



# wwPDB X-ray Structure Validation Summary Report

Jan 4, 2024 – 05:23 pm GMT

PDB ID : 4UTA  
Title : Crystal structure of dengue 2 virus envelope glycoprotein in complex with the Fab fragment of the broadly neutralizing human antibody EDE1 C8  
Authors : Rouvinski, A.; Guardado-Calvo, P.; Barba-Spaeth, G.; Duquerroy, S.; Vaney, M.C.; Rey, F.A.  
Deposited on : 2014-07-18  
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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

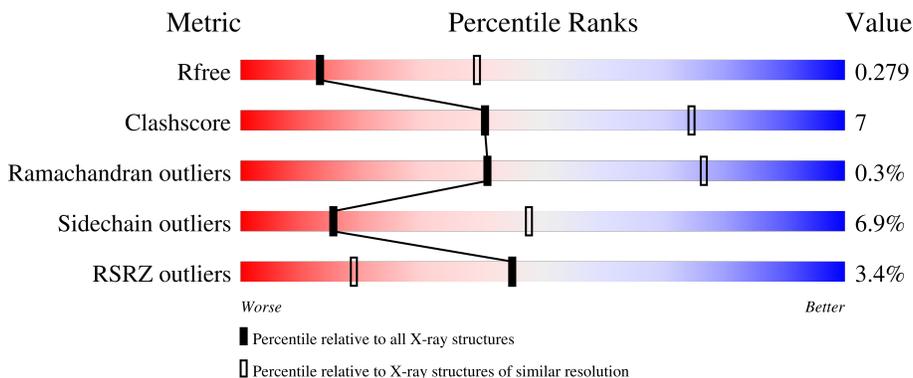
# 1 Overall quality at a glance

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.



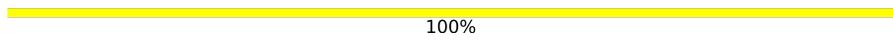
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	425	
1	B	425	
2	H	272	
2	I	272	
3	L	217	

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Mol	Chain	Length	Quality of chain
3	M	217	 11% 79% 18% ..
4	C	4	 100%
5	D	6	 67% 33%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 12683 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 ENVELOPE GLYCOPROTEIN E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	373	2898	1831	498	545	24	0	0	0
1	B	386	3009	1897	520	568	24	0	0	0

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	392	LEU	-	expression tag	UNP Q68Y26
A	393	ARG	-	expression tag	UNP Q68Y26
A	394	PRO	-	expression tag	UNP Q68Y26
A	395	LEU	-	expression tag	UNP Q68Y26
A	396	GLU	-	expression tag	UNP Q68Y26
A	397	SER	-	expression tag	UNP Q68Y26
A	398	ARG	-	expression tag	UNP Q68Y26
A	399	GLY	-	expression tag	UNP Q68Y26
A	400	PRO	-	expression tag	UNP Q68Y26
A	401	PHE	-	expression tag	UNP Q68Y26
A	402	GLU	-	expression tag	UNP Q68Y26
A	403	GLY	-	expression tag	UNP Q68Y26
A	404	LYS	-	expression tag	UNP Q68Y26
A	405	PRO	-	expression tag	UNP Q68Y26
A	406	ILE	-	expression tag	UNP Q68Y26
A	407	PRO	-	expression tag	UNP Q68Y26
A	408	ASN	-	expression tag	UNP Q68Y26
A	409	PRO	-	expression tag	UNP Q68Y26
A	410	LEU	-	expression tag	UNP Q68Y26
A	411	LEU	-	expression tag	UNP Q68Y26
A	412	GLY	-	expression tag	UNP Q68Y26
A	413	LEU	-	expression tag	UNP Q68Y26
A	414	ASP	-	expression tag	UNP Q68Y26
A	415	SER	-	expression tag	UNP Q68Y26
A	416	THR	-	expression tag	UNP Q68Y26

