



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2024 – 03:50 AM EDT

PDB ID : 5BR3  
Title : Crystal structure of hemagglutinin of A/Taiwan/2/2013 (H6N1) in complex with LSTa  
Authors : Ni, F.; Kondrashkina, E.; Wang, Q.  
Deposited on : 2015-05-29  
Resolution : 2.55 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>.

---

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 : 2.37.1  
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

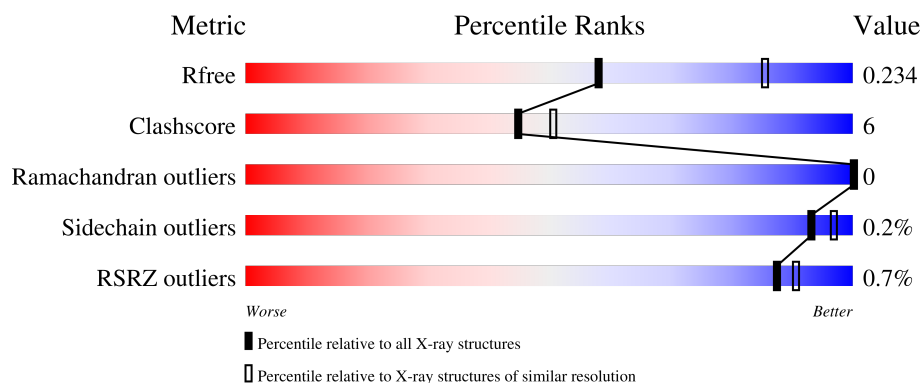
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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.





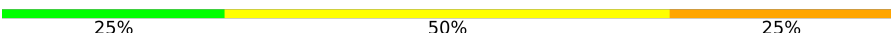
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	326	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -5px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>85%</span> <span>15%</span> </div> </div>
1	C	326	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -5px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>87%</span> <span>13%</span> </div> </div>
2	B	171	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -5px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>93%</span> <span>7%</span> </div> </div>
2	D	171	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -5px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>92%</span> <span>8%</span> </div> </div>
3	E	3	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> <span style="position: absolute; top: -5px; left: 0;">%</span> </div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>67%</span> <span>33%</span> </div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
4	F	6	 50% 50%
4	H	6	 50% 50%
5	G	4	 25% 50% 25%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	F	5	-	-	-	X
4	FUC	F	6	X	-	-	-
4	FUC	H	6	X	-	-	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8841 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.

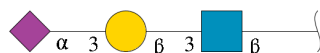
- Molecule 1 is a protein called HEMAGGLUTININ HA1 CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2577	1634	439	491	13			
1	C	326	Total	C	N	O	S	0	0	0
			2577	1634	439	491	13			

- Molecule 2 is a protein called HEMAGGLUTININ HA2 CHAIN.

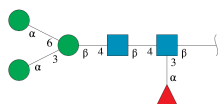
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	171	Total	C	N	O	S	0	0	0
			1381	860	242	272	7			
2	D	171	Total	C	N	O	S	0	0	0
			1381	860	242	272	7			

- Molecule 3 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	3	Total	C	N	O	0	0	0
			45	25	2	18			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	6	Total	C	N	O	0	0	0
			71	40	2	29			
4	H	6	Total	C	N	O	0	0	0
			71	40	2	29			

- Molecule 5 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	4	Total	C	N	O	0	0	0
			56	31	2	23			

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

*Continued on next page...*

*Continued from previous page...*

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

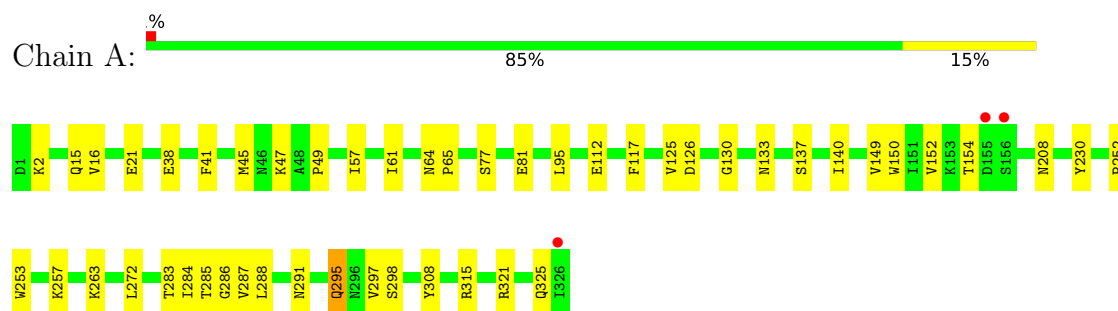
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	154	Total	O	0	0
			154	154		
7	B	136	Total	O	0	0
			136	136		
7	C	159	Total	O	0	0
			159	159		
7	D	121	Total	O	0	0
			121	121		

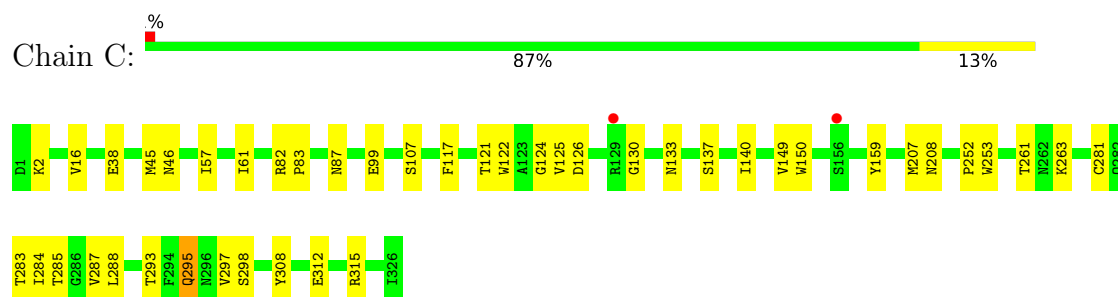
### 3 Residue-property plots

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.

