



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 03:48 PM BST

PDB ID : 6NRQ  
Title : Crystal structure of Dpr10 IG1 bound to DIP-alpha IG1  
Authors : Cheng, S.; Park, Y.J.; Kurleto, J.D.; Ozkan, E.  
Deposited on : 2019-01-24  
Resolution : 1.80 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.

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

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

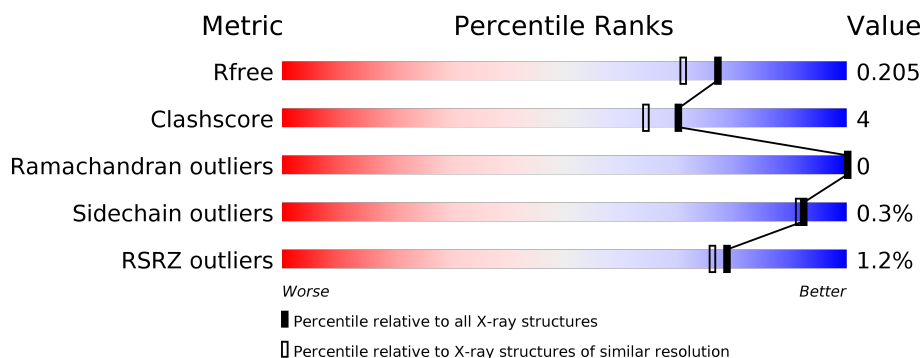
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	113	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>.</div> </div> </div>
1	C	113	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>.</div> </div> </div>
2	B	113	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>12%</div> <div>8%</div> </div> </div>
2	D	113	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>6%</div> <div>7%</div> </div> </div>
3	E	4	<div> <div></div> <div> <div>75%</div> <div>25%</div> </div> </div>
3	H	4	<div> <div></div> <div> <div>75%</div> <div>25%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	F	6	 17% 83%
4	G	6	 67% 33%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3999 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 Defective proboscis extension response 10, isoform A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	109	Total	C	N	O	S	0	0	0
			899	569	163	164	3			
1	C	108	Total	C	N	O	S	0	0	0
			894	566	162	163	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	GLY	-	expression tag	UNP Q9VT83
A	49	SER	-	expression tag	UNP Q9VT83
A	155	HIS	-	expression tag	UNP Q9VT83
A	156	HIS	-	expression tag	UNP Q9VT83
A	157	HIS	-	expression tag	UNP Q9VT83
A	158	HIS	-	expression tag	UNP Q9VT83
A	159	HIS	-	expression tag	UNP Q9VT83
A	160	HIS	-	expression tag	UNP Q9VT83
C	48	GLY	-	expression tag	UNP Q9VT83
C	49	SER	-	expression tag	UNP Q9VT83
C	155	HIS	-	expression tag	UNP Q9VT83
C	156	HIS	-	expression tag	UNP Q9VT83
C	157	HIS	-	expression tag	UNP Q9VT83
C	158	HIS	-	expression tag	UNP Q9VT83
C	159	HIS	-	expression tag	UNP Q9VT83
C	160	HIS	-	expression tag	UNP Q9VT83

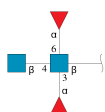
- Molecule 2 is a protein called Dpr-interacting protein alpha, isoform A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	104	Total	C	N	O	S	0	0	0
			812	511	145	152	4			
2	D	105	Total	C	N	O	S	0	0	0
			816	512	147	153	4			

There are 16 discrepancies between the modelled and reference sequences:

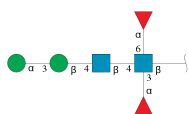
Chain	Residue	Modelled	Actual	Comment	Reference
B	37	SER	-	expression tag	UNP Q9W4R3
B	38	ARG	-	expression tag	UNP Q9W4R3
B	144	HIS	-	expression tag	UNP Q9W4R3
B	145	HIS	-	expression tag	UNP Q9W4R3
B	146	HIS	-	expression tag	UNP Q9W4R3
B	147	HIS	-	expression tag	UNP Q9W4R3
B	148	HIS	-	expression tag	UNP Q9W4R3
B	149	HIS	-	expression tag	UNP Q9W4R3
D	37	SER	-	expression tag	UNP Q9W4R3
D	38	ARG	-	expression tag	UNP Q9W4R3
D	144	HIS	-	expression tag	UNP Q9W4R3
D	145	HIS	-	expression tag	UNP Q9W4R3
D	146	HIS	-	expression tag	UNP Q9W4R3
D	147	HIS	-	expression tag	UNP Q9W4R3
D	148	HIS	-	expression tag	UNP Q9W4R3
D	149	HIS	-	expression tag	UNP Q9W4R3

- Molecule 3 is an oligosaccharide called alpha-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.



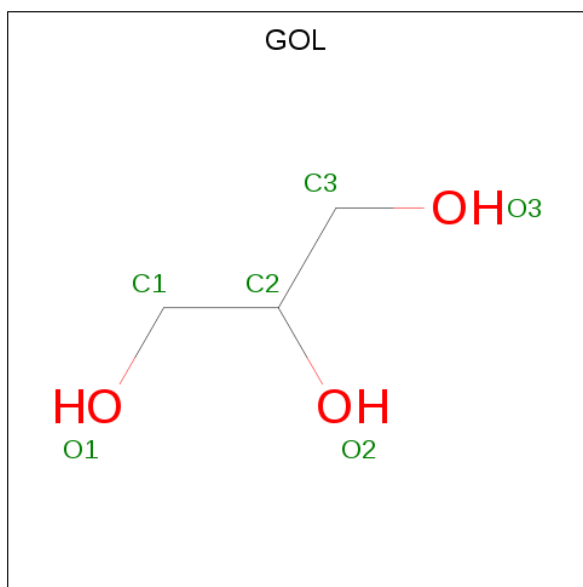
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	4	Total	C	N	O	0	0	0
			48	28	2	18			
3	H	4	Total	C	N	O	0	0	0
			48	28	2	18			

