



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 04:18 PM BST

PDB ID : 1MQN  
Title : BHA/LSTc  
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Deposited on : 2002-09-16  
Resolution : 3.20 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

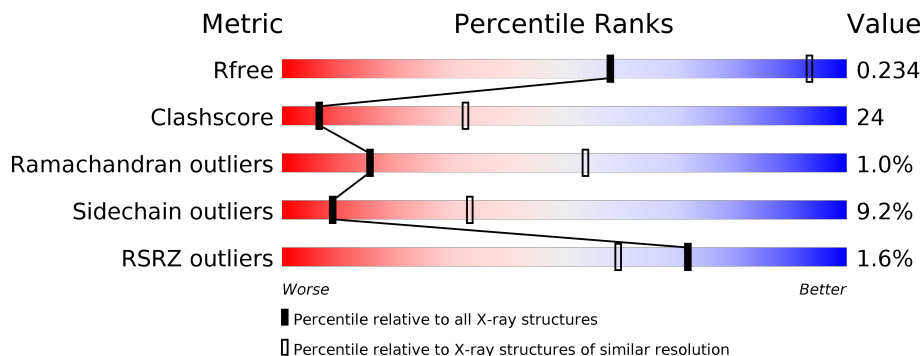
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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.



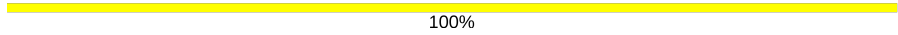
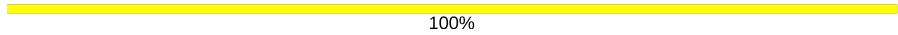
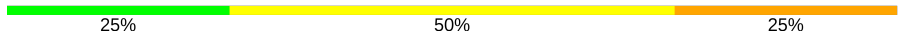


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	329	
1	D	329	
1	G	329	
2	B	221	
2	E	221	
2	H	221	

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Mol	Chain	Length	Quality of chain
3	C	2	 100%
3	I	2	 100%
4	F	4	 50% 25% 25%
4	K	4	 25% 50% 25%
4	M	4	 50% 50%
5	J	2	 50% 50%
5	L	2	 50% 50%

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
3	NAG	C	2	-	-	-	X
3	NAG	I	2	-	-	-	X
4	MAN	F	4	-	-	-	X
6	NAG	A	400	-	-	-	X
6	NAG	D	401	-	-	-	X
6	NAG	E	400	-	-	-	X
6	NAG	G	400	-	-	-	X
6	NAG	G	406	-	-	-	X
6	NAG	H	400	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 11982 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
			Total	C	N	O	S			
1	A	318	Total 2425	C 1522	N 424	O 466	S 13	0	0	0
1	D	318	Total 2432	C 1526	N 425	O 468	S 13	0	0	0
1	G	318	Total 2426	C 1523	N 424	O 466	S 13	0	0	0

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	172	Total 1398	C 867	N 247	O 278	S 6	0	0	0
2	E	172	Total 1401	C 869	N 248	O 278	S 6	0	0	0
2	H	172	Total 1404	C 871	N 249	O 278	S 6	0	0	0

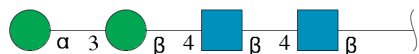
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	2	Total 28	C 16	N 2	O 10	0	0	0
3	I	2	Total 28	C 16	N 2	O 10	0	0	0

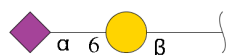
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

pyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	F	4	50	28	2	20	0	0	0
4	K	4	50	28	2	20	0	0	0
4	M	4	50	28	2	20	0	0	0

- Molecule 5 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	J	2	32	17	1	14	0	0	0
5	L	2	32	17	1	14	0	0	0

- 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
			Total	C	N	O		
6	A	1	14	8	1	5	0	0
6	B	1	14	8	1	5	0	0
6	D	1	14	8	1	5	0	0
6	D	1	14	8	1	5	0	0
6	E	1	14	8	1	5	0	0
6	G	1	14	8	1	5	0	0
6	G	1	14	8	1	5	0	0
6	G	1	14	8	1	5	0	0
6	H	1	14	8	1	5	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	20	Total	O	0	0
			20	20		
7	B	14	Total	O	0	0
			14	14		
7	D	22	Total	O	0	0
			22	22		

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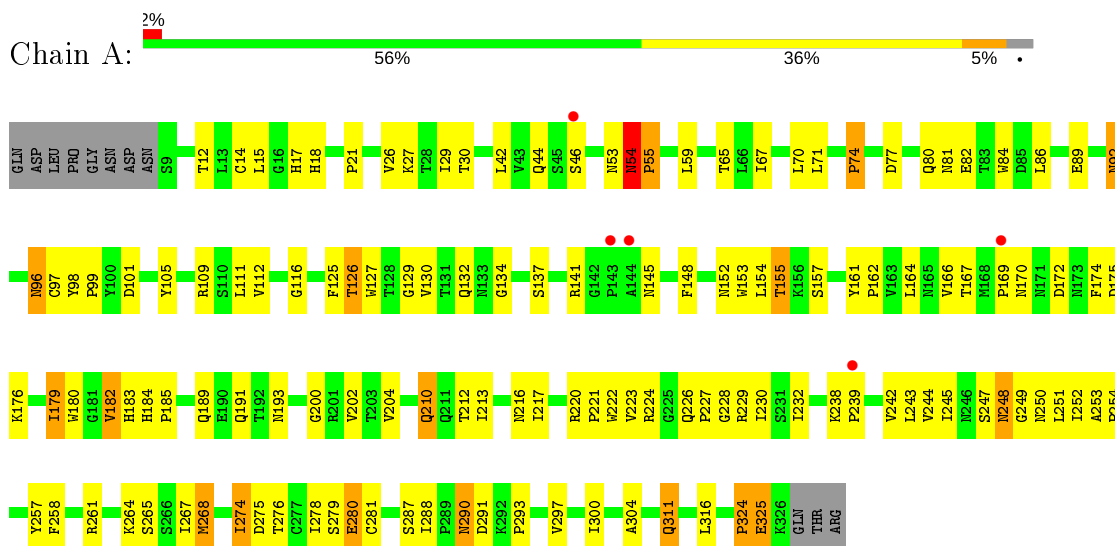
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
7	E	12	Total O 12 12	0	0
7	G	22	Total O 22 22	0	0
7	H	10	Total O 10 10	0	0

