



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 21, 2020 – 09:05 PM BST

PDB ID : 6WO5
Title : Structure of Hepatitis C Virus Envelope Glycoprotein E2 core from genotype 1a bound to neutralizing antibody 212.1.1 and non neutralizing antibody E1
Authors : Tzarum, N.; Wilson, I.A.; Law, M.
Deposited on : 2020-04-24
Resolution : 2.62 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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 : 2.14.6
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) : 2.14.6

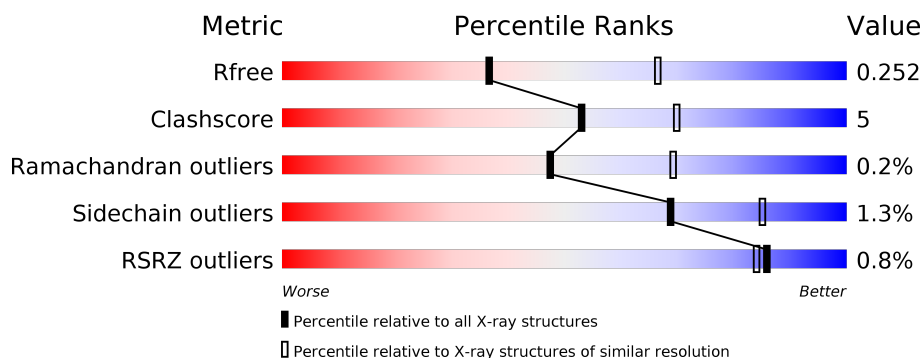
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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.








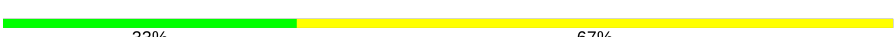



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 ≥ 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	227	<div> <div>78%</div> <div>15%</div> <div>7%</div> </div>
1	C	227	<div> <div>83%</div> <div>12%</div> <div>5%</div> </div>
2	B	221	<div> <div>83%</div> <div>15%</div> <div>.</div> </div>
2	D	221	<div> <div>%</div> <div>81%</div> <div>17%</div> <div>.</div> </div>
3	G	230	<div> <div>86%</div> <div>10%</div> <div>.</div> </div>
3	H	230	<div> <div>84%</div> <div>11%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
4	I	214	 87% 12%
4	L	214	 86% 13%
5	E	191	 3% 64% 13% 23%
5	F	191	 3% 62% 8% 28%
6	J	3	 100%
6	N	3	 33% 67%
7	K	2	 50% 50%
7	M	2	 100%
8	O	5	 100%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 15726 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 Fab E1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	0	0
			1583	1004	261	310	8			
1	C	216	Total	C	N	O	S	0	0	0
			1600	1011	264	317	8			

- Molecule 2 is a protein called Fab E1 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	221	Total	C	N	O	S	0	0	0
			1710	1071	294	340	5			
2	D	219	Total	C	N	O	S	0	0	0
			1697	1064	292	336	5			

- Molecule 3 is a protein called Fab 212.1.1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	219	Total	C	N	O	S	0	0	0
			1601	1009	268	316	8			
3	G	220	Total	C	N	O	S	0	0	0
			1610	1014	270	318	8			

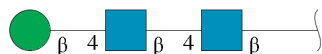
- Molecule 4 is a protein called Fab 212.1.1 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	212	Total	C	N	O	S	0	0	0
			1622	1016	273	328	5			
4	I	211	Total	C	N	O	S	0	0	0
			1618	1014	272	327	5			

- Molecule 5 is a protein called Envelope glycoprotein E2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	148	Total	C	N	O	S	0	0	0
			1141	730	196	202	13			
5	F	138	Total	C	N	O	S	0	0	0
			1064	679	185	188	12			

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



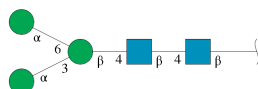
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	N	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 7 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
7	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
7	M	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 8 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)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 10 is beta-D-mannopyranose (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	L	1	Total	C	O	0	0
			11	6	5		

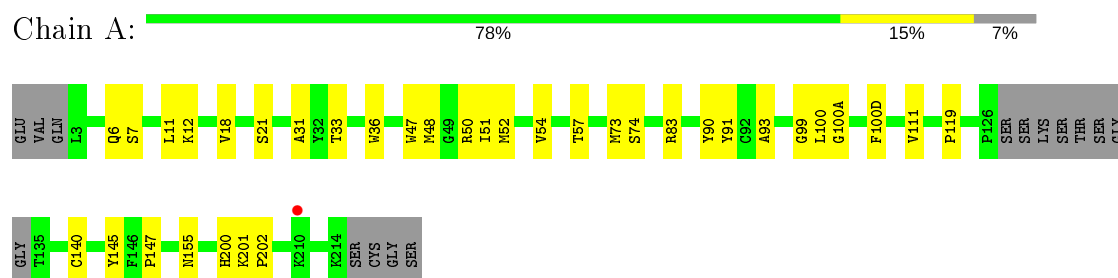
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	11	Total	O	0	0
			11	11		
11	B	29	Total	O	0	0
			29	29		
11	C	30	Total	O	0	0
			30	30		
11	D	13	Total	O	0	0
			13	13		
11	H	23	Total	O	0	0
			23	23		
11	L	32	Total	O	0	0
			32	32		
11	G	24	Total	O	0	0
			24	24		
11	I	19	Total	O	0	0
			19	19		
11	E	12	Total	O	0	0
			12	12		
11	F	11	Total	O	0	0
			11	11		

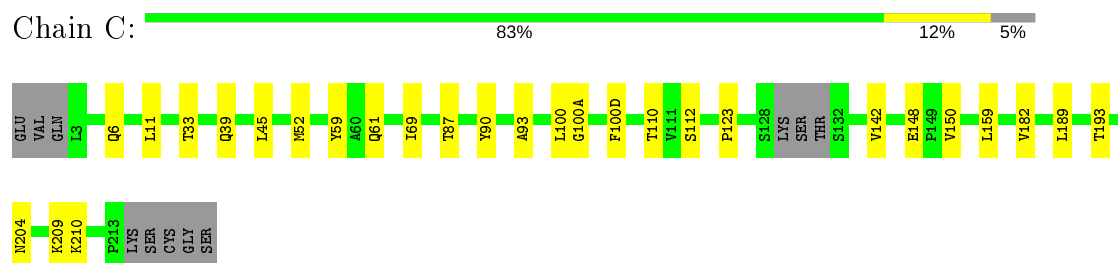
3 Residue-property plots [i](#)

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.