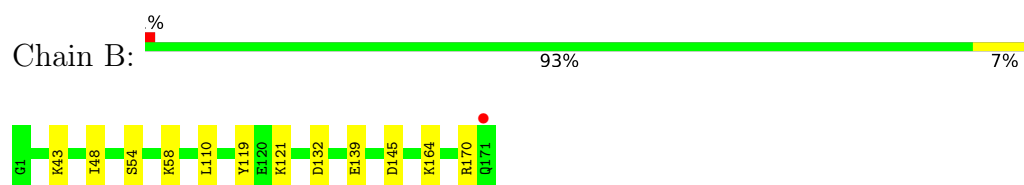
- Molecule 1: HEMAGGLUTININ HA1 CHAIN



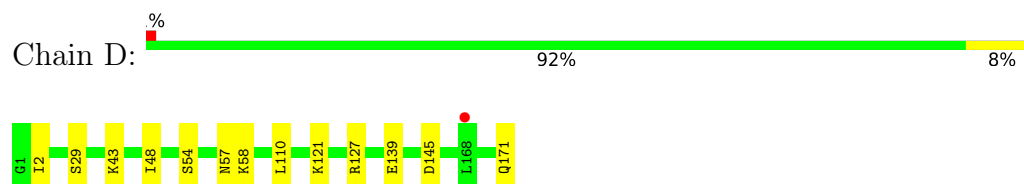
- Molecule 1: HEMAGGLUTININ HA1 CHAIN



- Molecule 2: HEMAGGLUTININ HA2 CHAIN



- Molecule 2: HEMAGGLUTININ HA2 CHAIN



- Molecule 3: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  67% 33%

HA01  
GAL2  
SIA3

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

Chain F:  50% 50%

HA01  
HA02  
BMA3  
MAN4  
MAN5  
FUC6

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

Chain H:  50% 50%

HA01  
HA02  
BMA3  
MAN4  
MAN5  
FUC6

- Molecule 5: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose

Chain G:  25% 50% 25%

GAL1  
HA02  
GAL3  
SIA4



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.01Å 114.01Å 163.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.24 – 2.55 42.24 – 2.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.24-2.55) 100.0 (42.24-2.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 2.54Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.201 , 0.228 0.210 , 0.234	Depositor DCC
$R_{free}$ test set	3871 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.7	Xtriage
Anisotropy	0.519	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 29.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.449 for -h,-k,l 0.146 for h,-h-k,-l 0.143 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8841	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% 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: GAL, SIA, MAN, 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	0.22	0/2638	0.41	0/3589
1	C	0.23	0/2638	0.41	0/3589
2	B	0.22	0/1409	0.36	0/1897
2	D	0.22	0/1409	0.35	0/1897
All	All	0.22	0/8094	0.39	0/10972

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	2577	0	2527	42	0
1	C	2577	0	2527	40	0
2	B	1381	0	1294	10	0
2	D	1381	0	1294	12	0
3	E	45	0	38	2	0
4	F	71	0	61	0	0
4	H	71	0	61	0	0
5	G	56	0	47	2	0
6	A	56	0	52	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	56	0	52	2	0
7	A	154	0	0	13	0
7	B	136	0	0	6	2
7	C	159	0	0	12	0
7	D	121	0	0	9	0
All	All	8841	0	7953	105	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 6.

The worst 5 of 105 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:43:LYS:NZ	7:B:401:HOH:O	1.98	0.96
1:C:38:GLU:OE2	7:C:501:HOH:O	1.94	0.83
1:A:81:GLU:OE2	7:A:502:HOH:O	1.97	0.82
1:A:295:GLN:HE21	1:A:298:SER:H	1.28	0.81
1:C:295:GLN:HE21	1:C:298:SER:H	1.31	0.79

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:452:HOH:O	7:B:487:HOH:O[3_455]	2.15	0.05
7:B:444:HOH:O	7:B:483:HOH:O[3_455]	2.16	0.04

## 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	324/326 (99%)	318 (98%)	6 (2%)	0	<b>100</b> <b>100</b>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	324/326 (99%)	317 (98%)	7 (2%)	0	100	100
2	B	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
2	D	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
All	All	986/994 (99%)	967 (98%)	19 (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	287/287 (100%)	286 (100%)	1 (0%)	92	96
1	C	287/287 (100%)	286 (100%)	1 (0%)	92	96
2	B	146/146 (100%)	146 (100%)	0	100	100
2	D	146/146 (100%)	146 (100%)	0	100	100
All	All	866/866 (100%)	864 (100%)	2 (0%)	93	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	295	GLN
1	C	295	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	ASN
1	A	295	GLN
1	C	133	ASN
1	C	295	GLN