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Chain	Residue	Modelled	Actual	Comment	Reference
A	417	ARG	-	expression tag	UNP Q68Y26
A	418	THR	-	expression tag	UNP Q68Y26
A	419	GLY	-	expression tag	UNP Q68Y26
A	420	HIS	-	expression tag	UNP Q68Y26
A	421	HIS	-	expression tag	UNP Q68Y26
A	422	HIS	-	expression tag	UNP Q68Y26
A	423	HIS	-	expression tag	UNP Q68Y26
A	424	HIS	-	expression tag	UNP Q68Y26
A	425	HIS	-	expression tag	UNP Q68Y26
A	118	LYS	MET	conflict	UNP Q68Y26
B	392	LEU	-	expression tag	UNP Q68Y26
B	393	ARG	-	expression tag	UNP Q68Y26
B	394	PRO	-	expression tag	UNP Q68Y26
B	395	LEU	-	expression tag	UNP Q68Y26
B	396	GLU	-	expression tag	UNP Q68Y26
B	397	SER	-	expression tag	UNP Q68Y26
B	398	ARG	-	expression tag	UNP Q68Y26
B	399	GLY	-	expression tag	UNP Q68Y26
B	400	PRO	-	expression tag	UNP Q68Y26
B	401	PHE	-	expression tag	UNP Q68Y26
B	402	GLU	-	expression tag	UNP Q68Y26
B	403	GLY	-	expression tag	UNP Q68Y26
B	404	LYS	-	expression tag	UNP Q68Y26
B	405	PRO	-	expression tag	UNP Q68Y26
B	406	ILE	-	expression tag	UNP Q68Y26
B	407	PRO	-	expression tag	UNP Q68Y26
B	408	ASN	-	expression tag	UNP Q68Y26
B	409	PRO	-	expression tag	UNP Q68Y26
B	410	LEU	-	expression tag	UNP Q68Y26
B	411	LEU	-	expression tag	UNP Q68Y26
B	412	GLY	-	expression tag	UNP Q68Y26
B	413	LEU	-	expression tag	UNP Q68Y26
B	414	ASP	-	expression tag	UNP Q68Y26
B	415	SER	-	expression tag	UNP Q68Y26
B	416	THR	-	expression tag	UNP Q68Y26
B	417	ARG	-	expression tag	UNP Q68Y26
B	418	THR	-	expression tag	UNP Q68Y26
B	419	GLY	-	expression tag	UNP Q68Y26
B	420	HIS	-	expression tag	UNP Q68Y26
B	421	HIS	-	expression tag	UNP Q68Y26
B	422	HIS	-	expression tag	UNP Q68Y26
B	423	HIS	-	expression tag	UNP Q68Y26

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Chain	Residue	Modelled	Actual	Comment	Reference
B	424	HIS	-	expression tag	UNP Q68Y26
B	425	HIS	-	expression tag	UNP Q68Y26
B	118	LYS	MET	conflict	UNP Q68Y26

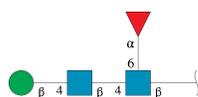
- Molecule 2 is a protein called BROADLY NEUTRALIZING HUMAN ANTIBODY EDE1 C8 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	221	Total	C	N	O	S	0	0	0
			1656	1047	271	331	7			
2	I	211	Total	C	N	O	S	0	0	0
			1594	1011	260	316	7			

- Molecule 3 is a protein called BROADLY NEUTRALIZING HUMAN ANTIBODY EDE1 C8 LIGHT CHAIN.

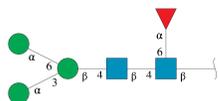
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	215	Total	C	N	O	S	0	1	0
			1675	1054	284	333	4			
3	M	213	Total	C	N	O	S	0	1	0
			1665	1049	282	330	4			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	C	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 5 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-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	D	6	71	40	2	29	0	0	0

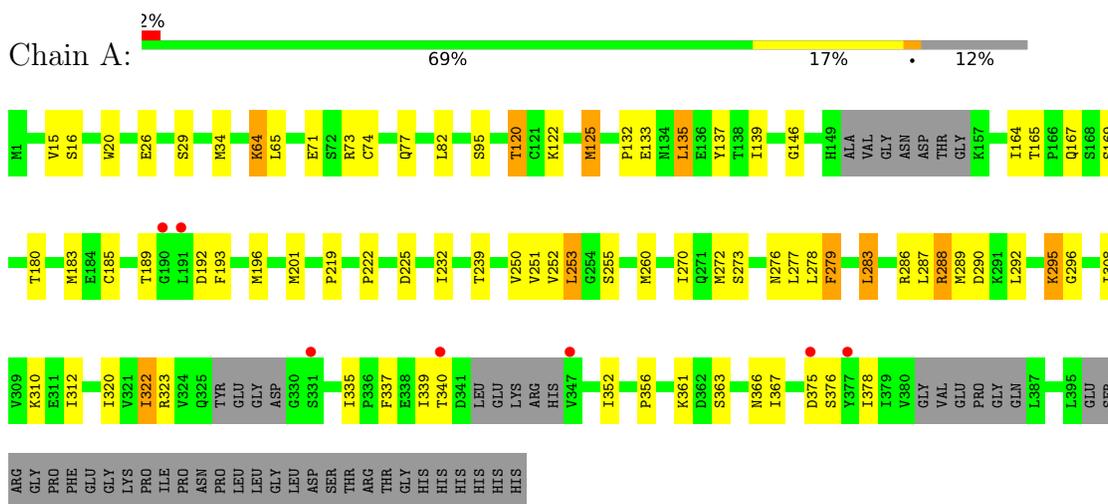
- Molecule 6 is water.