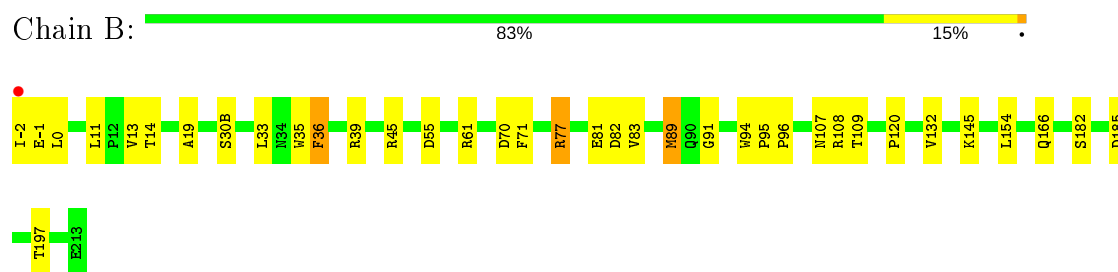
- Molecule 1: Fab E1 heavy chain



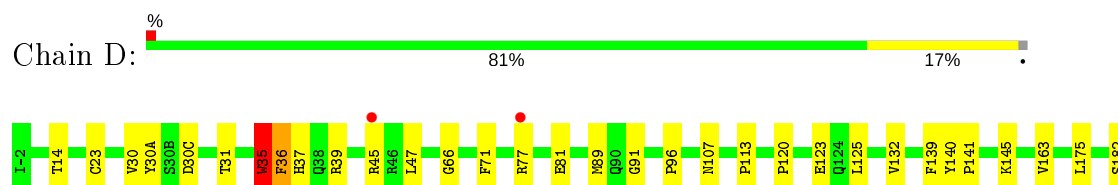
- Molecule 1: Fab E1 heavy chain



- Molecule 2: Fab E1 light chain



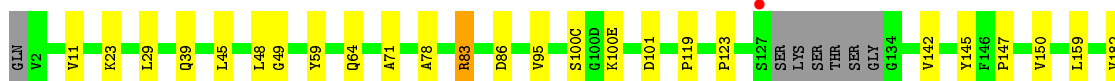
- Molecule 2: Fab E1 light chain





- Molecule 3: Fab 212.1.1 heavy chain

Chain H: 84% 11% 5%



- Molecule 3: Fab 212.1.1 heavy chain

Chain G: 86% 10% 4%



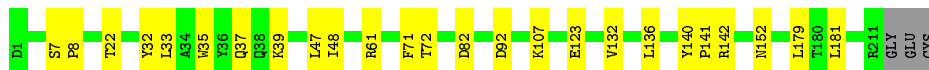
- Molecule 4: Fab 212.1.1 light chain

Chain L: 86% 13% 1%



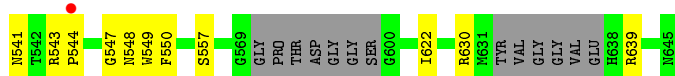
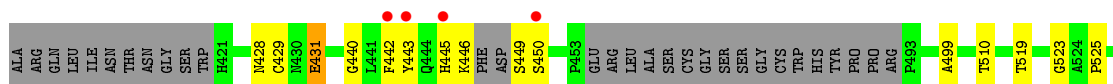
- Molecule 4: Fab 212.1.1 light chain

Chain I: 87% 12% 1%



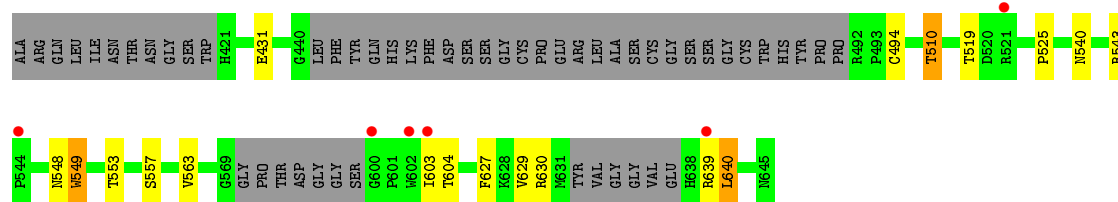
- Molecule 5: Envelope glycoprotein E2

Chain E: 3% 64% 13% 20%



- Molecule 5: Envelope glycoprotein E2

Chain F: 3% 62% 8% 27%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  100%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  33% 67%