### 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 ⓘ

19 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	3	14,14,15	0.66	1 (7%)	17,19,21	0.46	0
3	GAL	E	2	3	11,11,12	0.77	0	15,15,17	1.41	2 (13%)
3	SIA	E	3	3	20,20,21	1.22	4 (20%)	24,28,31	1.89	7 (29%)
4	NAG	F	1	4,2	14,14,15	0.43	0	17,19,21	0.46	0
4	NAG	F	2	4	14,14,15	0.19	0	17,19,21	0.45	0
4	BMA	F	3	4	11,11,12	0.63	0	15,15,17	0.79	0
4	MAN	F	4	4	11,11,12	0.96	1 (9%)	15,15,17	1.72	4 (26%)
4	MAN	F	5	4	11,11,12	0.75	0	15,15,17	1.30	2 (13%)
4	FUC	F	6	4	10,10,11	1.49	1 (10%)	14,14,16	1.78	3 (21%)
5	GAL	G	1	5	11,11,12	0.79	0	15,15,17	1.27	3 (20%)
5	NAG	G	2	5	14,14,15	0.49	0	17,19,21	0.72	0
5	GAL	G	3	5	11,11,12	0.63	0	15,15,17	1.32	2 (13%)
5	SIA	G	4	5	20,20,21	1.19	3 (15%)	24,28,31	1.84	7 (29%)
4	NAG	H	1	4,2	14,14,15	0.76	1 (7%)	17,19,21	0.74	0
4	NAG	H	2	4	14,14,15	0.20	0	17,19,21	0.46	0
4	BMA	H	3	4	11,11,12	0.58	0	15,15,17	0.89	0
4	MAN	H	4	4	11,11,12	0.85	0	15,15,17	1.05	2 (13%)
4	MAN	H	5	4	11,11,12	0.89	1 (9%)	15,15,17	1.85	4 (26%)
4	FUC	H	6	4	10,10,11	0.76	0	14,14,16	0.87	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	E	1	3	-	0/6/23/26	0/1/1/1
3	GAL	E	2	3	-	0/2/19/22	0/1/1/1
3	SIA	E	3	3	-	5/18/34/38	0/1/1/1
4	NAG	F	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1
4	MAN	F	5	4	-	1/2/19/22	1/1/1/1
4	FUC	F	6	4	1/1/4/5	-	0/1/1/1
5	GAL	G	1	5	-	0/2/19/22	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	GAL	G	3	5	-	0/2/19/22	0/1/1/1
5	SIA	G	4	5	-	3/18/34/38	0/1/1/1
4	NAG	H	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
4	MAN	H	4	4	-	1/2/19/22	1/1/1/1
4	MAN	H	5	4	-	2/2/19/22	0/1/1/1
4	FUC	H	6	4	1/1/4/5	-	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	6	FUC	C2-C3	3.39	1.57	1.52
4	H	1	NAG	O5-C1	-2.76	1.39	1.43
4	F	4	MAN	C1-C2	2.53	1.58	1.52
4	H	5	MAN	C1-C2	2.49	1.57	1.52
3	E	3	SIA	O6-C2	-2.46	1.40	1.43

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	3	SIA	O6-C2-C3	-4.97	103.63	110.46
4	F	6	FUC	C1-C2-C3	4.94	115.74	109.67
5	G	4	SIA	O6-C2-C3	-4.94	103.66	110.46
4	H	5	MAN	C1-O5-C5	4.47	118.25	112.19
5	G	4	SIA	O6-C2-C1	3.91	115.37	107.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	F	6	FUC	C1
4	H	6	FUC	C1

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	3	SIA	O8-C8-C9-O9
4	F	3	BMA	C4-C5-C6-O6
3	E	3	SIA	C11-C10-N5-C5
3	E	3	SIA	O10-C10-N5-C5
5	G	4	SIA	C11-C10-N5-C5

