



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:17 PM UTC

PDB ID : 5ELF / pdb\_00005elf  
Title : Cholera toxin El Tor B-pentamer in complex with A-pentasaccharide  
Authors : Heggelund, J.E.; Burschowsky, D.; Krenzel, U.  
Deposited on : 2015-11-04  
Resolution : 1.55 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

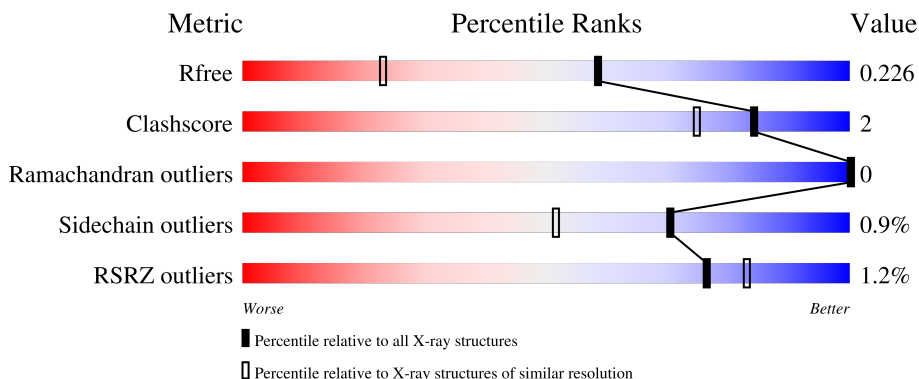
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.55 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.



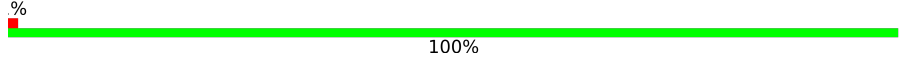
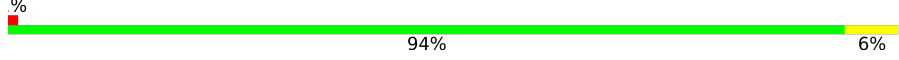
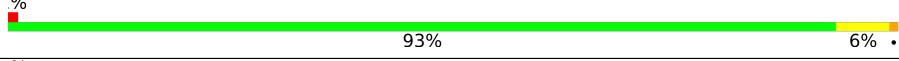
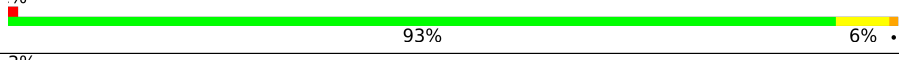
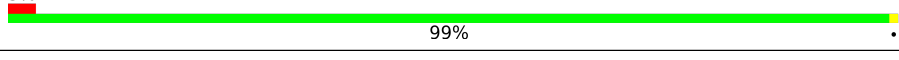
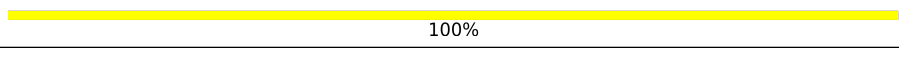
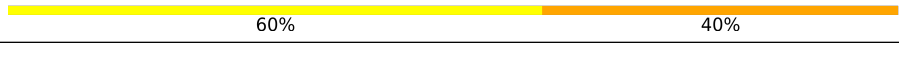
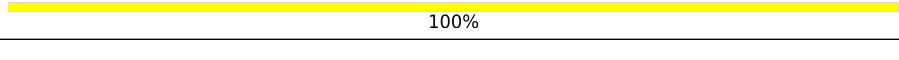
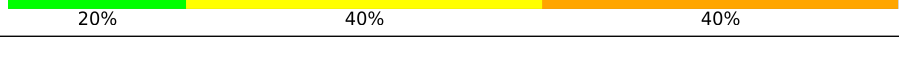



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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  $\geq 3$ , 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	103	99%
1	B	103	95% 5%
1	C	103	97% .
1	D	103	92% 7% .
1	E	103	95% 5%

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Mol	Chain	Length	Quality of chain
1	F	103	 100%
1	G	103	 94% 6%
1	H	103	 93% 6%
1	I	103	 93% 6%
1	J	103	 99%
2	K	5	 100%
2	M	5	 60% 40%
2	P	5	 100%
2	Q	5	 20% 40% 40%
3	L	5	 40% 60%
3	N	5	 20% 80%
3	O	5	 40% 60%

## 2 Entry composition i

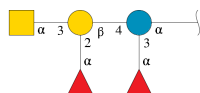
There are 9 unique types of molecules in this entry. The entry contains 10185 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Cholera enterotoxin subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	103	Total 829	C 525	N 142	O 157	S 5	0	2	0
1	B	103	Total 828	C 524	N 141	O 158	S 5	0	2	0
1	C	103	Total 834	C 531	N 142	O 156	S 5	0	3	0
1	D	103	Total 836	C 528	N 145	O 158	S 5	0	2	0
1	E	103	Total 823	C 521	N 141	O 156	S 5	0	1	0
1	F	103	Total 823	C 521	N 141	O 156	S 5	0	1	0
1	G	103	Total 826	C 522	N 142	O 157	S 5	0	1	0
1	H	103	Total 817	C 516	N 140	O 156	S 5	0	0	0
1	I	103	Total 817	C 516	N 140	O 156	S 5	0	0	0
1	J	103	Total 829	C 526	N 142	O 156	S 5	0	2	0

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



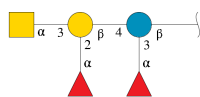
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	K	5	Total 57	C 32	N 1	O 24	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	M	5	Total	C	N	O	0	0	0
			57	32	1	24			
2	P	5	Total	C	N	O	0	0	0
			57	32	1	24			
2	Q	5	Total	C	N	O	0	5	0
			114	64	2	48			

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

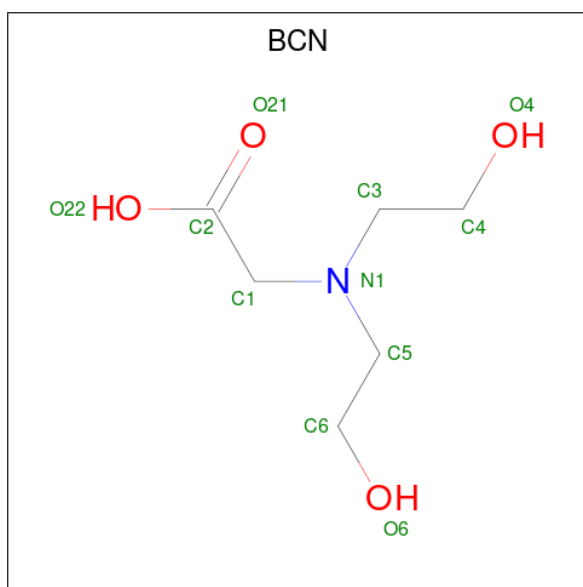


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	L	5	Total	C	N	O	0	5	0
			102	58	2	42			
3	N	5	Total	C	N	O	0	0	0
			57	32	1	24			
3	O	5	Total	C	N	O	0	5	0
			102	58	2	42			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

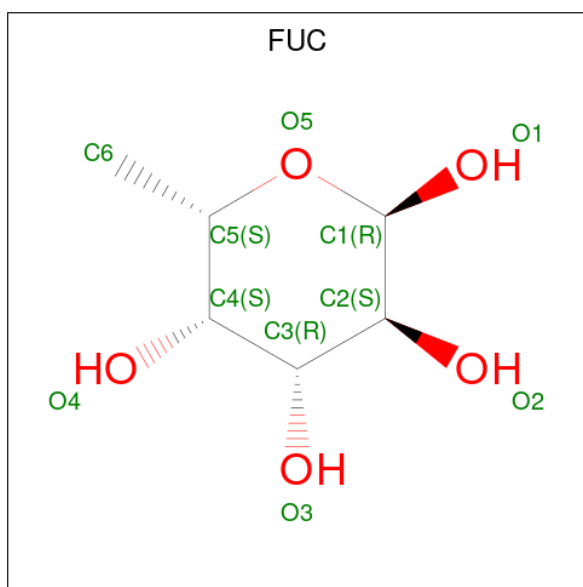
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Ca	0	0
			2	2		
4	B	2	Total	Ca	0	0
			2	2		
4	C	2	Total	Ca	0	0
			2	2		
4	D	2	Total	Ca	0	0
			2	2		
4	E	2	Total	Ca	0	0
			2	2		

- Molecule 5 is BICINE (CCD ID: BCN) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>).



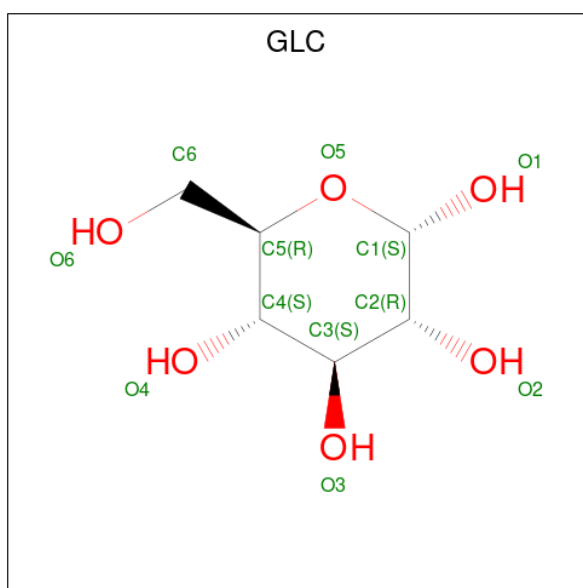
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	11	6	1	4	0	0
5	A	1	11	6	1	4	0	0
5	B	1	11	6	1	4	0	0
5	B	1	11	6	1	4	0	0
5	C	1	11	6	1	4	0	0
5	C	1	11	6	1	4	0	0
5	D	1	11	6	1	4	0	0
5	D	1	11	6	1	4	0	0
5	E	1	11	6	1	4	0	0
5	E	1	11	6	1	4	0	0

- Molecule 6 is alpha-L-fucopyranose (CCD ID: FUC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>5</sub>).



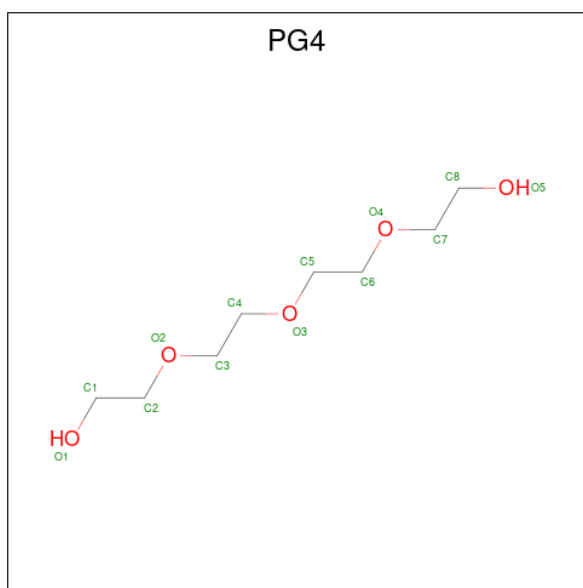
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			11	6	5		
6	H	1	Total	C	O	0	0
			11	6	5		

- Molecule 7 is alpha-D-glucopyranose (CCD ID: GLC) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	1
			12	6	6		
7	G	1	Total	C	O	0	1
			12	6	6		

- Molecule 8 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	F	1	Total	C O	0	0
			13	8 5		

- Molecule 9 is water.

