



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 10:53 AM EDT

PDB ID : 6MEJ  
Title : Crystal structure of Hepatitis C virus envelope glycoprotein E2 ectodomain in complex with human antibodies HEPC3 and HEPC46  
Authors : Flyak, A.I.; Bjorkman, P.J.  
Deposited on : 2018-09-06  
Resolution : 2.80 Å (reported)

This is a Full wwPDB X-ray Structure Validation 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 : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : **FAILED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

## 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 2.80 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8500 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 antibody HEPC46 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	1610	1013	275	315	7	0	0	0

- Molecule 2 is a protein called antibody HEPC46 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	212	1577	988	264	321	4	0	0	0

- Molecule 3 is a protein called E2 glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	234	1830	1162	325	324	19	0	0	0

- Molecule 4 is a protein called antibody HEPC3 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	225	1680	1056	282	334	8	0	0	0

- Molecule 5 is a protein called antibody HEPC3 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	L	213	1636	1017	281	333	5	0	0	0

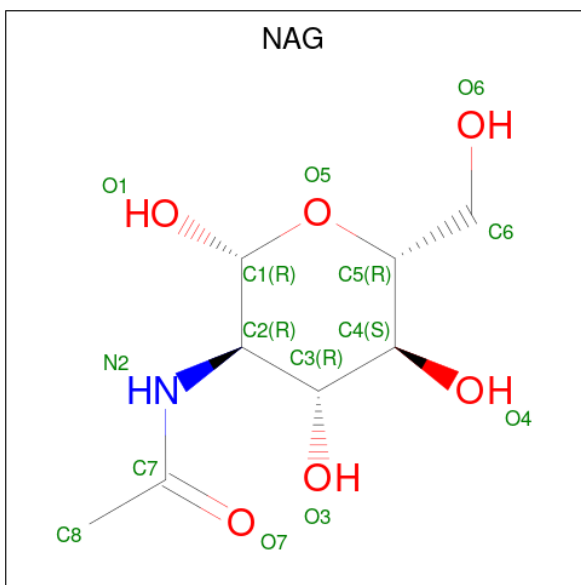
- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
6	D	5	61	34	2	25	0	0	0

- Molecule 7 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
7	E	4	50	28	2	20	0	0	0

- Molecule 8 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		
8	C	1	14	8	1	5	0	0
8	C	1	14	8	1	5	0	0
8	C	1	14	8	1	5	0	0
8	C	1	14	8	1	5	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

### 3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.44Å 76.64Å 118.26Å 90.00° 106.33° 90.00°	Depositor
Resolution (Å)	78.27 – 2.80	Depositor
% Data completeness (in resolution range)	99.7 (78.27-2.80)	Depositor
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.59 (at 2.82Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, $R_{free}$	0.198 , 0.271	Depositor
Wilson B-factor (Å <sup>2</sup> )	64.6	Xtrriage
Anisotropy	0.408	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8500	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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.

