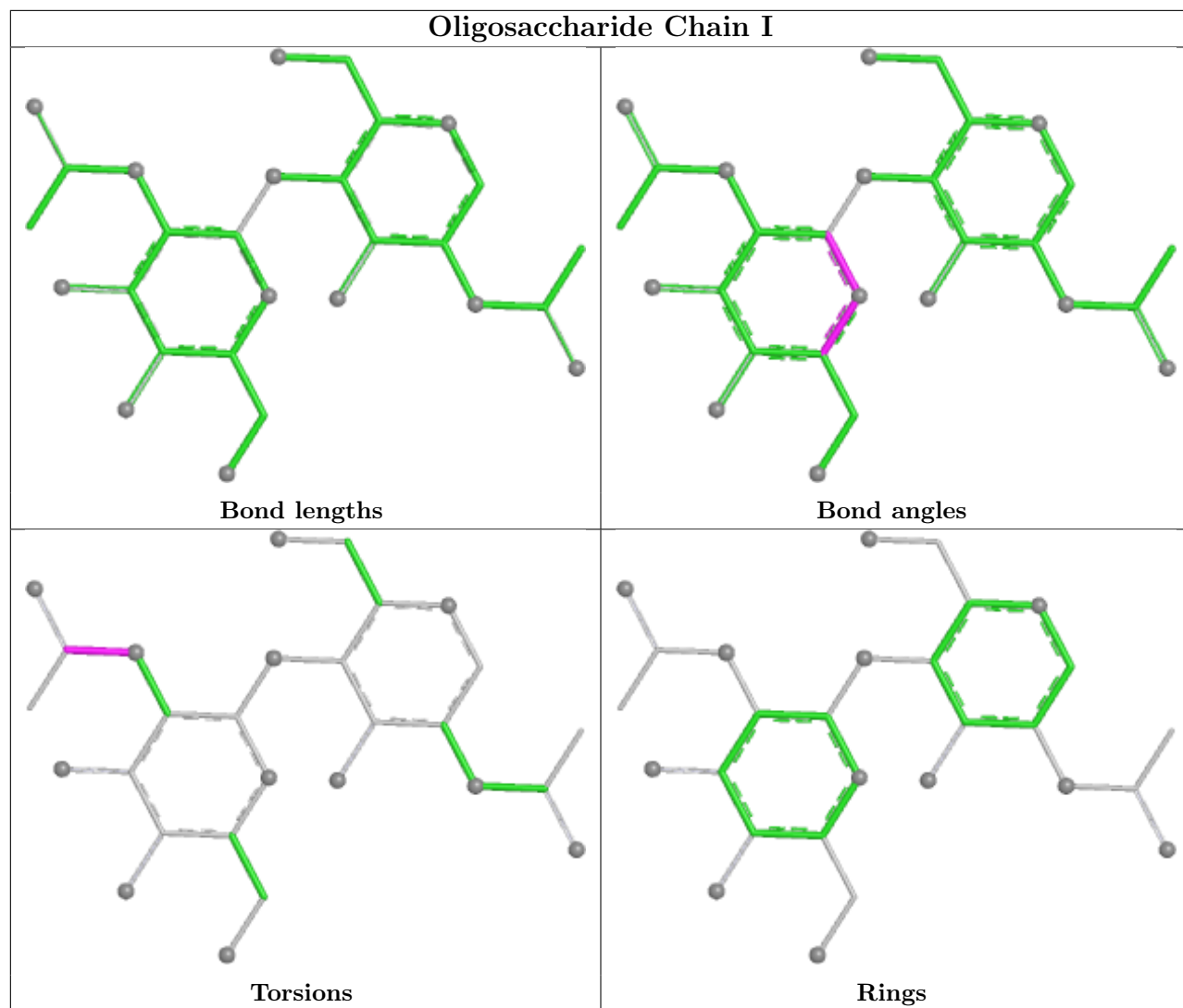
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