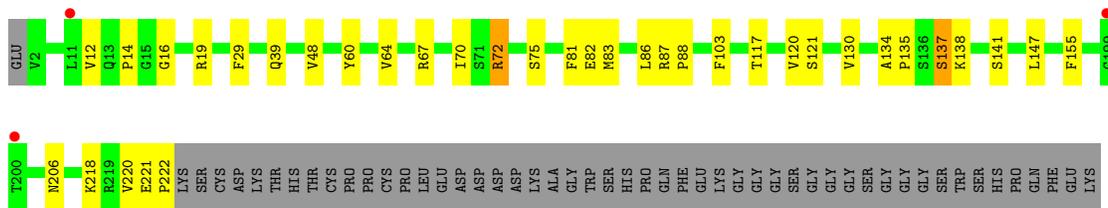
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	31	Total 31	O 31	0	0
6	B	18	Total 18	O 18	0	0
6	H	10	Total 10	O 10	0	0
6	I	3	Total 3	O 3	0	0
6	L	1	Total 1	O 1	0	0
6	M	3	Total 3	O 3	0	0

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

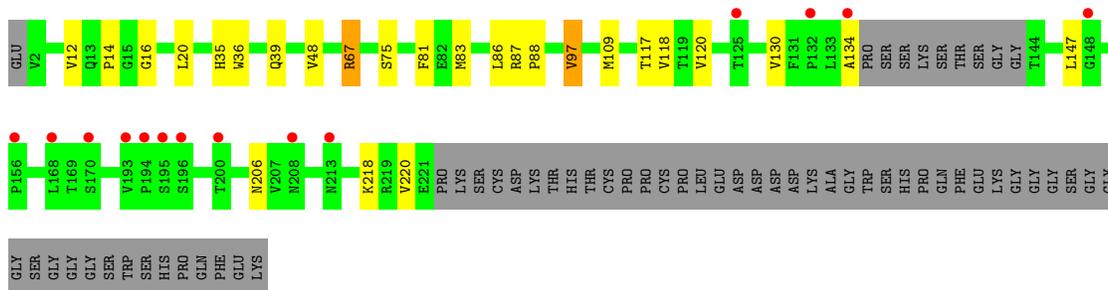
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: ENVELOPE GLYCOPROTEIN E

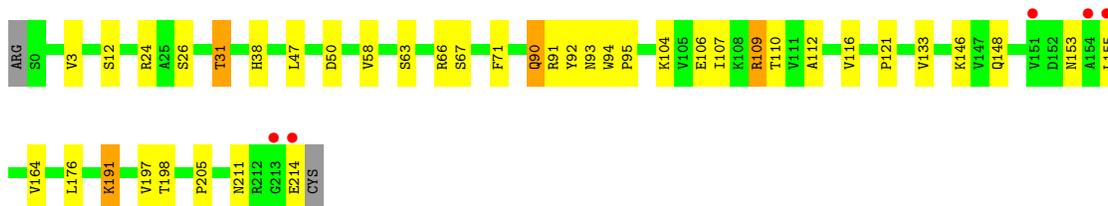
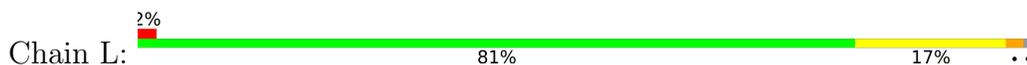




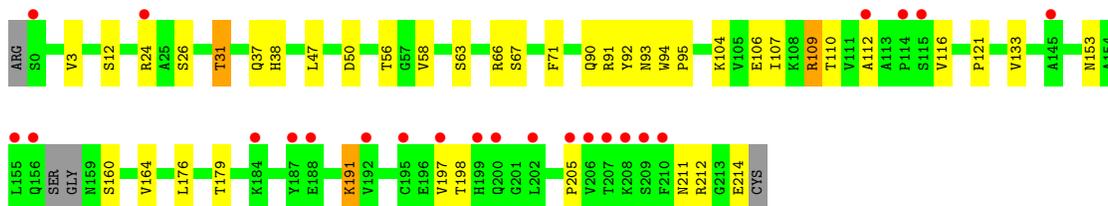
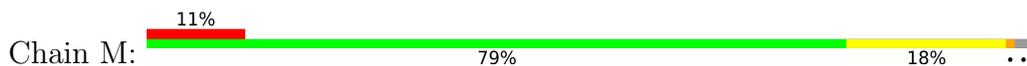
● Molecule 2: BROADLY NEUTRALIZING HUMAN ANTIBODY EDE1 C8 HEAVY CHAIN