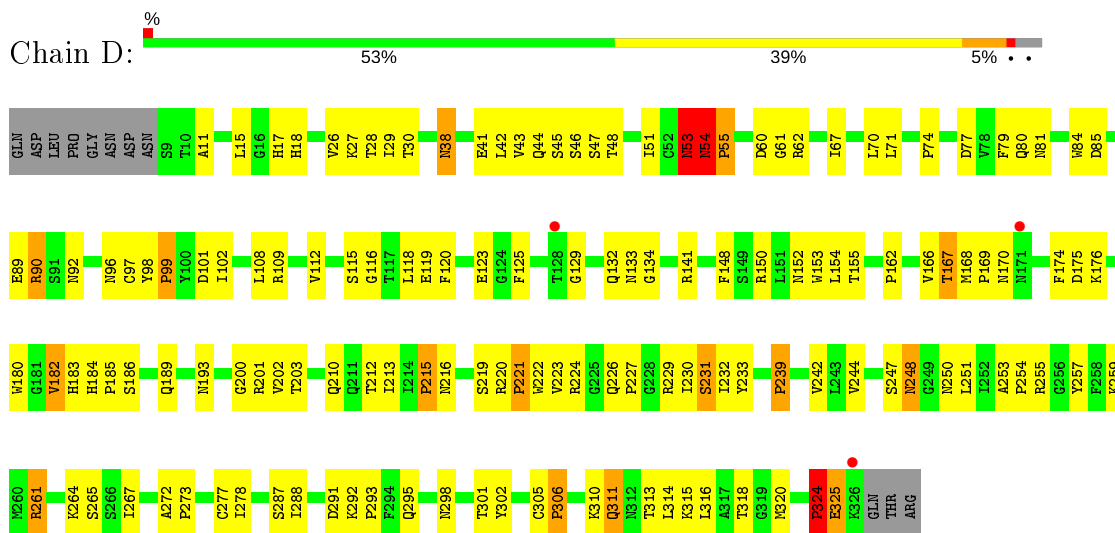
### 3 Residue-property plots

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



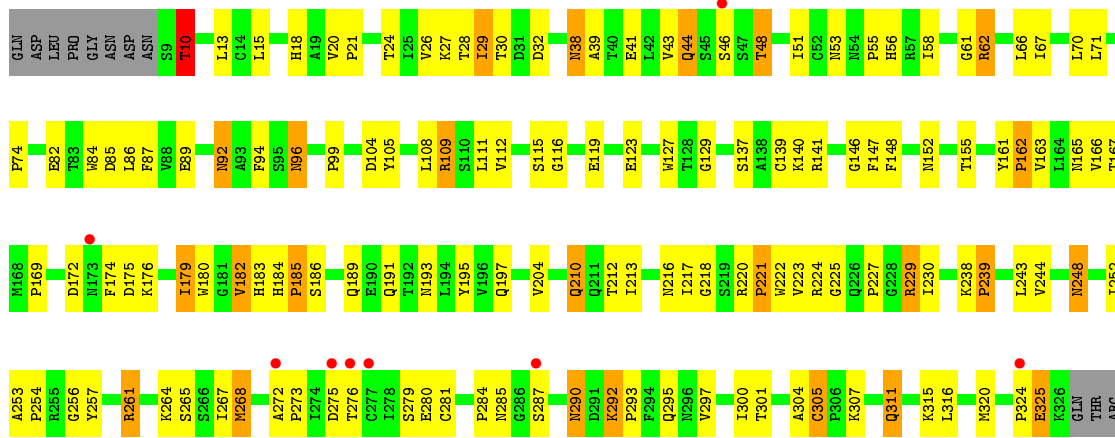
- Molecule 1: Hemagglutinin HA1 chain



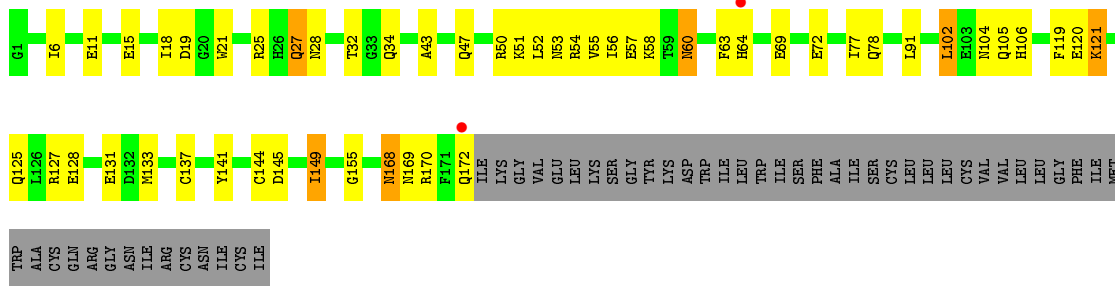
- Molecule 1: Hemagglutinin HA1 chain



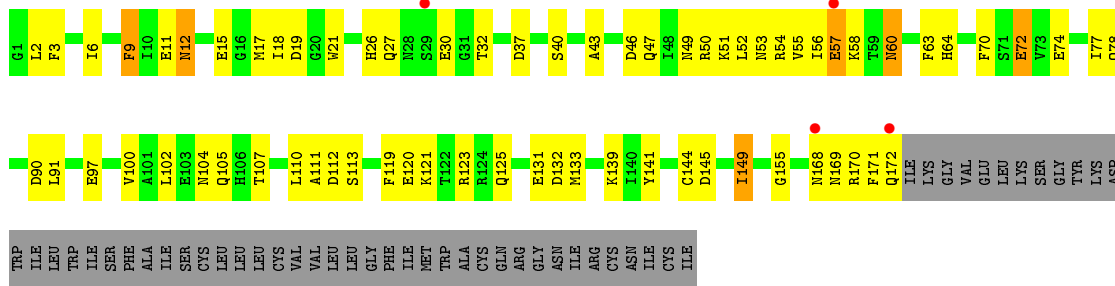




• Molecule 2: Hemagglutinin HA2 chain

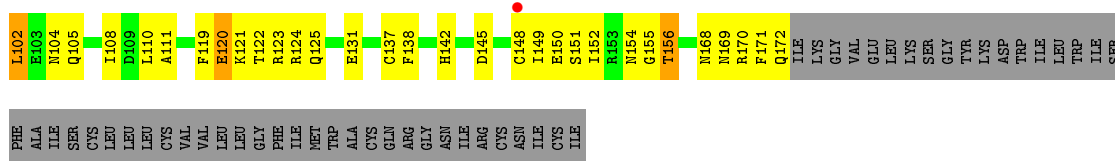


• Molecule 2: Hemagglutinin HA2 chain

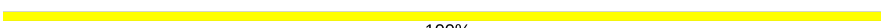


• Molecule 2: Hemagglutinin HA2 chain





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

Chain C:  100%

MAG1  
MAG2

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

Chain I:  100%

MAG1  
MAG2

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

Chain F:  50% 25% 25%

MAG1  
MAG2  
MAN3  
MAN4

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

Chain K:  25% 50% 25%

MAG1  
MAG2  
MAN3  
MAN4

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

Chain M:  50% 50%

MAG1  
MAG2  
MAN3  
MAN4

- Molecule 5: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose

Chain J:  50% 50%

GAL1  
S1A2

- Molecule 5: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose

Chain L: 

  
GAL1  
ST A2

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	147.32Å 148.43Å 250.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.20 38.74 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.20) 93.1 (38.74-3.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.98 (at 3.18Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.239 , 0.243 0.231 , 0.234	Depositor DCC
$R_{free}$ test set	2252 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.7	Xtrriage
Anisotropy	1.076	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 60.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.028 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	11982	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% 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, BMA, NAG, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.48	0/2482	0.81	4/3390 (0.1%)
1	D	0.56	0/2489	0.86	5/3398 (0.1%)
1	G	0.57	1/2483 (0.0%)	0.81	5/3391 (0.1%)
2	B	0.45	0/1422	0.62	0/1912
2	E	0.42	0/1425	0.65	0/1915
2	H	0.47	0/1428	0.73	1/1918 (0.1%)
All	All	0.51	1/11729 (0.0%)	0.77	15/15924 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	119	GLU	CB-CG	-5.32	1.42	1.52

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	54	ASN	C-N-CD	-20.24	76.08	120.60
1	A	54	ASN	C-N-CA	13.61	179.18	122.00
1	D	54	ASN	N-CA-C	11.37	141.70	111.00
1	D	54	ASN	C-N-CD	9.49	148.32	128.40
1	D	54	ASN	C-N-CA	-7.01	92.57	122.00

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	2425	0	2334	133	0
1	D	2432	0	2347	149	0
1	G	2426	0	2338	160	0
2	B	1398	0	1308	49	0
2	E	1401	0	1317	79	0
2	H	1404	0	1326	83	0
3	C	28	0	25	2	0
3	I	28	0	25	0	0
4	F	50	0	43	2	0
