



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 04:59 AM EDT

PDB ID : 2HMG  
Title : REFINEMENT OF THE INFLUENZA VIRUS HEMAGGLUTININ BY SIMULATED ANNEALING  
Authors : Weis, W.I.; Bruenger, A.T.; Skehel, J.J.; Wiley, D.C.  
Deposited on : 1989-09-11  
Resolution : 3.00 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

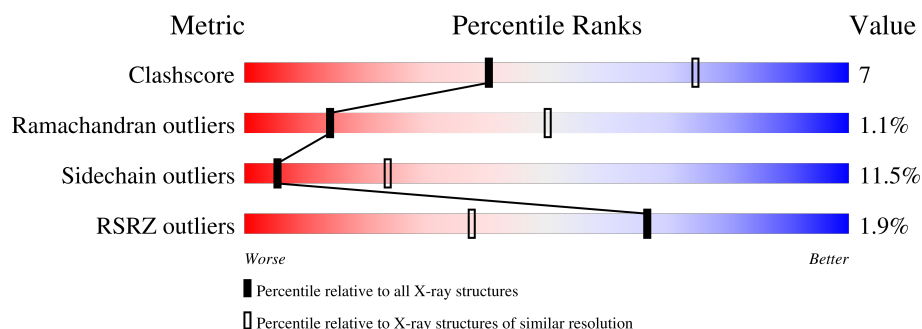
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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.



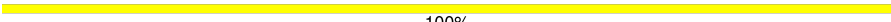

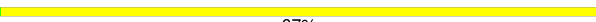
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	328	<div> <div>2%</div> <div>69%</div> <div>23%</div> <div>7%</div> </div>
1	C	328	<div> <div>2%</div> <div>70%</div> <div>23%</div> <div>6%</div> </div>
1	E	328	<div> <div>2%</div> <div>70%</div> <div>24%</div> <div>7%</div> </div>
2	B	175	<div> <div>%</div> <div>77%</div> <div>19%</div> <div>• •</div> </div>
2	D	175	<div> <div>%</div> <div>76%</div> <div>19%</div> <div>5% •</div> </div>
2	F	175	<div> <div>%</div> <div>74%</div> <div>21%</div> <div>• •</div> </div>
3	G	3	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	3	 100%
3	I	3	 33%  67%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12189 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called HEMAGGLUTININ (HA1 CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	0	0
			2536	1583	445	495	13			
1	C	328	Total	C	N	O	S	0	0	0
			2536	1583	445	495	13			
1	E	328	Total	C	N	O	S	0	0	0
			2536	1583	445	495	13			

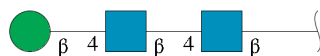
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	146	ASP	GLY	conflict	UNP P03437
C	146	ASP	GLY	conflict	UNP P03437
E	146	ASP	GLY	conflict	UNP P03437

- Molecule 2 is a protein called HEMAGGLUTININ (HA2 CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	175	Total	C	N	O	S	0	0	0
			1421	882	250	283	6			
2	D	175	Total	C	N	O	S	0	0	0
			1421	882	250	283	6			
2	F	175	Total	C	N	O	S	0	0	0
			1421	882	250	283	6			

- Molecule 3 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
3	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

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

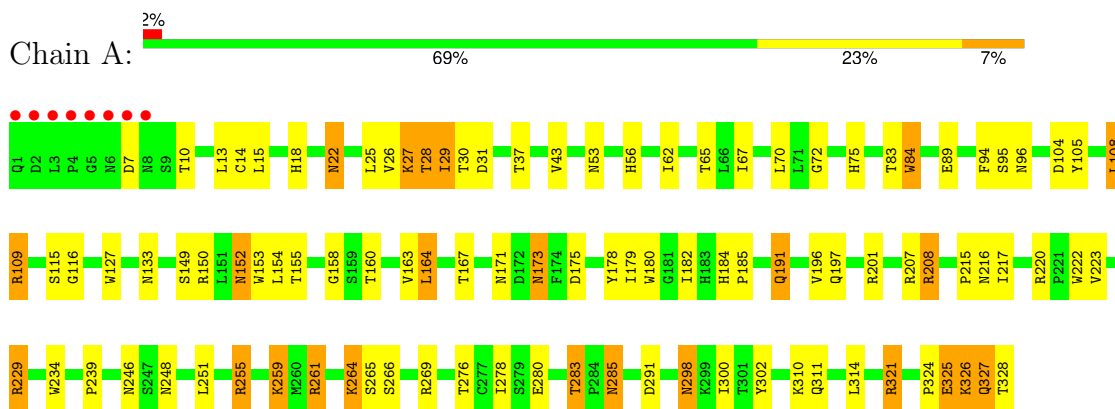
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	8	Total	O	0	0
			8	8		
5	B	3	Total	O	0	0
			3	3		
5	C	8	Total	O	0	0
			8	8		
5	D	3	Total	O	0	0
			3	3		
5	E	8	Total	O	0	0
			8	8		
5	F	3	Total	O	0	0
			3	3		