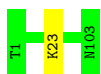
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	106	Total	O	0	0
			106	106		
9	B	102	Total	O	0	1
			103	103		
9	C	111	Total	O	0	0
			111	111		
9	D	128	Total	O	0	0
			128	128		
9	E	126	Total	O	0	0
			126	126		
9	F	123	Total	O	0	2
			125	125		
9	G	131	Total	O	0	1
			132	132		
9	H	115	Total	O	0	0
			115	115		
9	I	127	Total	O	0	0
			127	127		
9	J	125	Total	O	0	0
			125	125		

### 3 Residue-property plots [i](#)

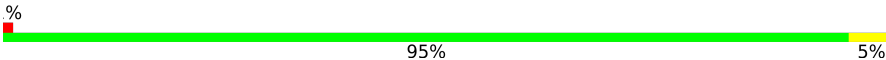
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

Chain A:  99%



- Molecule 1: Cholera enterotoxin subunit B

Chain B:  95%



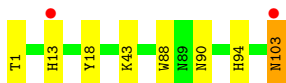
- Molecule 1: Cholera enterotoxin subunit B

Chain C:  97%



- Molecule 1: Cholera enterotoxin subunit B

Chain D:  92%



- Molecule 1: Cholera enterotoxin subunit B

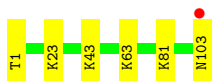
Chain E:  95%



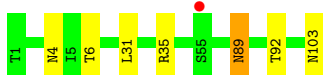
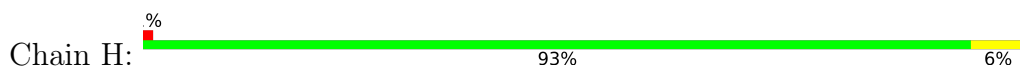
- Molecule 1: Cholera enterotoxin subunit B



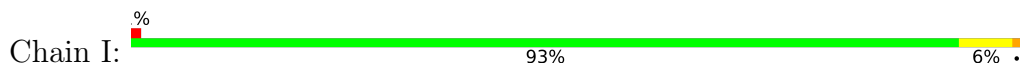
- Molecule 1: Cholera enterotoxin subunit B



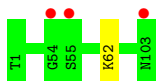
- Molecule 1: Cholera enterotoxin subunit B



- Molecule 1: Cholera enterotoxin subunit B



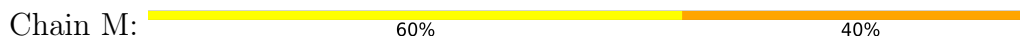
- Molecule 1: Cholera enterotoxin subunit B



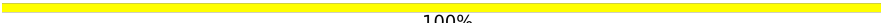
- Molecule 2: alpha-L-fucopyranose-(1-2)-[2-acetamido-2-deoxy-alpha-D-galactopyranose-(1-3)]beta-D-galactopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]alpha-D-glucopyranose



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

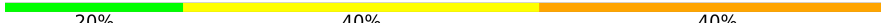


- Molecule 2: alpha-L-fucopyranose-(1-2)-[2-acetamido-2-deoxy-alpha-D-galactopyranose-(1-3)]beta-D-galactopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]alpha-D-glucopyranose

Chain P:  100%

GLC1  
GAL2  
FUC3  
A2G4  
FUC5

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

Chain Q:  20% 40% 40%

GLC1  
GAL2  
FUC3  
A2G4  
FUC5

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

Chain L:  40% 60%

BGC1  
GAL2  
FUC3  
A2G4  
FUC5

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

Chain N:  20% 80%

BGC1  
GAL2  
FUC3  
A2G4  
FUC5

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

Chain O:  40% 60%

BGC1  
GAL2  
FUC3  
A2G4  
FUC5

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.63Å 84.72Å 195.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.92 – 1.55 48.92 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.92-1.55) 99.7 (48.92-1.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.07 (at 1.55Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.179 , 0.220 0.189 , 0.226	Depositor DCC
$R_{free}$ test set	7666 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.4	Xtrriage
Anisotropy	0.641	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 42.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10185	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GLC, BCN, FUC, A2G, GAL, BGC, PG4, CA

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	0.95	0/849	0.94	0/1145
1	B	0.94	0/848	0.88	0/1144
1	C	0.97	0/857	0.89	0/1155
1	D	0.93	0/851	0.97	0/1148
1	E	1.00	0/840	0.93	0/1133
1	F	1.06	0/840	0.92	0/1133
1	G	1.03	0/840	0.92	0/1133
1	H	1.08	0/831	0.95	0/1122
1	I	1.02	0/831	0.92	0/1122
1	J	1.08	0/849	0.98	0/1144
All	All	1.01	0/8436	0.93	0/11379

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 [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	829	0	844	0	0
1	B	828	0	840	8	0
1	C	834	0	860	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	836	0	841	6	0
1	E	823	0	836	4	0
1	F	823	0	836	0	0
1	G	826	0	835	4	0
1	H	817	0	823	6	0
1	I	817	0	823	7	0
1	J	829	0	849	1	0
2	K	57	0	50	0	0
2	M	57	0	50	2	0
2	P	57	0	50	0	0
2	Q	114	0	100	2	0
3	L	102	0	85	5	0
3	N	57	0	50	0	0
3	O	102	0	86	3	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
5	A	22	0	20	0	0
5	B	22	0	20	0	0
5	C	22	0	20	0	0
5	D	22	0	20	0	0
5	E	22	0	20	0	0
6	B	11	0	12	1	0
6	H	11	0	12	0	0
7	D	12	0	5	3	0
7	G	12	0	6	0	0
8	F	13	0	18	0	0
9	A	106	0	0	0	0
9	B	103	0	0	1	0
9	C	111	0	0	1	0
9	D	128	0	0	2	0
9	E	126	0	0	1	0
9	F	125	0	0	0	0
9	G	132	0	0	2	0
9	H	115	0	0	2	0
9	I	127	0	0	2	0
9	J	125	0	0	0	0
All	All	10185	0	9011	42	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 42 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:D:103:ASN:O	1:G:43:LYS:NZ	2.30	0.65
1:B:103:ASN:HD21	1:I:23:LYS:CE	2.12	0.61
1:H:35:ARG:NH1	9:H:301:HOH:O	2.33	0.61
2:Q:1[A]:GLC:O6	2:Q:3[A]:FUC:H3	2.02	0.59
1:H:103:ASN:ND2	9:H:304:HOH:O	2.39	0.55

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	103/103 (100%)	102 (99%)	1 (1%)	0	100	100
1	B	103/103 (100%)	101 (98%)	2 (2%)	0	100	100
1	C	104/103 (101%)	103 (99%)	1 (1%)	0	100	100
1	D	103/103 (100%)	102 (99%)	1 (1%)	0	100	100
1	E	102/103 (99%)	101 (99%)	1 (1%)	0	100	100
1	F	102/103 (99%)	101 (99%)	1 (1%)	0	100	100
1	G	102/103 (99%)	101 (99%)	1 (1%)	0	100	100
1	H	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
1	I	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
1	J	103/103 (100%)	101 (98%)	2 (2%)	0	100	100
All	All	1024/1030 (99%)	1010 (99%)	14 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	91/89 (102%)	90 (99%)	1 (1%)	65	43
1	B	91/89 (102%)	91 (100%)	0	100	100
1	C	92/89 (103%)	92 (100%)	0	100	100
1	D	91/89 (102%)	89 (98%)	2 (2%)	45	18
1	E	90/89 (101%)	89 (99%)	1 (1%)	65	43
1	F	90/89 (101%)	90 (100%)	0	100	100
1	G	90/89 (101%)	89 (99%)	1 (1%)	65	43
1	H	89/89 (100%)	88 (99%)	1 (1%)	65	43
1	I	89/89 (100%)	87 (98%)	2 (2%)	45	18
1	J	91/89 (102%)	91 (100%)	0	100	100
All	All	904/890 (102%)	896 (99%)	8 (1%)	70	51

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	23	LYS
1	I	18	TYR
1	G	63	LYS
1	E	29	GLU
1	H	89	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	94	HIS
1	G	103	ASN
1	J	16	GLN
1	G	16	GLN
1	H	3	GLN