4	K	50	0	43	1	0
4	M	50	0	43	3	0
5	J	32	0	27	1	0
5	L	32	0	27	2	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0
6	D	28	0	26	0	0
6	E	14	0	13	0	0
6	G	42	0	39	11	0
6	H	14	0	13	2	0
7	A	20	0	0	2	0
7	B	14	0	0	0	0
7	D	22	0	0	2	0
7	E	12	0	0	0	0
7	G	22	0	0	4	0
7	H	10	0	0	1	0
All	All	11982	0	11320	549	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 24.

The worst 5 of 549 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:H:154:ASN:OD1	2:H:156:THR:HG22	1.43	1.15
1:D:81:ASN:OD1	1:D:119:GLU:HA	1.67	0.94
1:D:27:LYS:HB3	2:H:54:ARG:HH12	1.34	0.91
1:G:24:THR:OG1	6:G:400:NAG:H62	1.68	0.91
1:D:216:ASN:CB	1:G:212:THR:HG21	2.01	0.91

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	316/329 (96%)	282 (89%)	29 (9%)	5 (2%)	9	43
1	D	316/329 (96%)	289 (92%)	23 (7%)	4 (1%)	12	47
1	G	316/329 (96%)	292 (92%)	20 (6%)	4 (1%)	12	47
2	B	170/221 (77%)	155 (91%)	15 (9%)	0	100	100
2	E	170/221 (77%)	155 (91%)	14 (8%)	1 (1%)	25	64
2	H	170/221 (77%)	153 (90%)	17 (10%)	0	100	100
All	All	1458/1650 (88%)	1326 (91%)	118 (8%)	14 (1%)	15	54

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	PRO
1	A	324	PRO
1	A	325	GLU
1	D	324	PRO
1	D	325	GLU

### 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	268/288 (93%)	249 (93%)	19 (7%)	14	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	270/288 (94%)	241 (89%)	29 (11%)	6	27
1	G	268/288 (93%)	234 (87%)	34 (13%)	4	20
2	B	145/190 (76%)	135 (93%)	10 (7%)	15	49
2	E	146/190 (77%)	133 (91%)	13 (9%)	9	35
2	H	147/190 (77%)	137 (93%)	10 (7%)	16	49
All	All	1244/1434 (87%)	1129 (91%)	115 (9%)	9	33

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	261	ARG
2	E	64	HIS
2	H	19	ASP
1	D	273	PRO
2	E	9	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	226	GLN
2	E	26	HIS
2	H	105	GLN
1	D	248	ASN
1	D	311	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](#)

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	C	1	1,3	14,14,15	0.59	0	17,19,21	0.61	0
3	NAG	C	2	3	14,14,15	0.68	0	17,19,21	0.61	0
4	NAG	F	1	1,4	14,14,15	0.48	0	17,19,21	0.80	1 (5%)
4	NAG	F	2	4	14,14,15	0.59	0	17,19,21	0.67	0
4	BMA	F	3	4	11,11,12	0.81	0	15,15,17	1.31	1 (6%)
4	MAN	F	4	4	11,11,12	0.59	0	15,15,17	0.62	0
3	NAG	I	1	1,3	14,14,15	0.98	1 (7%)	17,19,21	1.29	1 (5%)
3	NAG	I	2	3	14,14,15	0.54	0	17,19,21	0.85	1 (5%)
5	GAL	J	1	5	12,12,12	0.83	1 (8%)	17,17,17	0.85	1 (5%)
5	SIA	J	2	5	17,20,21	0.63	0	21,28,31	0.84	1 (4%)
4	NAG	K	1	1,4	14,14,15	0.66	0	17,19,21	0.85	1 (5%)
4	NAG	K	2	4	14,14,15	0.74	0	17,19,21	0.73	0
4	BMA	K	3	4	11,11,12	0.51	0	15,15,17	1.53	4 (26%)
4	MAN	K	4	4	11,11,12	0.63	0	15,15,17	0.71	0
5	GAL	L	1	5	12,12,12	0.83	1 (8%)	17,17,17	0.86	1 (5%)
5	SIA	L	2	5	17,20,21	0.64	0	21,28,31	0.84	1 (4%)
4	NAG	M	1	1,4	14,14,15	0.46	0	17,19,21	0.86	1 (5%)
4	NAG	M	2	4	14,14,15	0.51	0	17,19,21	1.07	1 (5%)
4	BMA	M	3	4	11,11,12	0.79	0	15,15,17	1.21	1 (6%)
4	MAN	M	4	4	11,11,12	1.21	1 (9%)	15,15,17	1.29	3 (20%)