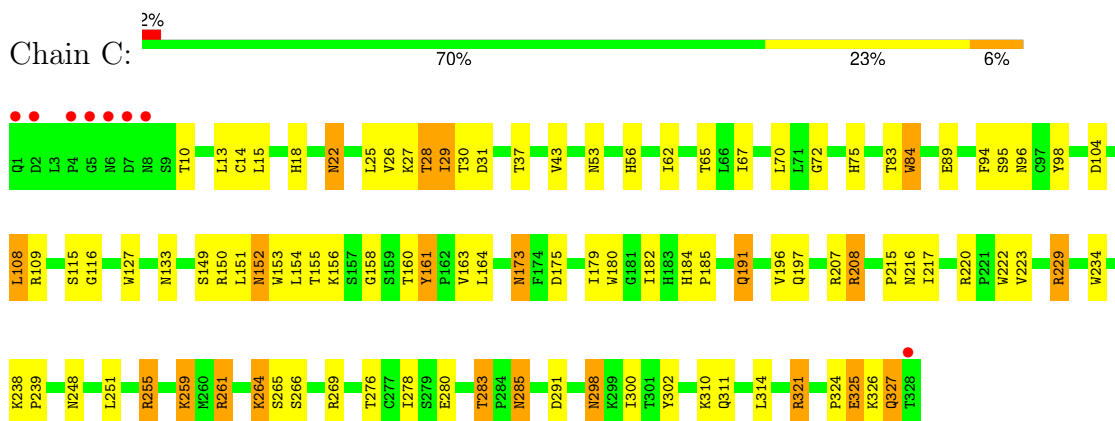
### 3 Residue-property plots

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.

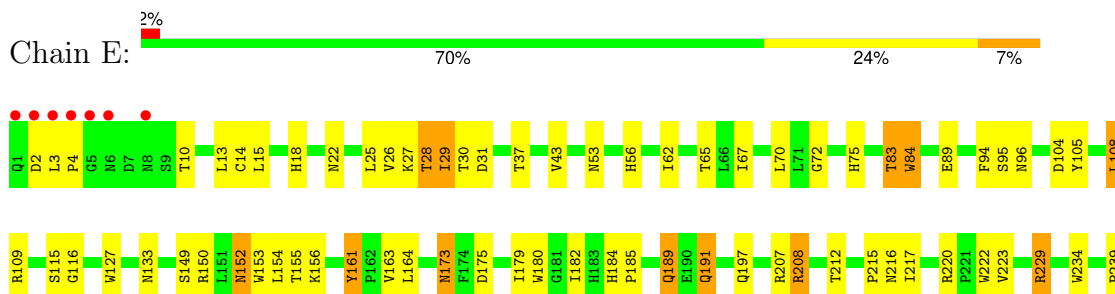
#### • Molecule 1: HEMAGGLUTININ (HA1 CHAIN)



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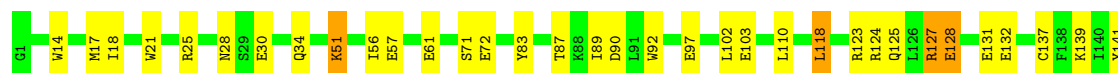


#### • Molecule 1: HEMAGGLUTININ (HA1 CHAIN)





• Molecule 2: HEMAGGLUTININ (HA2 CHAIN)



• Molecule 2: HEMAGGLUTININ (HA2 CHAIN)



• Molecule 2: HEMAGGLUTININ (HA2 CHAIN)



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



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





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

Chain I:  33% 67%

MAG1  
MAG2  
EMJ3

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.60Å 162.60Å 177.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.00 7.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00) 79.4 (7.00-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.222 , (Not available) 0.206 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.7	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 47.3	EDS
L-test for twinning <sup>1</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	12189	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</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

### 5.1 Standard geometry

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

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	0.92	0/2593	1.47	35/3533 (1.0%)
1	C	0.89	0/2593	1.47	35/3533 (1.0%)
1	E	0.93	1/2593 (0.0%)	1.47	37/3533 (1.0%)
2	B	0.95	0/1445	1.49	18/1939 (0.9%)
2	D	0.96	0/1445	1.49	18/1939 (0.9%)
2	F	0.98	0/1445	1.50	25/1939 (1.3%)
All	All	0.93	1/12114 (0.0%)	1.48	168/16416 (1.0%)

