wwPDB X-ray Structure Validation Summary Report (i)

Nov 7, 2023 – 11:14 AM EST

PDB ID	:	6W9G
Title	:	Crystal Structure of the Fab fragment of humanized 5c8 antibody containing the fluorescent non-canonical amino acid L-(7-hydroxycoumarin-4-yl)ethylglycine in complex with CD40L at pH 6.8
Authors	:	Henderson, J.N.; Simmons, C.R.; Mills, J.H.
Deposited on	:	2020-03-23
Resolution	:	1.82 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

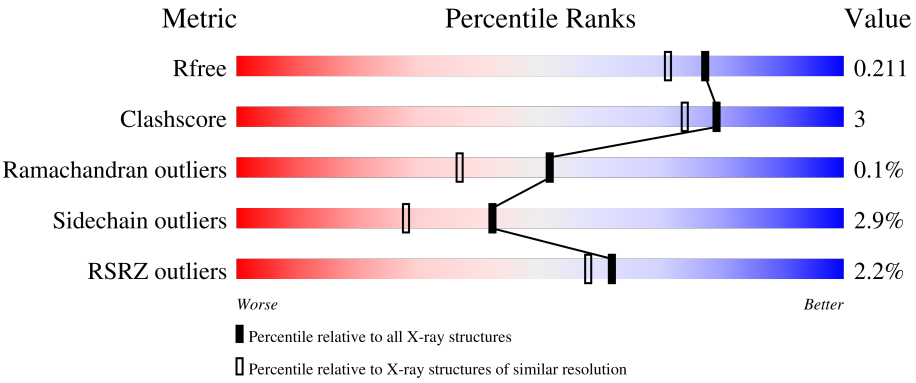
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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 >=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 <=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	146	82% 10% • 6%
1	B	146	84% 9% •• 6%
1	C	146	% 82% 13% 5%
2	H	226	4% 89% • 6%
2	K	226	% 89% • • 6%

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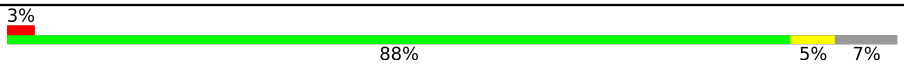
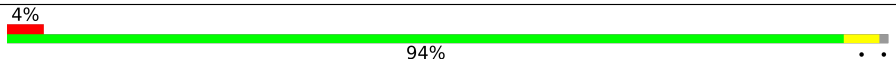
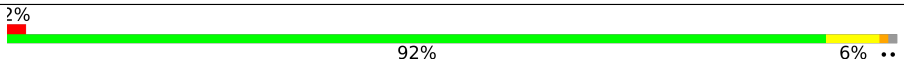
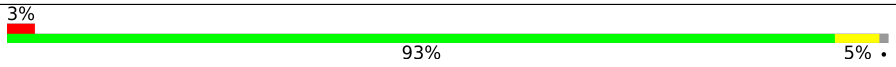
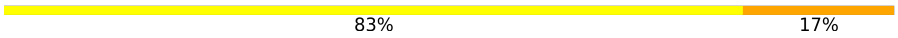
Mol	Chain	Length	Quality of chain
2	X	226	
3	L	218	
3	M	218	
3	Y	218	
4	D	6	
4	E	6	
4	F	6	

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 14802 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 CD40 ligand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	137	Total	C	N	O	S	0	10	0
			1096	701	185	205	5			
1	B	137	Total	C	N	O	S	0	9	0
			1095	698	189	204	4			
1	C	139	Total	C	N	O	S	0	14	0
			1130	725	188	212	5			

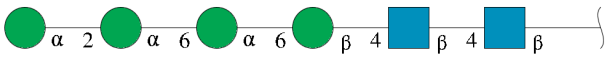
- Molecule 2 is a protein called 5c8* Fab (heavy chain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	212	Total	C	N	O	S	0	2	0
			1559	985	250	317	7			
2	K	213	Total	C	N	O	S	0	7	0
			1620	1023	262	328	7			
2	X	211	Total	C	N	O	S	0	1	0
			1562	985	253	317	7			

- Molecule 3 is a protein called 5c8* Fab (light chain).