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	C	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	1/2/19/22	0/1/1/1
3	NAG	I	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	I	2	3	-	4/6/23/26	0/1/1/1
5	GAL	J	1	5	-	0/2/22/22	0/1/1/1
5	SIA	J	2	5	-	0/14/34/38	0/1/1/1
4	NAG	K	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	BMA	K	3	4	-	2/2/19/22	0/1/1/1
4	MAN	K	4	4	-	2/2/19/22	0/1/1/1
5	GAL	L	1	5	-	0/2/22/22	0/1/1/1
5	SIA	L	2	5	-	0/14/34/38	0/1/1/1
4	NAG	M	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	M	2	4	-	2/6/23/26	0/1/1/1
4	BMA	M	3	4	-	2/2/19/22	0/1/1/1
4	MAN	M	4	4	-	2/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	4	MAN	O5-C5	2.71	1.48	1.43
5	L	1	GAL	O1-C1	-2.69	1.31	1.39
5	J	1	GAL	O1-C1	-2.67	1.31	1.39
3	I	1	NAG	C1-C2	2.64	1.56	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	3	BMA	C3-C4-C5	3.85	117.11	110.24
3	I	1	NAG	C4-C3-C2	-3.23	106.29	111.02
4	K	3	BMA	C1-C2-C3	-2.95	106.04	109.67
4	M	2	NAG	C2-N2-C7	-2.88	118.80	122.90
4	M	4	MAN	C2-C3-C4	2.84	115.81	110.89

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	C8-C7-N2-C2

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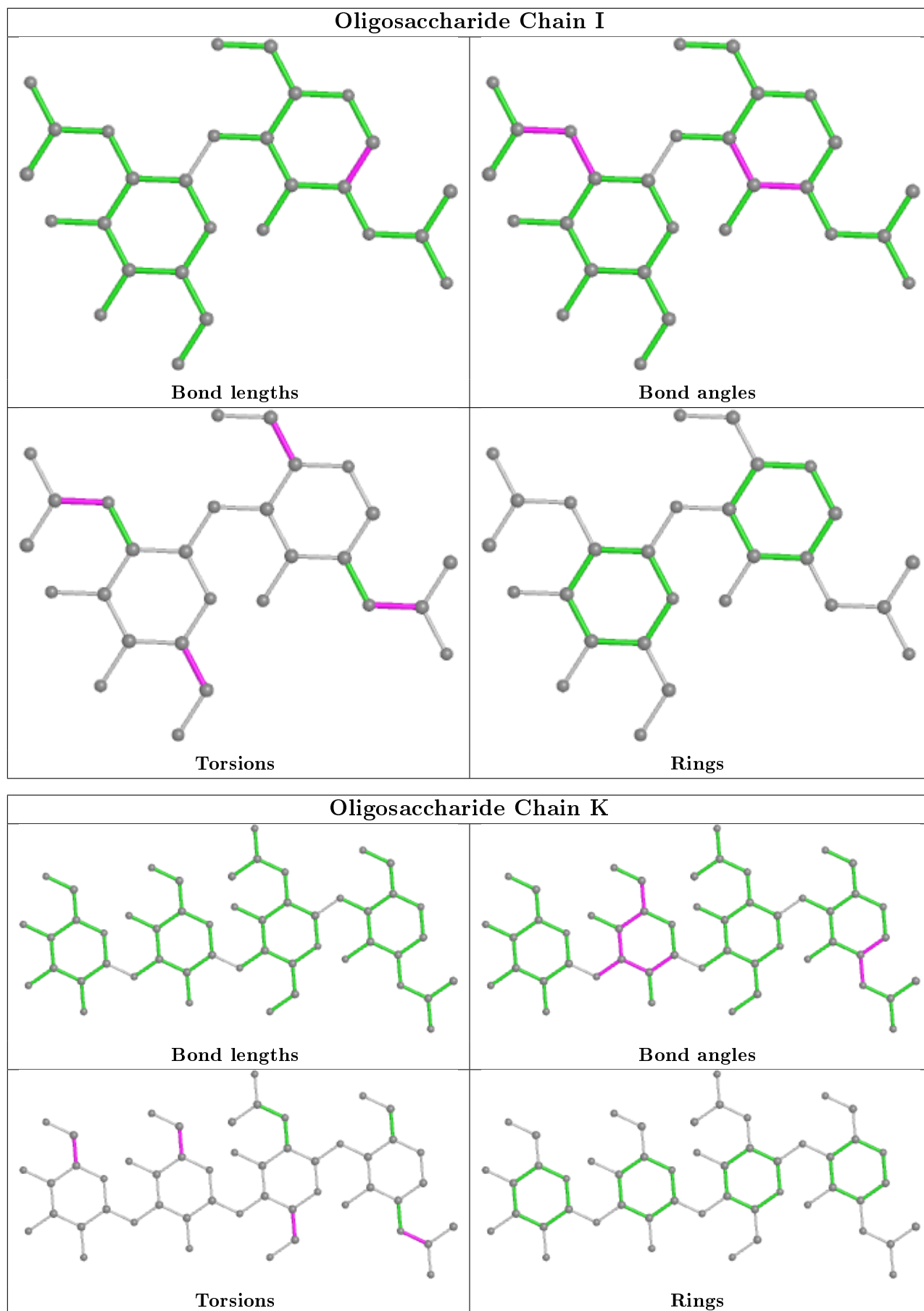
Mol	Chain	Res	Type	Atoms
3	C	2	NAG	O7-C7-N2-C2
4	F	1	NAG	C8-C7-N2-C2
4	F	1	NAG	O7-C7-N2-C2
3	I	2	NAG	C8-C7-N2-C2