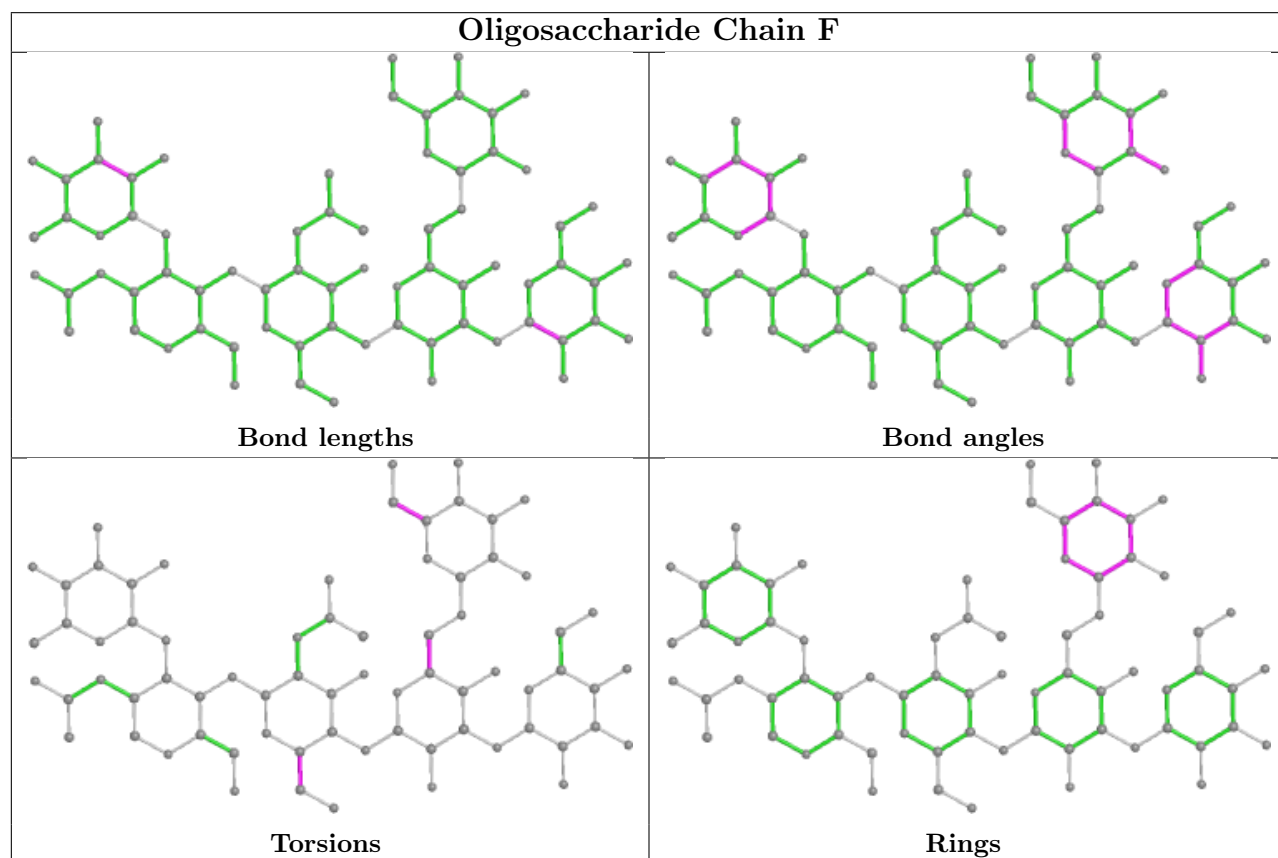
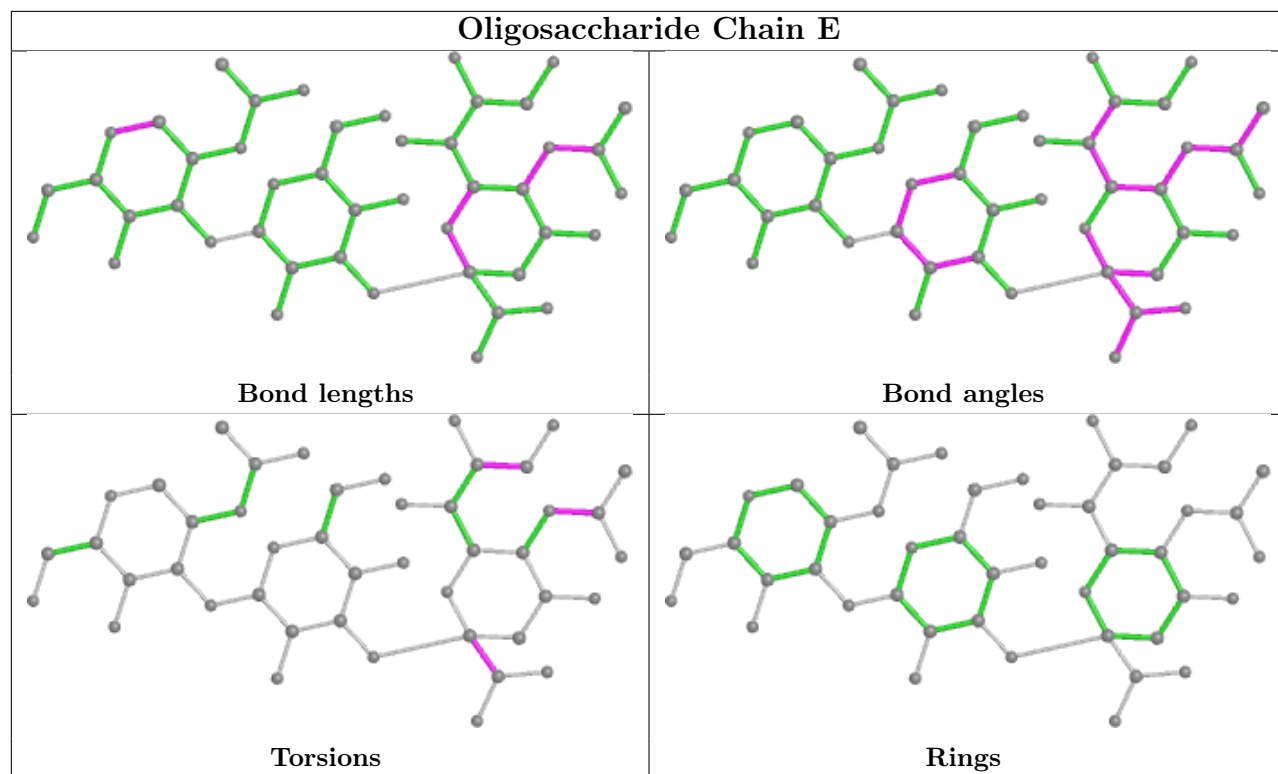
All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	4	MAN	C1-C2-C3-C4-C5-O5
4	F	5	MAN	C1-C2-C3-C4-C5-O5