● Molecule 3: BROADLY NEUTRALIZING HUMAN ANTIBODY EDE1 C8 LIGHT CHAIN



● Molecule 3: BROADLY NEUTRALIZING HUMAN ANTIBODY EDE1 C8 LIGHT CHAIN



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



- Molecule 5: 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-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:

67%

33%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.66Å 191.34Å 203.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.97 – 3.00 29.75 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.6 (19.97-3.00) 95.5 (29.75-3.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 3.00Å)	Xtrriage
Refinement program	BUSTER 2.11.4	Depositor
R, $R_{free}$	0.213 , 0.248 0.236 , 0.279	Depositor DCC
$R_{free}$ test set	2312 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	74.4	Xtrriage
Anisotropy	0.321	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 81.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	12683	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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: FUC, MAN, BMA, NAG

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	0.55	0/2952	0.78	1/3984 (0.0%)
1	B	0.60	0/3069	0.81	2/4145 (0.0%)
2	H	0.52	0/1699	0.73	0/2316
2	I	0.46	0/1634	0.72	0/2226
3	L	0.47	0/1719	0.72	0/2340
3	M	0.43	0/1708	0.70	0/2324
All	All	0.52	0/12781	0.76	3/17335 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	225	ASP	C-N-CA	6.05	136.82	121.70
1	B	279	PHE	C-N-CA	5.69	135.92	121.70
1	A	279	PHE	C-N-CA	5.26	134.84	121.70

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	2898	0	2907	45	0
1	B	3009	0	3012	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	1656	0	1589	24	0
2	I	1594	0	1528	18	0
3	L	1675	0	1630	26	0
3	M	1665	0	1621	26	0
4	C	49	0	43	0	0
5	D	71	0	61	1	0
6	A	31	0	0	0	0
6	B	18	0	0	0	0
6	H	10	0	0	0	0
6	I	3	0	0	0	0
6	L	1	0	0	0	0
6	M	3	0	0	0	0
All	All	12683	0	12391	181	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 181 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:A:295:LYS:C	1:A:296:GLY:HA3	1.74	1.08
1:B:310:LYS:HE2	3:M:31:THR:HG21	1.34	1.07
3:L:164:VAL:HG22	3:L:176:LEU:CD1	1.97	0.94
1:B:392:LEU:HG	1:B:392:LEU:O	1.68	0.93
1:A:312:ILE:HD11	1:A:320:ILE:HD13	1.51	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	361/425 (85%)	339 (94%)	21 (6%)	1 (0%)	41	76
1	B	380/425 (89%)	359 (94%)	18 (5%)	3 (1%)	19	57
2	H	219/272 (80%)	205 (94%)	14 (6%)	0	100	100
2	I	207/272 (76%)	194 (94%)	13 (6%)	0	100	100
3	L	214/217 (99%)	207 (97%)	7 (3%)	0	100	100
3	M	210/217 (97%)	201 (96%)	9 (4%)	0	100	100
All	All	1591/1828 (87%)	1505 (95%)	82 (5%)	4 (0%)	41	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	226	THR
1	B	280	THR
1	B	16	SER
1	A	16	SER

### 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	325/369 (88%)	298 (92%)	27 (8%)	11	39
1	B	337/369 (91%)	308 (91%)	29 (9%)	10	37
2	H	186/226 (82%)	176 (95%)	10 (5%)	22	57
2	I	178/226 (79%)	172 (97%)	6 (3%)	37	72
3	L	189/190 (100%)	176 (93%)	13 (7%)	15	48
3	M	188/190 (99%)	177 (94%)	11 (6%)	19	54
All	All	1403/1570 (89%)	1307 (93%)	96 (7%)	15	48

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	72	ARG

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Mol	Chain	Res	Type
2	I	206	ASN
2	H	81	PHE
2	H	206	ASN
3	L	50	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	386	GLN
3	L	38	HIS
3	M	38	HIS
3	L	90	GLN
1	B	27	HIS

### 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](#)

10 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	$\# Z  > 2$
4	NAG	C	1	1,4	14,14,15	0.44	0	17,19,21	1.24	2 (11%)
4	NAG	C	2	4	14,14,15	0.33	0	17,19,21	0.93	1 (5%)
4	BMA	C	3	4	11,11,12	0.28	0	15,15,17	0.67	1 (6%)
4	FUC	C	4	4	10,10,11	0.52	0	14,14,16	1.57	1 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	D	1	1,5	14,14,15	0.41	0	17,19,21	1.24	1 (5%)
5	NAG	D	2	5	14,14,15	0.36	0	17,19,21	1.05	1 (5%)
5	BMA	D	3	5	11,11,12	0.31	0	15,15,17	0.77	1 (6%)
5	MAN	D	4	5	11,11,12	0.55	0	15,15,17	1.29	1 (6%)
5	MAN	D	5	5	11,11,12	0.51	0	15,15,17	1.50	1 (6%)
5	FUC	D	6	5	10,10,11	0.55	0	14,14,16	1.55	3 (21%)