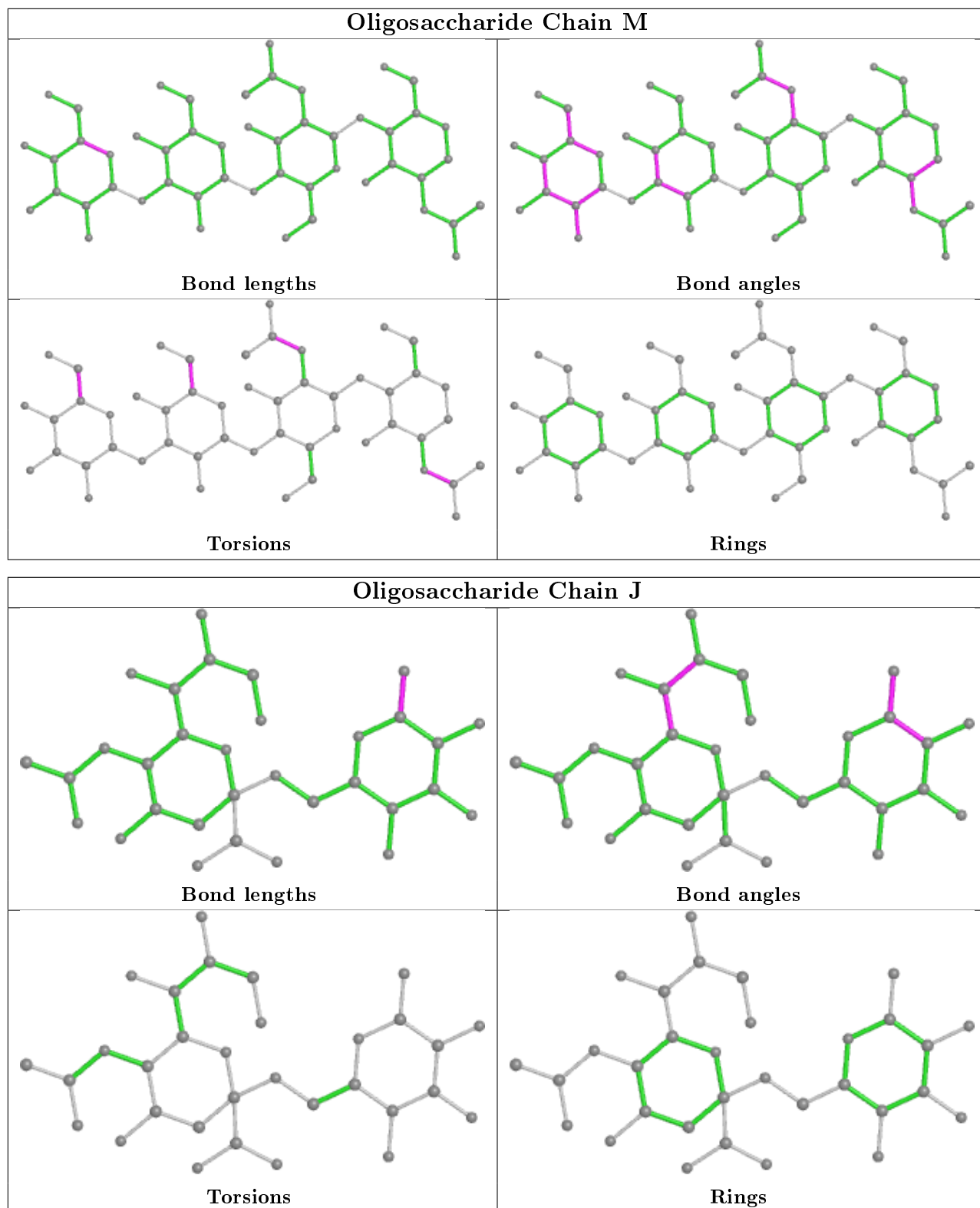
There are no ring outliers.

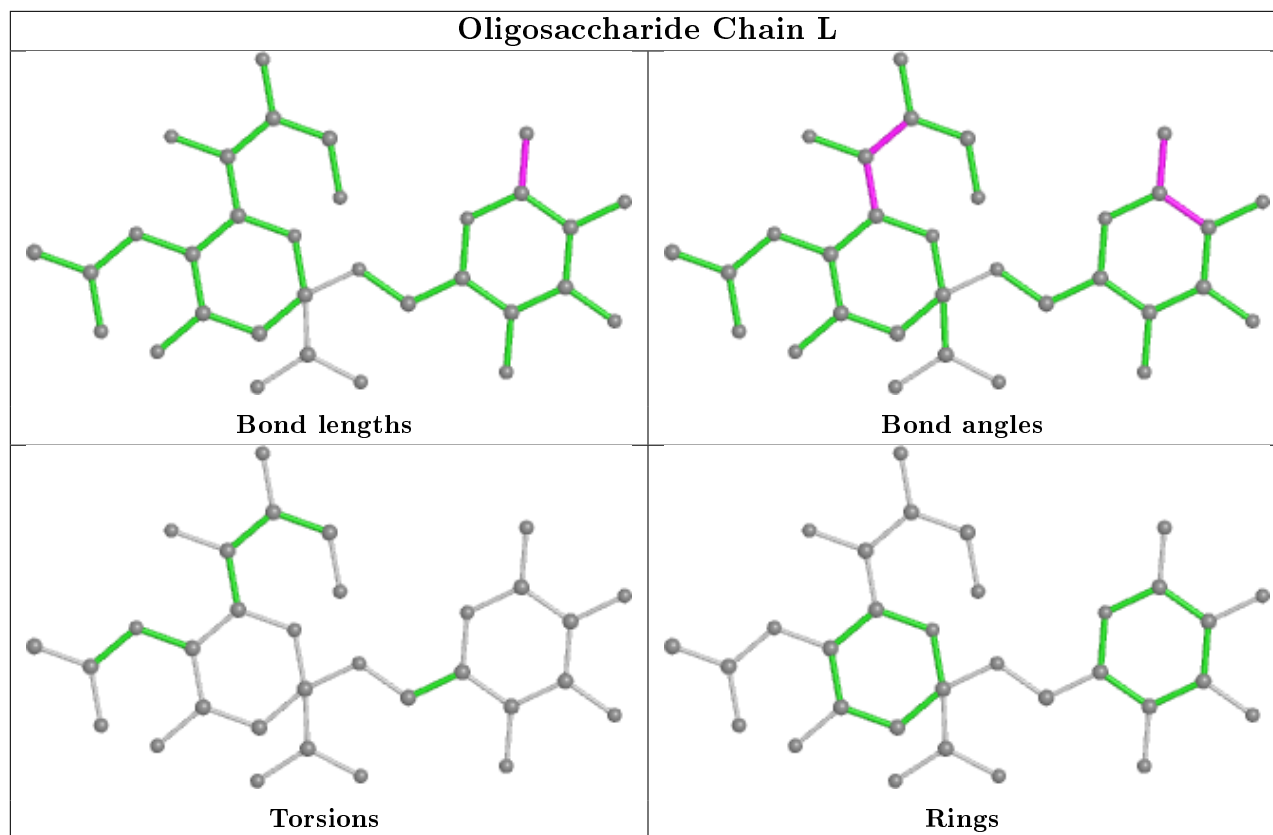
9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	NAG	1	0
4	F	1	NAG	2	0
5	L	2	SIA	2	0
5	J	2	SIA	1	0
4	M	2	NAG	2	0
4	K	1	NAG	1	0
4	K	2	NAG	1	0
4	M	1	NAG	3	0
3	C	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](#)