### 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](#)

48 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	GLC	K	1	2	12,12,12	0.97	1 (8%)	17,17,17	1.34	3 (17%)
2	GAL	K	2	2	11,11,12	0.98	0	15,15,17	1.57	1 (6%)
2	FUC	K	3	2	10,10,11	1.11	1 (10%)	14,14,16	0.87	1 (7%)
2	A2G	K	4	2	14,14,15	1.52	4 (28%)	17,19,21	2.05	4 (23%)
2	FUC	K	5	2	10,10,11	1.45	1 (10%)	14,14,16	1.14	2 (14%)
3	BGC	L	1[A]	3	12,12,12	0.83	1 (8%)	17,17,17	1.33	2 (11%)
3	GAL	L	2[A]	3	11,11,12	1.68	3 (27%)	15,15,17	1.82	4 (26%)
3	GAL	L	2[B]	3,7	11,11,12	1.08	0	15,15,17	1.33	2 (13%)
3	FUC	L	3[A]	3	10,10,11	0.94	0	14,14,16	0.74	0
3	FUC	L	3[B]	3	10,10,11	0.89	0	14,14,16	0.92	0
3	A2G	L	4[A]	3	14,14,15	0.88	1 (7%)	17,19,21	1.46	3 (17%)
3	A2G	L	4[B]	3	14,14,15	1.19	2 (14%)	17,19,21	1.35	2 (11%)
3	FUC	L	5[A]	3	10,10,11	1.21	1 (10%)	14,14,16	0.62	0
3	FUC	L	5[B]	7	10,10,11	0.79	0	14,14,16	0.90	0
2	GLC	M	1	2	12,12,12	0.65	0	17,17,17	1.25	2 (11%)
2	GAL	M	2	2	11,11,12	1.04	1 (9%)	15,15,17	1.05	1 (6%)
2	FUC	M	3	2	10,10,11	1.03	0	14,14,16	1.11	1 (7%)
2	A2G	M	4	2	14,14,15	1.82	4 (28%)	17,19,21	3.17	6 (35%)
2	FUC	M	5	2	10,10,11	1.46	1 (10%)	14,14,16	1.21	2 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	BGC	N	1	3	12,12,12	1.44	3 (25%)	17,17,17	1.29	2 (11%)
3	GAL	N	2	3	11,11,12	1.34	2 (18%)	15,15,17	1.47	2 (13%)
3	FUC	N	3	3	10,10,11	0.76	0	14,14,16	0.80	0
3	A2G	N	4	3	14,14,15	1.40	2 (14%)	17,19,21	1.51	2 (11%)
3	FUC	N	5	3	10,10,11	2.14	4 (40%)	14,14,16	0.52	0
3	BGC	O	1[B]	3	12,12,12	0.90	0	17,17,17	1.60	1 (5%)
3	GAL	O	2[A]	3,7	11,11,12	1.24	1 (9%)	15,15,17	1.15	0
3	GAL	O	2[B]	3	11,11,12	1.21	1 (9%)	15,15,17	1.04	1 (6%)
3	FUC	O	3[A]	3	10,10,11	0.97	0	14,14,16	0.92	1 (7%)
3	FUC	O	3[B]	3	10,10,11	0.73	0	14,14,16	1.07	1 (7%)
3	A2G	O	4[A]	3	14,14,15	1.50	4 (28%)	17,19,21	1.47	2 (11%)
3	A2G	O	4[B]	3	14,14,15	1.86	1 (7%)	17,19,21	2.46	4 (23%)
3	FUC	O	5[A]	7	10,10,11	1.31	2 (20%)	14,14,16	1.20	2 (14%)
3	FUC	O	5[B]	3	10,10,11	1.65	3 (30%)	14,14,16	1.61	2 (14%)
2	GLC	P	1	2	12,12,12	1.15	2 (16%)	17,17,17	1.33	2 (11%)
2	GAL	P	2	2	11,11,12	0.93	1 (9%)	15,15,17	1.40	1 (6%)
2	FUC	P	3	2	10,10,11	0.82	0	14,14,16	0.99	1 (7%)
2	A2G	P	4	2	14,14,15	1.50	2 (14%)	17,19,21	1.39	1 (5%)
2	FUC	P	5	2	10,10,11	1.35	2 (20%)	14,14,16	0.85	1 (7%)
2	GLC	Q	1[A]	2	12,12,12	0.98	1 (8%)	17,17,17	1.10	1 (5%)
2	GLC	Q	1[B]	2	12,12,12	0.90	0	17,17,17	1.82	3 (17%)
2	GAL	Q	2[A]	2	11,11,12	1.09	1 (9%)	15,15,17	1.43	4 (26%)
2	GAL	Q	2[B]	2	11,11,12	1.09	1 (9%)	15,15,17	0.96	1 (6%)
2	FUC	Q	3[A]	2	10,10,11	1.13	1 (10%)	14,14,16	1.48	2 (14%)
2	FUC	Q	3[B]	2	10,10,11	1.59	1 (10%)	14,14,16	1.36	2 (14%)
2	A2G	Q	4[A]	2	14,14,15	1.68	4 (28%)	17,19,21	1.67	3 (17%)
2	A2G	Q	4[B]	2	14,14,15	1.11	1 (7%)	17,19,21	1.67	4 (23%)
2	FUC	Q	5[A]	2	10,10,11	1.11	0	14,14,16	0.86	0
2	FUC	Q	5[B]	2	10,10,11	0.66	0	14,14,16	0.77	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	K	1	2	-	0/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GAL	K	2	2	-	1/2/19/22	0/1/1/1
2	FUC	K	3	2	-	-	0/1/1/1
2	A2G	K	4	2	-	2/6/23/26	0/1/1/1
2	FUC	K	5	2	-	-	0/1/1/1
3	BGC	L	1[A]	3	-	0/2/22/22	0/1/1/1
3	GAL	L	2[A]	3	-	1/2/19/22	0/1/1/1
3	GAL	L	2[B]	3,7	-	0/2/19/22	0/1/1/1
3	FUC	L	3[A]	3	-	-	0/1/1/1
3	FUC	L	3[B]	3	-	-	0/1/1/1
3	A2G	L	4[A]	3	-	2/6/23/26	0/1/1/1
3	A2G	L	4[B]	3	-	0/6/23/26	0/1/1/1
3	FUC	L	5[A]	3	-	-	0/1/1/1
3	FUC	L	5[B]	7	-	-	0/1/1/1
2	GLC	M	1	2	-	0/2/22/22	0/1/1/1
2	GAL	M	2	2	-	0/2/19/22	0/1/1/1
2	FUC	M	3	2	-	-	0/1/1/1
2	A2G	M	4	2	-	4/6/23/26	0/1/1/1
2	FUC	M	5	2	-	-	0/1/1/1
3	BGC	N	1	3	-	0/2/22/22	0/1/1/1
3	GAL	N	2	3	-	1/2/19/22	0/1/1/1
3	FUC	N	3	3	-	-	0/1/1/1
3	A2G	N	4	3	-	0/6/23/26	0/1/1/1
3	FUC	N	5	3	-	-	0/1/1/1
3	BGC	O	1[B]	3	-	0/2/22/22	0/1/1/1
3	GAL	O	2[A]	3,7	-	0/2/19/22	0/1/1/1
3	GAL	O	2[B]	3	-	1/2/19/22	0/1/1/1
3	FUC	O	3[A]	3	-	-	0/1/1/1
3	FUC	O	3[B]	3	-	-	0/1/1/1
3	A2G	O	4[A]	3	-	2/6/23/26	0/1/1/1
3	A2G	O	4[B]	3	-	2/6/23/26	0/1/1/1
3	FUC	O	5[A]	7	-	-	0/1/1/1
3	FUC	O	5[B]	3	-	-	0/1/1/1
2	GLC	P	1	2	-	0/2/22/22	0/1/1/1
2	GAL	P	2	2	-	0/2/19/22	0/1/1/1
2	FUC	P	3	2	-	-	0/1/1/1
2	A2G	P	4	2	-	2/6/23/26	0/1/1/1
2	FUC	P	5	2	-	-	0/1/1/1
2	GLC	Q	1[A]	2	-	2/2/22/22	0/1/1/1
2	GLC	Q	1[B]	2	-	0/2/22/22	0/1/1/1
2	GAL	Q	2[A]	2	-	1/2/19/22	0/1/1/1
2	GAL	Q	2[B]	2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FUC	Q	3[A]	2	-	-	0/1/1/1
2	FUC	Q	3[B]	2	-	-	0/1/1/1
2	A2G	Q	4[A]	2	-	0/6/23/26	0/1/1/1
2	A2G	Q	4[B]	2	-	2/6/23/26	0/1/1/1
2	FUC	Q	5[A]	2	-	-	0/1/1/1
2	FUC	Q	5[B]	2	-	-	0/1/1/1

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	O	4[B]	A2G	O3-C3	5.82	1.57	1.43
2	M	4	A2G	C1-C2	4.68	1.58	1.52
2	Q	3[B]	FUC	O5-C1	-4.53	1.36	1.43
2	P	4	A2G	O5-C5	4.03	1.51	1.43
3	N	5	FUC	C2-C3	3.42	1.57	1.52

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	4	A2G	C2-N2-C7	11.28	138.01	122.90
3	O	4[B]	A2G	C4-C3-C2	-6.15	102.01	111.02
3	O	1[B]	BGC	C1-O5-C5	-5.78	102.47	113.65
3	O	4[B]	A2G	C2-N2-C7	-5.58	115.42	122.90
2	K	4	A2G	C1-O5-C5	5.34	119.34	112.19

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	M	4	A2G	C3-C2-N2-C7
2	Q	4[B]	A2G	O5-C5-C6-O6
3	O	4[A]	A2G	C4-C5-C6-O6
2	Q	1[A]	GLC	O5-C5-C6-O6
2	P	4	A2G	O5-C5-C6-O6

There are no ring outliers.

11 monomers are involved in 12 short contacts:

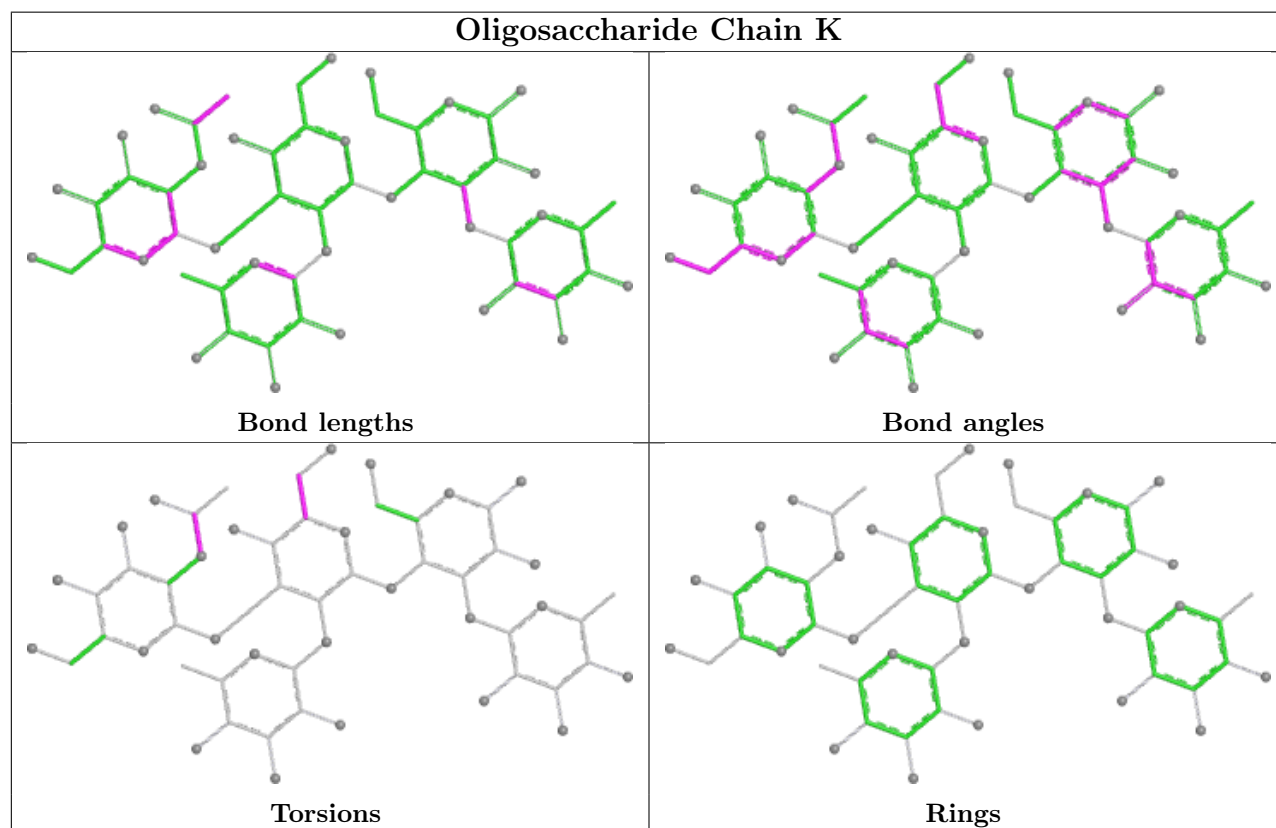
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Q	1[A]	GLC	2	0
3	O	4[B]	A2G	2	0