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

### 4.5 Carbohydrates [i](#)

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
6	NAG	D	1	3,6	14,14,15	0.66	0	17,19,21	2.54	6 (35%)
6	NAG	D	2	6	14,14,15	0.56	0	17,19,21	1.91	5 (29%)
6	BMA	D	3	6	11,11,12	1.08	1 (9%)	15,15,17	1.03	1 (6%)
6	MAN	D	4	6	11,11,12	0.64	0	15,15,17	1.22	2 (13%)
6	MAN	D	5	6	11,11,12	0.61	0	15,15,17	1.03	1 (6%)
7	NAG	E	1	3,7	14,14,15	0.41	0	17,19,21	1.06	1 (5%)
7	NAG	E	2	7	14,14,15	0.44	0	17,19,21	1.22	2 (11%)
7	BMA	E	3	7	11,11,12	1.22	2 (18%)	15,15,17	1.01	0
7	MAN	E	4	7	11,11,12	0.58	0	15,15,17	0.81	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
6	NAG	D	1	3,6	-	3/6/23/26	0/1/1/1
6	NAG	D	2	6	-	3/6/23/26	0/1/1/1
6	BMA	D	3	6	-	1/2/19/22	0/1/1/1
6	MAN	D	4	6	-	0/2/19/22	0/1/1/1
6	MAN	D	5	6	-	0/2/19/22	0/1/1/1
7	NAG	E	1	3,7	-	2/6/23/26	0/1/1/1
7	NAG	E	2	7	-	4/6/23/26	0/1/1/1
7	BMA	E	3	7	-	1/2/19/22	0/1/1/1
7	MAN	E	4	7	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	E	3	BMA	C4-C5	2.67	1.58	1.53
7	E	3	BMA	C4-C3	2.50	1.58	1.52
6	D	3	BMA	C1-C2	2.28	1.57	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	1	NAG	C1-C2-N2	-6.17	99.94	110.49
6	D	1	NAG	C2-N2-C7	5.01	130.04	122.90
6	D	2	NAG	C2-N2-C7	4.34	129.08	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	1	NAG	O3-C3-C4	-3.07	103.25	110.35
6	D	2	NAG	C4-C3-C2	3.01	115.43	111.02
7	E	1	NAG	C2-N2-C7	-2.76	118.98	122.90
7	E	2	NAG	C2-N2-C7	-2.75	118.99	122.90
6	D	4	MAN	C1-C2-C3	-2.51	106.58	109.67
6	D	1	NAG	O3-C3-C2	-2.48	104.34	109.47
6	D	1	NAG	O5-C5-C6	-2.41	103.42	107.20
6	D	2	NAG	O7-C7-N2	2.30	126.18	121.95
6	D	2	NAG	C6-C5-C4	2.21	118.18	113.00
7	E	2	NAG	O5-C1-C2	-2.17	107.86	111.29
6	D	1	NAG	C3-C4-C5	2.14	114.06	110.24
6	D	3	BMA	O2-C2-C3	-2.10	105.93	110.14
6	D	5	MAN	O5-C5-C6	2.05	110.41	107.20
6	D	4	MAN	C1-O5-C5	-2.02	109.46	112.19
6	D	2	NAG	C3-C4-C5	-2.01	106.65	110.24

There are no chirality outliers.

All (14) torsion outliers are listed below:

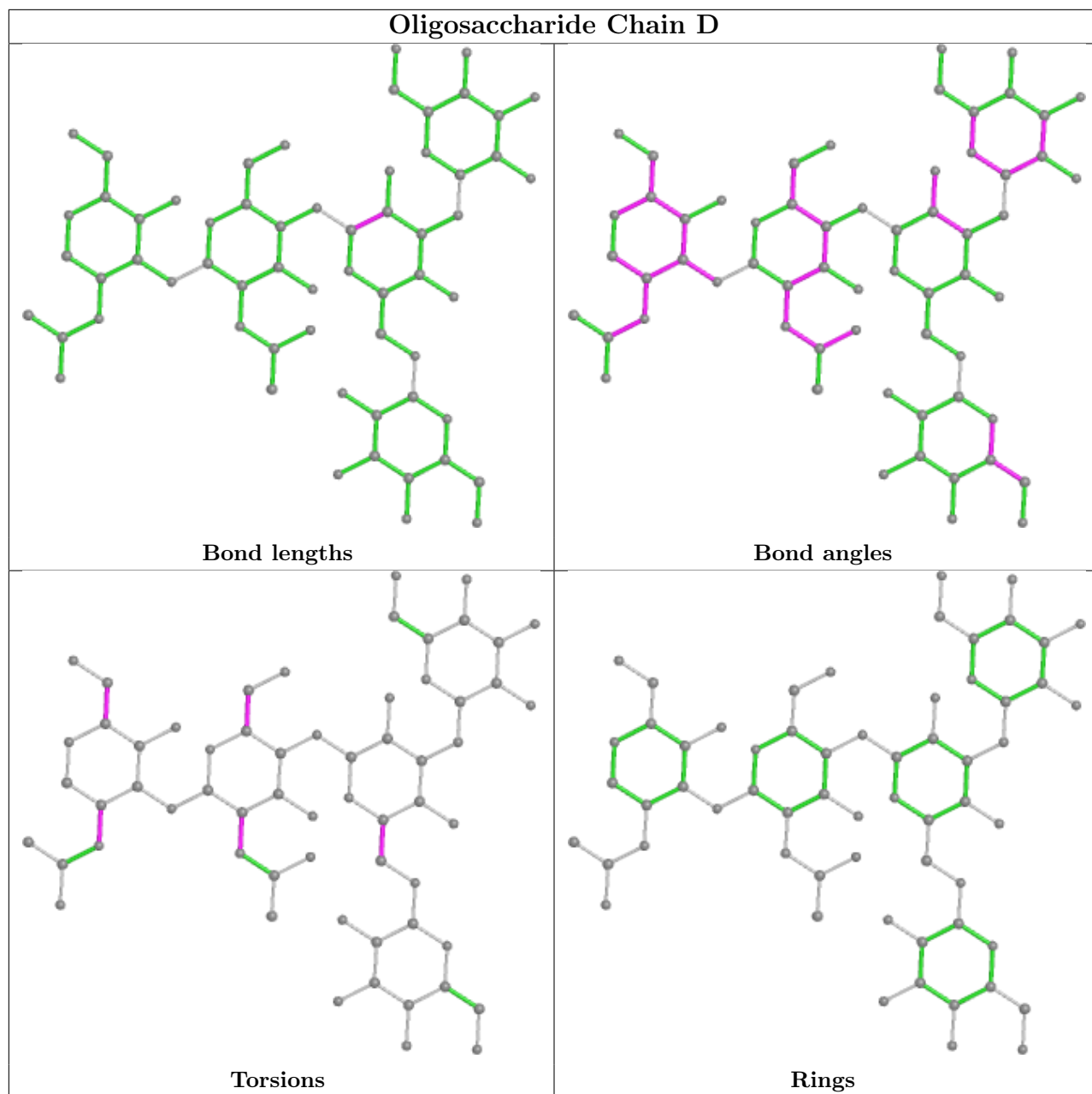
Mol	Chain	Res	Type	Atoms
6	D	1	NAG	C3-C2-N2-C7
6	D	1	NAG	O5-C5-C6-O6
6	D	1	NAG	C4-C5-C6-O6
7	E	3	BMA	O5-C5-C6-O6
7	E	2	NAG	C4-C5-C6-O6
7	E	2	NAG	O5-C5-C6-O6
6	D	3	BMA	O5-C5-C6-O6
6	D	2	NAG	O5-C5-C6-O6
7	E	1	NAG	C4-C5-C6-O6
7	E	2	NAG	C8-C7-N2-C2
6	D	2	NAG	C3-C2-N2-C7
7	E	2	NAG	O7-C7-N2-C2
7	E	1	NAG	O5-C5-C6-O6
6	D	2	NAG	C1-C2-N2-C7