- 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)-[alpha-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



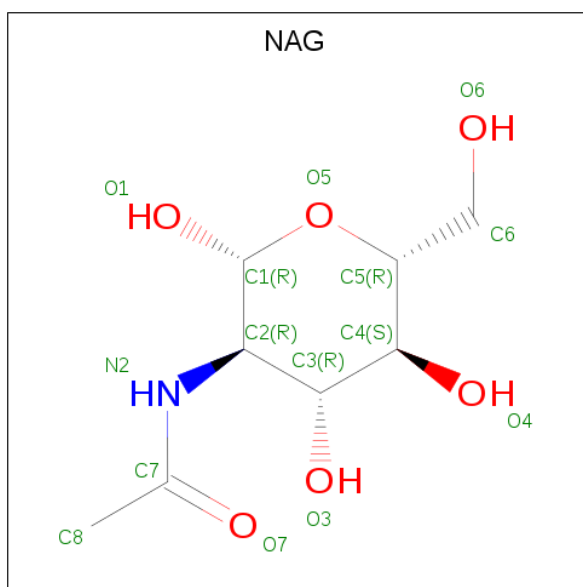
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	6	Total	C	N	O	0	0	0
			70	40	2	28			
4	G	6	Total	C	N	O	0	0	0
			70	40	2	28			

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

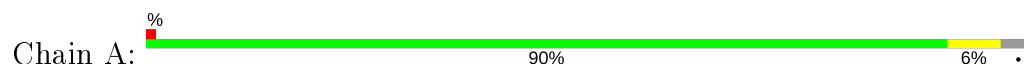
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	85	Total	O	0	0
			85	85		
7	B	78	Total	O	0	0
			78	78		
7	C	88	Total	O	0	0
			88	88		
7	D	45	Total	O	0	0
			45	45		

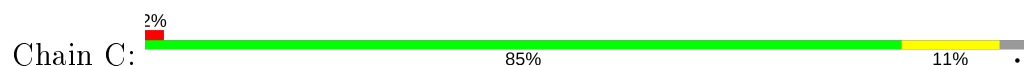
### 3 Residue-property plots [i](#)

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: Defective proboscis extension response 10, isoform A



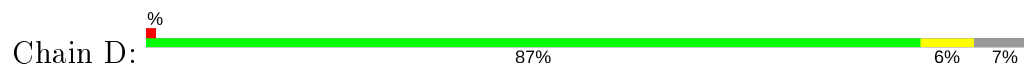
- Molecule 1: Defective proboscis extension response 10, isoform A



- Molecule 2: Dpr-interacting protein alpha, isoform A



- Molecule 2: Dpr-interacting protein alpha, isoform A



- Molecule 3: alpha-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



- Molecule 3: alpha-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 H:  75% 25%

MAG1  
FUC2  
MAG3  
FUC4

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

Chain F:  17% 83%

MAG1  
MAG2  
MAN3  
MAN4  
FUC5  
FUC6

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

Chain G:  67% 33%

MAG1  
MAG2  
MAN3  
MAN4  
FUC5  
FUC6

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.01Å 53.55Å 56.69Å 119.68° 103.77° 92.88°	Depositor
Resolution (Å)	48.55 – 1.80 48.55 – 1.80	Depositor EDS
% Data completeness (in resolution range)	87.2 (48.55-1.80) 87.3 (48.55-1.80)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.05 (at 1.79Å)	Xtriage
Refinement program	PHENIX dev_3112	Depositor
R, $R_{free}$	0.174 , 0.205 0.174 , 0.205	Depositor DCC
$R_{free}$ test set	2003 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.9	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 54.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3999	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.54% 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: MAN, GOL, BMA, NAG, FUC

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	0.44	0/923	0.57	0/1257
1	C	0.44	0/918	0.56	0/1250
2	B	0.39	0/830	0.57	0/1129
2	D	0.38	0/835	0.56	0/1138
All	All	0.41	0/3506	0.56	0/4774

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	899	0	864	5	0
1	C	894	0	862	10	0
2	B	812	0	783	9	0
2	D	816	0	778	4	0
3	E	48	0	43	0	0
3	H	48	0	43	0	0
4	F	70	0	61	0	0
4	G	70	0	61	0	0
5	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	6	0	8	0	0
5	C	6	0	8	1	0
6	C	14	0	13	0	0
6	D	14	0	13	0	0
7	A	85	0	0	1	1
7	B	78	0	0	3	1
7	C	88	0	0	3	1
7	D	45	0	0	0	1
All	All	3999	0	3545	26	2

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 4.

The worst 5 of 26 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)
2:B:41:GLN:NE2	7:B:1001:HOH:O	2.16	0.77
1:A:61:ARG:NH1	1:C:50:TRP:O	2.20	0.74
1:C:48:GLY:N	7:C:1001:HOH:O	2.25	0.69
2:B:89:ASN:ND2	7:B:1003:HOH:O	2.38	0.57
1:C:129:GLN:NE2	1:C:153:ILE:O	2.38	0.57

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:1074:HOH:O	7:C:1054:HOH:O[1_556]	2.06	0.14
7:A:1020:HOH:O	7:D:1041:HOH:O[1_566]	2.19	0.01