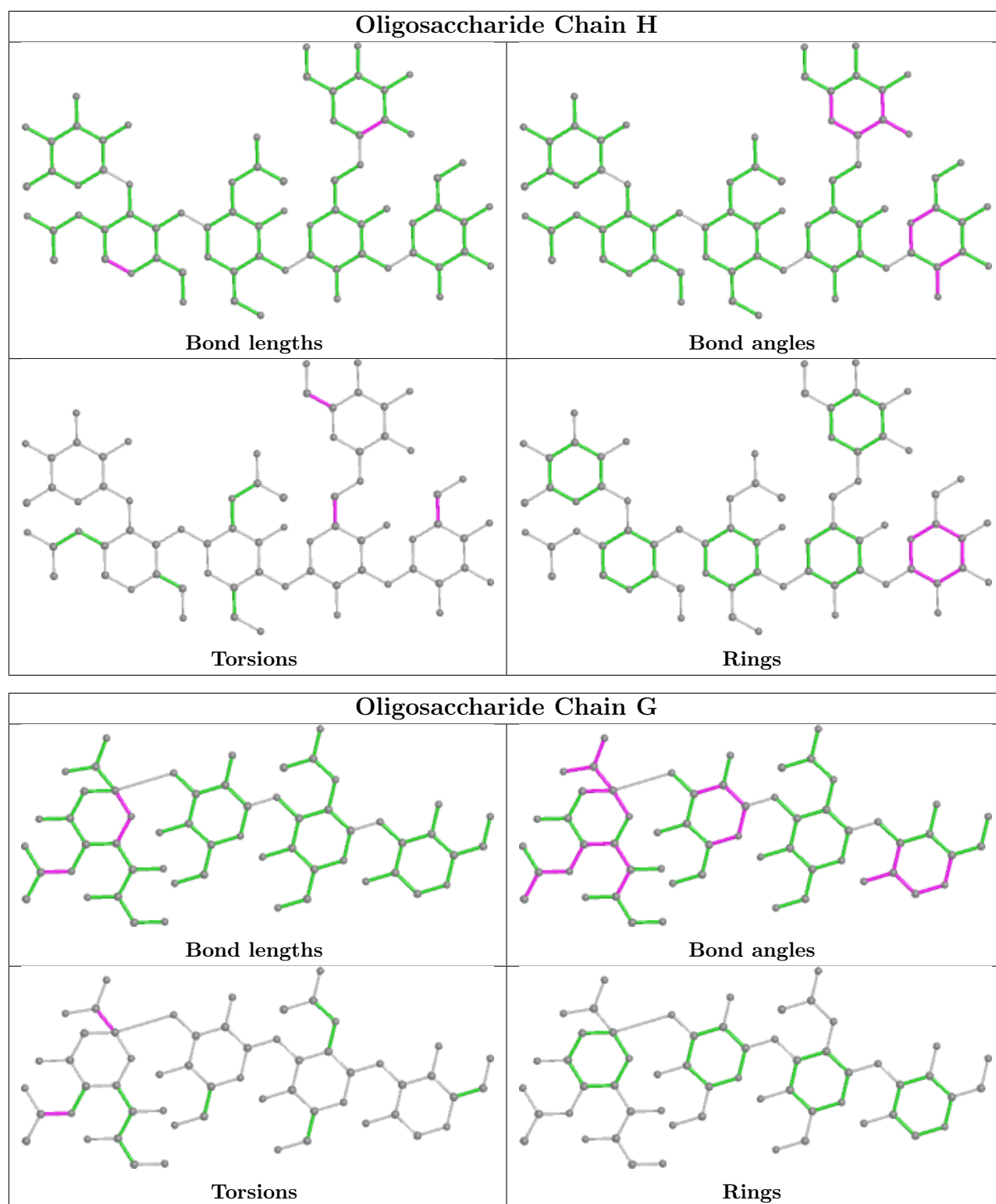
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	3	GAL	2	0
3	E	2	GAL	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](#)