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  50% 50%



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  100%



- Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.79Å 242.20Å 100.73Å 90.00° 98.31° 90.00°	Depositor
Resolution (Å)	47.44 – 2.62 47.44 – 2.62	Depositor EDS
% Data completeness (in resolution range)	96.7 (47.44-2.62) 96.6 (47.44-2.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.203 , 0.250 0.204 , 0.252	Depositor DCC
R_{free} test set	3791 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.607	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 32.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15726	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.30	0/1620	0.51	0/2206
1	C	0.28	0/1637	0.50	0/2229
2	B	0.32	1/1749 (0.1%)	0.68	3/2377 (0.1%)
2	D	0.34	1/1736 (0.1%)	0.74	3/2360 (0.1%)
3	G	0.28	0/1644	0.50	0/2235
3	H	0.28	0/1635	0.50	0/2223
4	I	0.28	0/1652	0.49	0/2245
4	L	0.45	2/1656 (0.1%)	0.71	6/2250 (0.3%)
5	E	0.28	0/1180	0.50	0/1614
5	F	0.26	0/1100	0.49	0/1508
All	All	0.31	4/15609 (0.0%)	0.58	12/21247 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
2	D	0	2
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	16	GLY	C-N	7.17	1.50	1.34
4	L	17	ASP	C-N	-7.15	1.17	1.34
2	D	35	TRP	C-N	-5.61	1.21	1.34
2	B	35	TRP	C-N	-5.39	1.21	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	35	TRP	O-C-N	-17.83	94.18	122.70
2	D	35	TRP	C-N-CA	17.27	164.88	121.70
2	B	35	TRP	C-N-CA	14.60	158.20	121.70
2	B	35	TRP	O-C-N	-14.60	99.35	122.70
2	D	35	TRP	CA-C-N	12.70	145.14	117.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	36	PHE	Mainchain
2	D	35	TRP	Peptide
2	D	36	PHE	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1583	0	1571	21	0
1	C	1600	0	1579	17	0
2	B	1710	0	1662	22	0
2	D	1697	0	1651	26	0
3	G	1610	0	1601	12	0
3	H	1601	0	1590	14	0
4	I	1618	0	1585	15	0
4	L	1622	0	1588	17	0
5	E	1141	0	1067	21	0
5	F	1064	0	1001	15	0
6	J	39	0	34	0	0
6	N	39	0	34	0	0
7	K	28	0	24	1	0
7	M	28	0	25	1	0
8	O	61	0	52	1	0
9	D	14	0	13	0	0
9	E	28	0	26	0	0
9	F	28	0	26	1	0
10	L	11	0	10	0	0
11	A	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	B	29	0	0	0	0
11	C	30	0	0	1	0
11	D	13	0	0	0	0
11	E	12	0	0	0	0
11	F	11	0	0	0	0
11	G	24	0	0	2	0
11	H	23	0	0	0	0
11	I	19	0	0	2	0
11	L	32	0	0	2	0
All	All	15726	0	15139	165	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 5.

The worst 5 of 165 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:GLN:NE2	1:C:90:TYR:O	2.20	0.73
4:L:155:GLN:HB3	4:L:158:ASN:HD21	1.54	0.73
4:L:61:ARG:NH2	4:L:82:ASP:OD2	2.20	0.72
4:L:18:ARG:NH1	11:L:402:HOH:O	2.24	0.71
2:B:-2:ILE:HD13	5:F:603:ILE:HG23	1.73	0.70

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	208/227 (92%)	198 (95%)	9 (4%)	1 (0%)	29 50
1	C	212/227 (93%)	206 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	219/221 (99%)	210 (96%)	9 (4%)	0	100	100
2	D	217/221 (98%)	212 (98%)	5 (2%)	0	100	100
3	G	216/230 (94%)	213 (99%)	3 (1%)	0	100	100
3	H	215/230 (94%)	207 (96%)	7 (3%)	1 (0%)	29	50
4	I	209/214 (98%)	203 (97%)	6 (3%)	0	100	100
4	L	210/214 (98%)	207 (99%)	3 (1%)	0	100	100
5	E	138/191 (72%)	134 (97%)	3 (2%)	1 (1%)	22	41
5	F	130/191 (68%)	123 (95%)	6 (5%)	1 (1%)	19	36
All	All	1974/2166 (91%)	1913 (97%)	57 (3%)	4 (0%)	47	69

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	ASN
3	H	48	LEU
5	F	510	THR
5	E	510	THR

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	178/190 (94%)	176 (99%)	2 (1%)	73	88
1	C	180/190 (95%)	179 (99%)	1 (1%)	86	94
2	B	194/194 (100%)	188 (97%)	6 (3%)	40	65
2	D	193/194 (100%)	192 (100%)	1 (0%)	88	95
3	G	180/188 (96%)	179 (99%)	1 (1%)	86	94
3	H	179/188 (95%)	177 (99%)	2 (1%)	73	88
4	I	185/187 (99%)	183 (99%)	2 (1%)	73	88
4	L	185/187 (99%)	184 (100%)	1 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	126/159 (79%)	123 (98%)	3 (2%)	49	72
5	F	117/159 (74%)	113 (97%)	4 (3%)	37	61
All	All	1717/1836 (94%)	1694 (99%)	23 (1%)	69	85

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	64	GLN
4	L	89	GLN
5	F	549	TRP
3	H	83	ARG
3	G	80	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

15 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	J	1	5,6	14,14,15	0.50	0	17,19,21	0.56	0
6	NAG	J	2	6	14,14,15	0.34	0	17,19,21	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	BMA	J	3	6	11,11,12	0.75	0	15,15,17	1.22	0
7	NAG	K	1	5,7	14,14,15	0.34	0	17,19,21	0.38	0
7	NAG	K	2	7	14,14,15	0.16	0	17,19,21	0.39	0
7	NAG	M	1	5,7	14,14,15	0.52	0	17,19,21	0.50	0
7	NAG	M	2	7	14,14,15	0.28	0	17,19,21	0.70	1 (5%)
6	NAG	N	1	5,6	14,14,15	0.78	1 (7%)	17,19,21	0.55	0
6	NAG	N	2	6	14,14,15	0.31	0	17,19,21	0.39	0
6	BMA	N	3	6	11,11,12	0.72	0	15,15,17	1.20	2 (13%)
8	NAG	O	1	8,5	14,14,15	0.24	0	17,19,21	0.57	0
8	NAG	O	2	8	14,14,15	0.34	0	17,19,21	0.81	1 (5%)
8	BMA	O	3	8	11,11,12	1.00	1 (9%)	15,15,17	1.41	2 (13%)
8	MAN	O	4	8	11,11,12	0.39	0	15,15,17	1.15	2 (13%)
8	MAN	O	5	8	11,11,12	1.13	1 (9%)	15,15,17	1.47	2 (13%)