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	C	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	C	2	4	-	0/6/23/26	0/1/1/1
4	BMA	C	3	4	-	0/2/19/22	0/1/1/1
4	FUC	C	4	4	-	-	0/1/1/1
5	NAG	D	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	D	2	5	-	0/6/23/26	0/1/1/1
5	BMA	D	3	5	-	2/2/19/22	0/1/1/1
5	MAN	D	4	5	-	1/2/19/22	0/1/1/1
5	MAN	D	5	5	-	0/2/19/22	1/1/1/1
5	FUC	D	6	5	-	-	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	5	MAN	C1-O5-C5	4.95	118.90	112.19
4	C	4	FUC	C3-C4-C5	4.42	116.65	109.77
5	D	4	MAN	C1-O5-C5	3.93	117.52	112.19
5	D	6	FUC	C3-C4-C5	3.52	115.26	109.77
5	D	2	NAG	C1-O5-C5	3.46	116.88	112.19

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	3	BMA	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	D	3	BMA	C4-C5-C6-O6
4	C	1	NAG	O5-C5-C6-O6
4	C	1	NAG	C4-C5-C6-O6
5	D	1	NAG	O5-C5-C6-O6

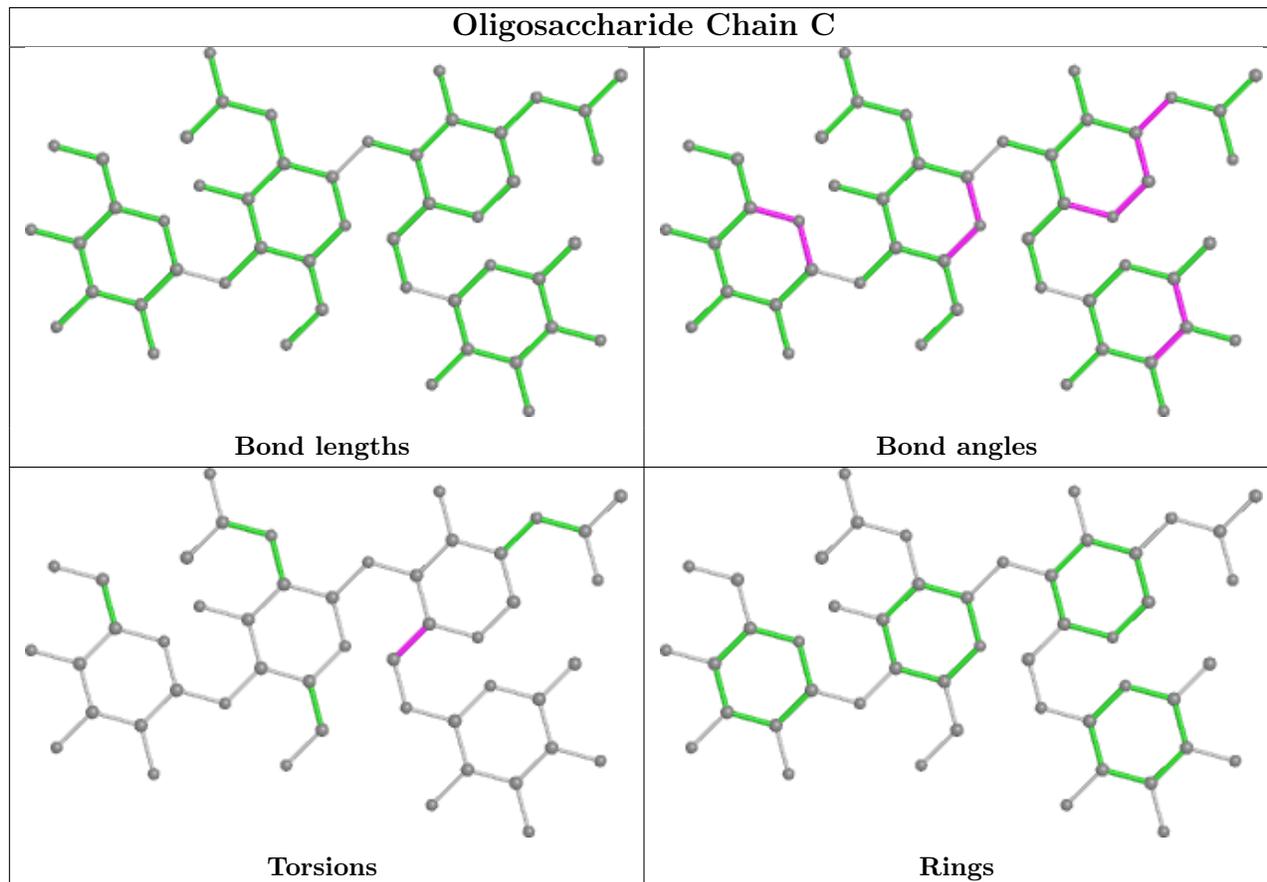
All (1) ring outliers are listed below:

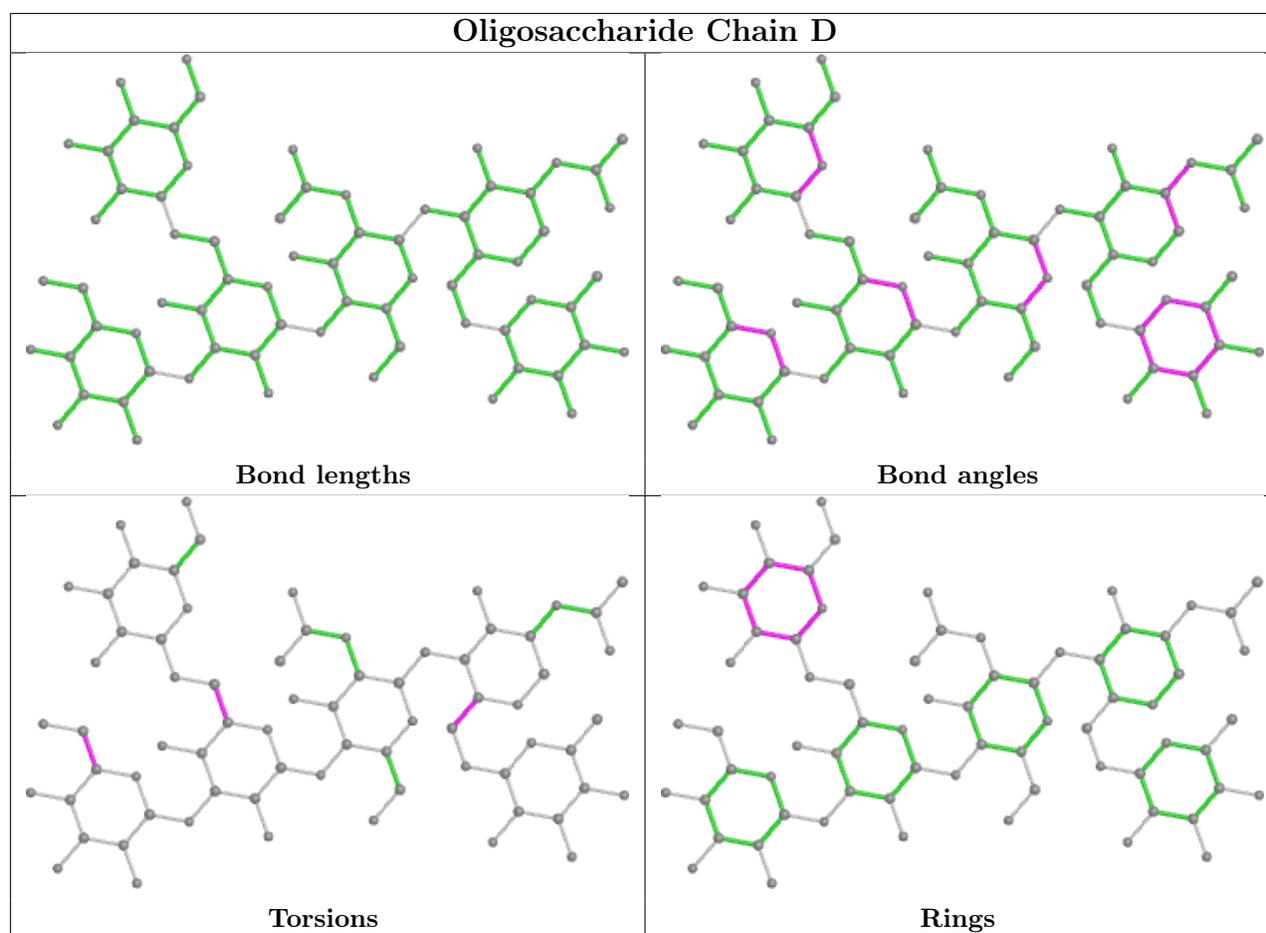
Mol	Chain	Res	Type	Atoms
5	D	5	MAN	C1-C2-C3-C4-C5-O5