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
1	C	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	234	TRP	CG-CD2	-5.16	1.34	1.43

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	321	ARG	NE-CZ-NH1	-10.01	115.30	120.30
1	E	321	ARG	NE-CZ-NH1	-9.94	115.33	120.30
1	A	321	ARG	NE-CZ-NH1	-9.75	115.42	120.30
1	C	229	ARG	NE-CZ-NH1	-9.70	115.45	120.30
2	F	124	ARG	NE-CZ-NH1	-9.67	115.47	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	161	TYR	Sidechain

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2536	0	2474	44	0
1	C	2536	0	2474	48	0
1	E	2536	0	2474	48	0
2	B	1421	0	1345	20	0
2	D	1421	0	1345	22	0
2	F	1421	0	1345	18	0
3	G	39	0	34	1	0
3	H	39	0	34	0	0
3	I	39	0	34	0	0
4	A	42	0	39	0	0
4	B	14	0	13	0	0
4	C	42	0	39	0	0
4	D	14	0	13	0	0
4	E	42	0	39	0	0
4	F	14	0	13	0	0
5	A	8	0	0	0	0
5	B	3	0	0	0	0
5	C	8	0	0	0	0
5	D	3	0	0	0	0
5	E	8	0	0	0	0
5	F	3	0	0	0	0
All	All	12189	0	11715	171	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 7.

The worst 5 of 171 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:325:GLU:HB2	2:D:12:ASN:ND2	2.04	0.72
2:D:25:ARG:HG2	2:D:34:GLN:HB3	1.72	0.70
2:B:51:LYS:HE3	2:B:103:GLU:OE2	1.93	0.69
2:D:51:LYS:HE3	2:D:103:GLU:OE2	1.92	0.69
1:E:29:ILE:HD11	2:F:102:LEU:HD23	1.75	0.69

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	326/328 (99%)	304 (93%)	18 (6%)	4 (1%)	13	48
1	C	326/328 (99%)	308 (94%)	14 (4%)	4 (1%)	13	48
1	E	326/328 (99%)	308 (94%)	16 (5%)	2 (1%)	25	64
2	B	173/175 (99%)	161 (93%)	10 (6%)	2 (1%)	13	48
2	D	173/175 (99%)	162 (94%)	9 (5%)	2 (1%)	13	48
2	F	173/175 (99%)	161 (93%)	10 (6%)	2 (1%)	13	48
All	All	1497/1509 (99%)	1404 (94%)	77 (5%)	16 (1%)	14	50

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	327	GLN
1	A	158	GLY
2	B	57	GLU
2	B	174	LYS
2	D	57	GLU

### 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	290/290 (100%)	250 (86%)	40 (14%)	3	17
1	C	290/290 (100%)	256 (88%)	34 (12%)	5	22
1	E	290/290 (100%)	252 (87%)	38 (13%)	4	18
2	B	149/149 (100%)	137 (92%)	12 (8%)	11	40
2	D	149/149 (100%)	136 (91%)	13 (9%)	10	37
2	F	149/149 (100%)	135 (91%)	14 (9%)	8	32
All	All	1317/1317 (100%)	1166 (88%)	151 (12%)	5	24

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	164	LEU
2	F	118	LEU
1	E	208	ARG
1	E	291	ASP
2	F	174	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	152	ASN
1	E	197	GLN
1	E	298	ASN
1	E	173	ASN
1	C	173	ASN

### 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 ⓘ

9 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	G	1	1,3	14,14,15	0.74	0	17,19,21	0.96	0
3	NAG	G	2	3	14,14,15	0.71	0	17,19,21	1.09	1 (5%)
3	BMA	G	3	3	11,11,12	0.76	0	15,15,17	1.21	2 (13%)
3	NAG	H	1	1,3	14,14,15	0.74	1 (7%)	17,19,21	0.93	1 (5%)
3	NAG	H	2	3	14,14,15	0.55	0	17,19,21	1.17	2 (11%)
3	BMA	H	3	3	11,11,12	0.94	1 (9%)	15,15,17	1.33	2 (13%)
3	NAG	I	1	1,3	14,14,15	0.62	0	17,19,21	0.99	1 (5%)
3	NAG	I	2	3	14,14,15	0.56	0	17,19,21	1.08	2 (11%)
3	BMA	I	3	3	11,11,12	0.56	0	15,15,17	1.07	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
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	BMA	H	3	3	-	0/2/19/22	0/1/1/1
3	NAG	I	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	I	3	3	-	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	3	BMA	C2-C3	2.29	1.56	1.52
3	H	1	NAG	O5-C1	-2.09	1.40	1.43