## 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	107/113 (95%)	105 (98%)	2 (2%)	0	100	100
1	C	106/113 (94%)	104 (98%)	2 (2%)	0	100	100
2	B	102/113 (90%)	100 (98%)	2 (2%)	0	100	100
2	D	103/113 (91%)	99 (96%)	4 (4%)	0	100	100
All	All	418/452 (92%)	408 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	98/103 (95%)	97 (99%)	1 (1%)	76	71
1	C	98/103 (95%)	98 (100%)	0	100	100
2	B	89/99 (90%)	89 (100%)	0	100	100
2	D	89/99 (90%)	89 (100%)	0	100	100
All	All	374/404 (93%)	373 (100%)	1 (0%)	92	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

20 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	$\# Z  > 2$
3	NAG	E	1	1,3	14,14,15	0.35	0	17,19,21	0.57	0
3	FUC	E	2	3	10,10,11	0.82	0	14,14,16	0.85	0
3	NAG	E	3	3	14,14,15	0.57	0	17,19,21	0.44	0
3	FUC	E	4	3	10,10,11	1.14	1 (10%)	14,14,16	1.90	3 (21%)
4	NAG	F	1	1,4	14,14,15	0.65	0	17,19,21	0.76	1 (5%)
4	NAG	F	2	4	14,14,15	0.24	0	17,19,21	0.52	0
4	BMA	F	3	4	11,11,12	1.28	2 (18%)	15,15,17	1.01	1 (6%)
4	MAN	F	4	4	11,11,12	1.25	1 (9%)	15,15,17	1.88	3 (20%)
4	FUC	F	5	4	10,10,11	0.86	1 (10%)	14,14,16	0.71	0
4	FUC	F	6	4	10,10,11	1.35	1 (10%)	14,14,16	0.95	1 (7%)
4	NAG	G	1	2,4	14,14,15	0.15	0	17,19,21	0.58	0
4	NAG	G	2	4	14,14,15	0.34	0	17,19,21	0.51	0
4	BMA	G	3	4	11,11,12	0.68	0	15,15,17	0.87	0
4	MAN	G	4	4	11,11,12	0.85	0	15,15,17	1.10	1 (6%)
4	FUC	G	5	4	10,10,11	0.72	0	14,14,16	1.08	1 (7%)
4	FUC	G	6	4	10,10,11	0.91	0	14,14,16	0.86	0
3	NAG	H	1	1,3	14,14,15	0.43	0	17,19,21	0.50	0
3	FUC	H	2	3	10,10,11	0.57	0	14,14,16	0.90	0
3	NAG	H	3	3	14,14,15	0.35	0	17,19,21	0.43	0
3	FUC	H	4	3	10,10,11	0.75	0	14,14,16	1.15	2 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	FUC	E	2	3	-	-	0/1/1/1
3	NAG	E	3	3	-	0/6/23/26	0/1/1/1
3	FUC	E	4	3	-	-	0/1/1/1
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	MAN	F	4	4	-	2/2/19/22	0/1/1/1
4	FUC	F	5	4	-	-	0/1/1/1
4	FUC	F	6	4	-	-	0/1/1/1
4	NAG	G	1	2,4	-	1/6/23/26	0/1/1/1
4	NAG	G	2	4	-	1/6/23/26	0/1/1/1
4	BMA	G	3	4	-	2/2/19/22	0/1/1/1
4	MAN	G	4	4	-	0/2/19/22	0/1/1/1
4	FUC	G	5	4	-	-	0/1/1/1
4	FUC	G	6	4	-	-	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	FUC	H	2	3	-	-	0/1/1/1
3	NAG	H	3	3	-	0/6/23/26	0/1/1/1
3	FUC	H	4	3	-	-	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)
4	F	4	MAN	C1-C2	3.87	1.61	1.52
4	F	6	FUC	C2-C3	3.18	1.57	1.52
3	E	4	FUC	C1-C2	2.72	1.58	1.52
4	F	3	BMA	O5-C5	2.29	1.48	1.43
4	F	5	FUC	O5-C1	-2.09	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	4	MAN	C1-O5-C5	4.95	118.90	112.19
3	E	4	FUC	O5-C1-C2	4.02	116.98	110.77
3	E	4	FUC	C1-O5-C5	3.64	121.04	112.78
4	F	4	MAN	C1-C2-C3	3.60	114.09	109.67
3	E	4	FUC	C1-C2-C3	3.39	113.83	109.67

There are no chirality outliers.