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	5	MAN	1	0
5	D	2	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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	295:LYS	C	296:GLY	N	3.18

## 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	373/425 (87%)	-0.07	7 (1%) 66 37	42, 74, 130, 141	0
1	B	386/425 (90%)	-0.24	3 (0%) 86 65	36, 69, 121, 131	0
2	H	221/272 (81%)	0.01	3 (1%) 75 49	39, 83, 119, 138	0
2	I	211/272 (77%)	0.46	14 (6%) 18 5	45, 105, 152, 160	0
3	L	215/217 (99%)	-0.10	5 (2%) 60 31	50, 73, 118, 155	0
3	M	213/217 (98%)	0.60	23 (10%) 5 2	58, 117, 164, 175	0
All	All	1619/1828 (88%)	0.05	55 (3%) 45 19	36, 85, 142, 175	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	M	187	TYR	4.8
3	M	206	VAL	4.8
2	I	200	THR	4.7
3	M	209	SER	4.7
3	M	197[A]	VAL	4.2

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

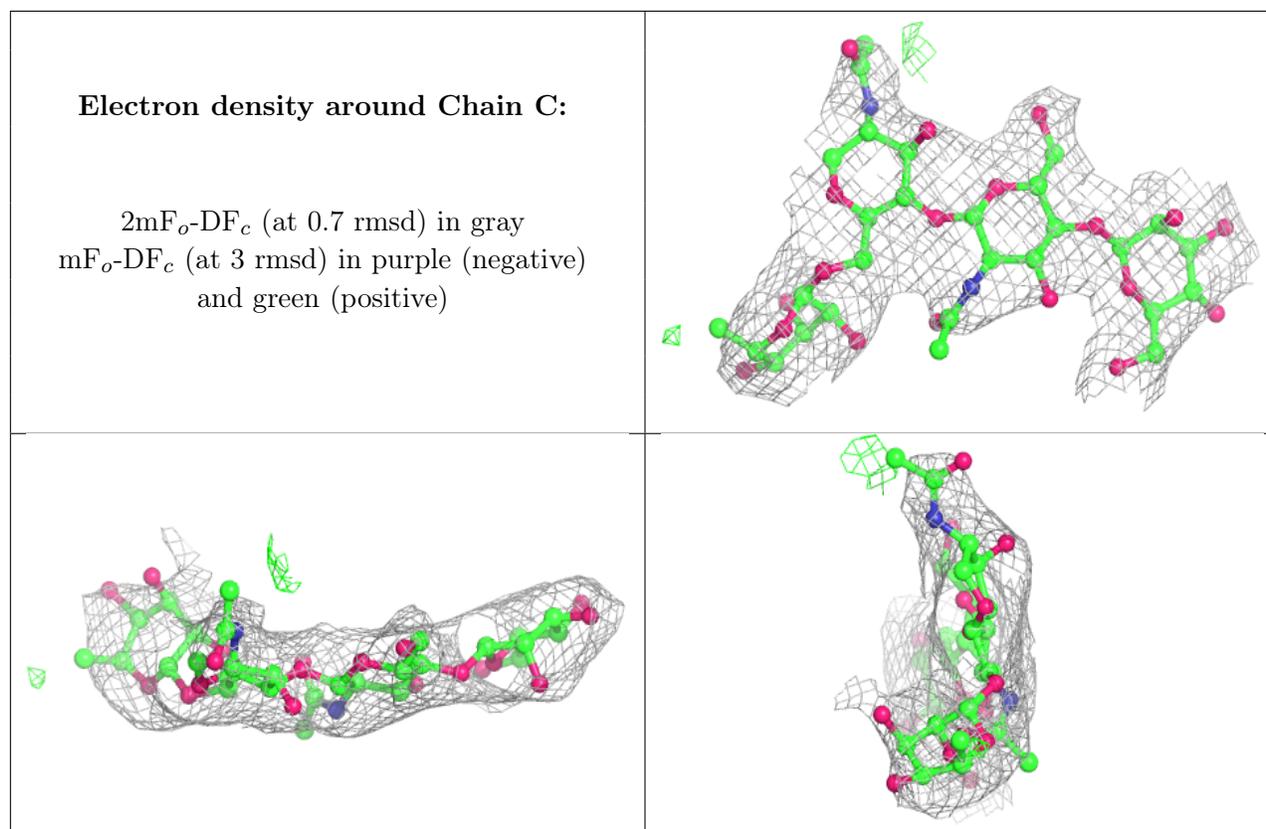
There are no non-standard protein/DNA/RNA residues in this entry.