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	3	BMA	C1-O5-C5	3.10	116.34	112.19
3	H	3	BMA	C2-C3-C4	-2.67	106.17	110.86
3	H	3	BMA	O3-C3-C2	2.63	115.42	110.05
3	H	2	NAG	C1-C2-N2	2.54	114.44	110.43
3	I	1	NAG	C1-C2-N2	2.33	114.11	110.43

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	1	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6

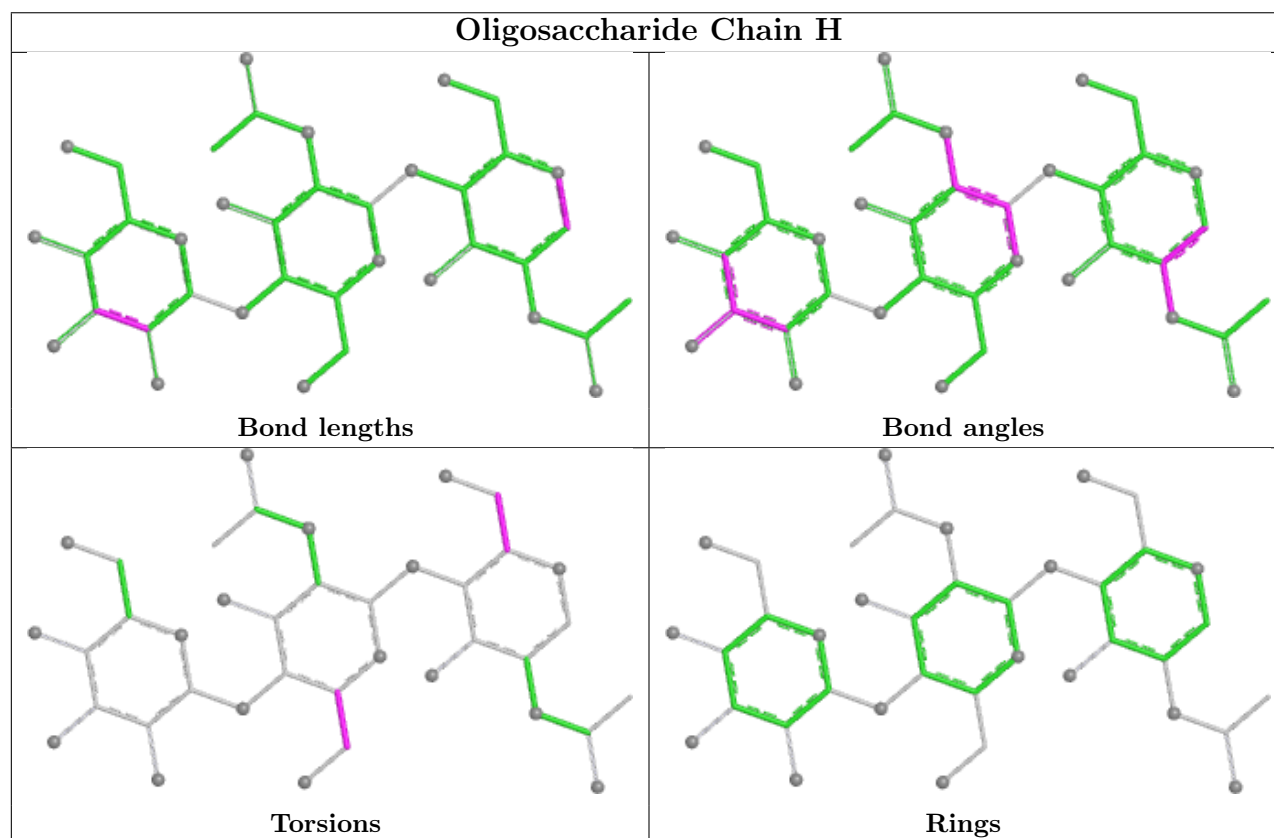
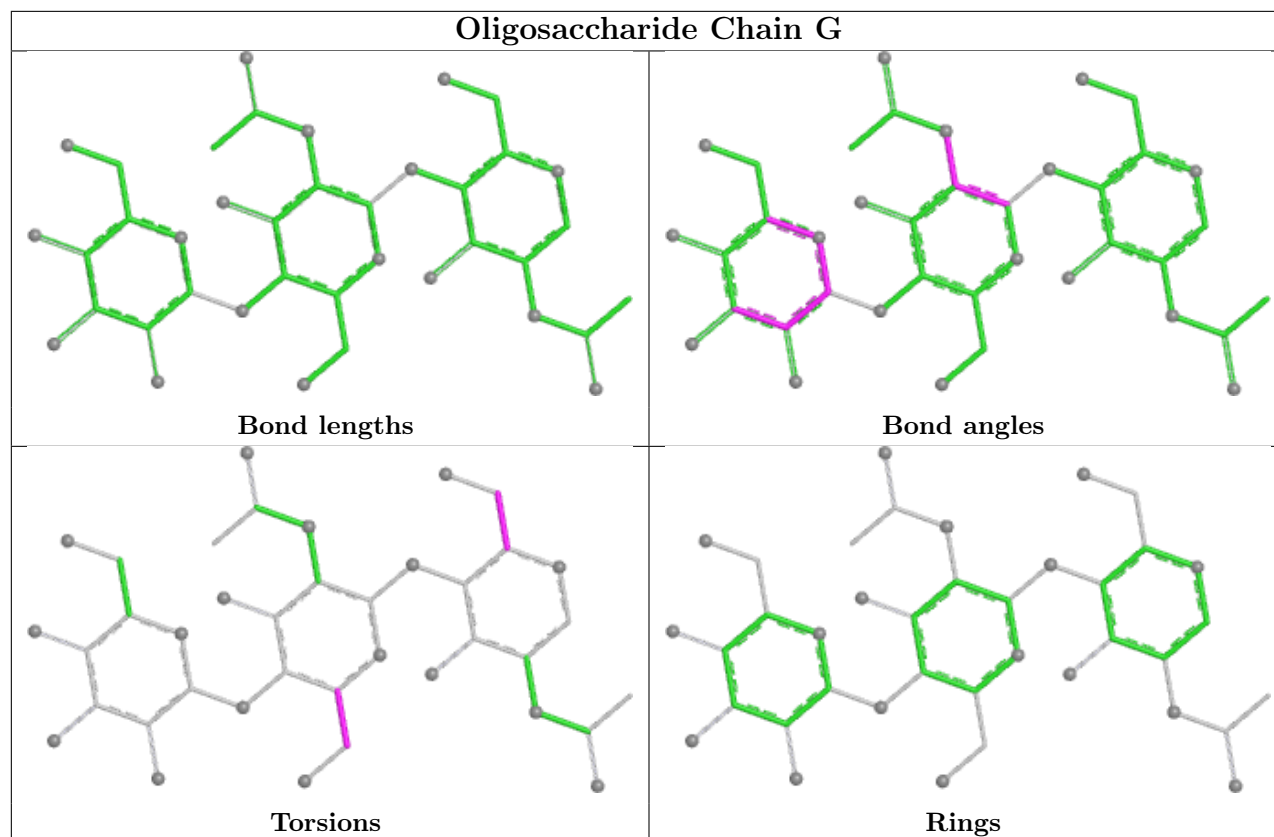
There are no ring outliers.