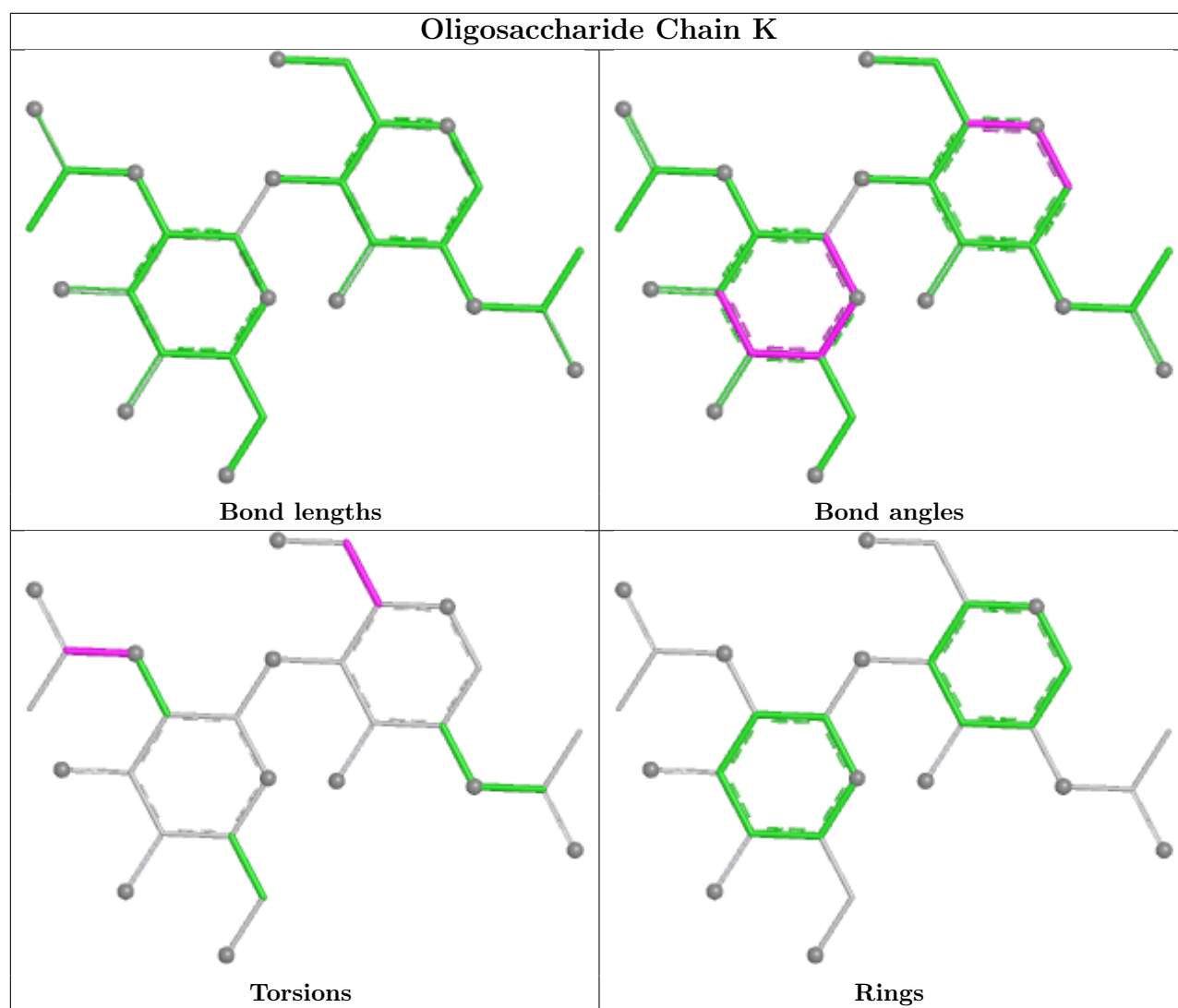




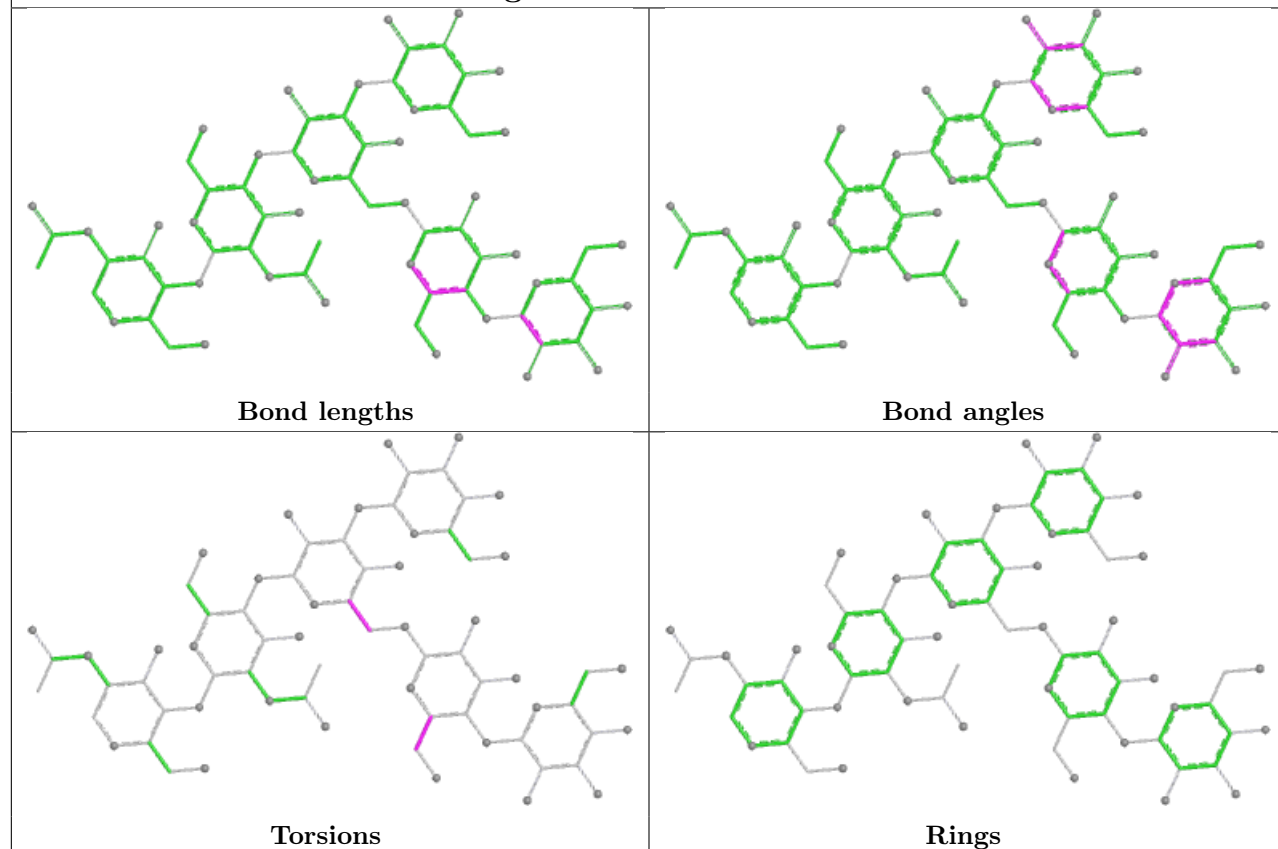




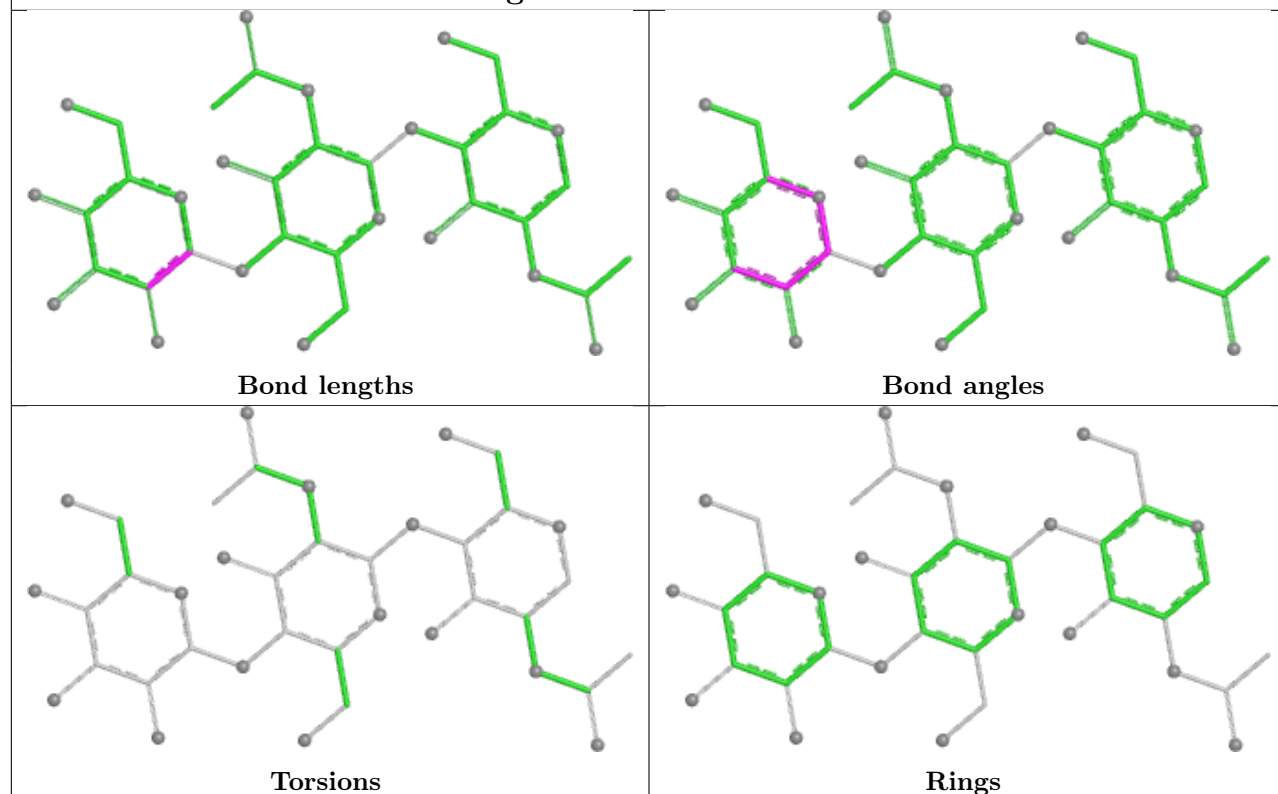


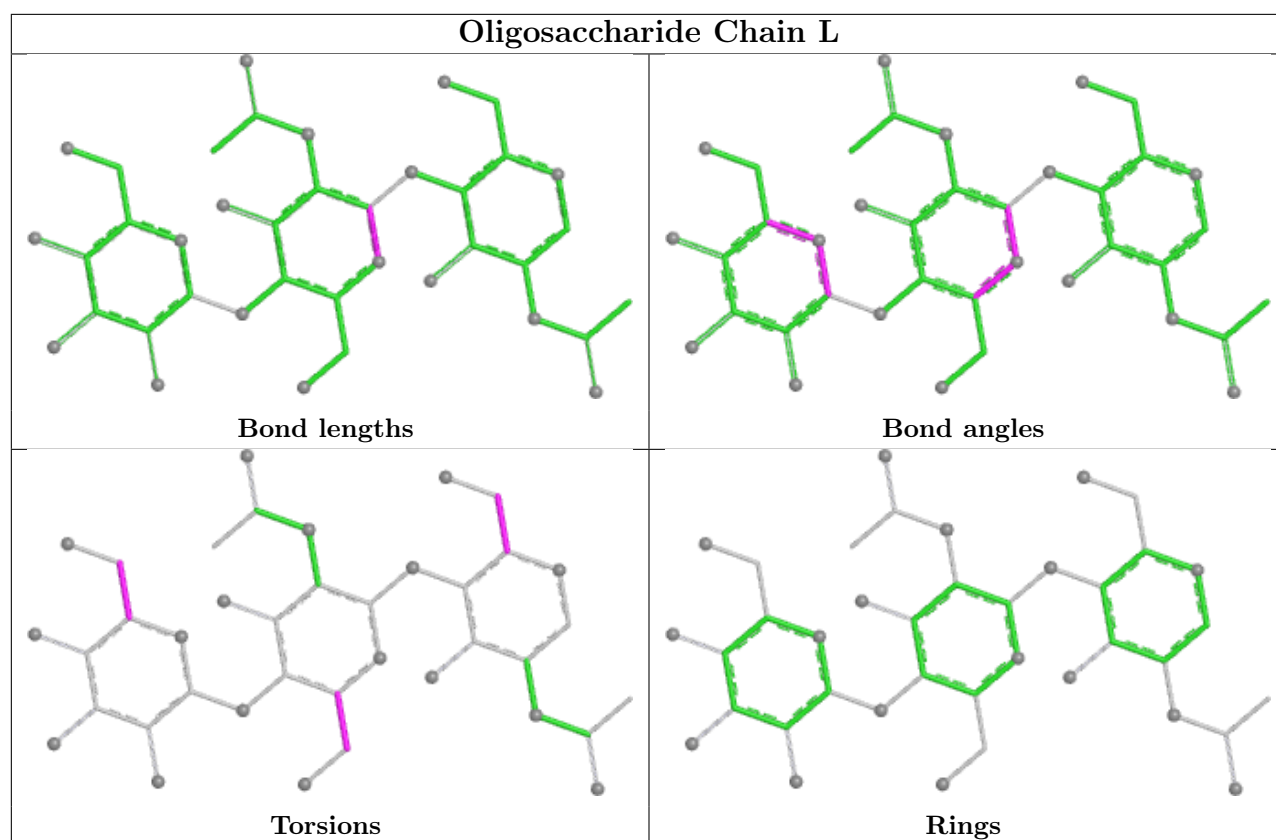


Oligosaccharide Chain F



Oligosaccharide Chain J





5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 8 are monoatomic - leaving 5 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	$\# Z > 2$
8	NAG	B	701	2	14,14,15	0.76	1 (7%)	17,19,21	1.23	1 (5%)
8	NAG	B	702	2	14,14,15	0.35	0	17,19,21	0.62	0
8	NAG	A	1001	1	14,14,15	0.27	0	17,19,21	0.46	0
8	NAG	A	1002	1	14,14,15	0.85	1 (7%)	17,19,21	1.22	1 (5%)
8	NAG	A	1003	1	14,14,15	0.27	0	17,19,21	0.53	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