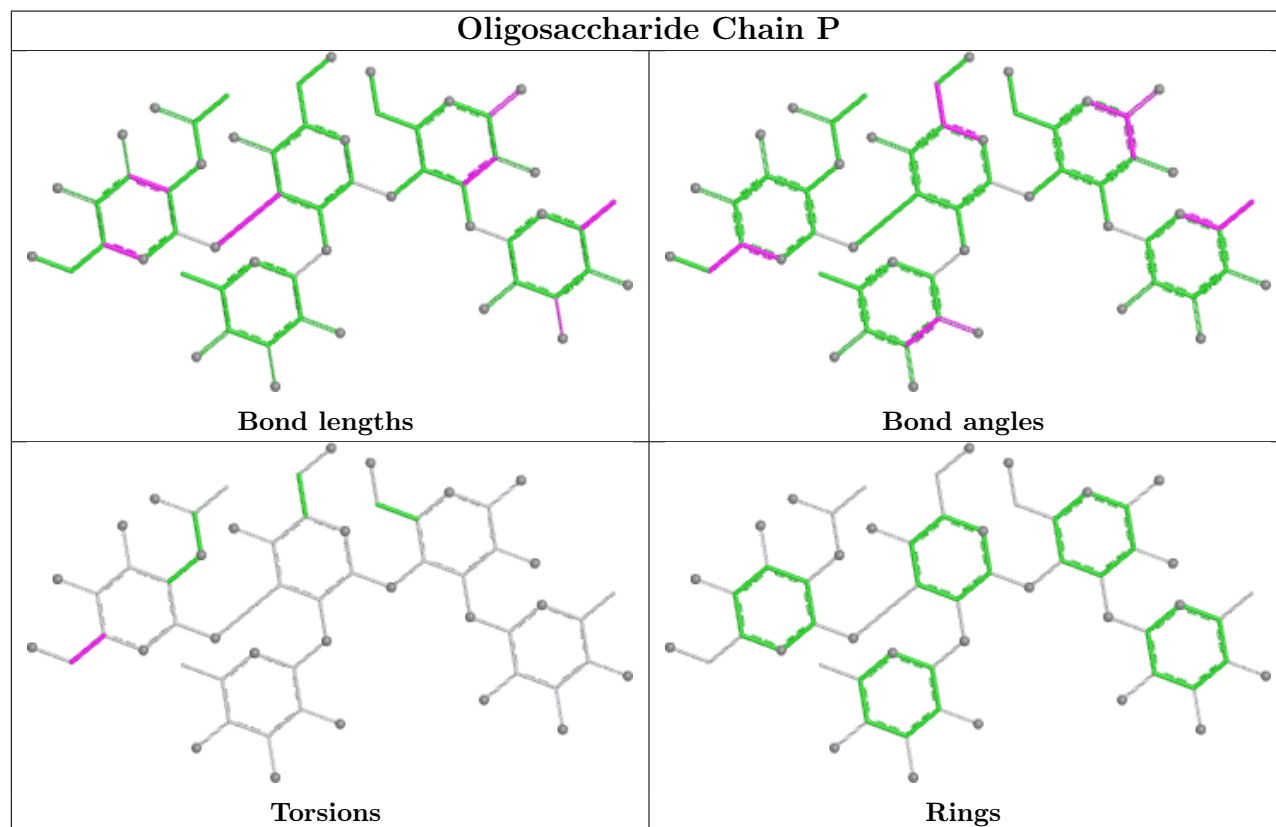
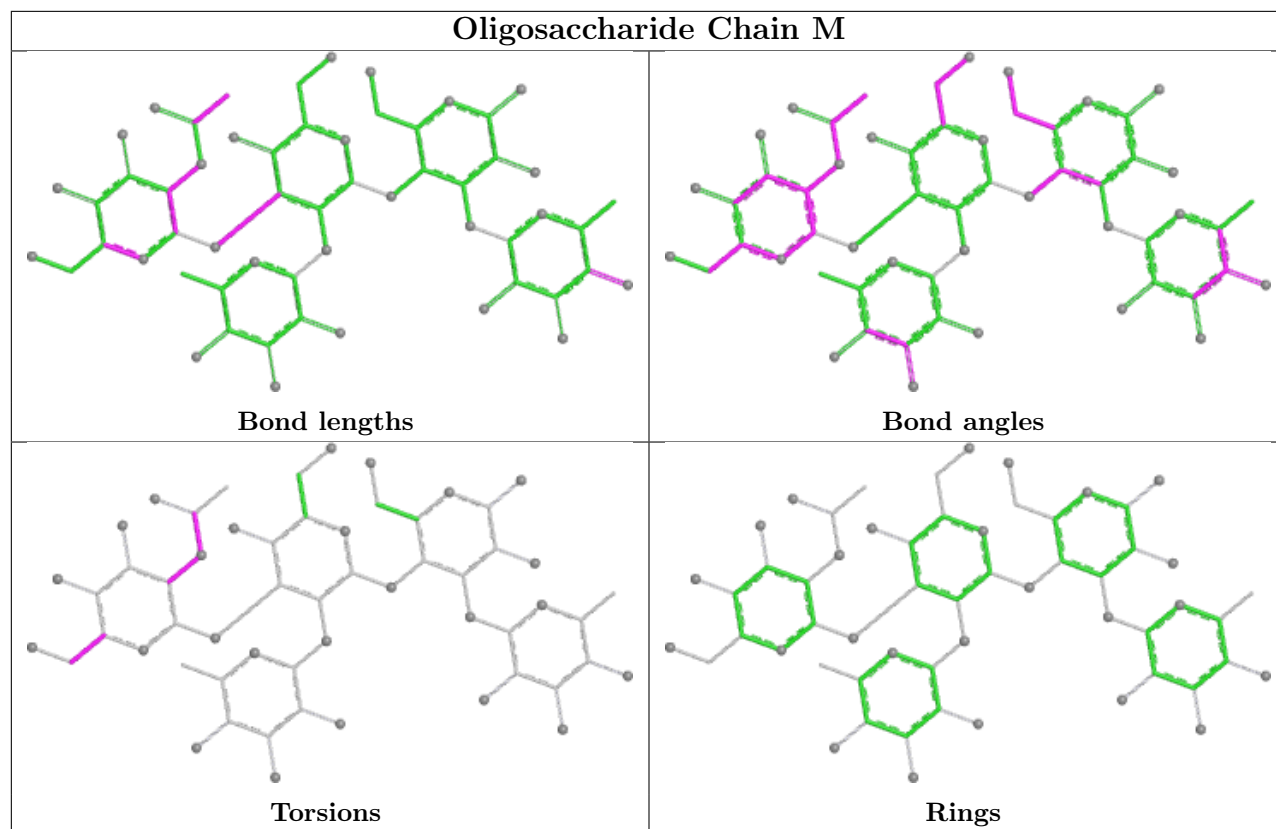
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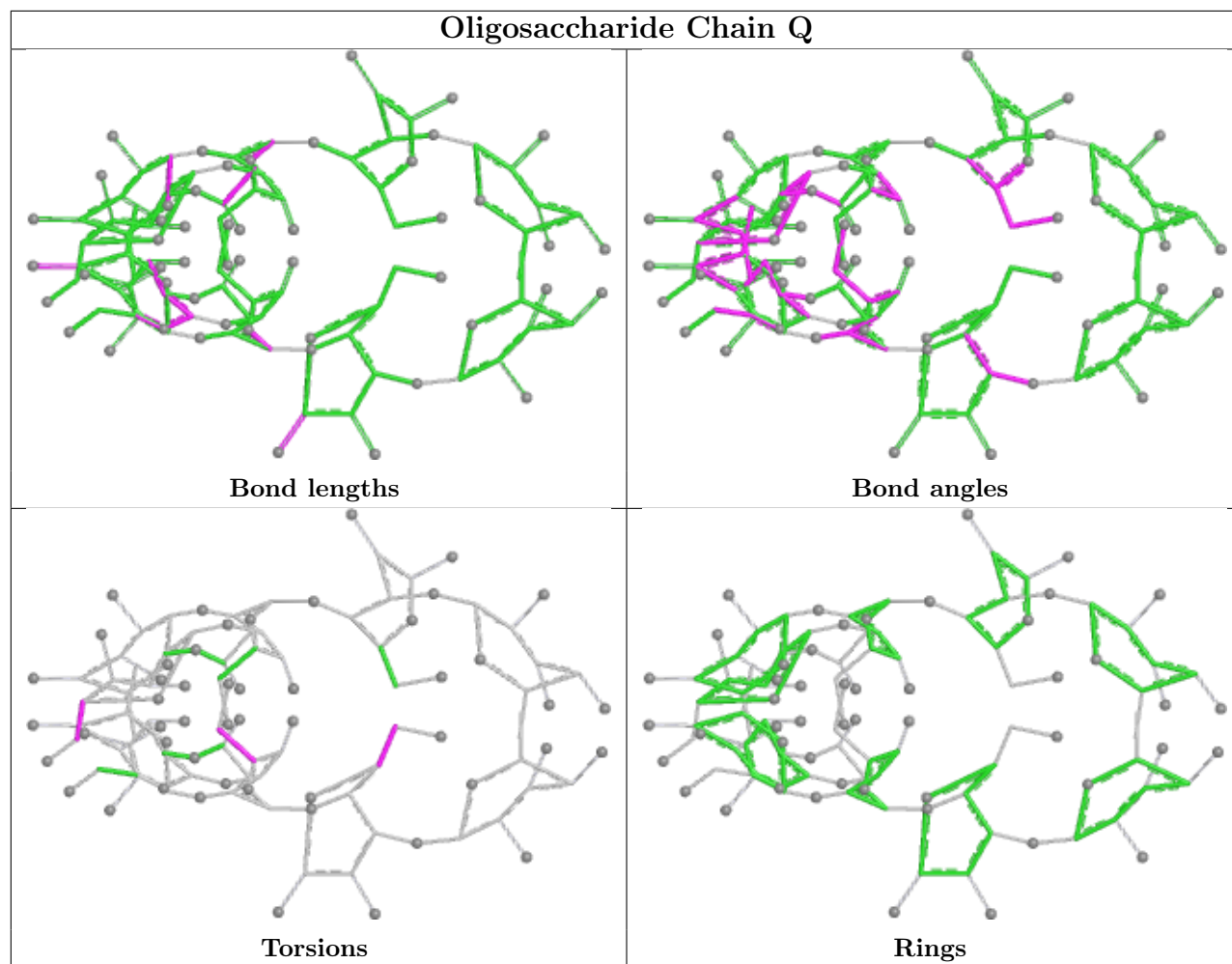
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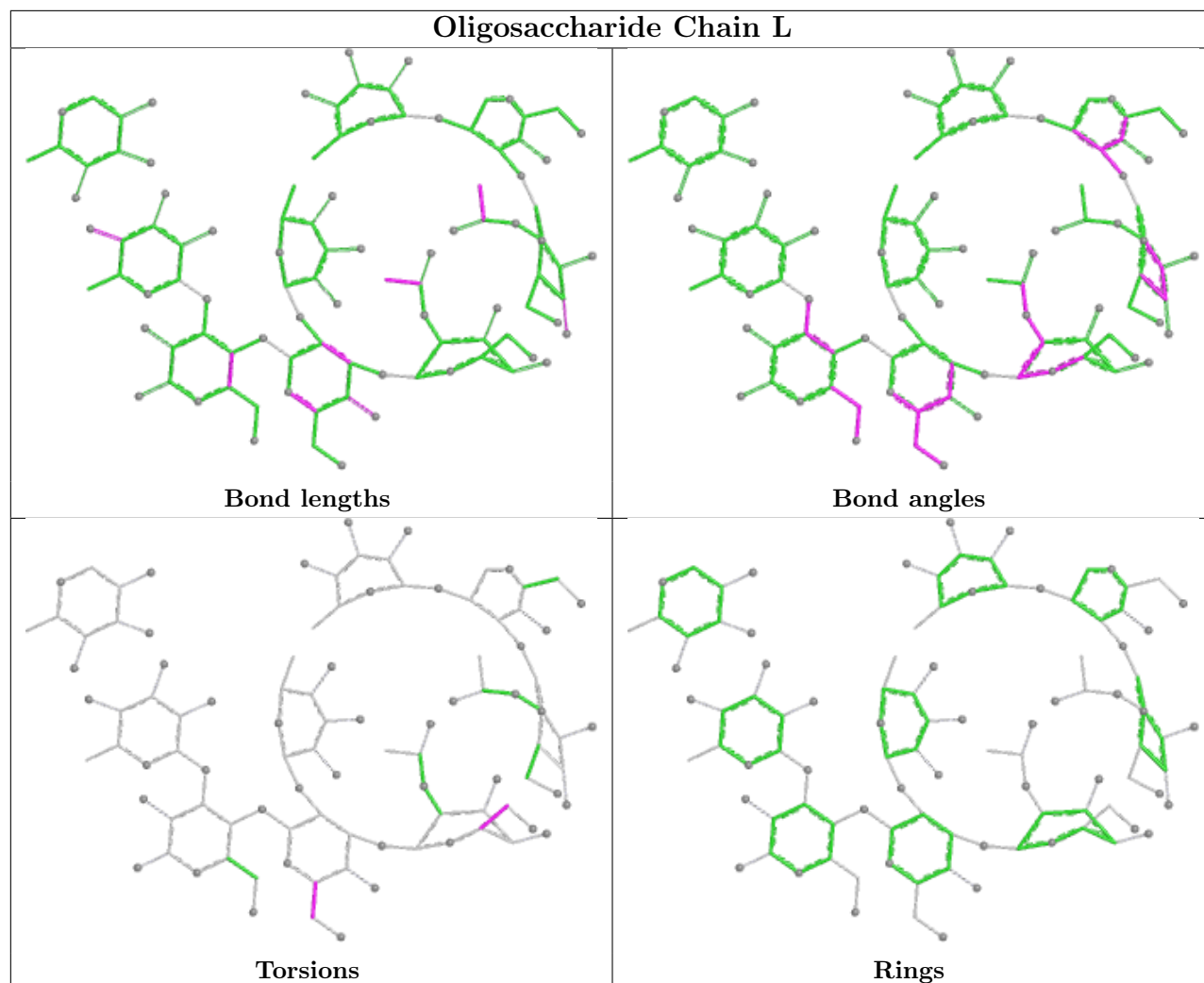
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Q	3[A]	FUC	2	0
3	L	2[B]	GAL	1	0
3	L	4[B]	A2G	1	0
3	O	5[B]	FUC	1	0
2	M	4	A2G	2	0
3	L	5[A]	FUC	1	0
2	M	2	GAL	1	0
3	O	1[B]	BGC	1	0
3	L	3[B]	FUC	2	0