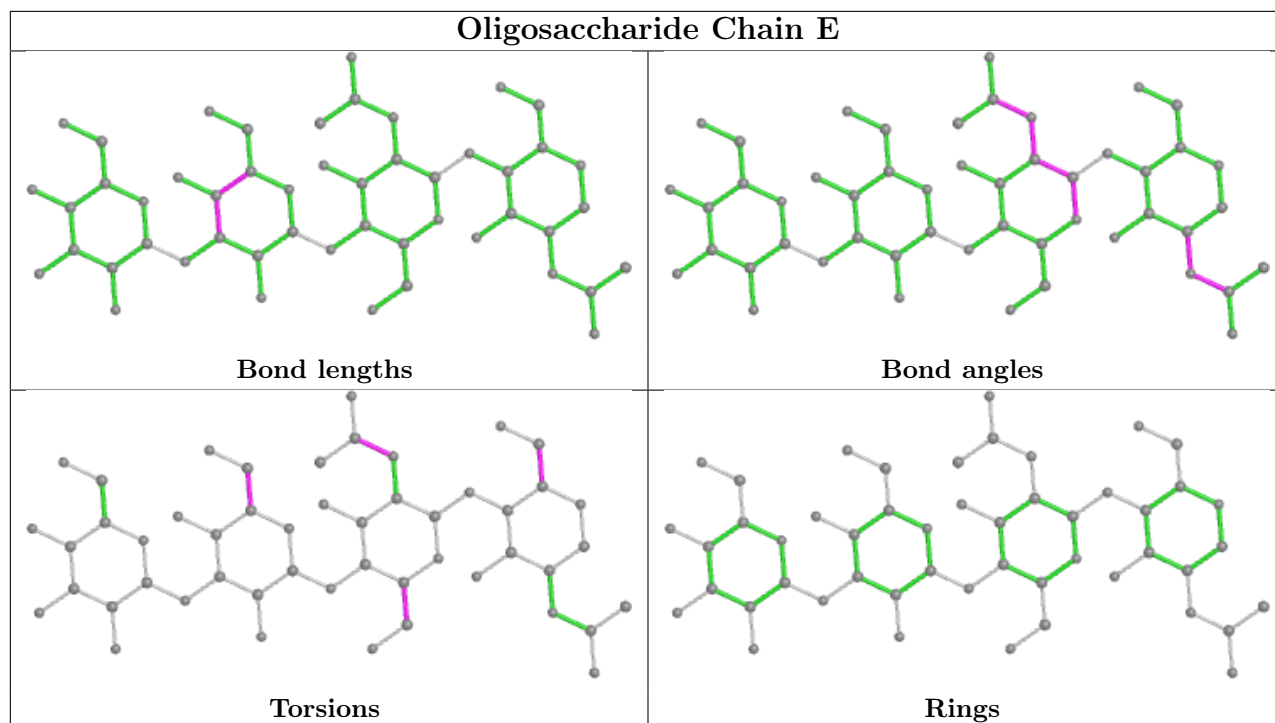
There are no ring outliers.

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.







## 4.6 Ligand geometry [i](#)

4 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	$\# Z  > 2$
8	NAG	C	4311	3	14,14,15	0.62	0	17,19,21	1.82	5 (29%)
8	NAG	C	4301	3	14,14,15	0.53	0	17,19,21	0.90	0
8	NAG	C	4313	3	14,14,15	0.49	0	17,19,21	1.04	1 (5%)
8	NAG	C	4312	3	14,14,15	0.67	0	17,19,21	0.94	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
8	NAG	C	4311	3	-	4/6/23/26	0/1/1/1
8	NAG	C	4301	3	-	6/6/23/26	0/1/1/1
8	NAG	C	4313	3	-	0/6/23/26	0/1/1/1
8	NAG	C	4312	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	4311	NAG	C6-C5-C4	-3.44	104.94	113.00
8	C	4311	NAG	O5-C1-C2	-2.99	106.57	111.29
8	C	4311	NAG	C4-C3-C2	-2.99	106.64	111.02
8	C	4311	NAG	C1-O5-C5	2.49	115.57	112.19
8	C	4311	NAG	O7-C7-N2	2.36	126.30	121.95
8	C	4312	NAG	C1-O5-C5	2.23	115.22	112.19
8	C	4313	NAG	O5-C5-C6	2.08	110.47	107.20

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	C	4301	NAG	C1-C2-N2-C7
8	C	4301	NAG	C8-C7-N2-C2
8	C	4301	NAG	O7-C7-N2-C2
8	C	4311	NAG	C8-C7-N2-C2
8	C	4311	NAG	O7-C7-N2-C2
8	C	4311	NAG	O5-C5-C6-O6
8	C	4301	NAG	O5-C5-C6-O6
8	C	4311	NAG	C4-C5-C6-O6
8	C	4301	NAG	C4-C5-C6-O6
8	C	4301	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

## 4.7 Other polymers [i](#)

There are no such residues in this entry.

## 4.8 Polymer linkage issues

There are no chain breaks in this entry.

## 5 Fit of model and data

### 5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

### 5.4 Ligands

EDS failed to run properly - this section is therefore empty.

### 5.5 Other polymers

EDS failed to run properly - this section is therefore empty.