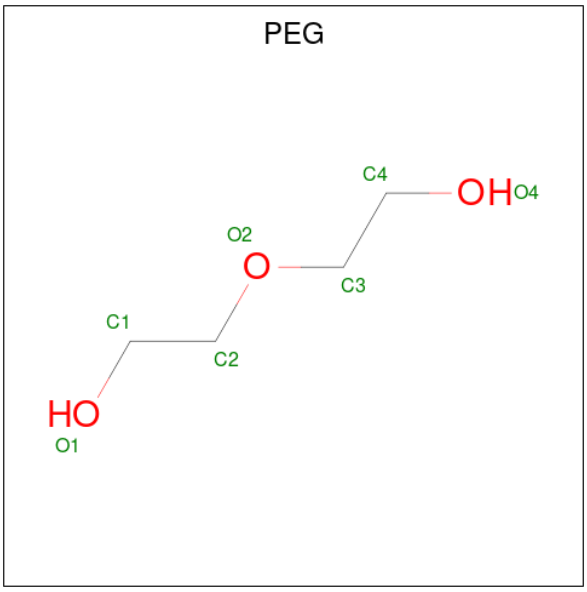
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	215	Total	C	N	O	S	0	5	0
			1669	1053	276	335	5			
3	M	216	Total	C	N	O	S	0	2	0
			1660	1044	273	338	5			
3	Y	216	Total	C	N	O	S	0	4	0
			1685	1062	277	341	5			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-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
4	D	6	Total C N O 86 48 3 35	0	6	0
4	E	6	Total C N O 86 48 3 35	0	6	0
4	F	6	Total C N O 86 48 3 35	0	6	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	L	1	Total C O 7 4 3	0	0
5	Y	1	Total C O 7 4 3	0	0

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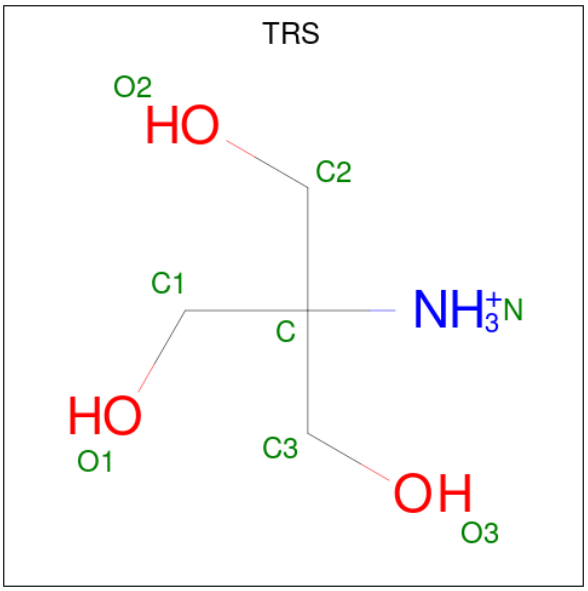
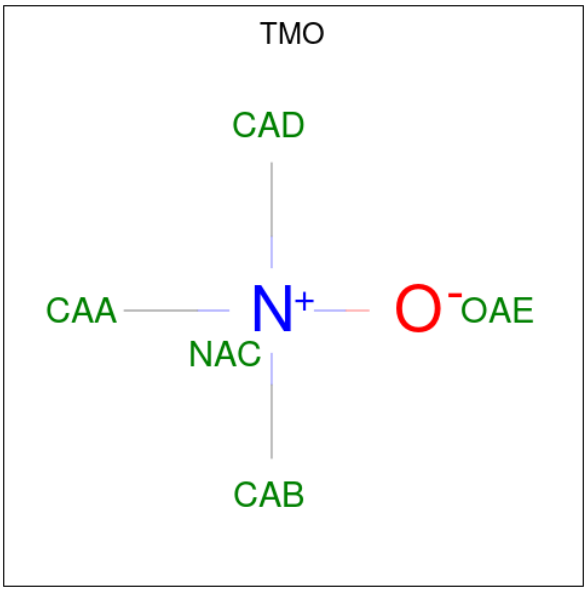
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Y	1	Total C O 7 4 3	0	0
5	Y	1	Total C O 7 4 3	0	0

- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O 8 4 1 3	0	0
6	A	1	Total C N O 8 4 1 3	0	0

- Molecule 7 is trimethylamine oxide (three-letter code: TMO) (formula: C_3H_9NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			5	3	1	1		
7	B	1	Total	C	N	O	0	0
			5	3	1	1		
7	C	1	Total	C	N	O	0	0
			5	3	1	1		
7	H	1	Total	C	N	O	0	0
			5	3	1	1		
7	H	1	Total	C	N	O	0	0
			5	3	1	1		
7	L	1	Total	C	N	O	0	0
			5	3	1	1		
7	L	1	Total	C	N	O	0	0
			5	3	1	1		
7	L	1	Total	C	N	O	0	0
			5	3	1	1		
7	L	1	Total	C	N	O	0	0
			5	3	1	1		
7	K	1	Total	C	N	O	0	0
			5	3	1	1		
7	K	1	Total	C	N	O	0	0
			5	3	1	1		
7	K	1	Total	C	N	O	0	0
			5	3	1	1		
7	K	1	Total	C	N	O	0	0
			5	3	1	1		
7	M	1	Total	C	N	O	0	0
			5	3	1	1		

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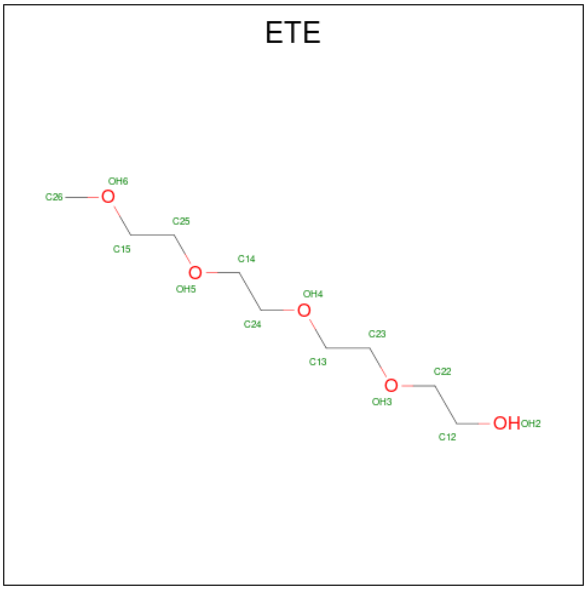
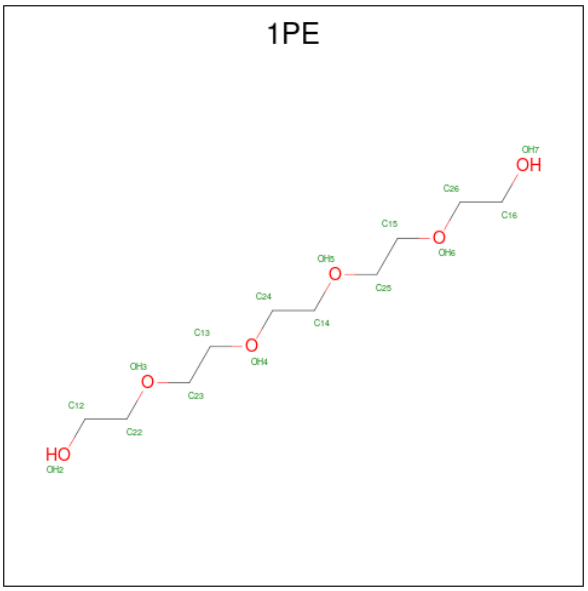
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	M	1	Total C N O 5 3 1 1	0	0
7	M	1	Total C N O 5 3 1 1	0	0
7	M	1	Total C N O 5 3 1 1	0	0
7	X	1	Total C N O 5 3 1 1	0	0
7	X	1	Total C N O 5 3 1 1	0	0
7	Y	1	Total C N O 5 3 1 1	0	0
7	Y	1	Total C N O 5 3 1 1	0	0