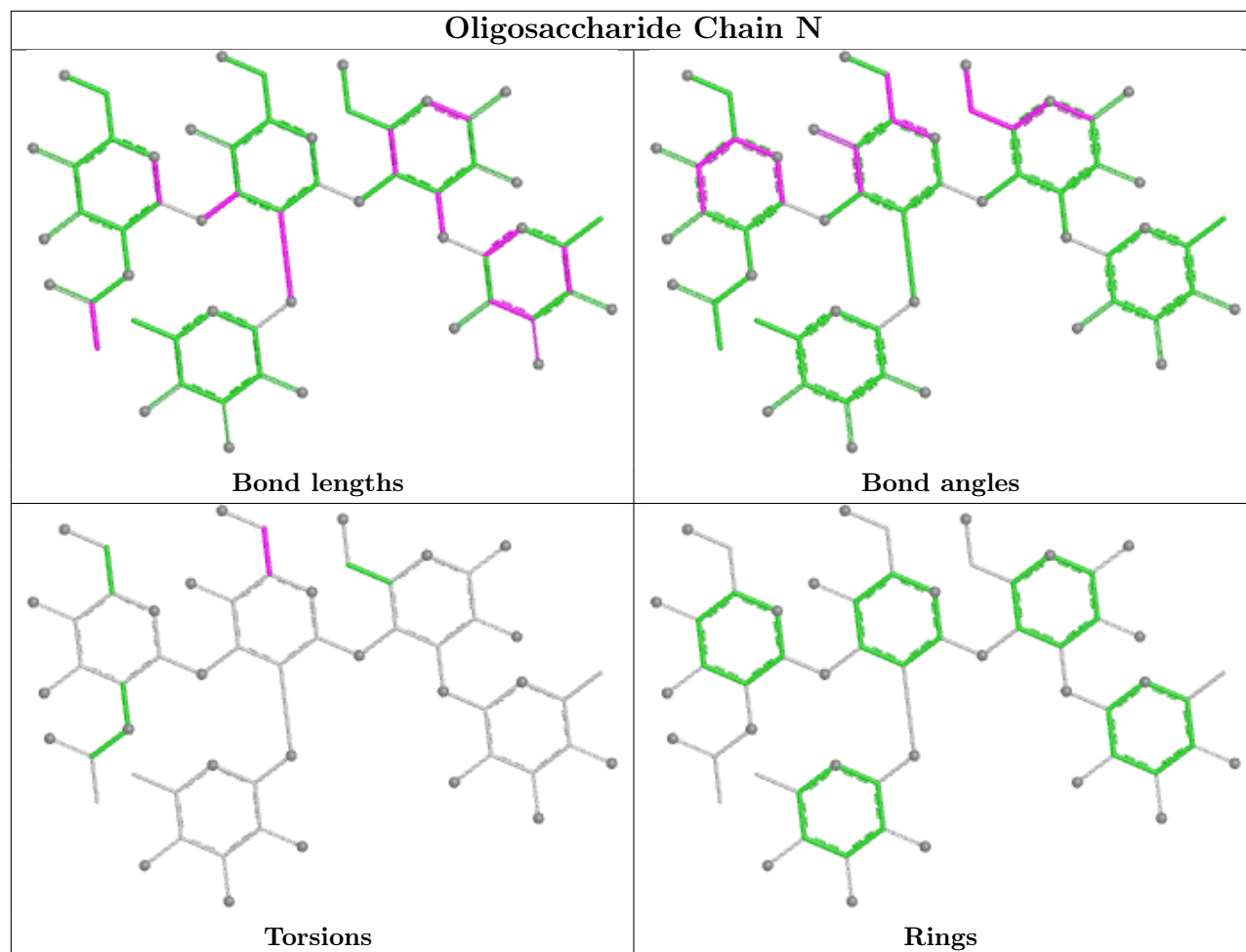
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