8 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$
6	NAG	A	402	1	14,14,15	0.80	1 (7%)	17,19,21	1.69	3 (17%)
6	NAG	A	404	1	14,14,15	0.19	0	17,19,21	0.53	0
6	NAG	C	403	1	14,14,15	0.80	1 (7%)	17,19,21	1.31	1 (5%)
6	NAG	C	404	1	14,14,15	0.23	0	17,19,21	0.58	0
6	NAG	C	402	1	14,14,15	0.18	0	17,19,21	0.46	0
6	NAG	A	403	1	14,14,15	0.28	0	17,19,21	0.57	0
6	NAG	A	401	1	14,14,15	0.43	0	17,19,21	0.37	0
6	NAG	C	401	1	14,14,15	0.98	1 (7%)	17,19,21	1.15	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
6	NAG	A	402	1	-	4/6/23/26	0/1/1/1
6	NAG	A	404	1	-	0/6/23/26	0/1/1/1
6	NAG	C	403	1	-	2/6/23/26	0/1/1/1
6	NAG	C	404	1	-	0/6/23/26	0/1/1/1
6	NAG	C	402	1	-	2/6/23/26	0/1/1/1
6	NAG	A	403	1	-	1/6/23/26	0/1/1/1
6	NAG	A	401	1	-	2/6/23/26	0/1/1/1
6	NAG	C	401	1	-	3/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	401	NAG	O5-C1	3.22	1.48	1.43
6	C	403	NAG	O5-C1	2.91	1.48	1.43
6	A	402	NAG	O5-C1	-2.11	1.40	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	403	NAG	C1-O5-C5	5.15	119.16	112.19
6	A	402	NAG	C1-O5-C5	4.93	118.88	112.19
6	C	401	NAG	C1-O5-C5	4.40	118.16	112.19
6	A	402	NAG	C3-C4-C5	3.66	116.77	110.24
6	A	402	NAG	O5-C5-C4	2.26	116.34	110.83

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	401	NAG	O5-C5-C6-O6
6	C	402	NAG	O5-C5-C6-O6
6	C	403	NAG	O5-C5-C6-O6
6	C	401	NAG	C1-C2-N2-C7
6	A	402	NAG	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	402	NAG	1	0
6	C	402	NAG	1	0
6	A	403	NAG	1	0
6	C	401	NAG	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	326/326 (100%)	-0.03	3 (0%) 84 88	20, 40, 64, 99	0
1	C	326/326 (100%)	-0.04	2 (0%) 89 92	19, 41, 63, 100	0
2	B	171/171 (100%)	-0.04	1 (0%) 89 92	17, 30, 51, 93	0
2	D	171/171 (100%)	-0.03	1 (0%) 89 92	17, 30, 51, 86	0
All	All	994/994 (100%)	-0.03	7 (0%) 87 90	17, 36, 62, 100	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	171	GLN	3.6
1	A	155	ASP	2.5
1	A	156	SER	2.4
2	D	168	LEU	2.3
1	C	156	SER	2.3

### 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.

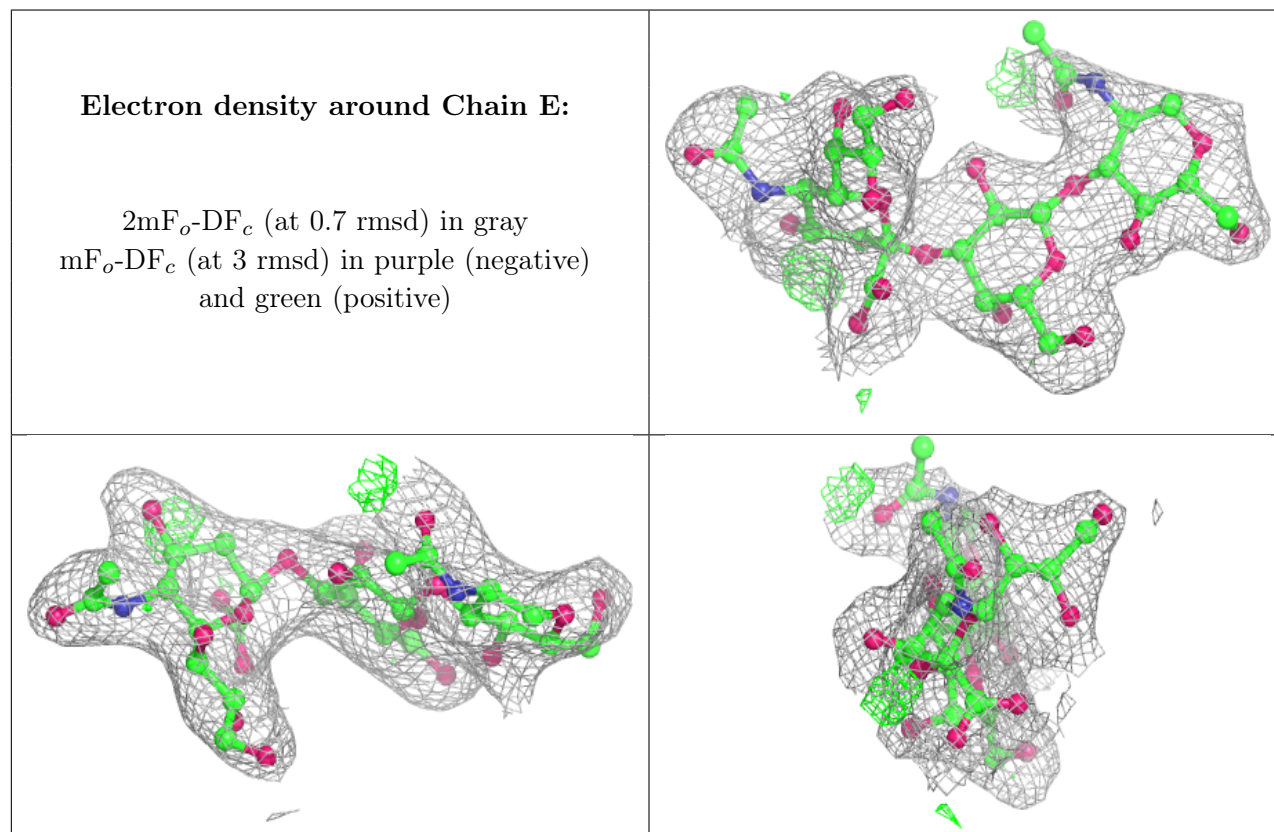
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	MAN	F	5	11/12	0.50	0.48	84,98,107,112	0
4	MAN	F	4	11/12	0.77	0.22	78,85,90,91	0

*Continued on next page...*

Continued from previous page...