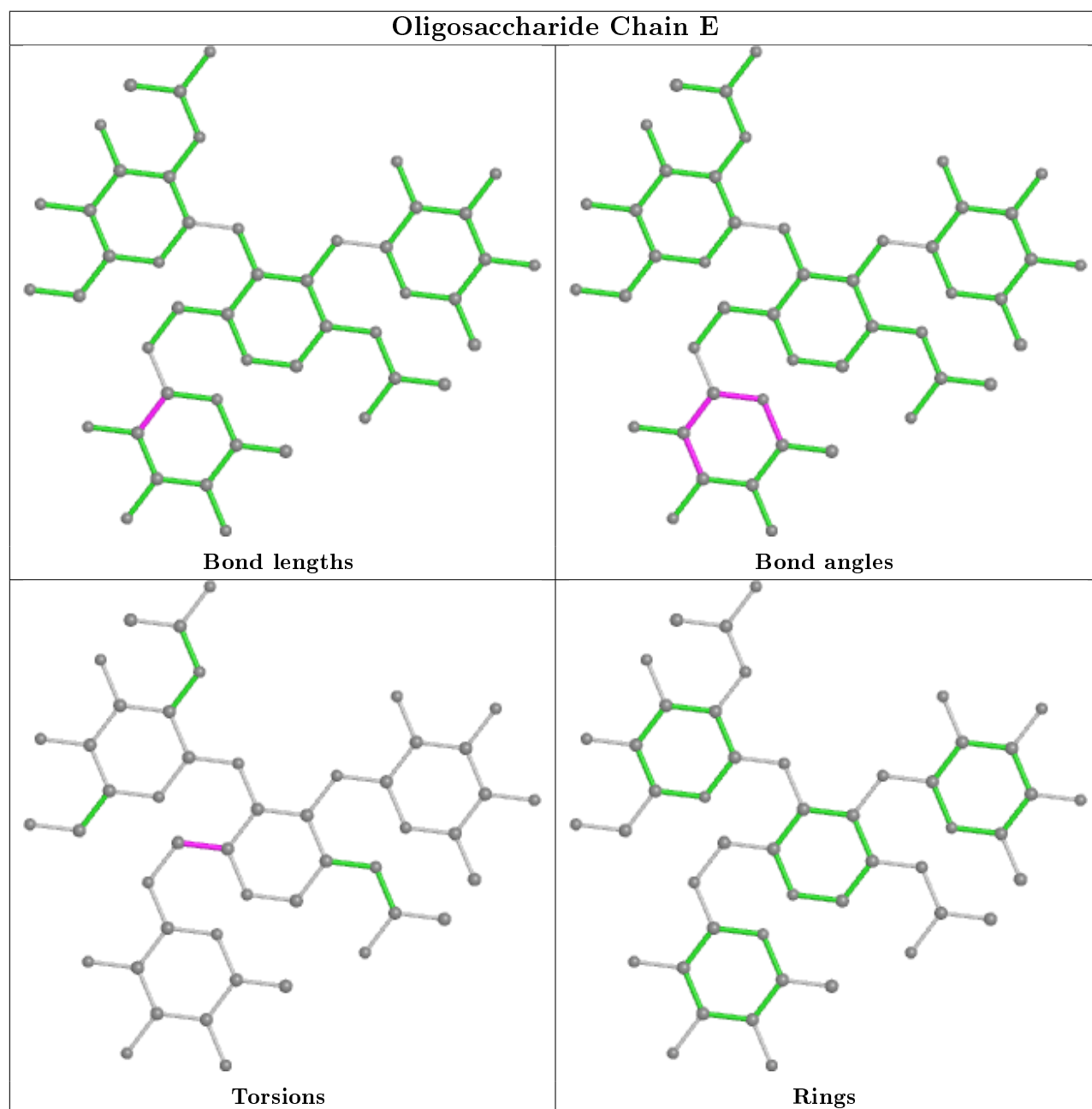
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	1	NAG	O5-C5-C6-O6
4	F	4	MAN	C4-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
4	F	4	MAN	O5-C5-C6-O6
4	G	3	BMA	O5-C5-C6-O6

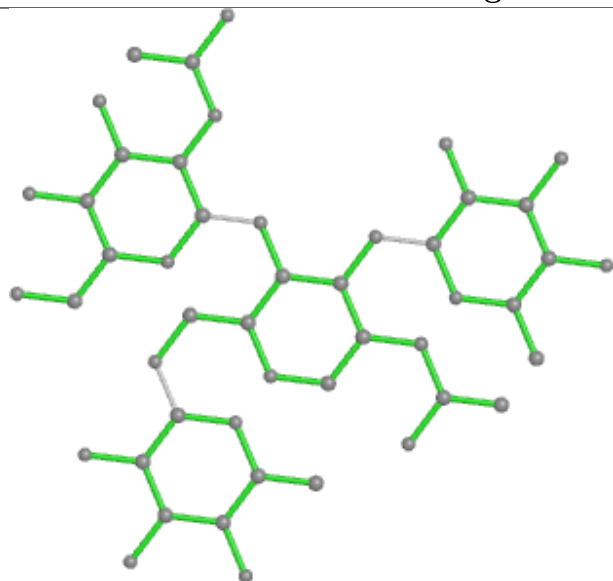
There are no ring outliers.

No monomer is involved in short contacts.

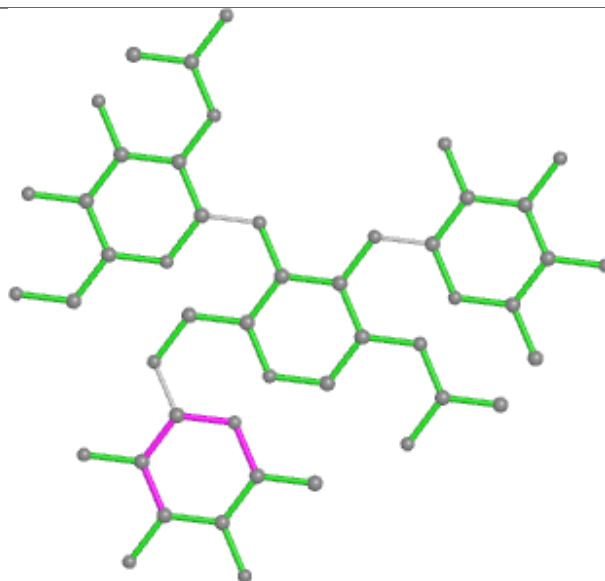
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