9 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	H	400	2	14,14,15	1.32	3 (21%)	17,19,21	1.25	2 (11%)
6	NAG	G	400	1	14,14,15	1.22	1 (7%)	17,19,21	2.56	5 (29%)
6	NAG	D	400	1	14,14,15	1.17	2 (14%)	17,19,21	2.01	4 (23%)
6	NAG	B	400	2	14,14,15	0.66	0	17,19,21	0.89	1 (5%)
6	NAG	G	406	1	14,14,15	0.86	1 (7%)	17,19,21	1.14	1 (5%)
6	NAG	G	401	1	14,14,15	0.73	0	17,19,21	1.27	2 (11%)
6	NAG	D	401	1	14,14,15	0.94	1 (7%)	17,19,21	1.40	3 (17%)
6	NAG	E	400	2	14,14,15	0.61	0	17,19,21	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	NAG	A	400	1	14,14,15	0.72	0	17,19,21	0.75	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	H	400	2	-	4/6/23/26	0/1/1/1
6	NAG	G	400	1	-	2/6/23/26	0/1/1/1
6	NAG	D	400	1	-	6/6/23/26	0/1/1/1
6	NAG	B	400	2	-	2/6/23/26	0/1/1/1
6	NAG	G	406	1	-	3/6/23/26	0/1/1/1
6	NAG	G	401	1	-	1/6/23/26	0/1/1/1
6	NAG	D	401	1	-	4/6/23/26	0/1/1/1
6	NAG	E	400	2	-	2/6/23/26	0/1/1/1
6	NAG	A	400	1	-	6/6/23/26	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	400	NAG	C1-C2	3.24	1.57	1.52
6	D	400	NAG	O5-C5	2.94	1.49	1.43
6	G	400	NAG	C1-C2	2.76	1.56	1.52
6	H	400	NAG	C8-C7	2.35	1.55	1.50
6	H	400	NAG	C4-C5	2.24	1.57	1.53

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	400	NAG	C6-C5-C4	-6.09	98.73	113.00
6	D	400	NAG	C1-C2-N2	-4.88	102.15	110.49
6	D	400	NAG	O5-C5-C6	4.38	114.07	107.20
6	G	400	NAG	C1-O5-C5	4.28	117.99	112.19
6	G	400	NAG	C2-N2-C7	-3.91	117.33	122.90

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	G	400	NAG	C8-C7-N2-C2
6	G	400	NAG	O7-C7-N2-C2
6	D	400	NAG	C1-C2-N2-C7
6	D	400	NAG	O7-C7-N2-C2
6	B	400	NAG	C8-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	400	NAG	2	0
6	G	400	NAG	5	0
6	G	406	NAG	6	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	318/329 (96%)	-0.03	5 (1%) 72 59	23, 41, 61, 79	0
1	D	318/329 (96%)	-0.14	3 (0%) 84 75	13, 35, 54, 77	0
1	G	318/329 (96%)	-0.02	8 (2%) 57 43	19, 38, 59, 93	0
2	B	172/221 (77%)	-0.27	2 (1%) 79 67	10, 37, 57, 85	0
2	E	172/221 (77%)	-0.05	4 (2%) 60 47	16, 40, 64, 82	0
2	H	172/221 (77%)	-0.04	2 (1%) 79 67	15, 39, 61, 84	0
All	All	1470/1650 (89%)	-0.08	24 (1%) 72 59	10, 38, 60, 93	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	143	PRO	3.4
2	E	57	GLU	3.0
2	H	29	SER	2.9
1	G	277	CYS	2.7
1	A	144	ALA	2.7