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	J	1	5,6	-	0/6/23/26	0/1/1/1
6	NAG	J	2	6	-	0/6/23/26	0/1/1/1
6	BMA	J	3	6	-	0/2/19/22	0/1/1/1
7	NAG	K	1	5,7	-	0/6/23/26	0/1/1/1
7	NAG	K	2	7	-	0/6/23/26	0/1/1/1
7	NAG	M	1	5,7	-	0/6/23/26	0/1/1/1
7	NAG	M	2	7	-	1/6/23/26	0/1/1/1
6	NAG	N	1	5,6	-	0/6/23/26	0/1/1/1
6	NAG	N	2	6	-	0/6/23/26	0/1/1/1
6	BMA	N	3	6	-	1/2/19/22	0/1/1/1
8	NAG	O	1	8,5	-	1/6/23/26	0/1/1/1
8	NAG	O	2	8	-	2/6/23/26	0/1/1/1
8	BMA	O	3	8	-	2/2/19/22	0/1/1/1
8	MAN	O	4	8	-	2/2/19/22	0/1/1/1
8	MAN	O	5	8	-	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)
8	O	5	MAN	O5-C1	-3.52	1.38	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	O	3	BMA	C1-C2	2.58	1.58	1.52
6	N	1	NAG	C1-C2	2.10	1.55	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	O	5	MAN	C1-O5-C5	3.87	117.44	112.19
8	O	3	BMA	O2-C2-C3	-2.96	104.20	110.14
8	O	3	BMA	C3-C4-C5	-2.66	105.49	110.24
8	O	2	NAG	C1-O5-C5	2.50	115.57	112.19
8	O	4	MAN	C1-O5-C5	2.44	115.49	112.19

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

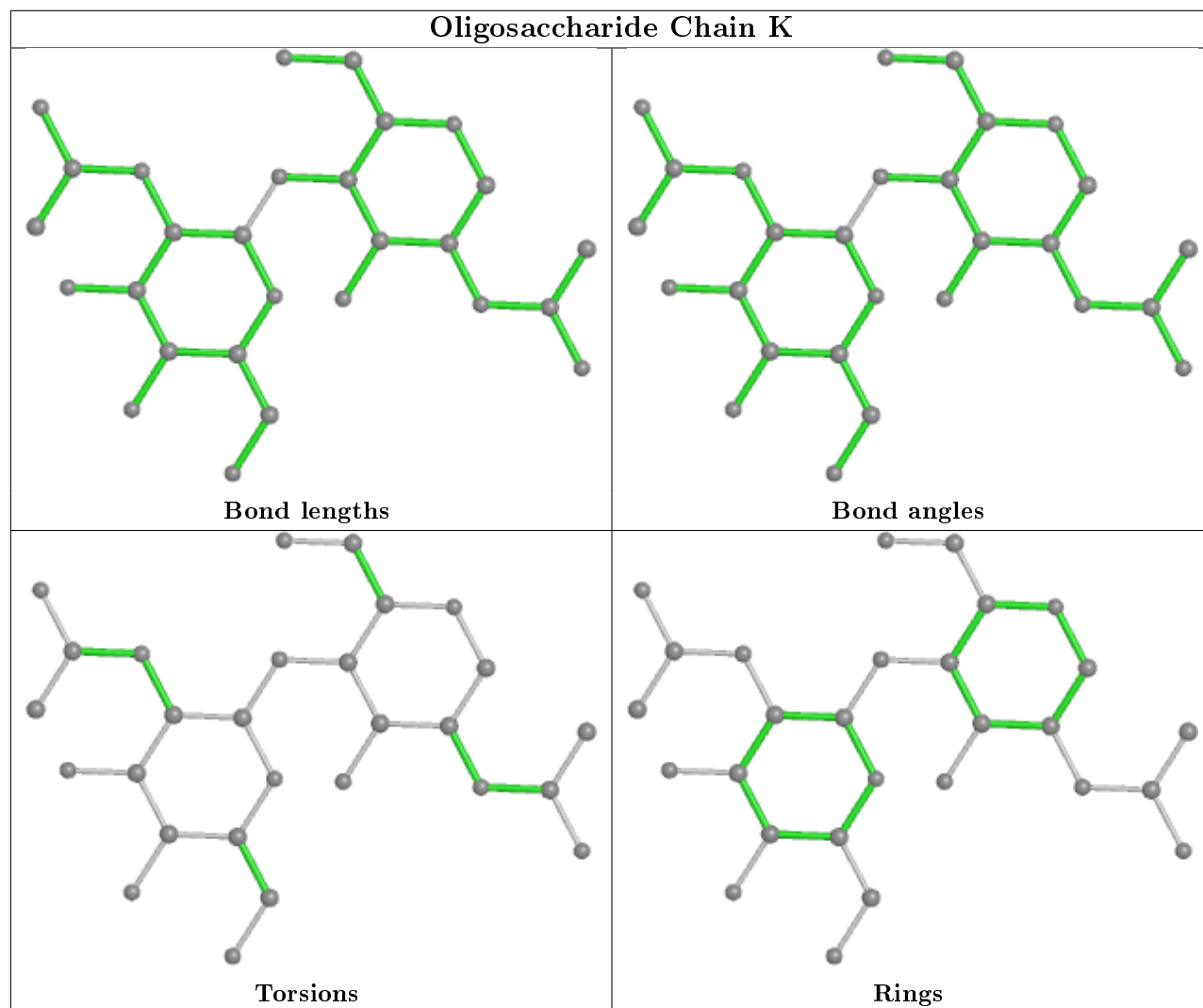
Mol	Chain	Res	Type	Atoms
8	O	4	MAN	O5-C5-C6-O6
8	O	4	MAN	C4-C5-C6-O6
8	O	2	NAG	O5-C5-C6-O6
8	O	2	NAG	C4-C5-C6-O6
7	M	2	NAG	O5-C5-C6-O6