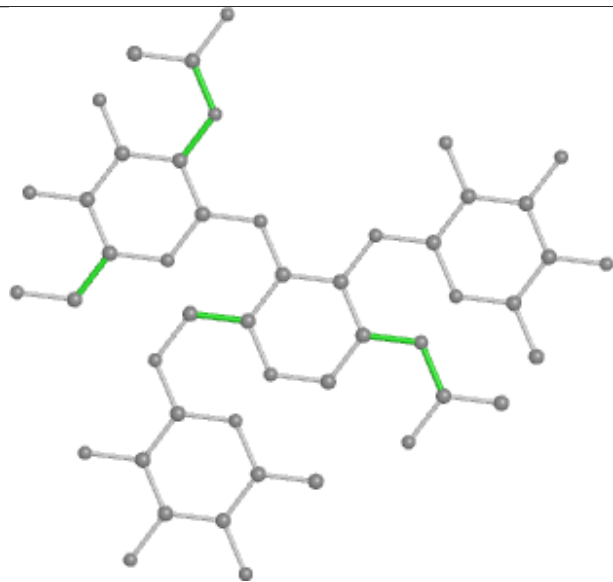
## Oligosaccharide Chain H



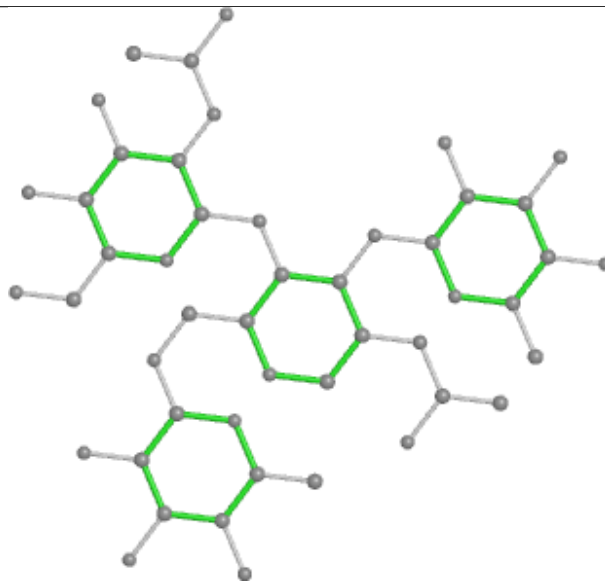
Bond lengths



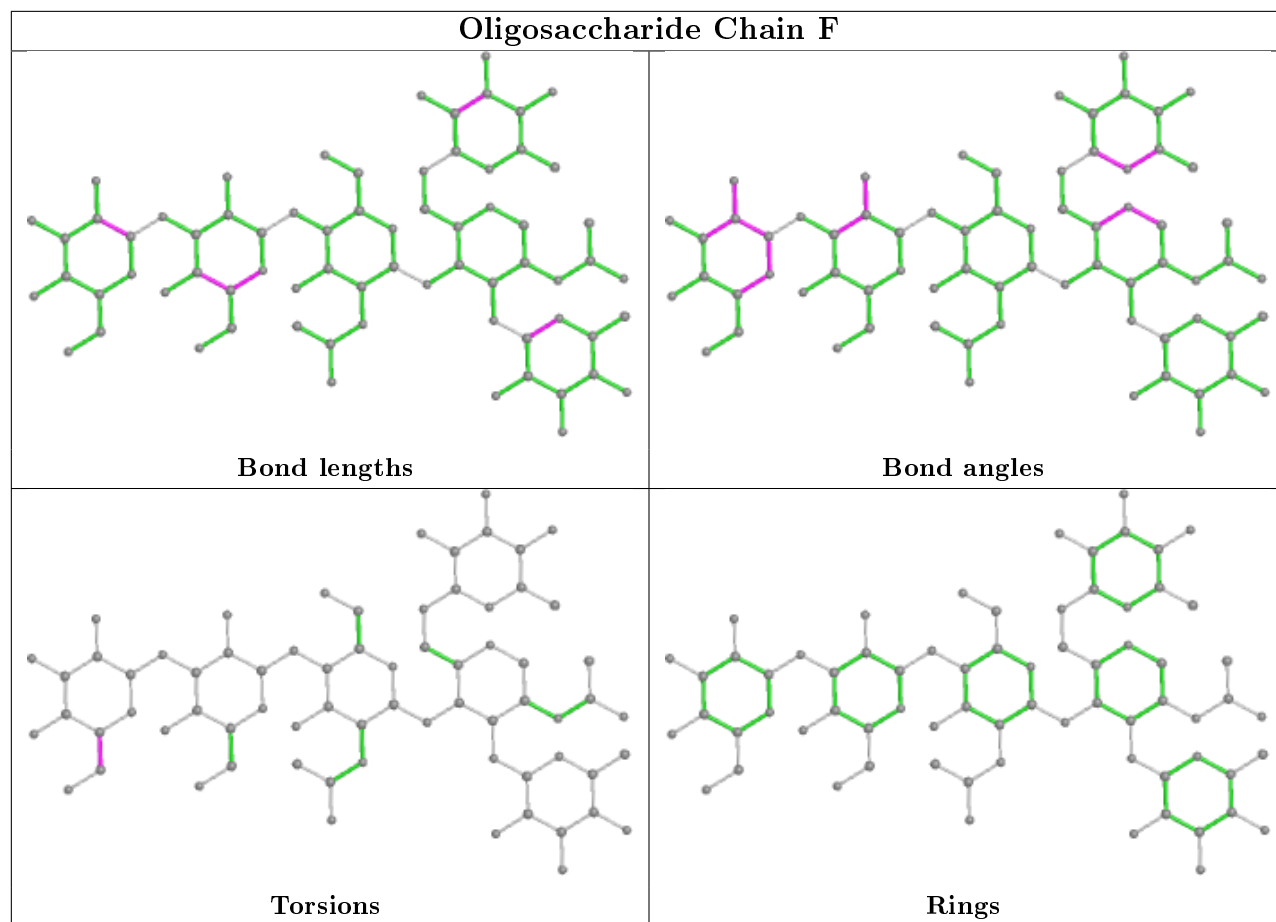
Bond angles

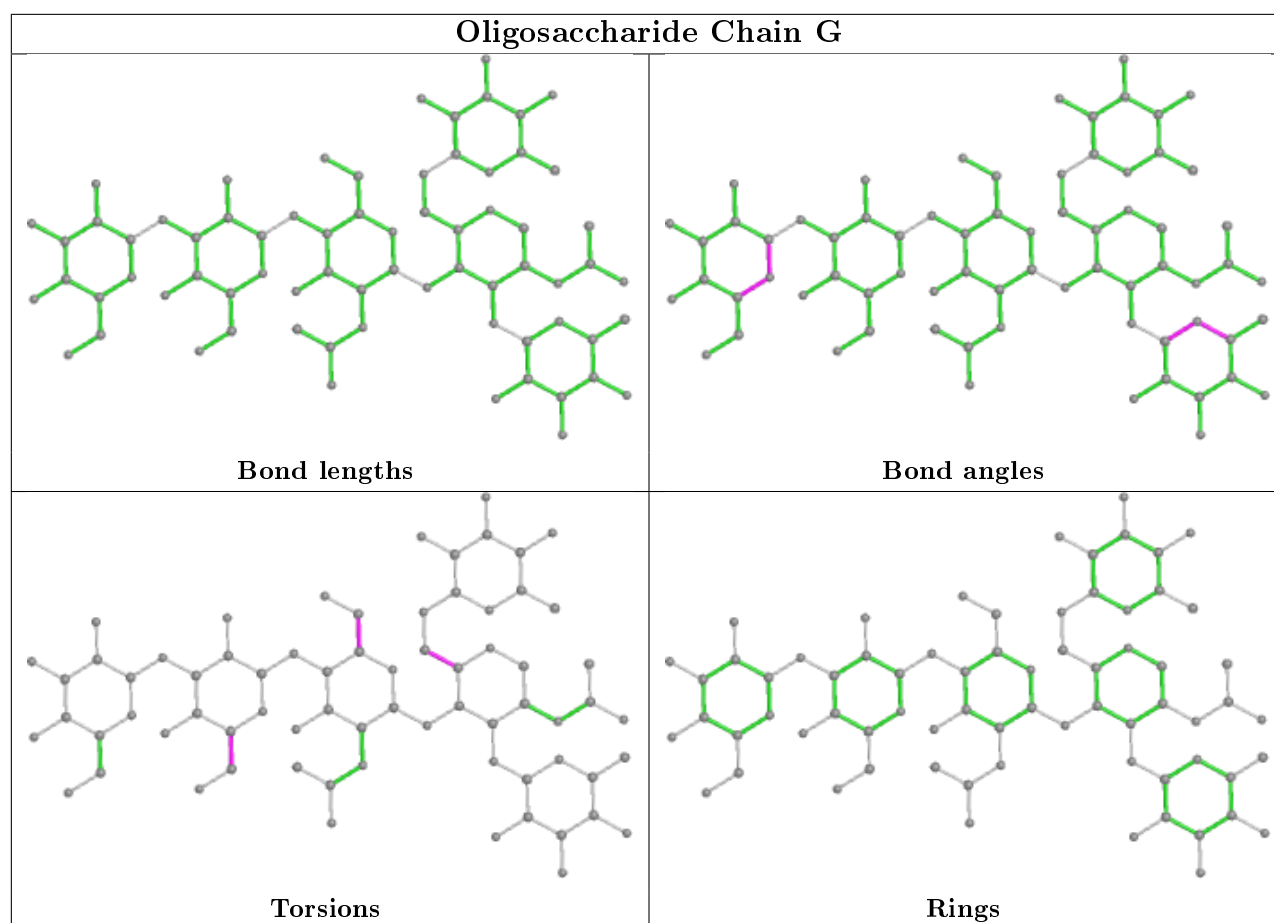


Torsions



Rings





## 5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	GOL	B	907	-	5,5,5	0.75	0	5,5,5	1.12	1 (20%)
6	NAG	C	905	1	14,14,15	0.28	0	17,19,21	0.50	0
5	GOL	A	911	-	5,5,5	0.99	0	5,5,5	0.80	0
5	GOL	C	906	-	5,5,5	0.87	0	5,5,5	0.97	0
6	NAG	D	901	2	14,14,15	0.78	1 (7%)	17,19,21	0.73	1 (5%)

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
5	GOL	B	907	-	-	0/4/4/4	-
6	NAG	C	905	1	-	0/6/23/26	0/1/1/1
5	GOL	A	911	-	-	2/4/4/4	-
5	GOL	C	906	-	-	4/4/4/4	-
6	NAG	D	901	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	901	NAG	O5-C1	2.36	1.47	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	901	NAG	C1-O5-C5	2.54	115.64	112.19
5	B	907	GOL	C3-C2-C1	-2.09	103.58	111.70

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	906	GOL	O1-C1-C2-C3
5	C	906	GOL	C1-C2-C3-O3
6	D	901	NAG	O5-C5-C6-O6
6	D	901	NAG	C4-C5-C6-O6
5	A	911	GOL	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	906	GOL	1	0

## 5.7 Other polymers [i](#)

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, 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	109/113 (96%)	-0.12	1 (0%) 84 82	26, 35, 69, 88	0
1	C	108/113 (95%)	-0.09	2 (1%) 66 63	25, 33, 54, 88	0
2	B	104/113 (92%)	-0.12	1 (0%) 82 80	27, 37, 62, 79	0
2	D	105/113 (92%)	0.03	1 (0%) 82 80	27, 45, 73, 84	0
All	All	426/452 (94%)	-0.08	5 (1%) 79 76	25, 37, 69, 88	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	142	ILE	3.9
2	D	102	LEU	3.9
1	C	49	SER	3.4
1	C	48	GLY	3.4
1	A	49	SER	3.1

### 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
4	MAN	F	4	11/12	0.69	0.26	64,68,69,72	0
4	BMA	G	3	11/12	0.72	0.17	56,64,71,71	0