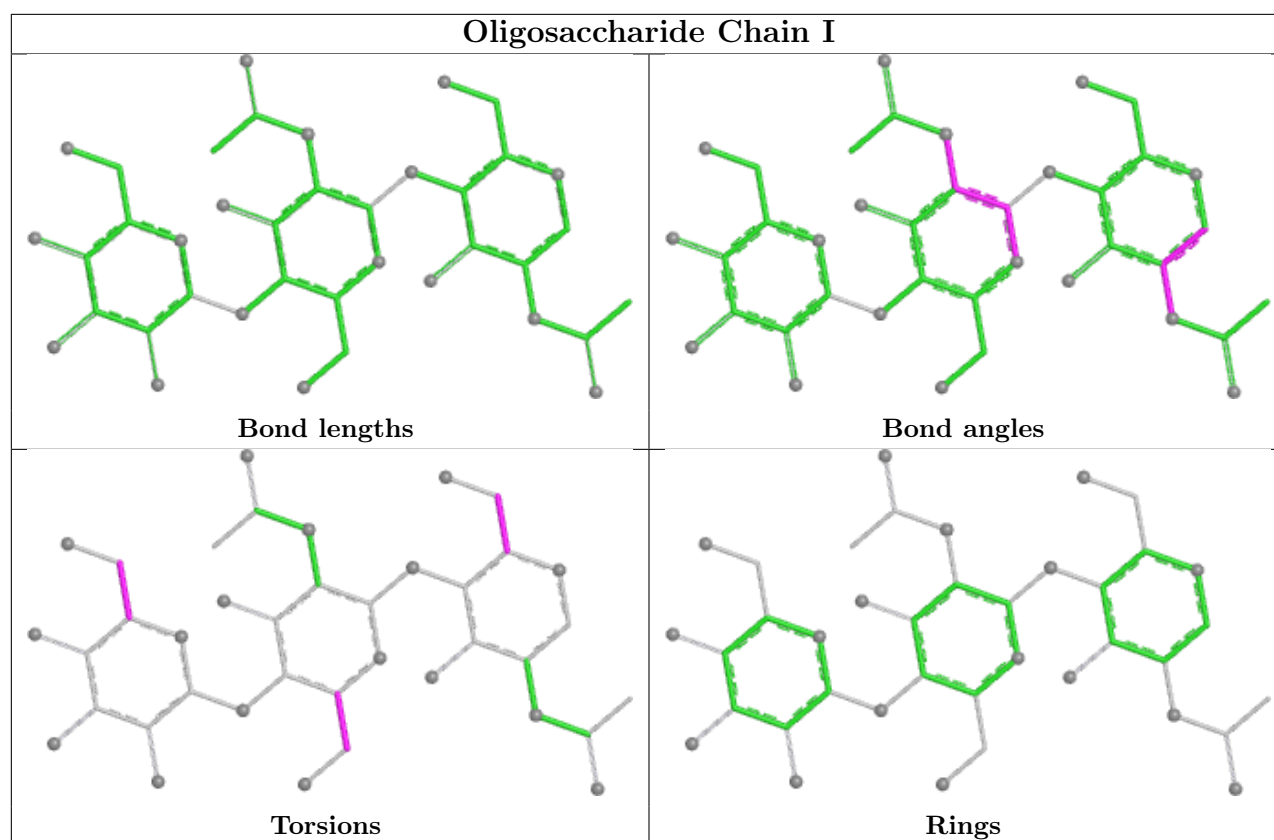
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	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.