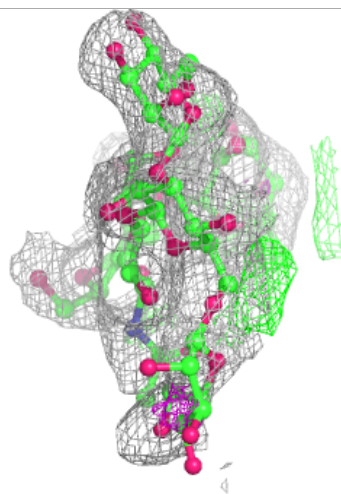
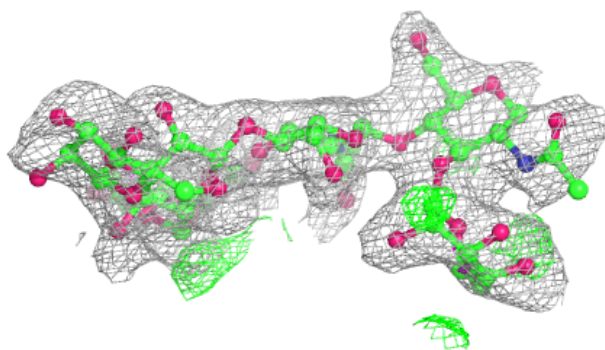
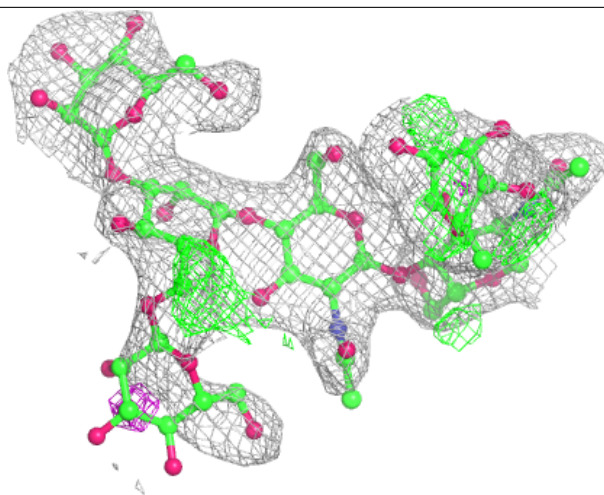
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	E	1	14/15	0.83	0.27	79,86,93,94	0
4	FUC	F	6	10/11	0.83	0.17	64,73,88,92	0
4	BMA	F	3	11/12	0.84	0.16	81,90,94,97	0
4	MAN	H	5	11/12	0.86	0.22	68,72,75,75	0
4	FUC	H	6	10/11	0.88	0.16	51,52,53,54	0
5	GAL	G	1	11/12	0.88	0.19	98,106,111,117	0
4	BMA	H	3	11/12	0.89	0.16	64,66,69,70	0
4	MAN	H	4	11/12	0.90	0.30	67,68,69,69	0
5	NAG	G	2	14/15	0.90	0.19	76,89,97,103	0
4	NAG	F	2	14/15	0.91	0.16	64,72,76,78	0
4	NAG	F	1	14/15	0.92	0.15	55,62,69,71	0
3	GAL	E	2	11/12	0.92	0.13	46,66,75,79	0
4	NAG	H	2	14/15	0.92	0.17	56,60,63,64	0
5	GAL	G	3	11/12	0.92	0.13	47,62,72,80	0
3	SIA	E	3	20/21	0.93	0.13	43,55,70,71	0
4	NAG	H	1	14/15	0.95	0.12	44,47,51,53	0
5	SIA	G	4	20/21	0.95	0.15	48,56,66,67	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 F:**