### 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](#)

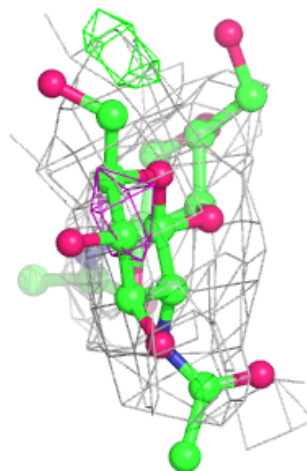
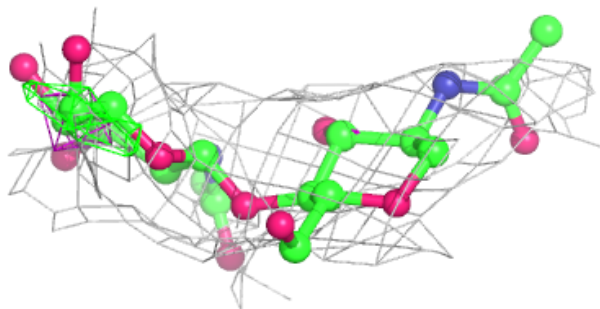
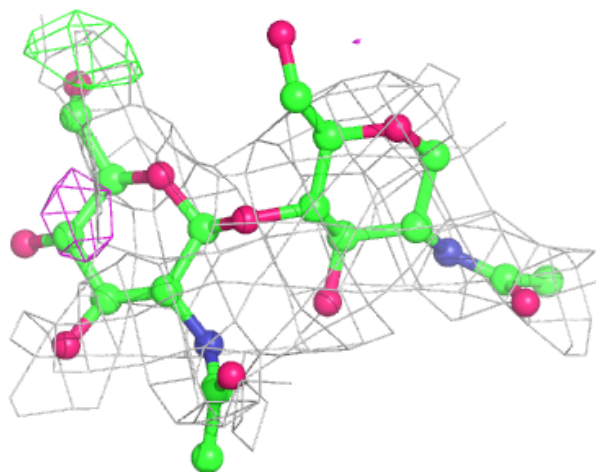
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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	NAG	C	2	14/15	0.55	0.58	103,105,107,107	0
3	NAG	I	2	14/15	0.58	0.49	100,104,106,107	0
4	MAN	K	4	11/12	0.65	0.39	92,96,99,99	0
4	MAN	F	4	11/12	0.69	0.51	93,95,97,97	0
3	NAG	C	1	14/15	0.79	0.33	87,92,98,99	0
4	MAN	M	4	11/12	0.82	0.38	84,87,88,88	0
4	BMA	F	3	11/12	0.82	0.36	77,80,83,89	0
4	BMA	M	3	11/12	0.83	0.30	62,66,70,77	0
5	GAL	J	1	12/12	0.83	0.37	65,82,83,84	0
5	GAL	L	1	12/12	0.85	0.46	59,78,81,82	0
4	BMA	K	3	11/12	0.87	0.32	78,81,83,88	0
4	NAG	F	1	14/15	0.87	0.29	52,55,58,61	0
5	SIA	J	2	20/21	0.89	0.28	53,56,64,64	0
3	NAG	I	1	14/15	0.89	0.46	76,81,90,93	0
4	NAG	M	1	14/15	0.92	0.27	28,31,36,38	0
4	NAG	K	1	14/15	0.92	0.32	49,53,57,59	0
5	SIA	L	2	20/21	0.92	0.28	40,45,53,55	0
4	NAG	K	2	14/15	0.92	0.26	60,62,64,71	0
4	NAG	F	2	14/15	0.93	0.36	61,63,68,74	0
4	NAG	M	2	14/15	0.95	0.19	38,42,45,53	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.

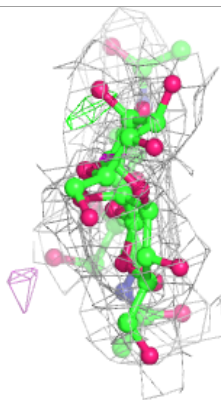
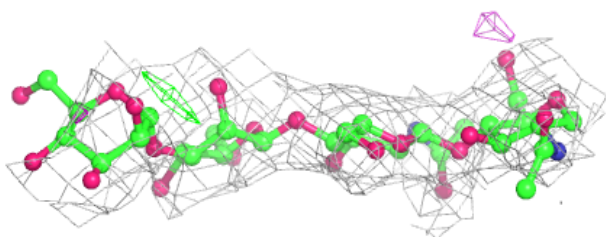
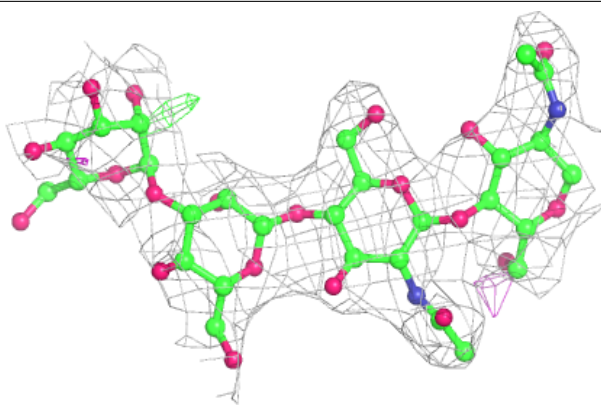
**Electron density around Chain I:**

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

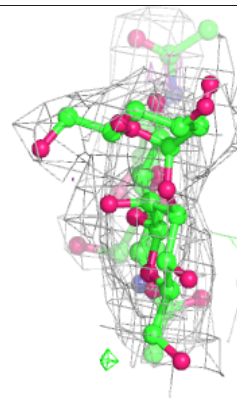
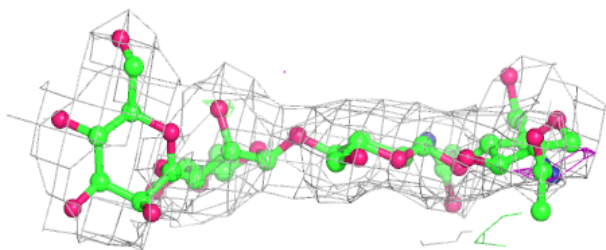
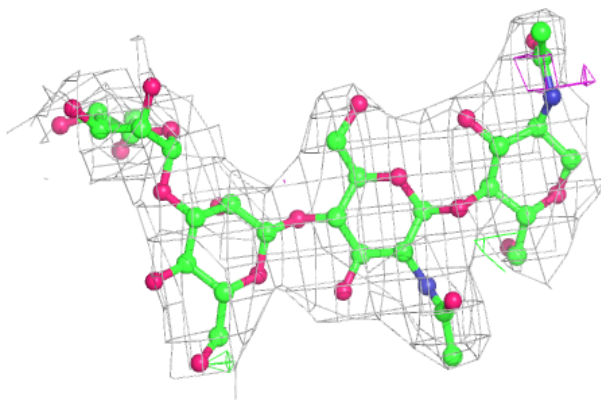