## 5.6 Ligand geometry [i](#)

12 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
4	NAG	A	334	1	14,14,15	0.78	0	17,19,21	1.18	2 (11%)
4	NAG	D	401	2	14,14,15	0.80	1 (7%)	17,19,21	1.15	2 (11%)
4	NAG	C	348	1	14,14,15	0.62	0	17,19,21	1.22	2 (11%)
4	NAG	E	334	1	14,14,15	0.75	0	17,19,21	1.19	1 (5%)
4	NAG	A	329	1	14,14,15	0.98	1 (7%)	17,19,21	0.78	0
4	NAG	B	401	2	14,14,15	0.62	0	17,19,21	1.03	1 (5%)
4	NAG	C	334	1	14,14,15	0.67	0	17,19,21	1.20	2 (11%)
4	NAG	C	329	1	14,14,15	0.81	0	17,19,21	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	E	348	1	14,14,15	0.68	0	17,19,21	1.18	1 (5%)
4	NAG	E	329	1	14,14,15	1.15	1 (7%)	17,19,21	0.86	1 (5%)
4	NAG	A	348	1	14,14,15	0.72	0	17,19,21	1.08	1 (5%)
4	NAG	F	401	2	14,14,15	0.72	0	17,19,21	1.07	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
4	NAG	A	334	1	-	2/6/23/26	0/1/1/1
4	NAG	D	401	2	-	0/6/23/26	0/1/1/1
4	NAG	C	348	1	-	0/6/23/26	0/1/1/1
4	NAG	E	334	1	-	2/6/23/26	0/1/1/1
4	NAG	A	329	1	-	0/6/23/26	0/1/1/1
4	NAG	B	401	2	-	0/6/23/26	0/1/1/1
4	NAG	C	334	1	-	2/6/23/26	0/1/1/1
4	NAG	C	329	1	-	0/6/23/26	0/1/1/1
4	NAG	E	348	1	-	0/6/23/26	0/1/1/1
4	NAG	E	329	1	-	0/6/23/26	0/1/1/1
4	NAG	A	348	1	-	0/6/23/26	0/1/1/1
4	NAG	F	401	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	329	NAG	C1-C2	-3.19	1.48	1.52
4	A	329	NAG	C1-C2	-2.26	1.49	1.52
4	D	401	NAG	C1-C2	-2.00	1.49	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	334	NAG	C1-O5-C5	2.90	116.07	112.19
4	E	334	NAG	C1-O5-C5	2.85	116.00	112.19
4	C	334	NAG	C1-O5-C5	2.80	115.94	112.19
4	D	401	NAG	C1-O5-C5	2.38	115.38	112.19
4	B	401	NAG	C3-C4-C5	-2.34	106.00	110.23