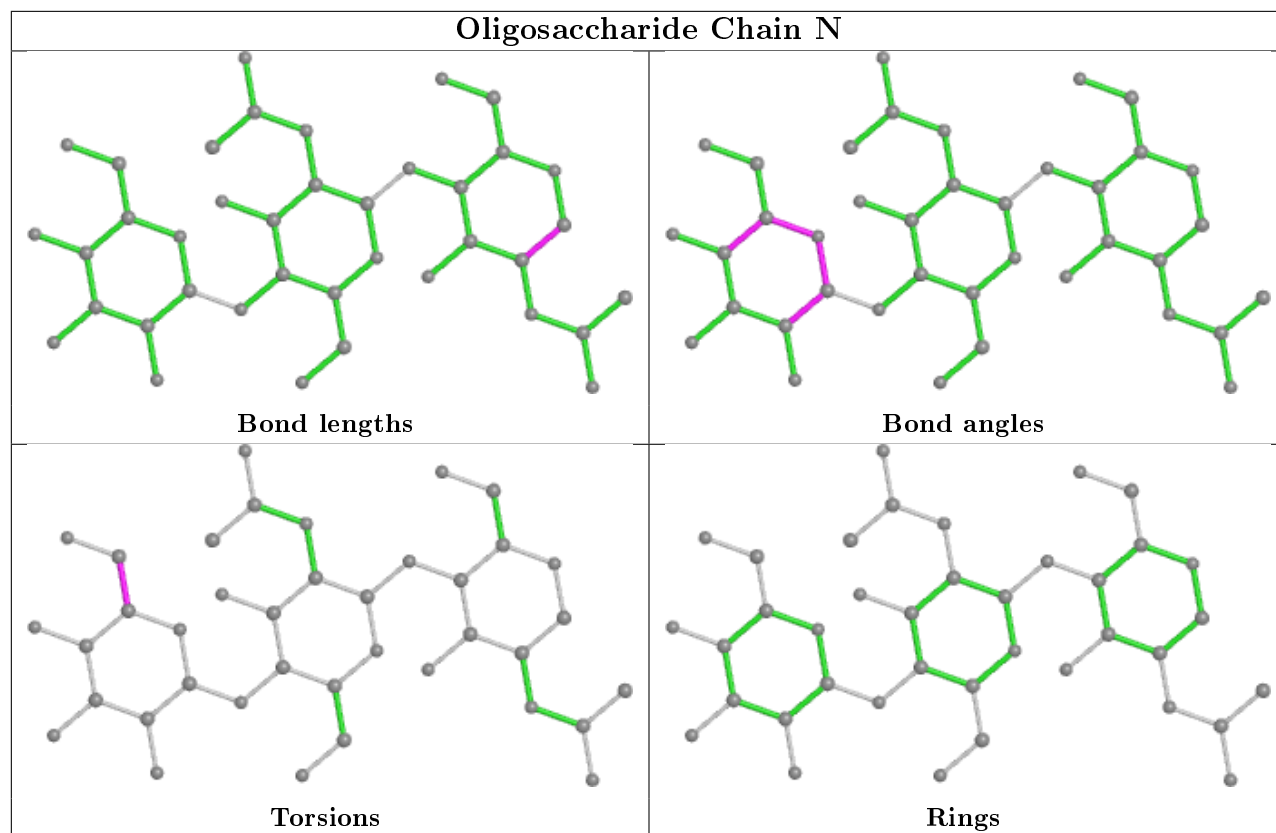
There are no ring outliers.

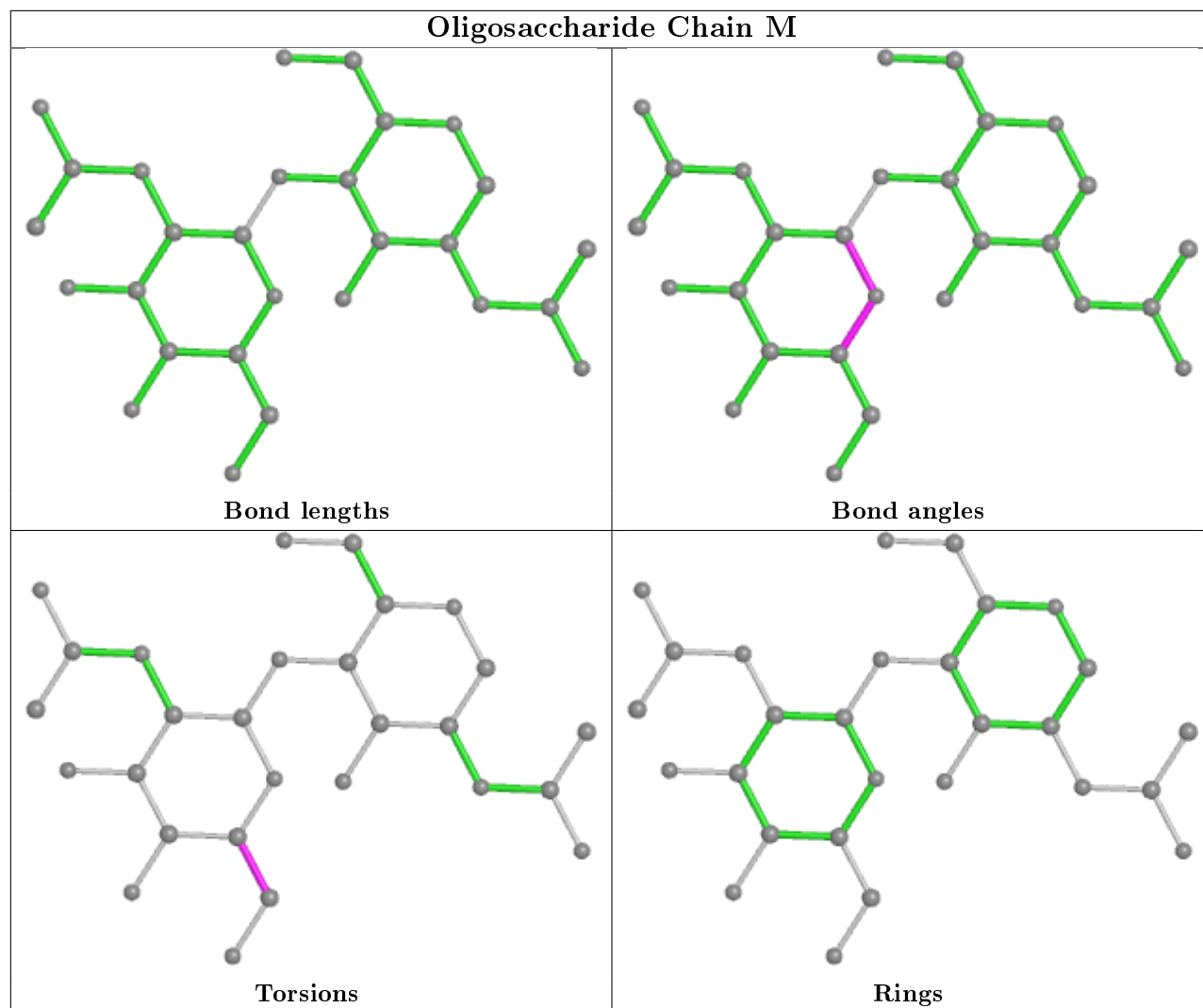
3 monomers are involved in 3 short contacts:

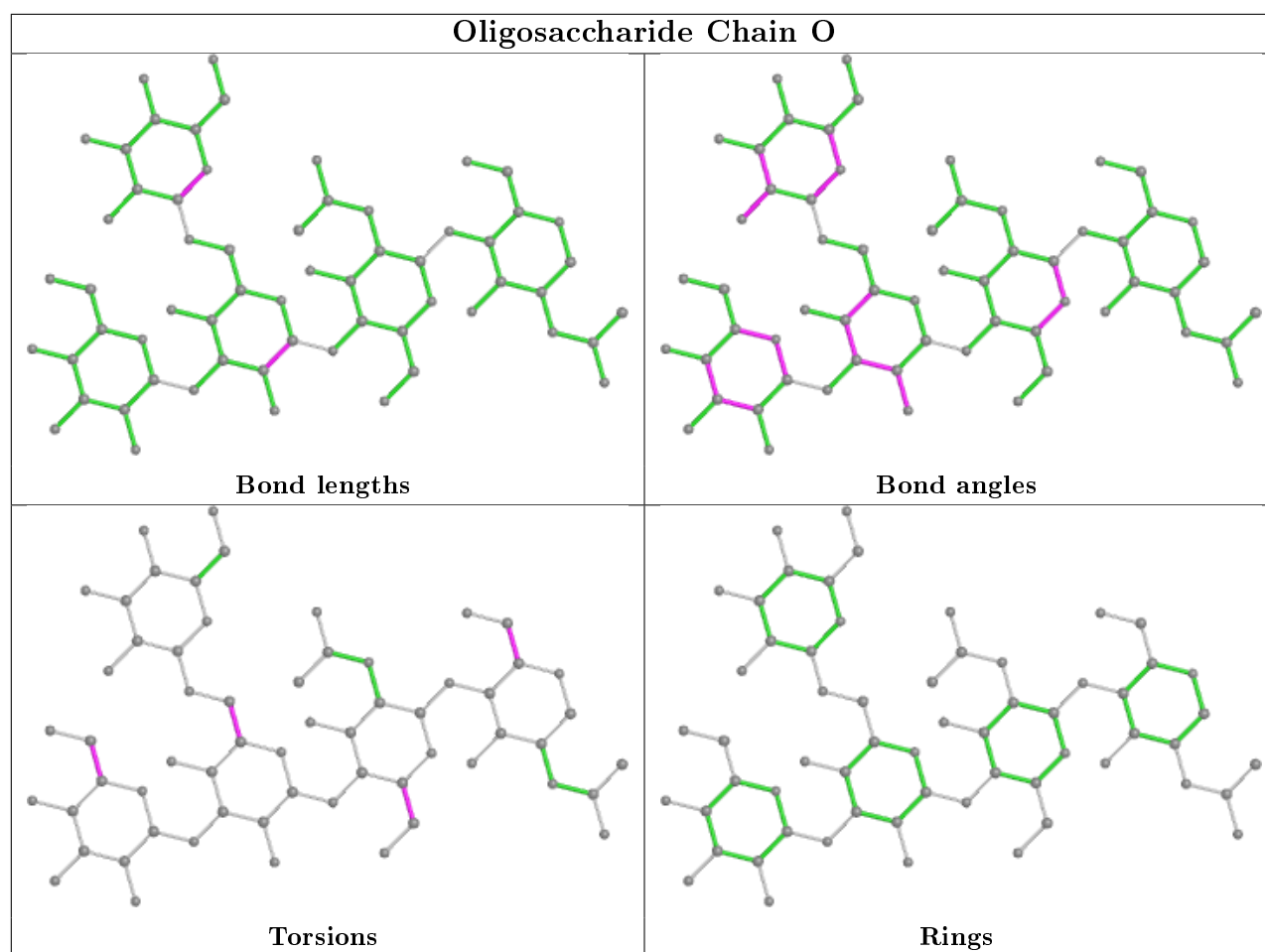
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	K	1	NAG	1	0
7	M	1	NAG	1	0
8	O	1	NAG	1	0

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](#)

6 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	$\# Z > 2$
9	NAG	D	1000	2	14,14,15	0.34	0	17,19,21	1.03	2 (11%)
9	NAG	E	706	5	14,14,15	0.29	0	17,19,21	0.63	0
9	NAG	E	707	5	14,14,15	0.23	0	17,19,21	0.50	0
9	NAG	F	910	5	14,14,15	0.22	0	17,19,21	0.63	1 (5%)
9	NAG	F	909	5	14,14,15	0.29	0	17,19,21	0.67	1 (5%)
10	BMA	L	301	-	11,11,12	0.65	0	15,15,17	0.82	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
9	NAG	D	1000	2	-	0/6/23/26	0/1/1/1
9	NAG	E	706	5	-	0/6/23/26	0/1/1/1
9	NAG	E	707	5	-	0/6/23/26	0/1/1/1
9	NAG	F	910	5	-	2/6/23/26	0/1/1/1
9	NAG	F	909	5	-	0/6/23/26	0/1/1/1
10	BMA	L	301	-	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	D	1000	NAG	O5-C5-C6	3.08	112.03	107.20
9	F	909	NAG	C1-O5-C5	2.15	115.11	112.19
9	F	910	NAG	C1-O5-C5	2.12	115.06	112.19
9	D	1000	NAG	C2-N2-C7	-2.04	120.00	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	F	910	NAG	O5-C5-C6-O6
9	F	910	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	F	910	NAG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	17:ASP	C	18:ARG	N	1.17