8	NAG	B	701	2	-	1/6/23/26	0/1/1/1
8	NAG	B	702	2	-	2/6/23/26	0/1/1/1
8	NAG	A	1001	1	-	2/6/23/26	0/1/1/1
8	NAG	A	1002	1	-	1/6/23/26	0/1/1/1
8	NAG	A	1003	1	-	1/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1002	NAG	O5-C1	2.99	1.48	1.43
8	B	701	NAG	O5-C1	2.70	1.48	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	701	NAG	C1-O5-C5	4.84	118.68	112.19
8	A	1002	NAG	C1-O5-C5	4.80	118.62	112.19

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1001	NAG	O5-C5-C6-O6
8	A	1001	NAG	C4-C5-C6-O6
8	B	702	NAG	O5-C5-C6-O6
8	B	702	NAG	C4-C5-C6-O6
8	B	701	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	702	NAG	2	0
8	A	1002	NAG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	924/959 (96%)	-0.15	11 (1%) 76 64	48, 83, 135, 155	0
2	B	690/692 (99%)	0.16	26 (3%) 44 33	50, 96, 190, 224	1 (0%)
3	C	93/98 (94%)	0.88	12 (12%) 9 9	70, 186, 307, 319	0
All	All	1707/1749 (97%)	0.03	49 (2%) 54 39	48, 90, 187, 319	1 (0%)

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	1505	ILE	4.0
2	B	677	SER	3.7
1	A	550	ASP	3.7
3	C	1428	ALA	3.6
2	B	37	ARG	3.5

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MAN	D	4	11/12	0.34	0.10	157,165,170,173	0
7	BMA	J	3	11/12	0.37	0.13	160,166,175,175	0
4	MAN	G	4	11/12	0.45	0.12	144,152,158,162	0