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	334	NAG	C4-C5-C6-O6
4	C	334	NAG	C4-C5-C6-O6
4	E	334	NAG	C4-C5-C6-O6
4	A	334	NAG	O5-C5-C6-O6
4	C	334	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 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	328/328 (100%)	-0.82	8 (2%) 59 30	4, 23, 55, 137	0
1	C	328/328 (100%)	-0.88	8 (2%) 59 30	4, 23, 50, 132	0
1	E	328/328 (100%)	-0.91	8 (2%) 59 30	5, 22, 48, 134	0
2	B	175/175 (100%)	-0.98	1 (0%) 89 72	2, 17, 48, 102	0
2	D	175/175 (100%)	-1.02	1 (0%) 89 72	3, 16, 42, 103	0
2	F	175/175 (100%)	-0.98	2 (1%) 80 56	2, 16, 42, 103	0
All	All	1509/1509 (100%)	-0.91	28 (1%) 66 37	2, 21, 51, 137	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	175	GLY	7.0
1	E	2	ASP	5.1
1	E	4	PRO	5.0
1	A	1	GLN	4.8
1	C	1	GLN	4.4

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

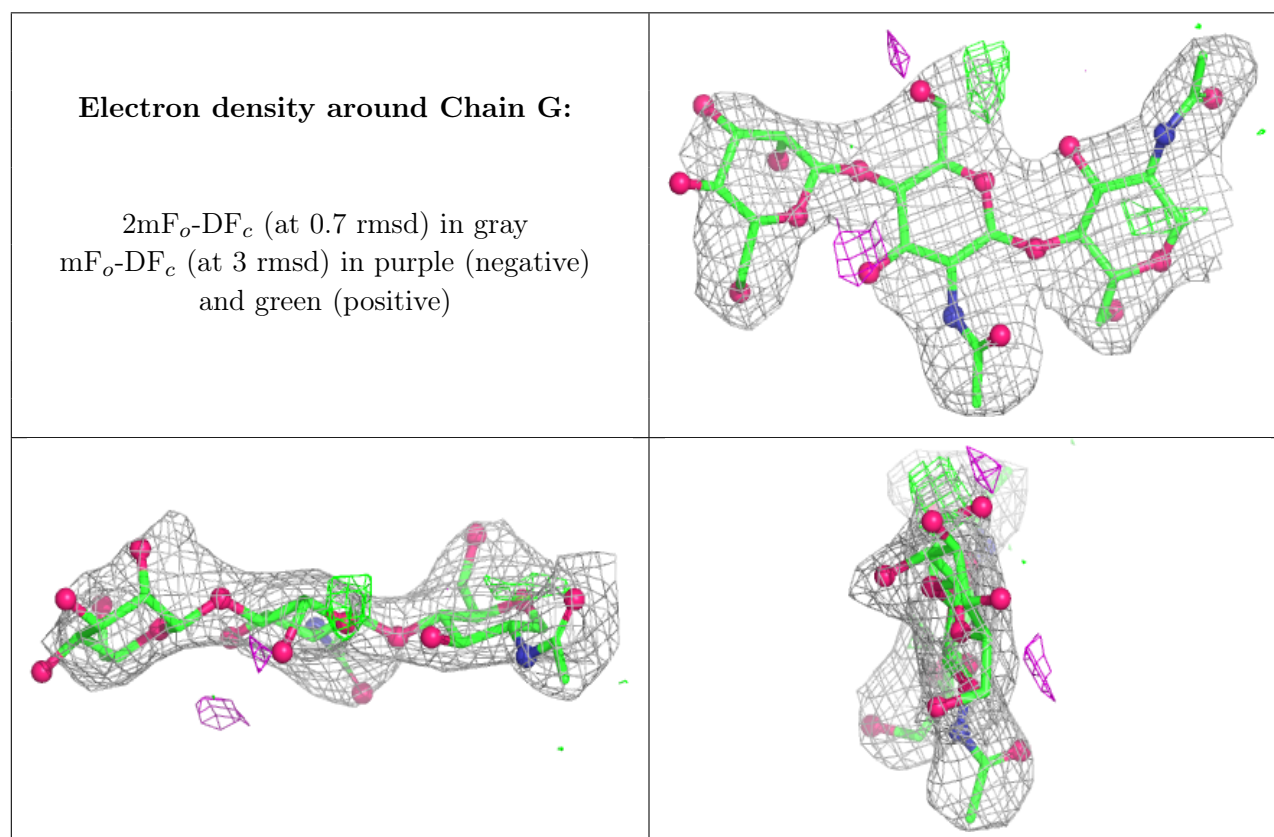
There are no non-standard protein/DNA/RNA residues in this entry.