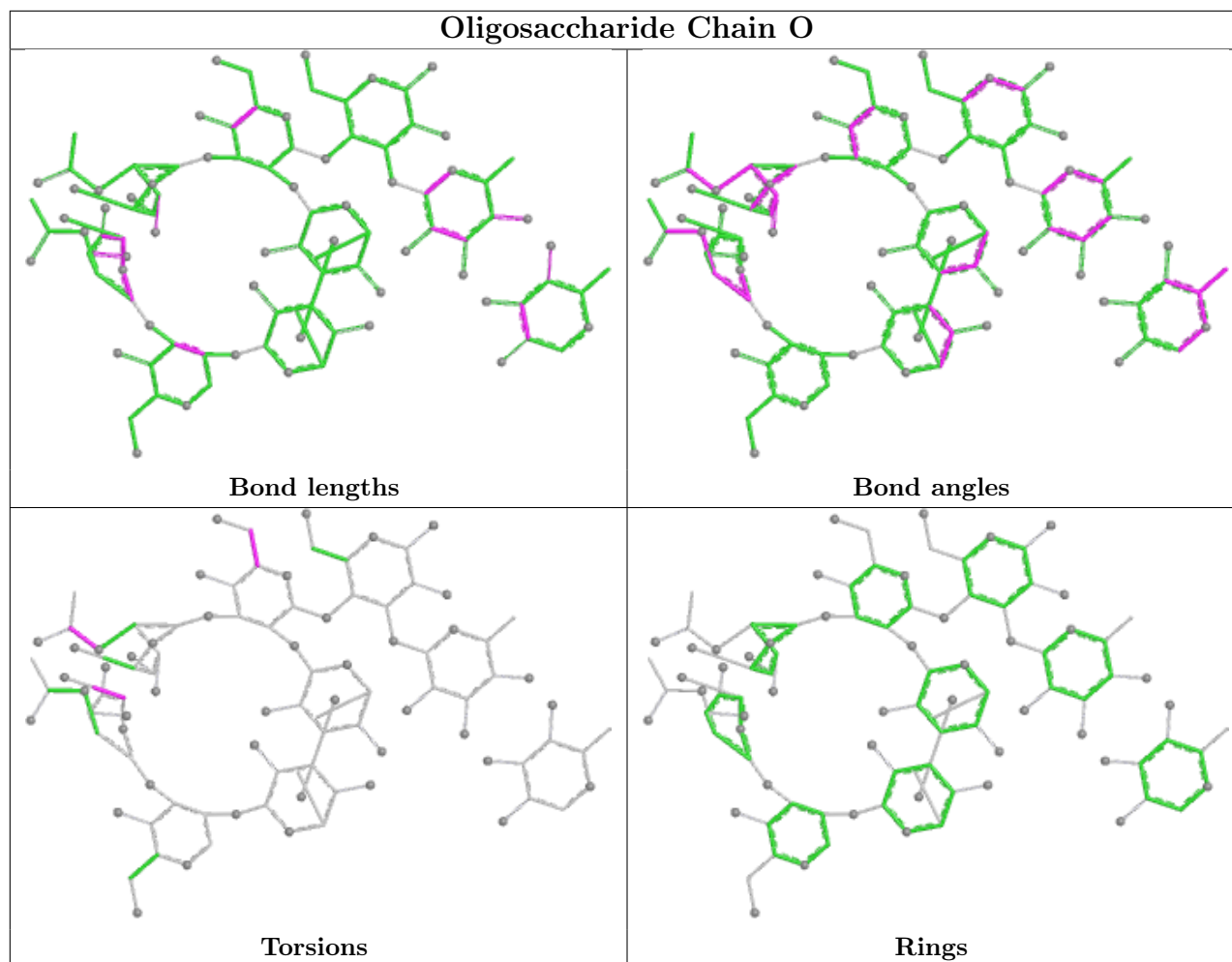












## 5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 10 are monoatomic - leaving 15 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	$\# Z  > 2$
7	GLC	D	210[B]	3	12,12,12	0.84	0	17,17,17	1.26	3 (17%)
7	GLC	G	206[A]	3	12,12,12	1.63	3 (25%)	17,17,17	1.02	1 (5%)
5	BCN	C	202	4	10,10,10	0.87	0	11,11,11	0.69	0
5	BCN	C	203	4	10,10,10	0.82	0	11,11,11	1.10	0
5	BCN	B	201	4	10,10,10	1.11	1 (10%)	11,11,11	2.76	5 (45%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	BCN	D	203	4	10,10,10	0.80	0	11,11,11	1.04	1 (9%)
8	PG4	F	201	-	12,12,12	0.32	0	11,11,11	0.42	0
5	BCN	A	202	4	10,10,10	0.89	0	11,11,11	0.85	0
5	BCN	D	202	4	10,10,10	0.94	1 (10%)	11,11,11	0.80	0
6	FUC	B	203	-	11,11,11	1.05	1 (9%)	16,16,16	1.41	4 (25%)
5	BCN	B	204	4	10,10,10	0.82	0	11,11,11	0.88	0
5	BCN	A	204	4	10,10,10	0.63	0	11,11,11	2.44	4 (36%)
5	BCN	E	203	4	10,10,10	0.86	0	11,11,11	2.37	5 (45%)
6	FUC	H	201	-	11,11,11	0.89	0	16,16,16	1.32	2 (12%)
5	BCN	E	201	4	10,10,10	0.76	0	11,11,11	2.44	6 (54%)

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. <sup>1,2</sup> means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GLC	D	210[B]	3	-	0/2/22/22	0/1/1/1
7	GLC	G	206[A]	3	-	0/2/22/22	0/1/1/1
5	BCN	C	202	4	-	1/10/10/10	-
5	BCN	C	203	4	-	2/10/10/10	-
5	BCN	B	201	4	-	6/10/10/10	-
5	BCN	D	203	4	-	1/10/10/10	-
8	PG4	F	201	-	-	4/10/10/10	-
5	BCN	A	202	4	-	2/10/10/10	-
5	BCN	D	202	4	-	0/10/10/10	-
6	FUC	B	203	-	-	-	0/1/1/1
5	BCN	B	204	4	-	1/10/10/10	-
5	BCN	A	204	4	-	4/10/10/10	-
5	BCN	E	203	4	-	7/10/10/10	-
6	FUC	H	201	-	-	-	0/1/1/1
5	BCN	E	201	4	-	3/10/10/10	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	206[A]	GLC	C4-C3	3.29	1.60	1.52
5	B	201	BCN	C1-N1	3.05	1.53	1.47
7	G	206[A]	GLC	O2-C2	2.66	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	202	BCN	O22-C2	-2.26	1.23	1.30
7	G	206[A]	GLC	O1-C1	2.03	1.46	1.39

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	201	BCN	C1-N1-C3	5.61	125.45	111.91
5	E	203	BCN	C5-N1-C3	4.77	122.81	111.44
5	A	204	BCN	C1-N1-C3	4.67	123.17	111.91
5	B	201	BCN	C2-C1-N1	4.60	128.35	113.77
5	A	204	BCN	C2-C1-N1	4.30	127.40	113.77

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	204	BCN	C4-C3-N1-C1
5	E	203	BCN	C2-C1-N1-C3
5	E	203	BCN	C6-C5-N1-C1
5	E	203	BCN	N1-C1-C2-O22
5	B	201	BCN	C4-C3-N1-C1

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	210[B]	GLC	3	0
6	B	203	FUC	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	103/103 (100%)	0.01	0 100 100	11, 20, 33, 38	2 (1%)
1	B	103/103 (100%)	0.16	1 (0%) 79 85	13, 23, 35, 51	2 (1%)
1	C	103/103 (100%)	-0.13	1 (0%) 79 85	9, 18, 30, 44	3 (2%)
1	D	103/103 (100%)	-0.11	2 (1%) 66 75	9, 17, 30, 43	2 (1%)
1	E	103/103 (100%)	-0.05	1 (0%) 79 85	11, 18, 31, 44	1 (0%)
1	F	103/103 (100%)	-0.38	1 (0%) 79 85	12, 15, 24, 39	1 (0%)
1	G	103/103 (100%)	-0.22	1 (0%) 79 85	8, 16, 29, 45	1 (0%)
1	H	103/103 (100%)	-0.05	1 (0%) 79 85	12, 18, 31, 44	0
1	I	103/103 (100%)	-0.22	1 (0%) 79 85	12, 16, 29, 34	0
1	J	103/103 (100%)	-0.30	3 (2%) 53 62	10, 15, 25, 43	2 (1%)
All	All	1030/1030 (100%)	-0.13	12 (1%) 76 83	8, 17, 31, 51	14 (1%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	103	ASN	3.2
1	E	55	SER	3.0
1	F	103	ASN	3.0
1	C	103	ASN	2.9
1	D	103	ASN	2.8

### 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, 95<sup>th</sup> 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.

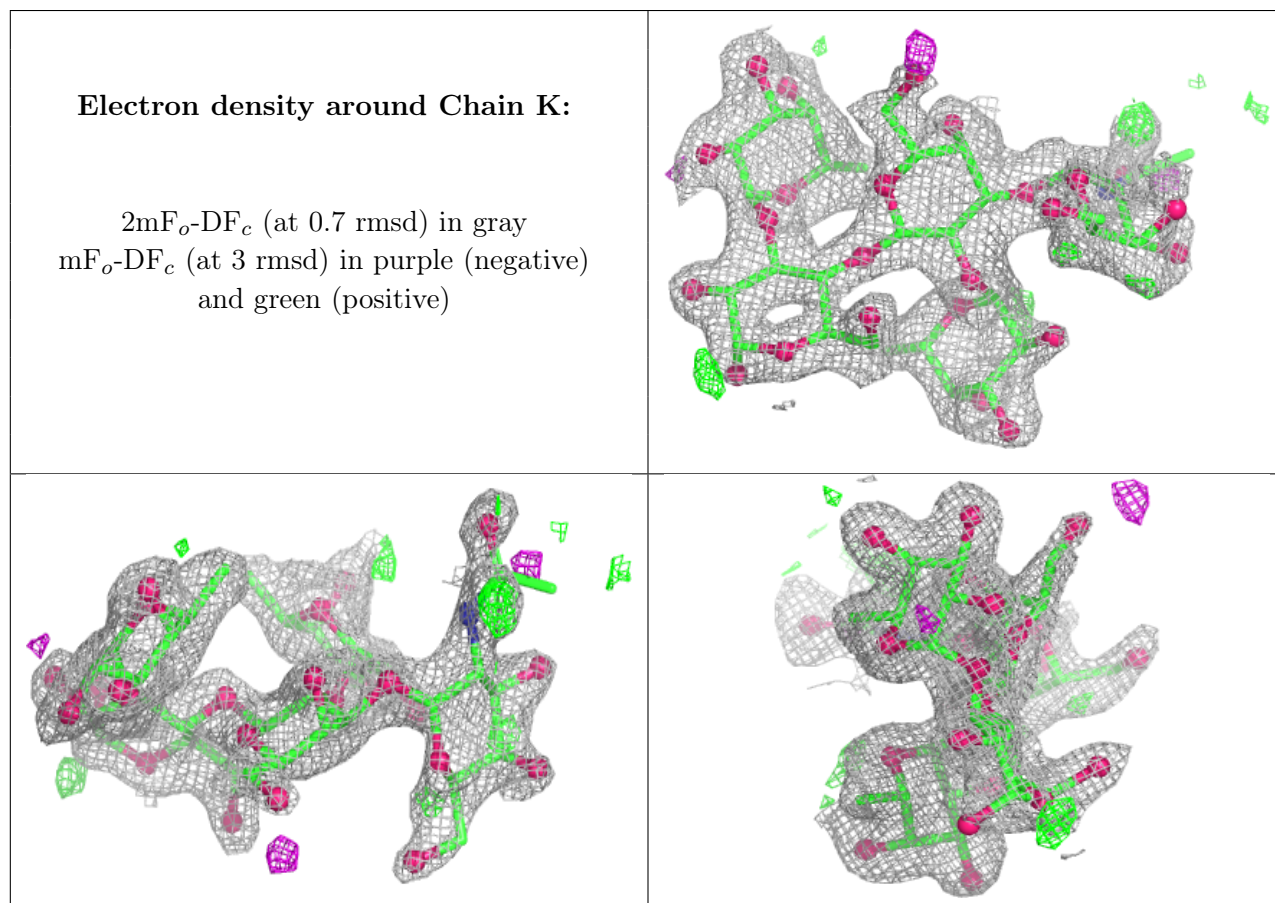
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	A2G	K	4	14/15	0.64	0.19	43,47,57,60	14
2	GLC	M	1	12/12	0.71	0.15	31,38,43,44	12
2	A2G	M	4	14/15	0.72	0.15	34,39,42,43	14
2	FUC	M	3	10/11	0.78	0.14	37,40,43,43	10
2	GAL	M	2	11/12	0.78	0.15	37,40,43,47	11
3	A2G	O	4[A]	14/15	0.80	0.14	26,29,33,38	14
3	A2G	O	4[B]	14/15	0.80	0.14	19,21,24,27	14
2	A2G	Q	4[B]	14/15	0.82	0.11	20,21,22,22	14
2	GAL	K	2	11/12	0.82	0.12	37,39,40,41	11
2	A2G	Q	4[A]	14/15	0.82	0.11	24,27,29,30	14
2	GLC	K	1	12/12	0.83	0.12	28,36,40,40	12
3	A2G	N	4	14/15	0.83	0.11	33,38,42,44	0
2	FUC	Q	3[B]	10/11	0.84	0.09	19,21,22,22	10
2	FUC	Q	3[A]	10/11	0.84	0.09	20,23,23,24	10
2	FUC	K	3	10/11	0.85	0.11	35,39,41,45	10
3	FUC	N	3	10/11	0.89	0.09	26,30,32,33	0
3	A2G	L	4[A]	14/15	0.90	0.09	18,19,21,21	14
3	A2G	L	4[B]	14/15	0.90	0.09	17,17,19,19	14
2	FUC	K	5	10/11	0.90	0.10	23,27,29,30	10
2	FUC	M	5	10/11	0.91	0.10	22,26,27,28	10
3	BGC	N	1	12/12	0.91	0.08	22,27,33,34	0
2	FUC	P	3	10/11	0.92	0.08	26,30,35,36	0
3	BGC	O	1[B]	12/12	0.92	0.08	13,14,14,17	12
3	GAL	N	2	11/12	0.92	0.07	23,26,30,30	0
3	BGC	L	1[A]	12/12	0.92	0.07	14,16,17,18	12
2	GLC	P	1	12/12	0.93	0.09	16,26,35,36	0
3	GAL	L	2[A]	11/12	0.93	0.07	16,17,17,19	11
3	GAL	L	2[B]	11/12	0.93	0.07	14,14,15,15	11
2	A2G	P	4	14/15	0.93	0.08	24,27,33,35	0
2	GAL	Q	2[A]	11/12	0.93	0.07	20,21,21,23	11
2	GAL	Q	2[B]	11/12	0.93	0.07	18,19,20,20	11
2	GLC	Q	1[B]	12/12	0.94	0.07	15,16,17,17	12
3	GAL	O	2[A]	11/12	0.94	0.06	16,18,19,21	11
3	GAL	O	2[B]	11/12	0.94	0.06	11,13,13,15	11
2	GLC	Q	1[A]	12/12	0.94	0.07	19,23,26,31	12
3	FUC	N	5	10/11	0.94	0.07	18,22,24,25	0
3	FUC	L	3[A]	10/11	0.96	0.05	16,17,17,18	10