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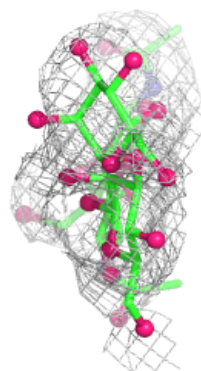
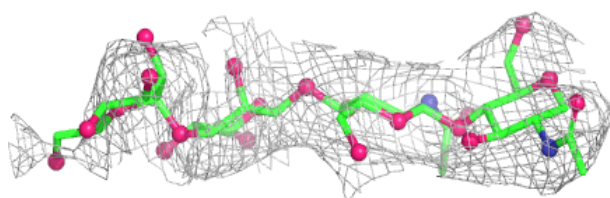
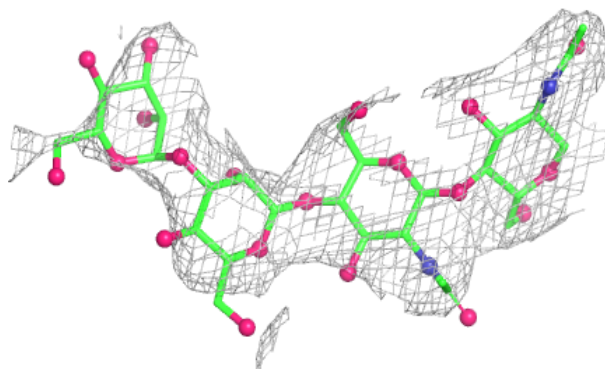
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	NAG	J	2	14/15	0.49	0.13	121,137,156,169	0
4	BMA	G	3	11/12	0.53	0.13	145,147,159,167	0
4	NAG	G	2	14/15	0.60	0.14	122,138,152,159	0
5	NAG	H	2	14/15	0.60	0.11	126,135,138,141	0
4	BMA	D	3	11/12	0.62	0.09	140,150,154,161	0
5	NAG	I	2	14/15	0.64	0.11	137,144,154,156	0
5	NAG	E	2	14/15	0.66	0.12	127,136,146,150	0
6	MAN	F	6	11/12	0.67	0.10	109,121,135,136	0
5	NAG	K	2	14/15	0.73	0.14	134,138,153,158	0
7	BMA	L	3	11/12	0.74	0.11	103,112,118,119	0
5	NAG	I	1	14/15	0.75	0.11	107,127,143,146	0
6	BMA	F	4	11/12	0.75	0.12	90,106,127,128	0
5	NAG	H	1	14/15	0.76	0.11	111,127,138,141	0
5	NAG	E	1	14/15	0.80	0.10	101,119,128,137	0
5	NAG	K	1	14/15	0.83	0.12	91,117,137,141	0
4	NAG	G	1	14/15	0.85	0.11	108,126,140,148	0
6	MAN	F	5	11/12	0.85	0.10	100,107,116,117	0
6	BMA	F	3	11/12	0.85	0.07	88,95,111,122	0
4	NAG	D	2	14/15	0.87	0.09	100,112,117,135	0
7	NAG	L	2	14/15	0.88	0.14	96,111,123,123	0
7	NAG	J	1	14/15	0.92	0.07	76,100,118,120	0
4	NAG	D	1	14/15	0.94	0.09	75,86,101,106	0
6	NAG	F	2	14/15	0.96	0.07	47,62,87,94	0
7	NAG	L	1	14/15	0.96	0.07	75,100,107,107	0
6	NAG	F	1	14/15	0.97	0.06	45,60,89,90	0

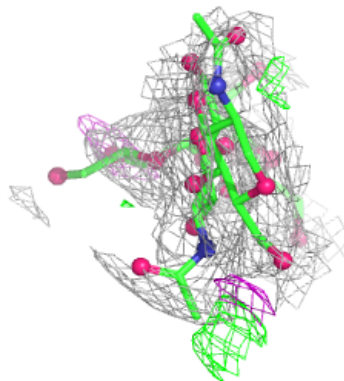
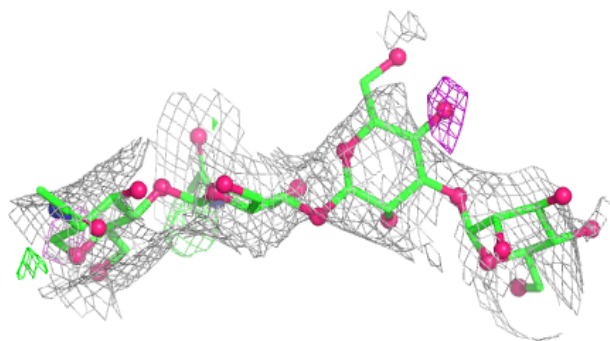
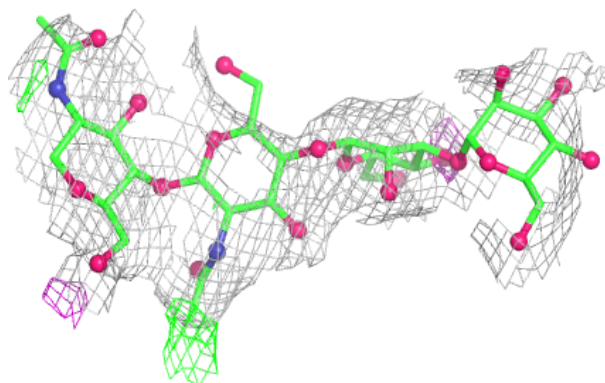
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain D:

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

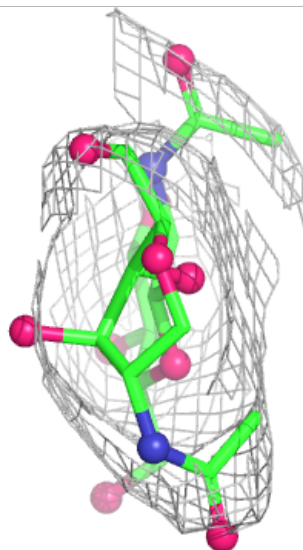
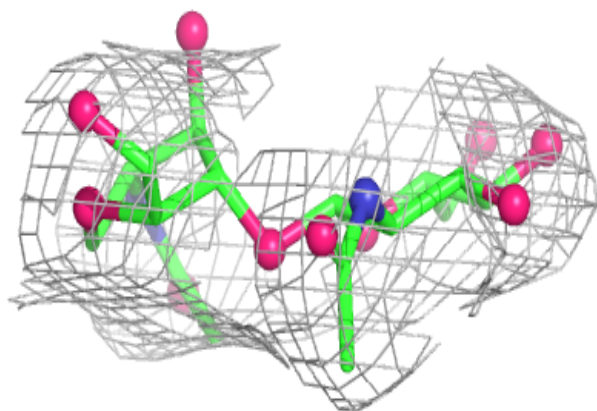
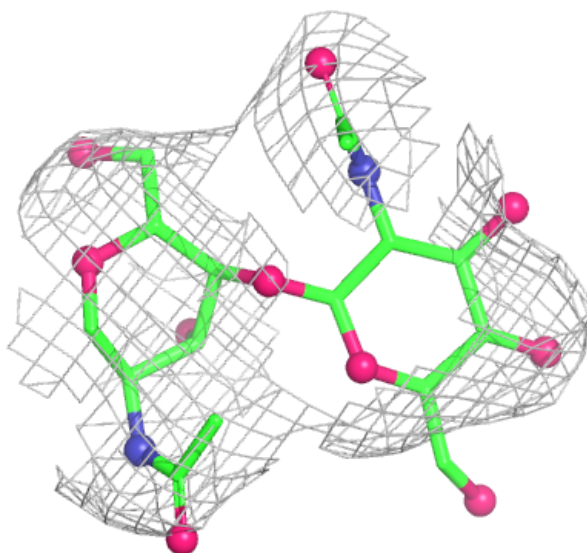
**Electron density around Chain G:**

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



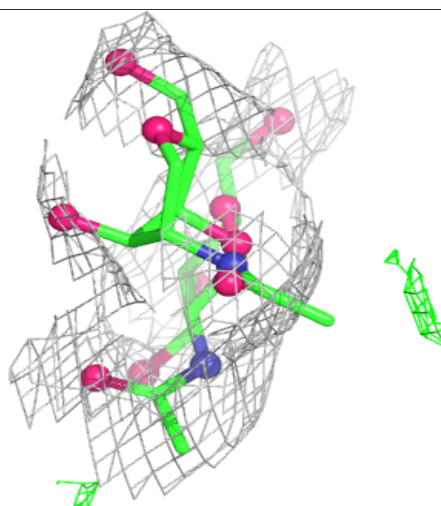
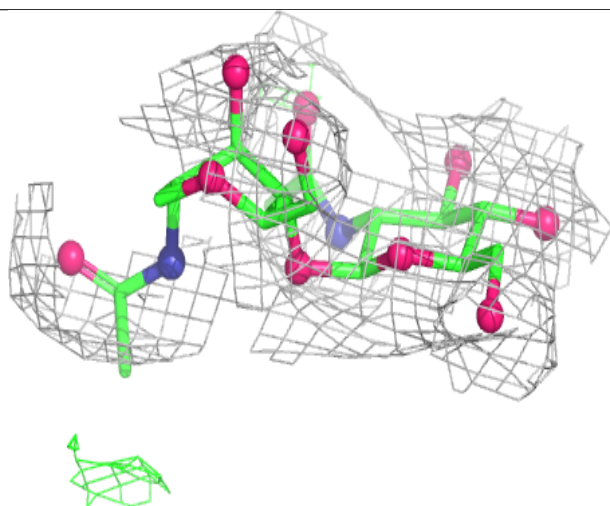
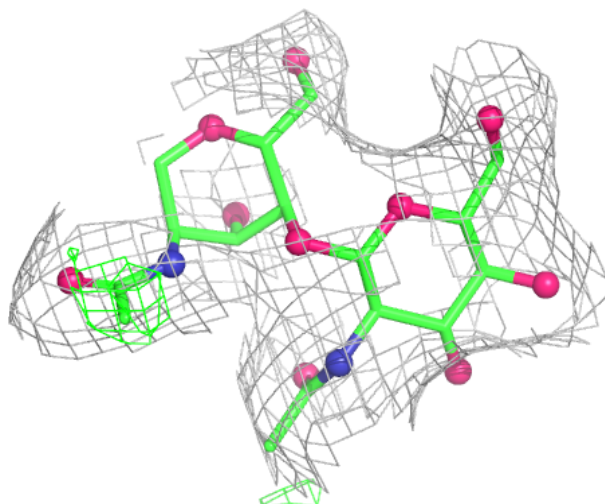
Electron density around Chain E:

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



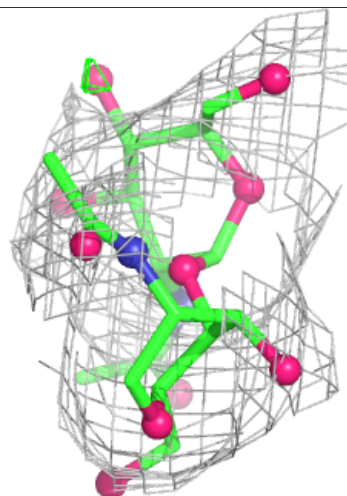
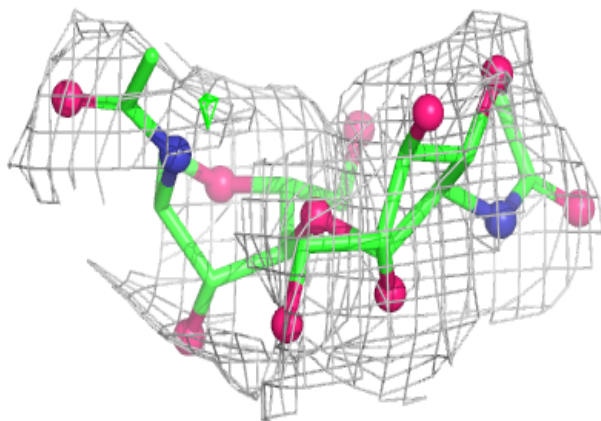
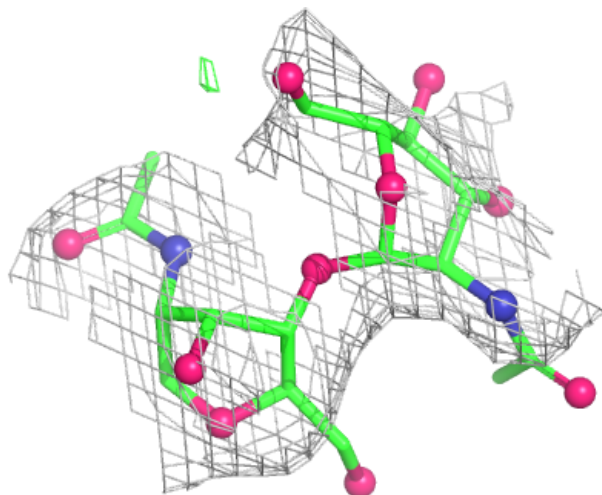
Electron density around Chain H:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



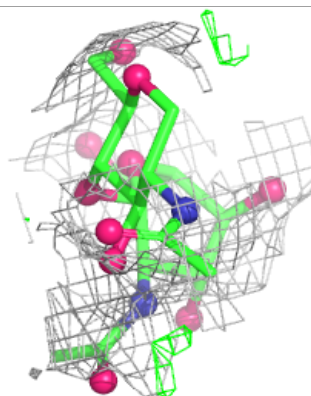
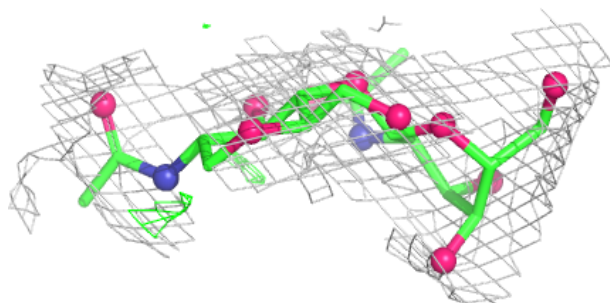
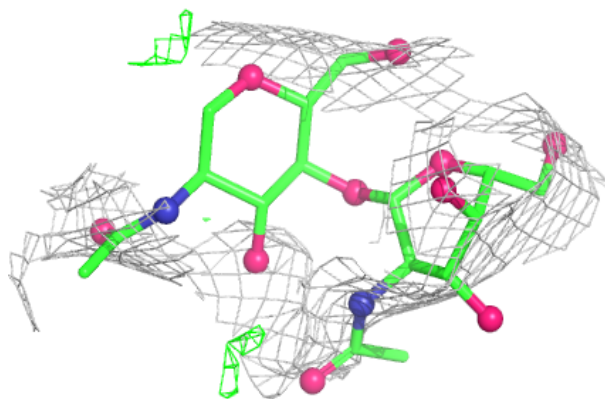
Electron density around Chain I:

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

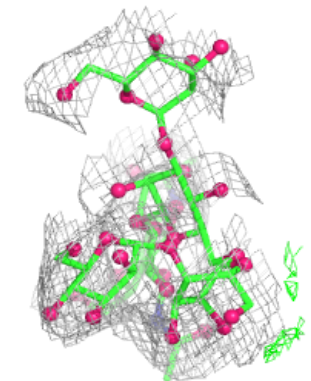
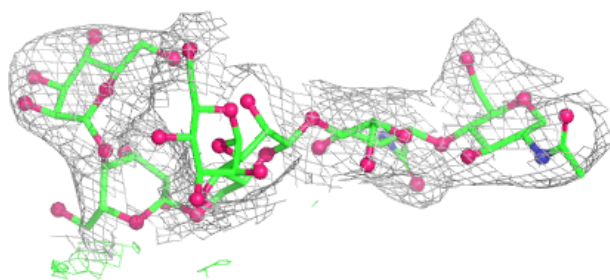
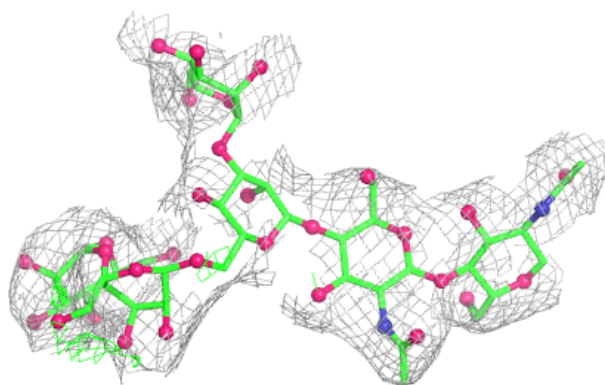