### 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.

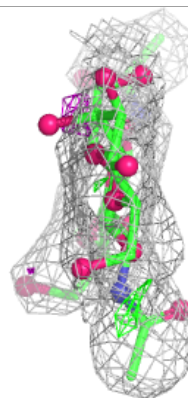
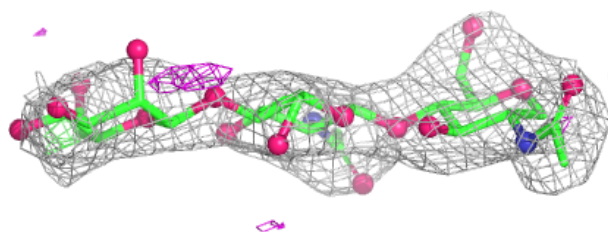
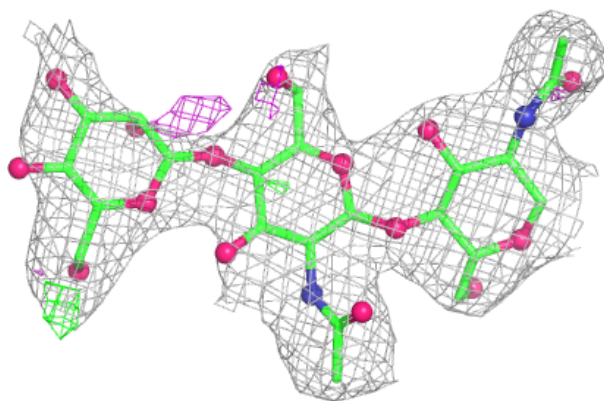
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	BMA	H	3	11/12	0.85	0.28	55,57,58,58	0
3	NAG	H	2	14/15	0.88	0.25	47,50,51,53	0
3	BMA	G	3	11/12	0.90	0.23	54,56,57,58	0
3	BMA	I	3	11/12	0.91	0.24	56,58,59,59	0
3	NAG	H	1	14/15	0.92	0.19	39,42,44,46	0
3	NAG	I	2	14/15	0.92	0.17	46,49,51,53	0
3	NAG	G	2	14/15	0.92	0.19	46,49,51,52	0
3	NAG	G	1	14/15	0.93	0.18	39,42,45,45	0
3	NAG	I	1	14/15	0.96	0.13	38,41,43,44	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.

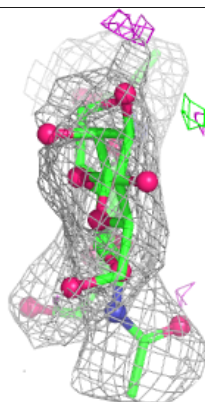
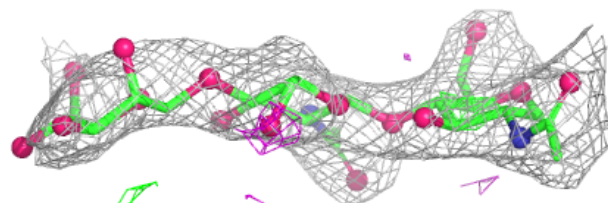
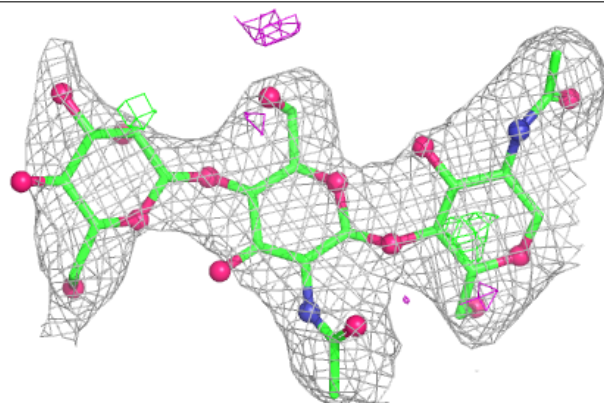


**Electron density around Chain H:**

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

**Electron density around Chain I:**

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





## 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( $\text{\AA}^2$ )	Q<0.9
4	NAG	B	401	14/15	0.86	0.28	48,52,53,56	0
4	NAG	F	401	14/15	0.86	0.28	48,51,53,54	0
4	NAG	E	348	14/15	0.88	0.25	35,40,42,43	0
4	NAG	A	334	14/15	0.89	0.20	37,40,42,43	0
4	NAG	E	329	14/15	0.91	0.23	36,40,42,42	0
4	NAG	E	334	14/15	0.91	0.19	37,40,42,42	0
4	NAG	A	348	14/15	0.91	0.19	35,39,41,41	0
4	NAG	D	401	14/15	0.91	0.23	48,52,54,54	0
4	NAG	C	348	14/15	0.92	0.20	35,39,41,42	0
4	NAG	A	329	14/15	0.93	0.21	36,40,41,42	0
4	NAG	C	329	14/15	0.94	0.16	35,39,40,40	0
4	NAG	C	334	14/15	0.94	0.17	38,41,43,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.