*Continued on next page...*

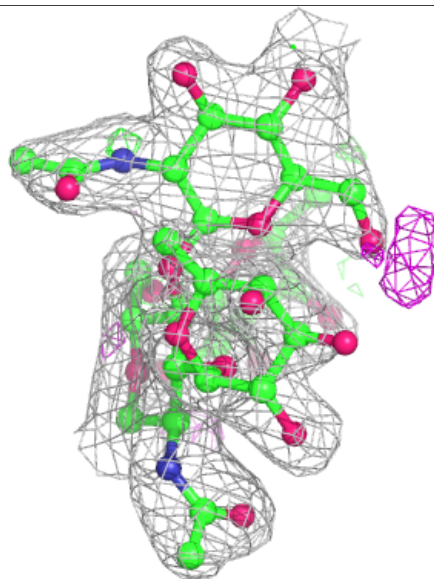
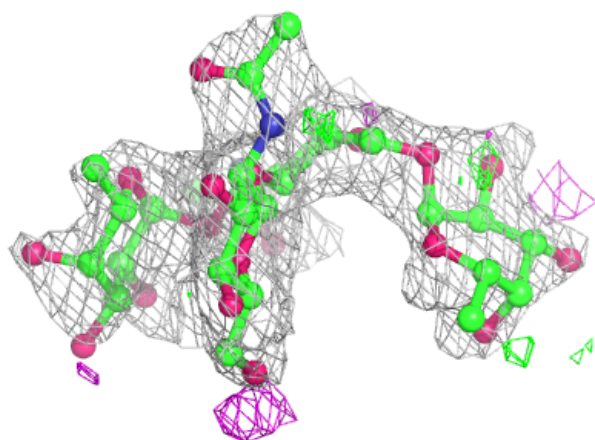
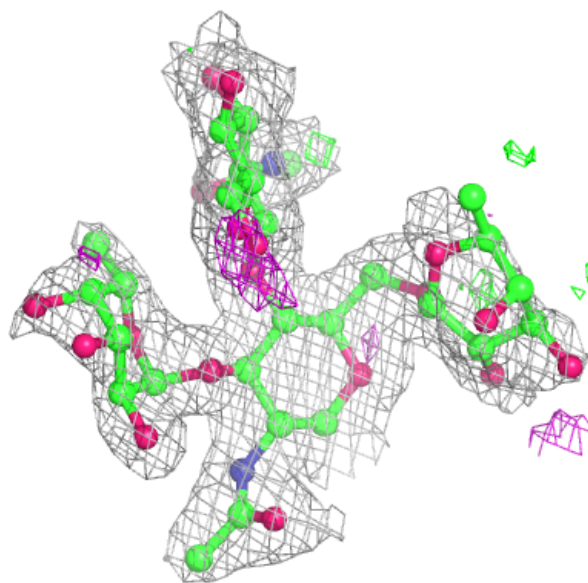
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	FUC	G	6	10/11	0.79	0.23	70,75,78,80	0
3	FUC	E	4	10/11	0.81	0.24	64,70,72,73	0
4	MAN	G	4	11/12	0.82	0.18	51,57,61,65	0
4	BMA	F	3	11/12	0.82	0.25	63,71,80,84	0
3	FUC	E	2	10/11	0.87	0.24	56,65,70,72	0
3	FUC	H	2	10/11	0.89	0.21	64,70,74,75	0
4	NAG	G	2	14/15	0.89	0.15	61,63,68,72	0
3	NAG	E	3	14/15	0.89	0.15	49,55,59,64	0
3	NAG	E	1	14/15	0.92	0.13	30,44,50,56	0
3	NAG	H	1	14/15	0.92	0.13	34,43,54,55	0
4	FUC	F	6	10/11	0.92	0.13	37,40,45,47	0
4	NAG	F	1	14/15	0.93	0.14	31,40,49,50	0
3	NAG	H	3	14/15	0.93	0.12	49,62,69,74	0
4	NAG	F	2	14/15	0.93	0.14	42,47,52,52	0
4	FUC	F	5	10/11	0.94	0.11	40,44,50,55	0
4	FUC	G	5	10/11	0.94	0.23	63,68,69,72	0
4	NAG	G	1	14/15	0.94	0.09	40,53,62,65	0
3	FUC	H	4	10/11	0.94	0.11	44,56,61,68	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.

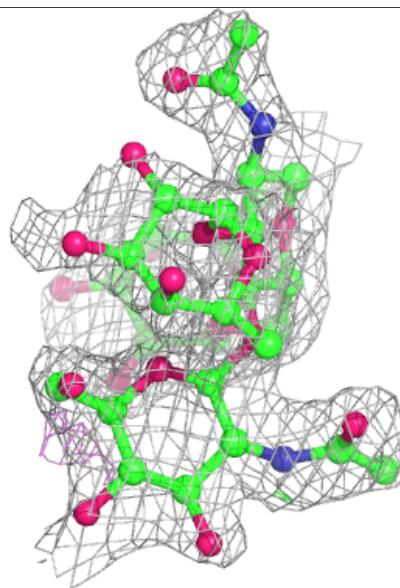
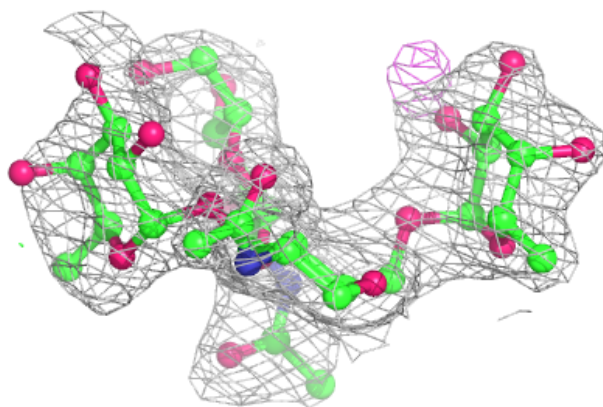
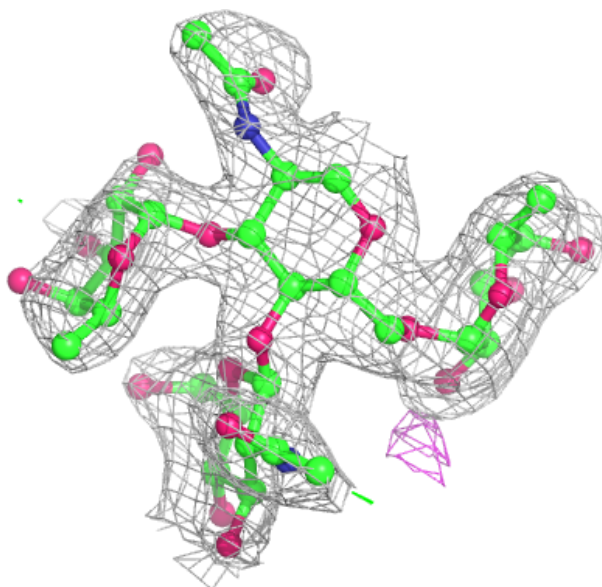
**Electron density around Chain E:**