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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 ²)	Q<0.9
1	A	212/227 (93%)	-0.23	1 (0%) 91 89	39, 53, 72, 88	0
1	C	216/227 (95%)	-0.27	0 100 100	36, 49, 67, 78	0
2	B	221/221 (100%)	-0.24	1 (0%) 91 89	33, 48, 68, 88	0
2	D	219/221 (99%)	-0.09	2 (0%) 84 82	33, 51, 73, 83	0
3	G	220/230 (95%)	-0.35	0 100 100	33, 48, 67, 80	0
3	H	219/230 (95%)	-0.26	1 (0%) 91 89	33, 47, 69, 87	0
4	I	211/214 (98%)	-0.26	0 100 100	35, 52, 73, 82	0
4	L	212/214 (99%)	-0.34	0 100 100	33, 47, 64, 76	0
5	E	148/191 (77%)	-0.11	5 (3%) 45 38	34, 48, 89, 114	0
5	F	138/191 (72%)	0.06	6 (4%) 35 29	36, 50, 75, 92	0
All	All	2016/2166 (93%)	-0.22	16 (0%) 86 84	33, 50, 71, 114	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	443	TYR	5.2
3	H	127	SER	4.1
2	B	-2	ILE	3.9
5	E	450	SER	3.9
5	E	442	PHE	3.8

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

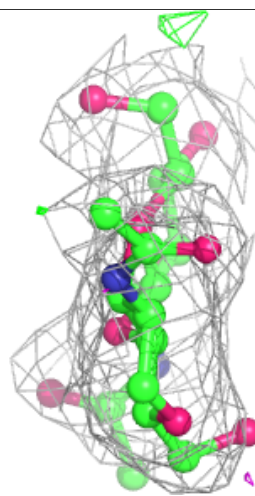
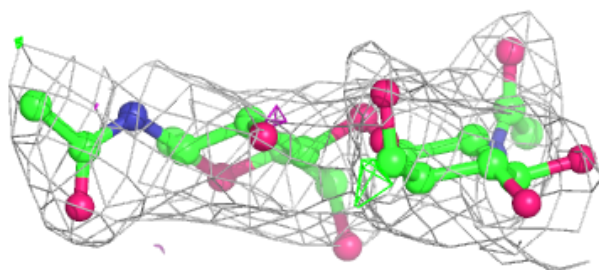
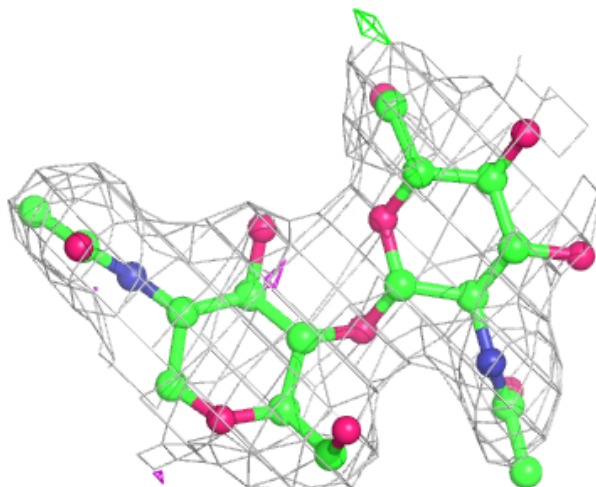
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	MAN	O	5	11/12	0.70	0.21	70,76,88,91	0
6	BMA	J	3	11/12	0.72	0.36	107,117,130,135	0
6	NAG	J	2	14/15	0.80	0.24	77,96,107,114	0
8	MAN	O	4	11/12	0.80	0.32	81,86,92,94	0
8	NAG	O	1	14/15	0.83	0.17	61,66,74,94	0
6	BMA	N	3	11/12	0.84	0.13	78,86,96,101	0
7	NAG	M	2	14/15	0.86	0.36	68,82,104,106	0
8	NAG	O	2	14/15	0.87	0.21	65,70,78,80	0
7	NAG	K	1	14/15	0.88	0.16	57,66,81,83	0
7	NAG	K	2	14/15	0.89	0.15	68,77,84,89	0
6	NAG	J	1	14/15	0.89	0.19	58,69,81,88	0
8	BMA	O	3	11/12	0.90	0.14	67,74,80,83	0
6	NAG	N	1	14/15	0.94	0.13	48,59,66,66	0
6	NAG	N	2	14/15	0.95	0.10	56,66,75,77	0
7	NAG	M	1	14/15	0.96	0.13	47,53,69,71	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.

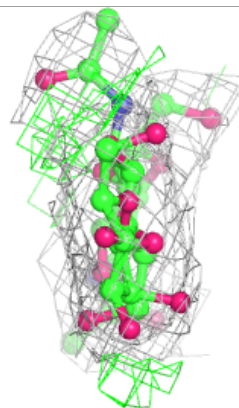
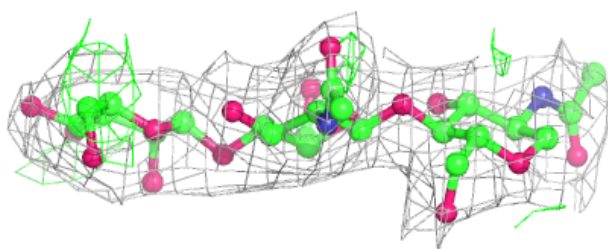
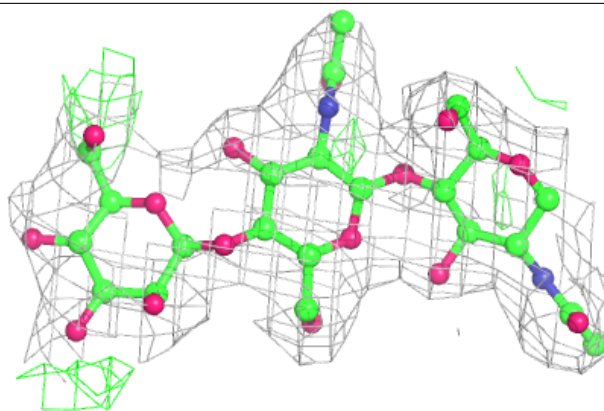
Electron density around Chain K:

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



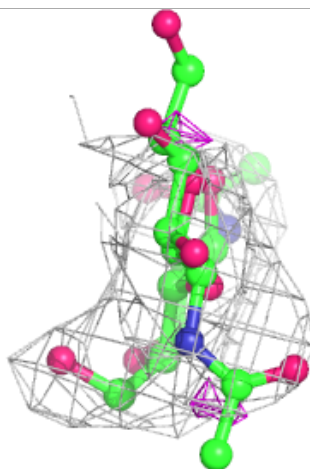
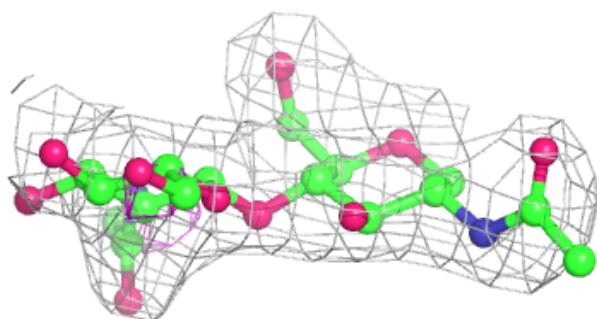
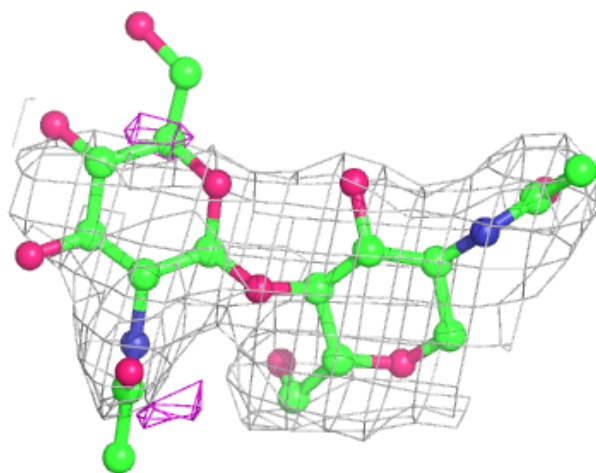
Electron density around Chain N:

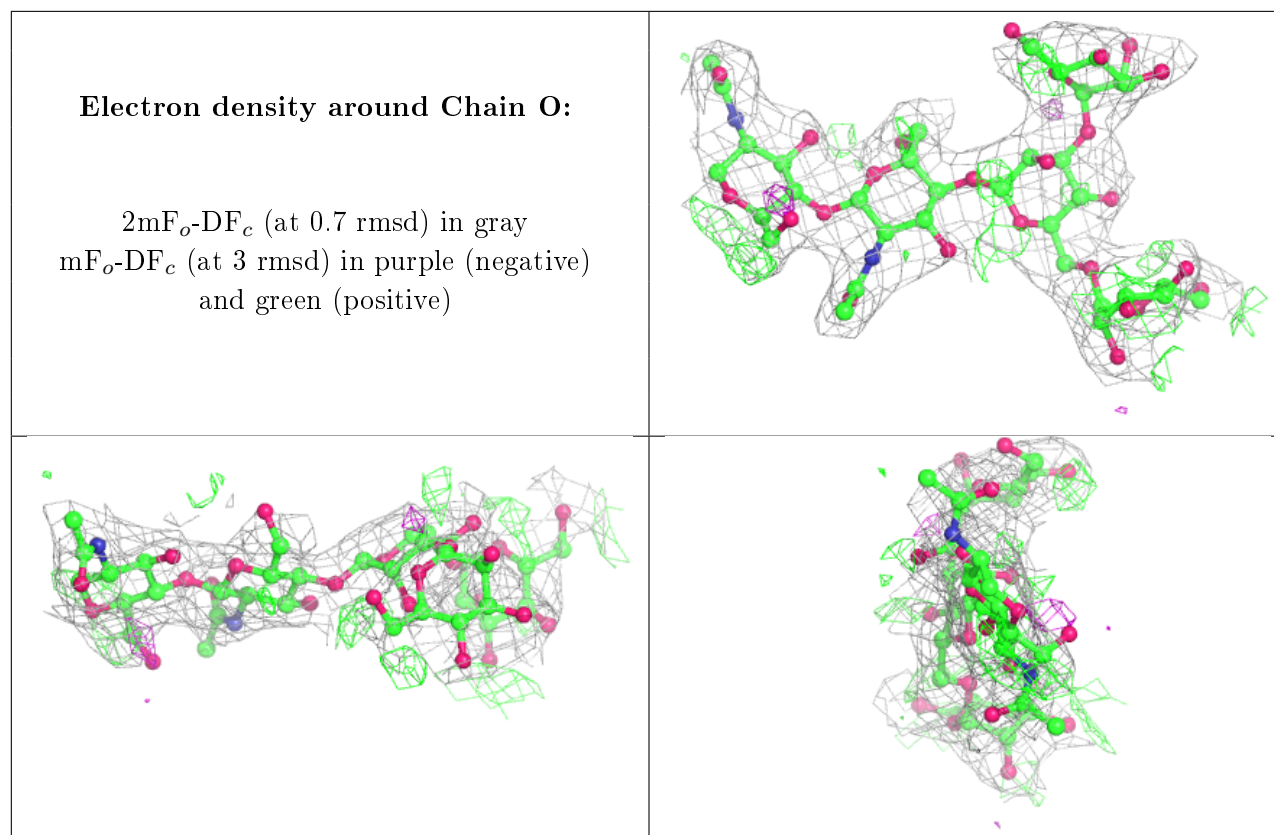
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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, 95th 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 ²)	Q<0.9
9	NAG	D	1000	14/15	0.65	0.27	70,80,96,110	0
10	BMA	L	301	11/12	0.83	0.19	75,82,96,100	0
9	NAG	E	706	14/15	0.85	0.23	83,94,101,103	0
9	NAG	F	909	14/15	0.91	0.12	39,61,73,74	0
9	NAG	F	910	14/15	0.92	0.18	55,66,72,85	0
9	NAG	E	707	14/15	0.93	0.14	33,53,65,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.