- Molecule 8 is 2-{2-[2-2-(METHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHANOL (three-letter code: ETE) (formula: $C_9H_{20}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 13 8 5	0	0
8	B	1	Total C O 14 9 5	0	0
8	M	1	Total C O 10 6 4	0	0

- Molecule 9 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	C	1	Total C O 16 10 6	0	0

- Molecule 10 is water.

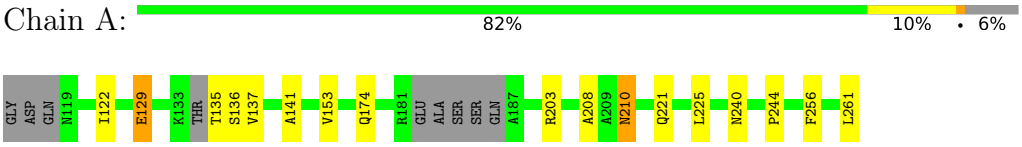
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	115	Total O 115 115	0	18
10	B	117	Total O 117 117	0	16
10	C	96	Total O 96 96	0	14
10	H	87	Total O 87 87	0	2
10	L	191	Total O 191 191	0	4
10	K	133	Total O 133 133	0	2
10	M	202	Total O 202 202	0	0
10	X	102	Total O 102 102	0	4
10	Y	195	Total O 195 195	0	2

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.

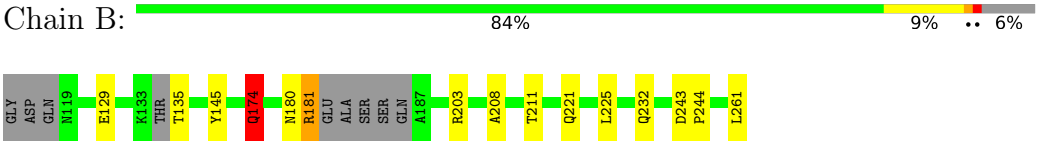
• Molecule 1: CD40 ligand

Chain A:



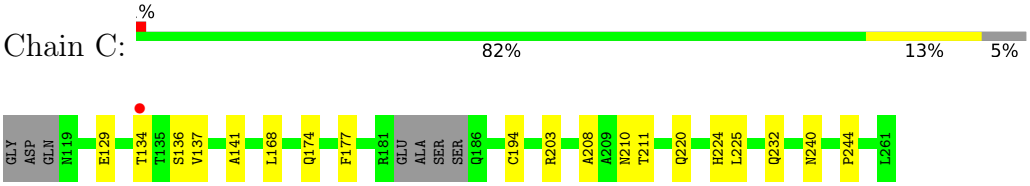
• Molecule 1: CD40 ligand

Chain B:



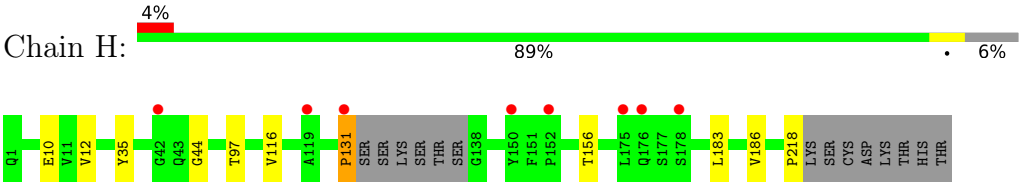
• Molecule 1: CD40 ligand

Chain C:



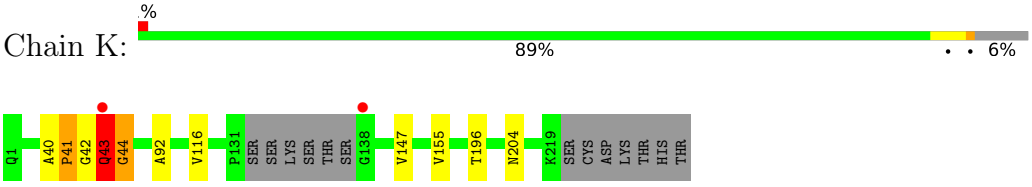
• Molecule 2: 5c8* Fab (heavy chain)

Chain H:



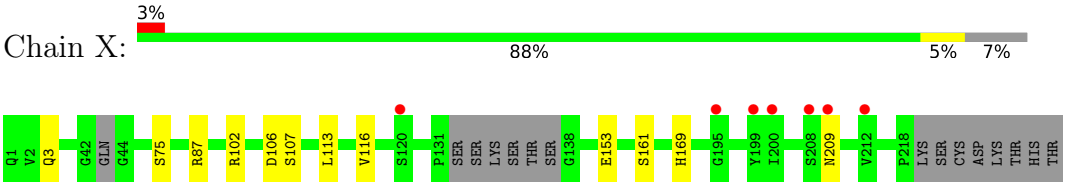
• Molecule 2: 5c8* Fab (heavy chain)

Chain K:



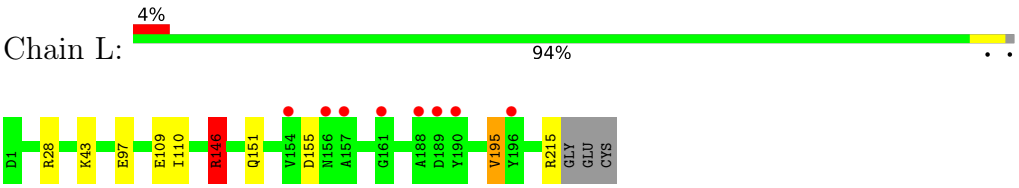
• Molecule 2: 5c8* Fab (heavy chain)

Chain X:



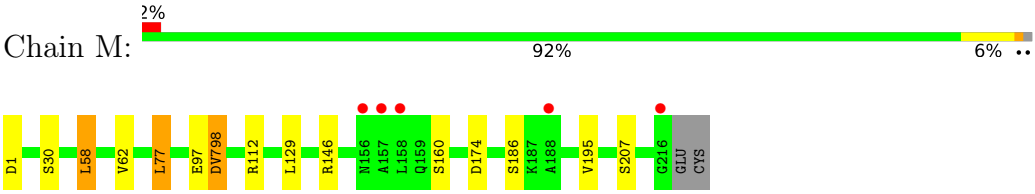
• Molecule 3: 5c8* Fab (light chain)

Chain L:



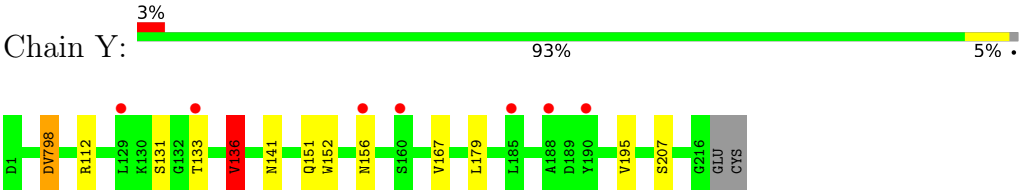
• Molecule 3: 5c8* Fab (light chain)

Chain M:



• Molecule 3: 5c8* Fab (light chain)

Chain Y:

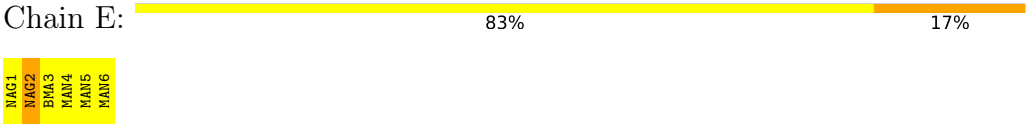


• Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:

• Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-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 E:



• Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-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 F:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	226.68Å 131.20Å 97.56Å 90.00° 108.82° 90.00°	Depositor
Resolution (Å)	48.47 – 1.82 48.47 – 1.82	Depositor EDS
% Data completeness (in resolution range)	97.1 (48.47-1.82) 97.1 (48.47-1.82)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.67 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.179 , 0.207 0.187 , 0.211	Depositor DCC
R_{free} test set	11697 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	23.0	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 50.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	14802	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MAN, BMA, NAG, PEG, 1PE, TRS, TMO, DV7, ETE

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	0.86	0/1144	0.97	5/1548 (0.3%)
1	B	0.89	0/1143	1.02	5/1546 (0.3%)
1	C	0.84	0/1194	0.93	0/1620
2	H	0.73	0/1601	0.85	1/2187 (0.0%)
2	K	0.74	0/1663	0.85	0/2268
2	X	0.75	0/1600	0.83	2/2181 (0.1%)
3	L	0.75	1/1703 (0.1%)	0.89	2/2318 (0.1%)
3	M	0.84	2/1684 (0.1%)	0.92	4/2293 (0.2%)
3	Y	0.80	0/1700	0.90	3/2313 (0.1%)
All	All	0.79	3/13432 (0.0%)	0.90	22/18274 (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	K	0	1
3	M	0	2
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	97	GLU	CD-OE1	5.66	1.31	1.25
3	L	97	GLU	CD-OE2	5.49	1.31	1.25
3	M	30	SER	CB-OG	-5.22	1.35	1.42

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	Y	112	ARG	NE-CZ-NH2	8.27	124.43	120.30
3	Y	112	ARG	NE-CZ-NH1	-7.18	116.71	120.30
3	L	146[A]	ARG	NE-CZ-NH1	6.88	123.74	120.30
3	L	146[B]	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	B	243	ASP	CB-CG-OD1	6.35	124.02	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	K	44[B]	GLY	Peptide
3	M	160	SER	Peptide
3	M	98[A]	DV7	Peptide

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	1096	0	1093	10	0
1	B	1095	0	1098	11	0
1	C	1130	0	1145	15	0
2	H	1559	0	1480	4	0
2	K	1620	0	1560	18	0
2	X	1562	0	1494	3	0
3	L	1669	0	1580	7	0
3	M	1660	0	1552	4	0
3	Y	1685	0	1572	6	0
4	D	86	0	74	4	0
4	E	86	0	74	1	0
4	F	86	0	74	3	0
5	A	7	0	10	0	0
5	B	7	0	10	0	0
5	C	14	0	20	0	0
5	L	7	0	10	0	0
5	Y	21	0	30	0	0
6	A	16	0	24	0	0
7	A	5	0	9	0	0
7	B	5	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	5	0	9	0	0
7	H	10	0	18	0	0
7	K	20	0	36	0	0
7	L	20	0	36	0	0
7	M	20	0	36	0	0
7	X	10	0	18	0	0
7	Y	10	0	18	1	0
8	A	13	0	17	0	0
8	B	14	0	20	0	0
8	M	10	0	13	0	0
9	C	16	0	22	0	0
10	A	115	0	0	0	0
10	B	117	0	0	2	0
10	C	96	0	0	0	0
10	H	87	0	0	0	0
10	K	133	0	0	0	0
10	L	191	0	0	3	0
10	M	202	0	0	3	0
10	X	102	0	0	1	0
10	Y	195	0	0	1	0
All	All	14802	0	13161	76	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 3.