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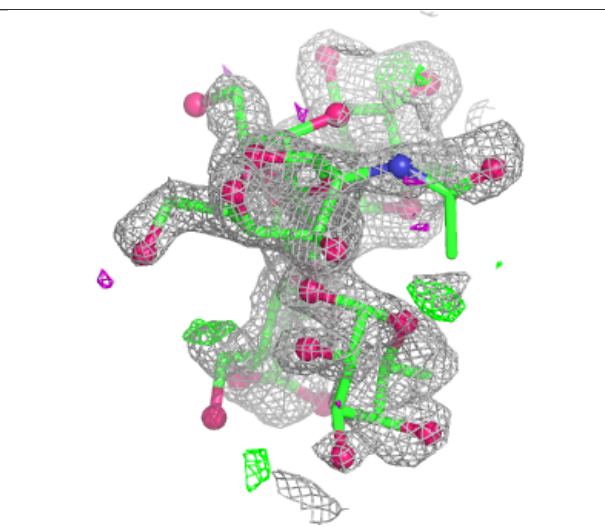
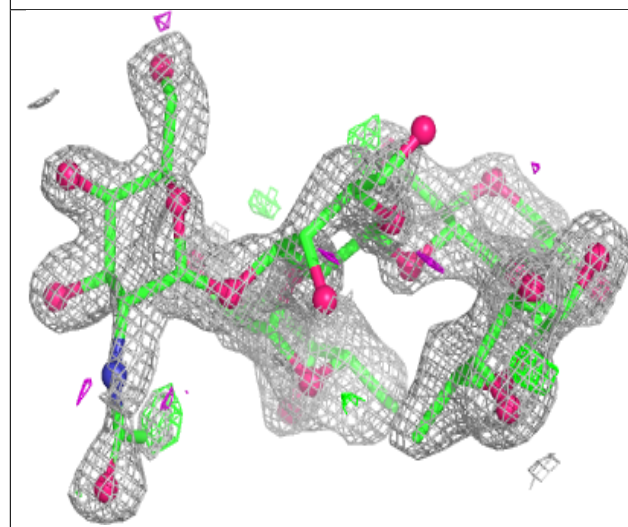
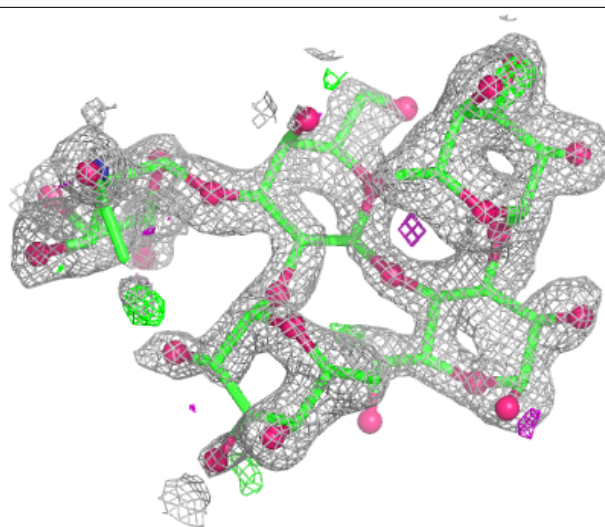
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	FUC	L	3[B]	10/11	0.96	0.05	14,15,16,16	10
2	FUC	Q	5[B]	10/11	0.96	0.05	13,14,15,16	10
2	GAL	P	2	11/12	0.96	0.05	18,20,22,24	0
3	FUC	L	5[A]	10/11	0.96	0.05	11,13,13,14	10
3	FUC	L	5[B]	10/11	0.96	0.05	13,14,15,15	10
3	FUC	O	3[A]	10/11	0.96	0.05	14,14,15,15	10
3	FUC	O	3[B]	10/11	0.96	0.05	11,11,12,12	10
2	FUC	P	5	10/11	0.96	0.06	14,15,16,17	0
2	FUC	Q	5[A]	10/11	0.96	0.05	14,15,17,17	10
3	FUC	O	5[A]	10/11	0.98	0.04	11,12,12,13	10
3	FUC	O	5[B]	10/11	0.98	0.04	12,13,13,14	10

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.



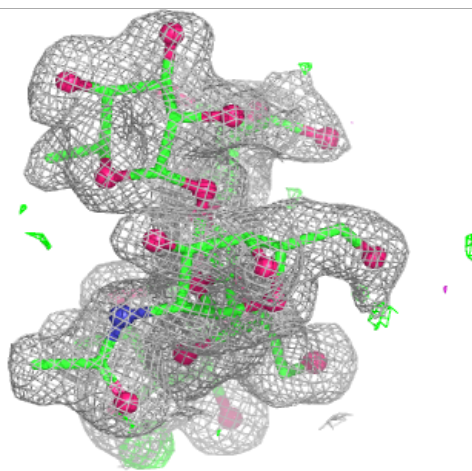
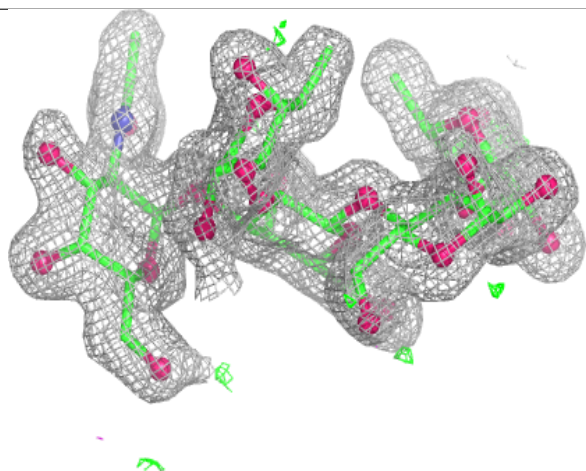
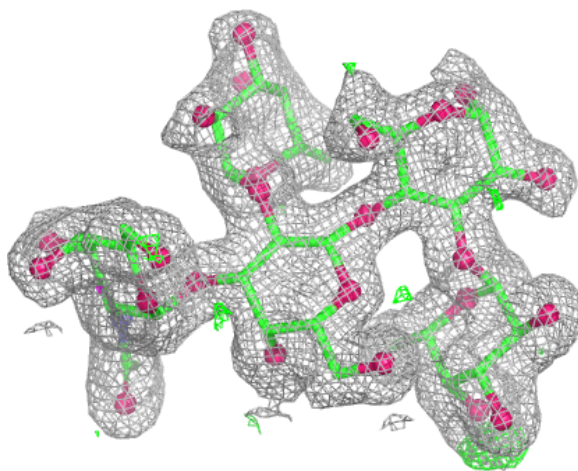
**Electron density around Chain M:**

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



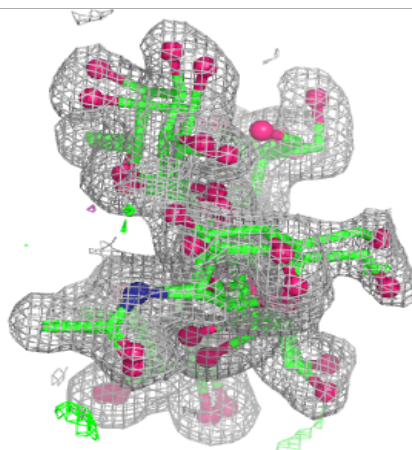
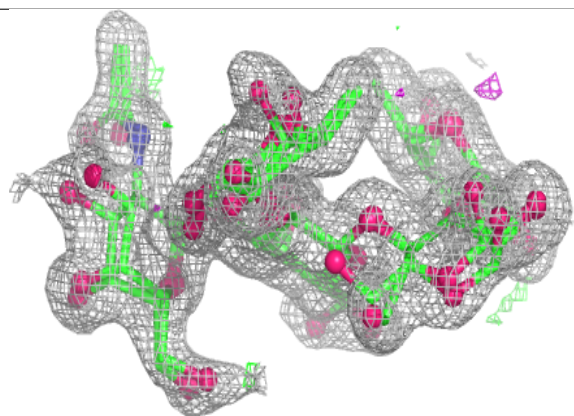
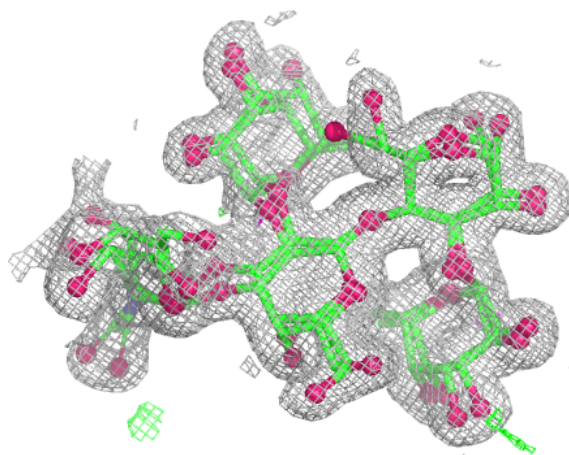
**Electron density around Chain P:**