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



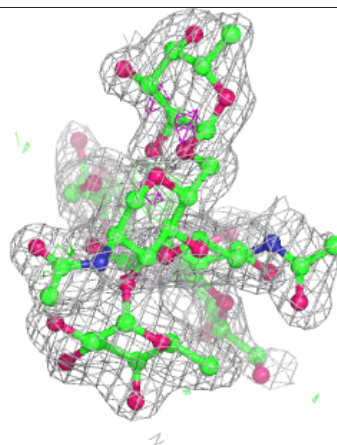
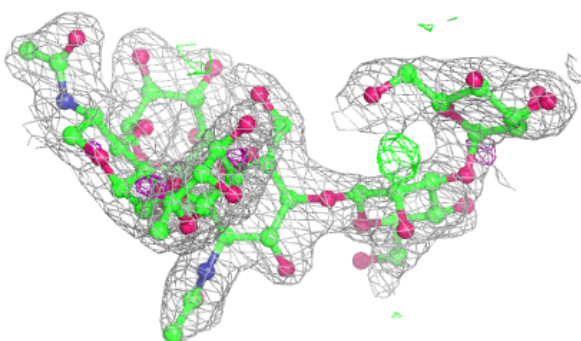
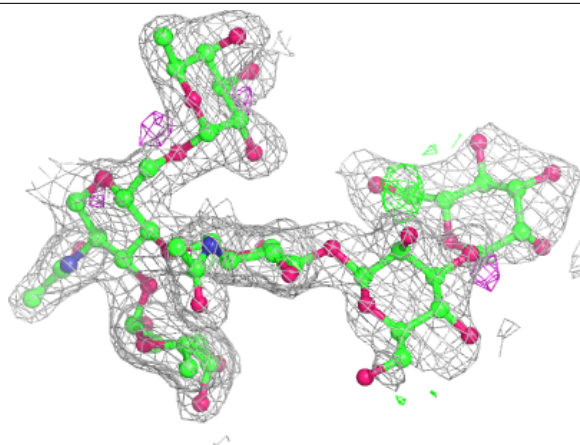
**Electron density around Chain H:**

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

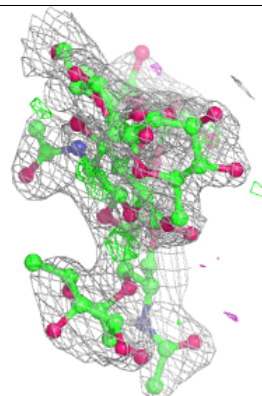
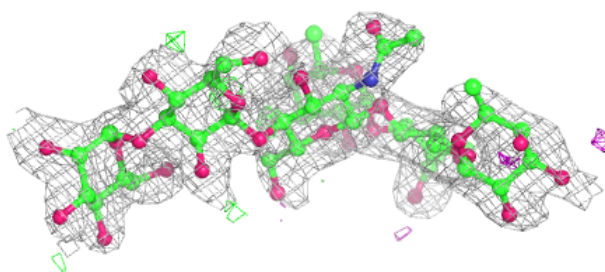
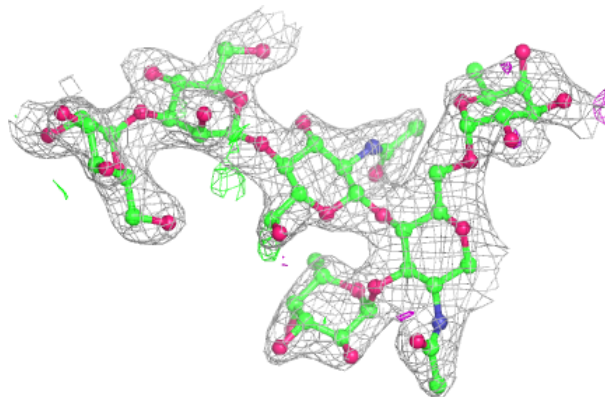


**Electron density around Chain F:**

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

**Electron density around Chain G:**

$2mF_o-DF_c$  (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
5	GOL	A	911	6/6	0.84	0.14	49,51,55,57	0
6	NAG	D	901	14/15	0.84	0.14	44,60,67,73	0
6	NAG	C	905	14/15	0.86	0.19	54,73,83,84	0
5	GOL	C	906	6/6	0.91	0.13	56,57,61,62	0
5	GOL	B	907	6/6	0.96	0.10	42,48,52,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.