Electron density around Chain K:

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

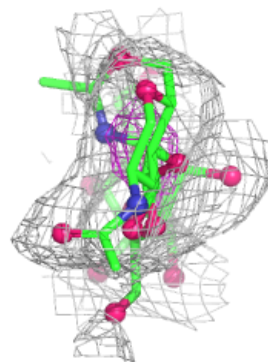
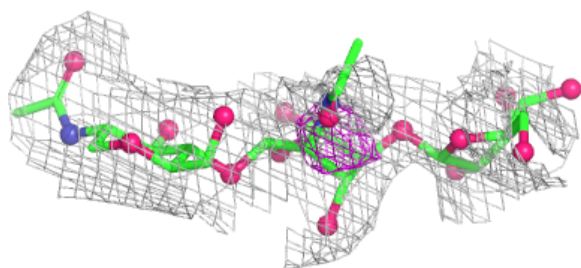
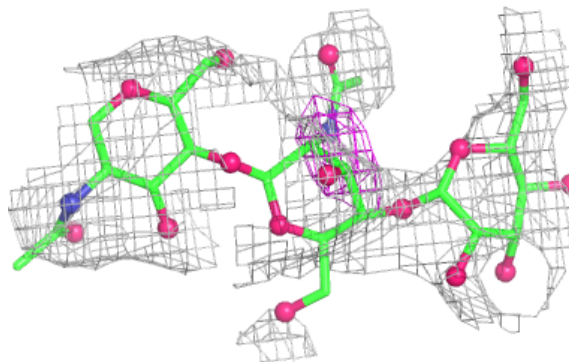
**Electron density around Chain F:**

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

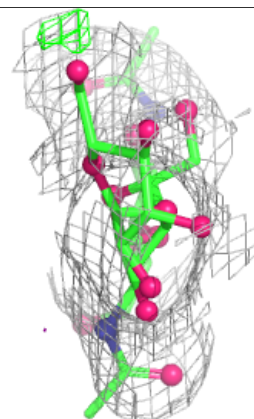
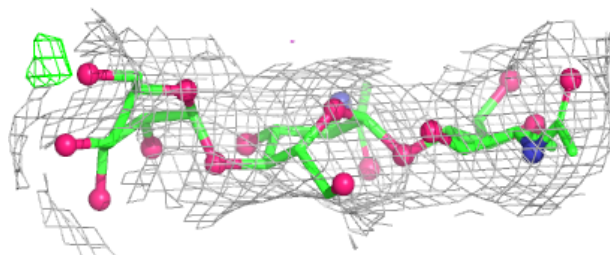
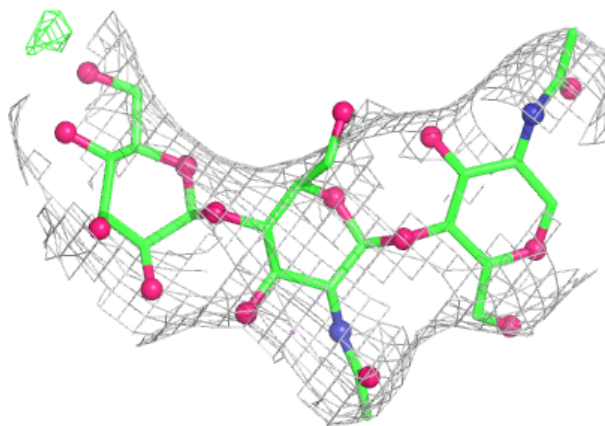


Electron density around Chain J:

$2mF_o-DF_c$ (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)



6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	NAG	A	1002	14/15	0.58	0.11	164,180,187,187	0
8	NAG	A	1001	14/15	0.63	0.12	143,162,169,172	0
8	NAG	B	701	14/15	0.64	0.13	101,128,137,148	0
8	NAG	A	1003	14/15	0.77	0.11	93,108,117,120	0
8	NAG	B	702	14/15	0.87	0.09	80,95,106,114	0
9	MN	A	1004	1/1	0.92	0.08	96,96,96,96	0
9	MN	A	1005	1/1	0.95	0.06	84,84,84,84	0
9	MN	A	1006	1/1	0.97	0.09	119,119,119,119	0
9	MN	B	704	1/1	0.97	0.05	81,81,81,81	0
9	MN	A	1007	1/1	0.98	0.09	114,114,114,114	0
9	MN	A	1008	1/1	0.99	0.03	92,92,92,92	0
9	MN	B	705	1/1	0.99	0.02	55,55,55,55	0
9	MN	B	703	1/1	1.00	0.02	57,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.