**Electron density around Chain K:**

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

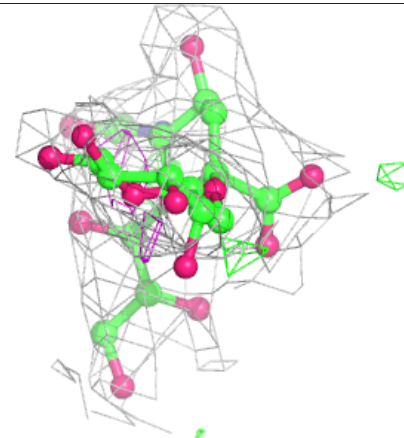
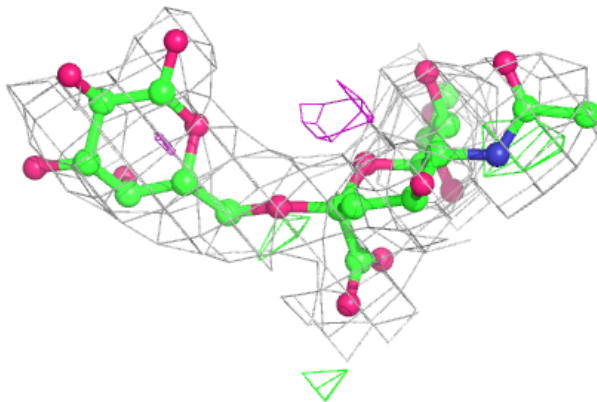
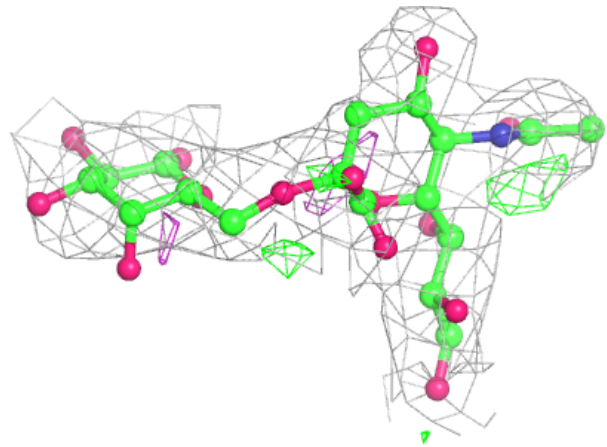
**Electron density around Chain M:**

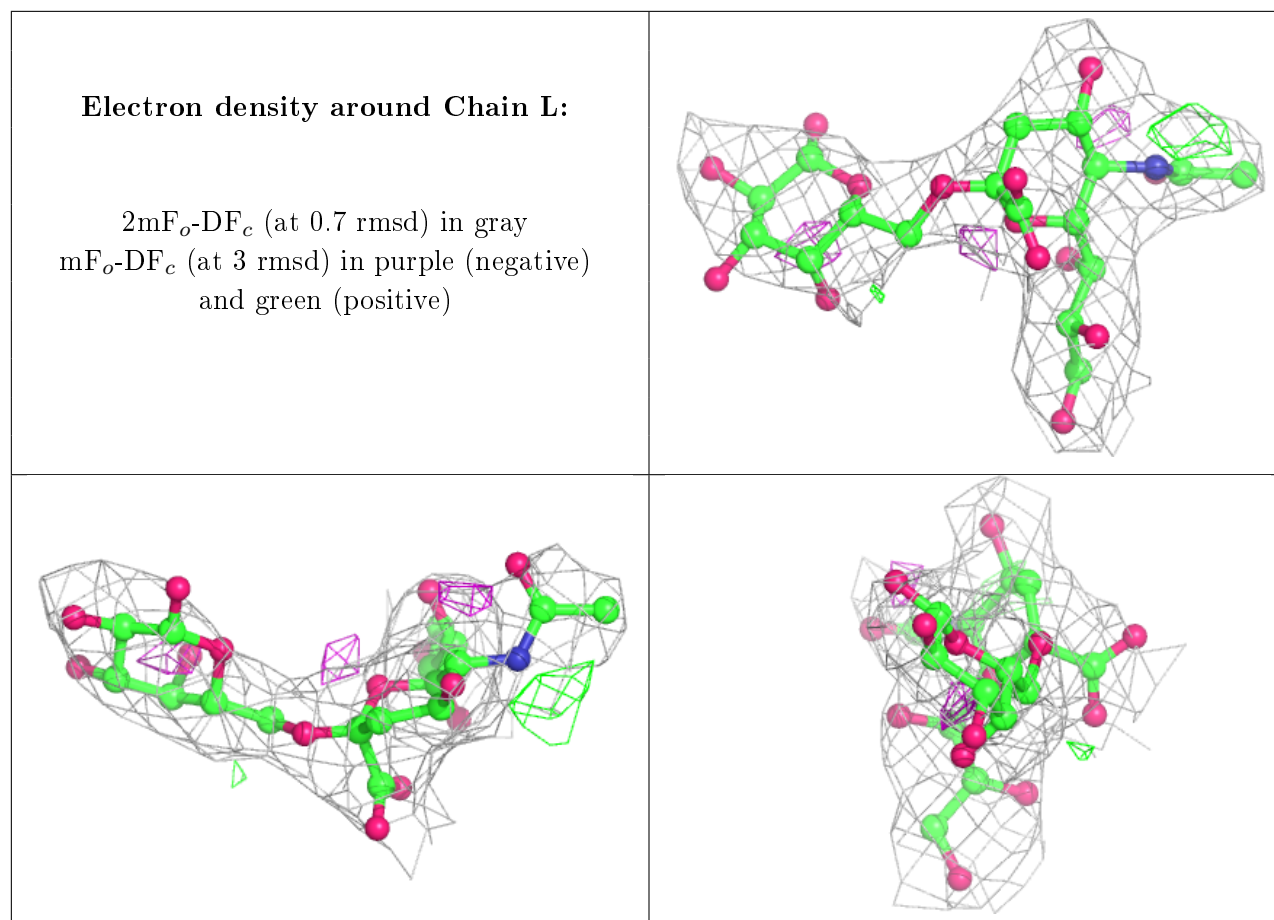
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain J:**

$2mF_o-DF_c$  (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	NAG	G	400	14/15	0.53	0.52	90,97,99,101	0
6	NAG	G	406	14/15	0.74	0.44	75,79,83,84	0
6	NAG	D	401	14/15	0.74	0.45	82,88,92,93	0
6	NAG	E	400	14/15	0.74	0.72	88,93,95,96	0
6	NAG	H	400	14/15	0.77	0.55	86,89,90,92	0
6	NAG	A	400	14/15	0.77	0.48	74,79,83,83	0
6	NAG	G	401	14/15	0.78	0.34	64,68,70,72	0
6	NAG	D	400	14/15	0.81	0.27	71,74,77,78	0
6	NAG	B	400	14/15	0.86	0.59	77,82,83,83	0

## 6.5 Other polymers

There are no such residues in this entry.