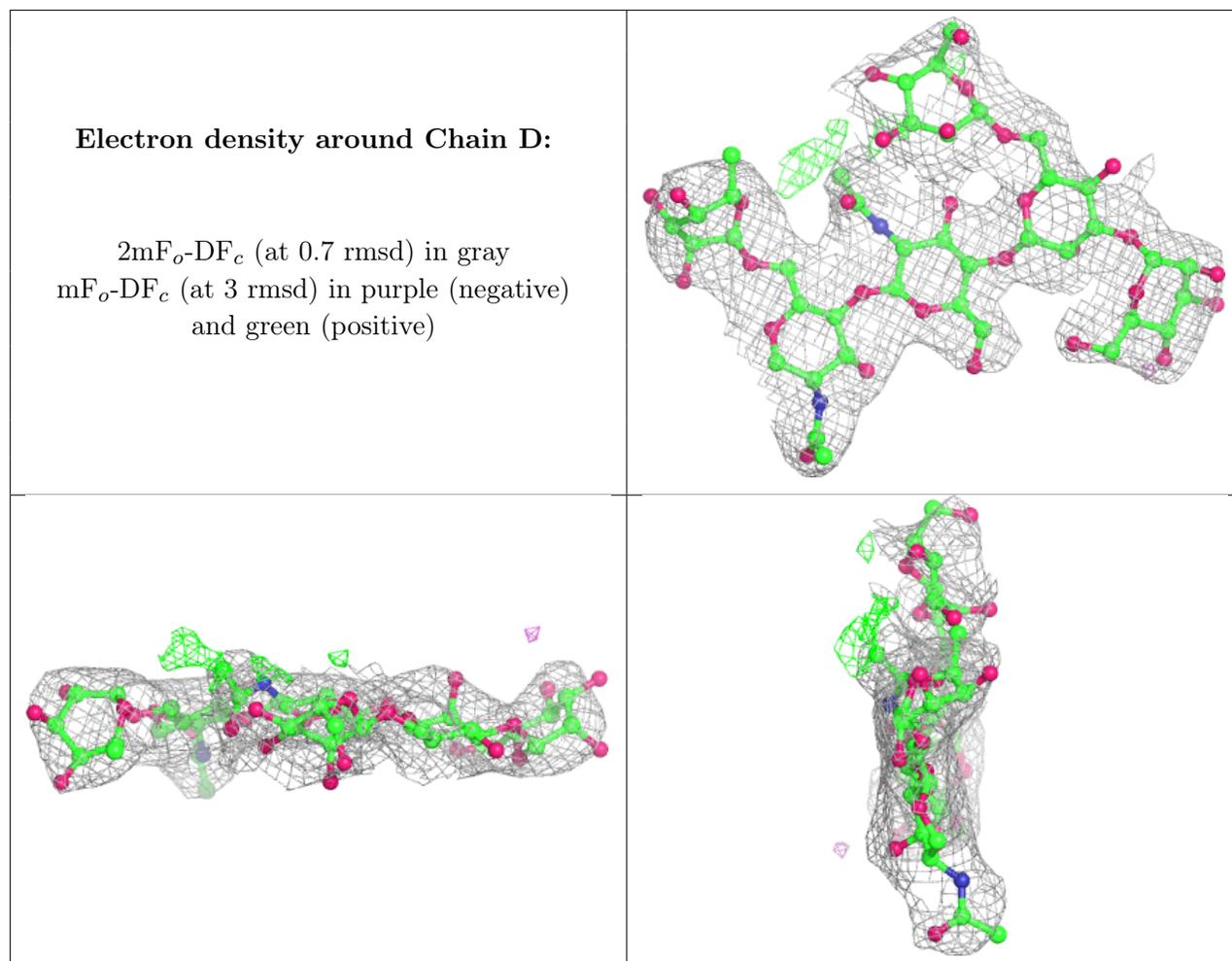
### 6.3 Carbohydrates [i](#)

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
5	MAN	D	5	11/12	0.69	0.28	151,154,156,157	0
5	BMA	D	3	11/12	0.83	0.31	122,129,137,143	0
4	FUC	C	4	10/11	0.83	0.27	111,112,116,119	0
4	BMA	C	3	11/12	0.84	0.28	122,129,130,131	0
4	NAG	C	2	14/15	0.86	0.29	121,124,127,128	0
5	NAG	D	2	14/15	0.86	0.27	90,103,107,115	0
4	NAG	C	1	14/15	0.92	0.18	96,102,108,114	0
5	MAN	D	4	11/12	0.93	0.42	123,129,131,132	0
5	NAG	D	1	14/15	0.94	0.16	75,81,88,92	0
5	FUC	D	6	10/11	0.94	0.20	82,87,89,89	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.





## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.