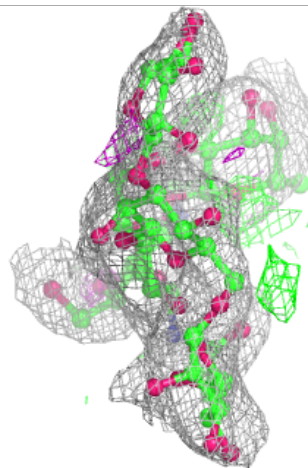
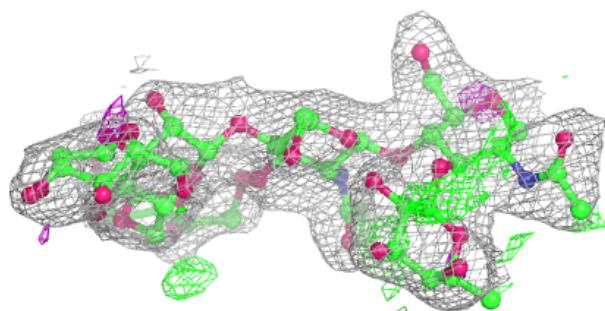
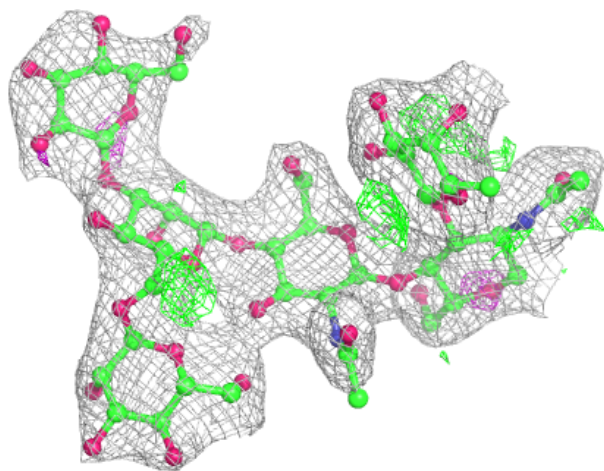
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

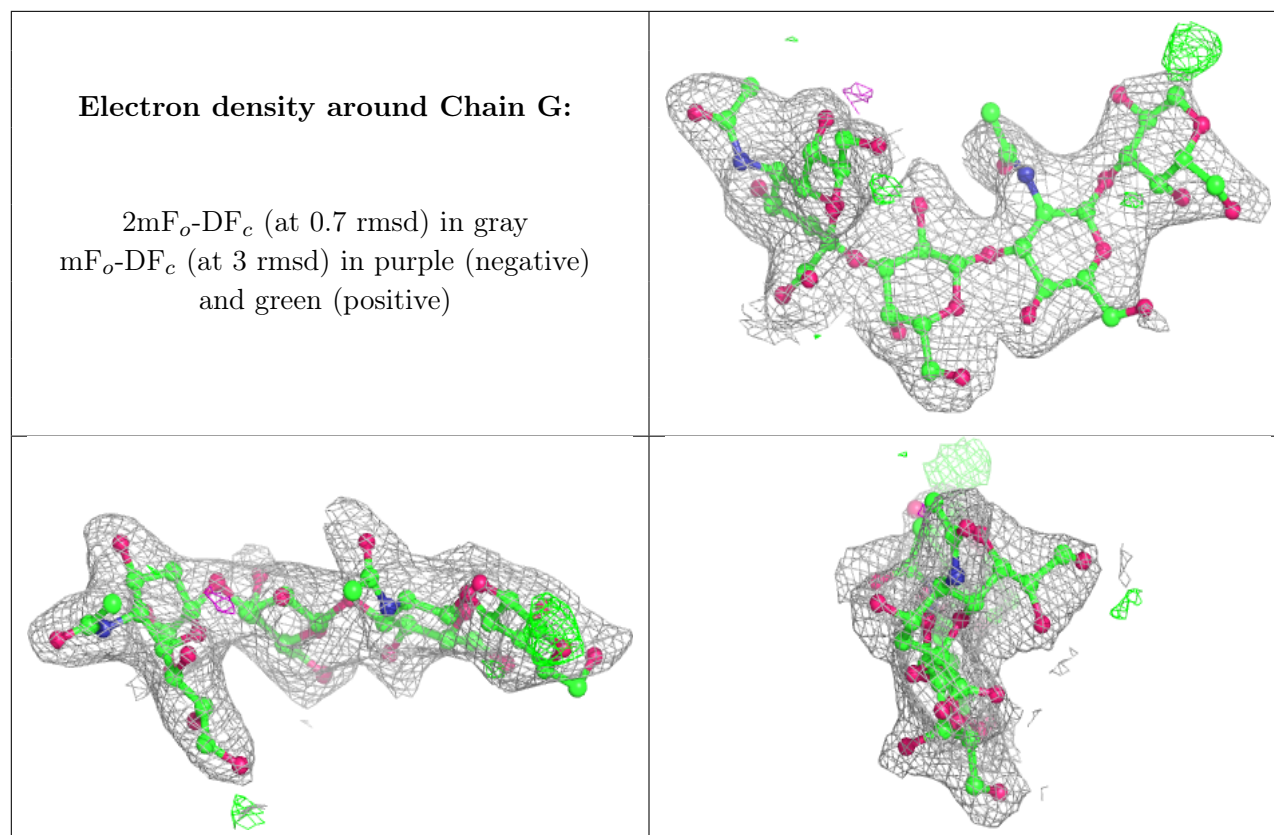




**Electron density around Chain H:**

$2mF_o-DF_c$  (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
6	NAG	A	402	14/15	0.75	0.24	42,44,44,44	0
6	NAG	A	404	14/15	0.76	0.36	51,54,55,56	0
6	NAG	A	401	14/15	0.78	0.20	37,38,39,39	0
6	NAG	C	402	14/15	0.78	0.27	42,45,45,45	0
6	NAG	C	404	14/15	0.82	0.38	43,49,51,51	0
6	NAG	C	403	14/15	0.86	0.19	48,49,50,50	0
6	NAG	C	401	14/15	0.88	0.23	35,37,38,38	0
6	NAG	A	403	14/15	0.93	0.12	46,47,47,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.