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



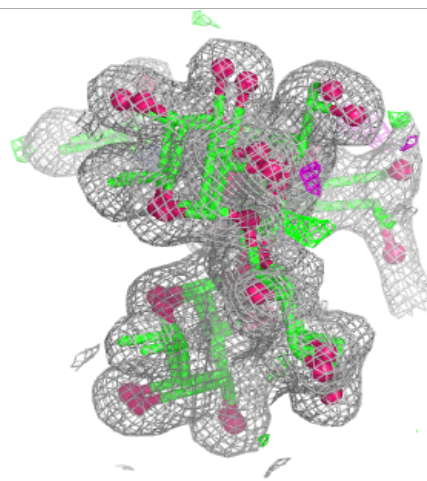
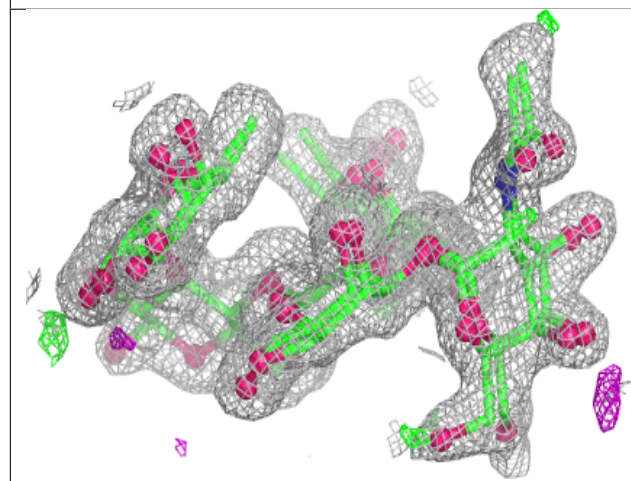
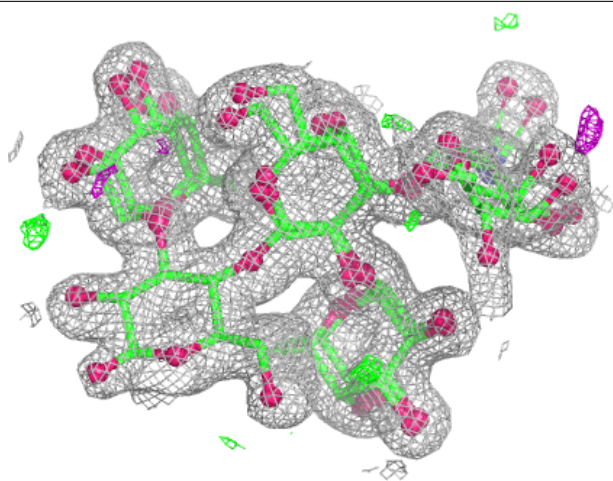
**Electron density around Chain Q:**

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



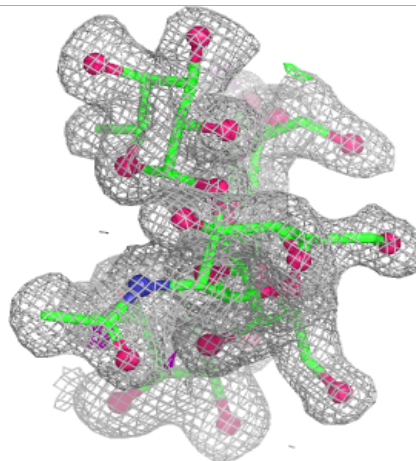
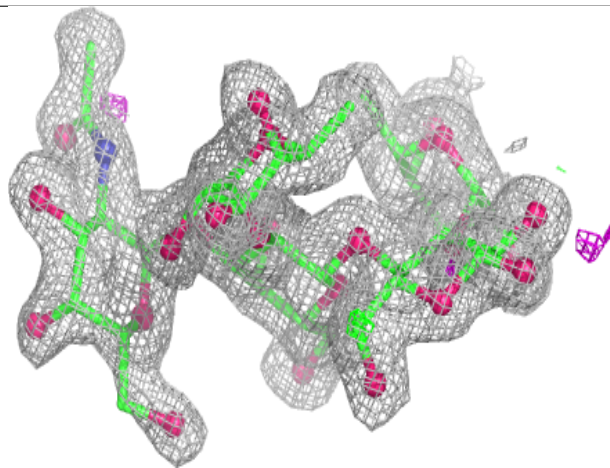
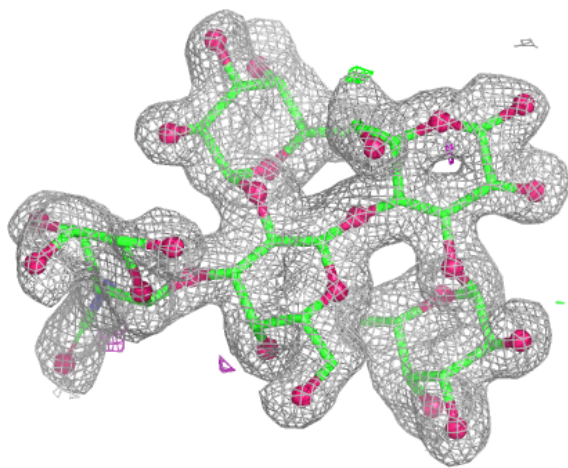
**Electron density around Chain L:**

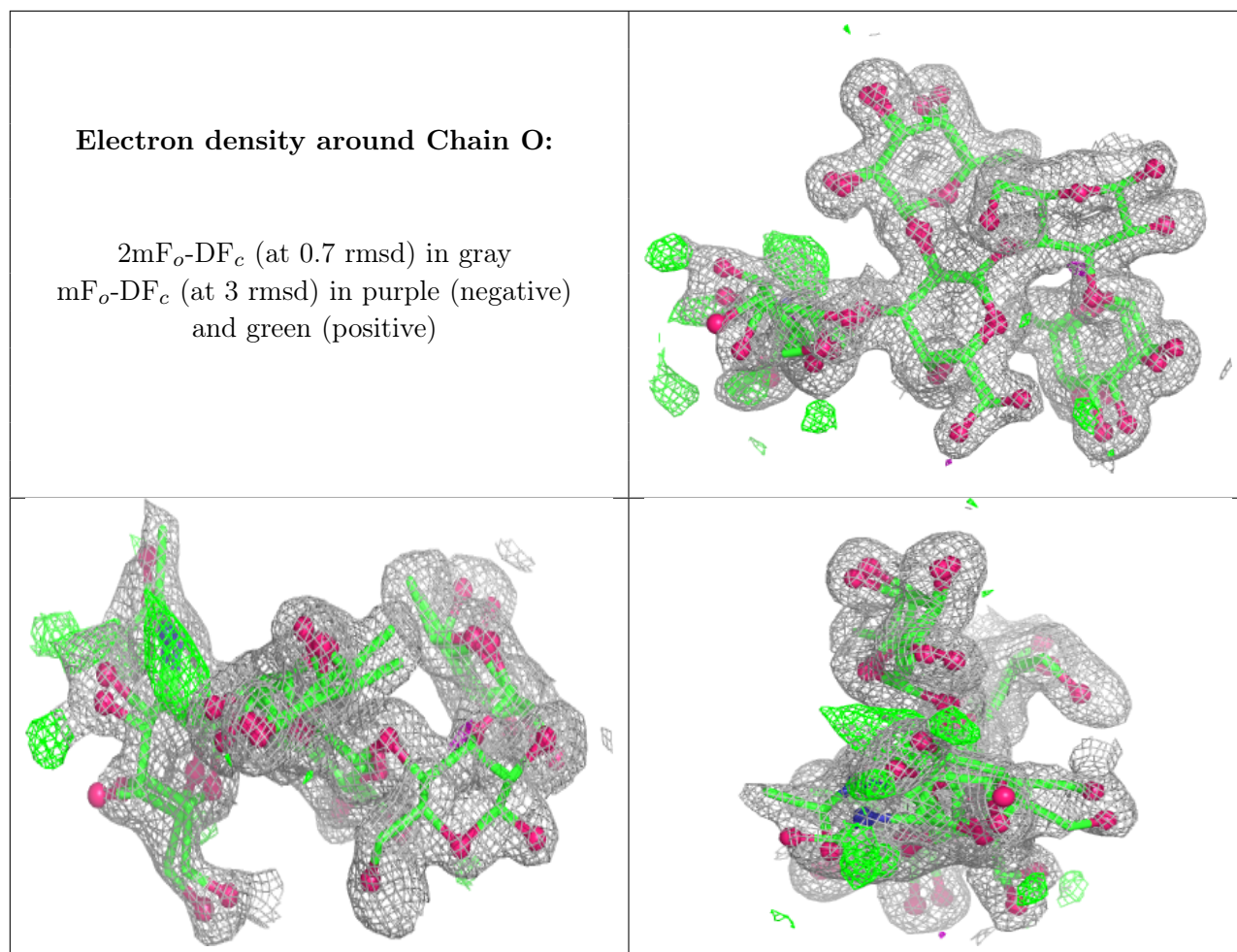
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	FUC	B	203	11/11	0.74	0.15	39,46,50,52	0
6	FUC	H	201	11/11	0.82	0.14	31,39,42,44	0
8	PG4	F	201	13/13	0.91	0.12	29,35,41,45	0
5	BCN	B	201	11/11	0.92	0.10	19,24,30,32	0
5	BCN	C	202	11/11	0.93	0.08	17,22,25,26	0
7	GLC	D	210[B]	12/12	0.93	0.07	15,17,18,19	12
5	BCN	A	204	11/11	0.93	0.09	18,23,26,28	0
5	BCN	A	202	11/11	0.94	0.07	18,21,25,26	0
5	BCN	E	203	11/11	0.94	0.09	17,23,26,27	0
5	BCN	B	204	11/11	0.94	0.09	20,24,28,29	0
5	BCN	D	202	11/11	0.95	0.07	16,23,25,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	BCN	E	201	11/11	0.96	0.07	17,19,23,24	0
5	BCN	C	203	11/11	0.96	0.07	16,22,25,26	0
7	GLC	G	206[A]	12/12	0.96	0.05	14,15,15,17	12
5	BCN	D	203	11/11	0.96	0.07	17,22,27,27	0
4	CA	A	203	1/1	0.99	0.03	15,15,15,15	0
4	CA	B	205	1/1	0.99	0.02	15,15,15,15	0
4	CA	D	201	1/1	0.99	0.03	14,14,14,14	0
4	CA	D	204	1/1	0.99	0.02	15,15,15,15	0
4	CA	E	202	1/1	0.99	0.02	14,14,14,14	0
4	CA	E	204	1/1	0.99	0.04	14,14,14,14	0
4	CA	A	201	1/1	0.99	0.02	13,13,13,13	0
4	CA	C	201	1/1	1.00	0.02	15,15,15,15	0
4	CA	C	204	1/1	1.00	0.02	16,16,16,16	0
4	CA	B	202	1/1	1.00	0.03	15,15,15,15	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.