The worst 5 of 76 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:K:43[B]:GLN:HG3	2:K:44[B]:GLY:N	1.62	1.14
2:K:43[B]:GLN:HG3	2:K:44[B]:GLY:H	0.92	1.06
2:K:43[B]:GLN:CG	2:K:44[B]:GLY:N	2.12	1.06
2:K:43[B]:GLN:CG	2:K:44[B]:GLY:H	1.65	1.01
1:B:221[A]:GLN:OE1	1:C:210:ASN:OD1	1.83	0.96

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	141/146 (97%)	139 (99%)	2 (1%)	0	100	100
1	B	140/146 (96%)	139 (99%)	1 (1%)	0	100	100
1	C	149/146 (102%)	146 (98%)	3 (2%)	0	100	100
2	H	210/226 (93%)	207 (99%)	3 (1%)	0	100	100
2	K	216/226 (96%)	207 (96%)	5 (2%)	4 (2%)	8	1
2	X	206/226 (91%)	200 (97%)	6 (3%)	0	100	100
3	L	216/218 (99%)	211 (98%)	5 (2%)	0	100	100
3	M	214/218 (98%)	208 (97%)	6 (3%)	0	100	100
3	Y	216/218 (99%)	210 (97%)	6 (3%)	0	100	100
All	All	1708/1770 (96%)	1667 (98%)	37 (2%)	4 (0%)	51	33

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	K	43[A]	GLN
2	K	43[B]	GLN
2	K	41[A]	PRO
2	K	41[B]	PRO

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	121/122 (99%)	116 (96%)	5 (4%)	30	15
1	B	122/122 (100%)	117 (96%)	5 (4%)	30	15
1	C	128/122 (105%)	125 (98%)	3 (2%)	50	37
2	H	171/194 (88%)	166 (97%)	5 (3%)	42	28
2	K	179/194 (92%)	174 (97%)	5 (3%)	43	29
2	X	174/194 (90%)	166 (95%)	8 (5%)	27	12
3	L	184/191 (96%)	179 (97%)	5 (3%)	44	30
3	M	182/191 (95%)	176 (97%)	6 (3%)	38	23
3	Y	185/191 (97%)	178 (96%)	7 (4%)	33	18
All	All	1446/1521 (95%)	1397 (97%)	49 (3%)	42	22

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	M	58	LEU
2	X	75	SER
3	M	77[A]	LEU
3	M	195	VAL
2	X	107	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	X	209	ASN
3	Y	141	ASN
3	Y	156	ASN
1	A	221	GLN
1	A	210	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

4 non-standard protein/DNA/RNA residues 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	DV7	Y	98[B]	-	18,19,20	0.98	1 (5%)	21,26,28	1.75	3 (14%)
3	DV7	M	98[A]	3	18,19,20	0.81	1 (5%)	21,26,28	1.17	2 (9%)
3	DV7	Y	98[A]	-	18,19,20	0.95	0	21,26,28	1.35	1 (4%)

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	DV7	Y	98[B]	-	-	0/6/7/9	0/2/2/2
3	DV7	M	98[A]	3	-	1/6/7/9	0/2/2/2
3	DV7	Y	98[A]	-	-	1/6/7/9	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Y	98[B]	DV7	OH1-CZ1	-2.58	1.33	1.38
3	M	98[A]	DV7	CE2-CD	-2.00	1.42	1.46

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	Y	98[B]	DV7	CG-CD-CE2	4.57	123.93	118.62
3	Y	98[A]	DV7	OH1-CZ1-OH2	-3.97	111.39	116.44
3	Y	98[B]	DV7	OH1-CZ1-OH2	-3.93	111.44	116.44
3	M	98[A]	DV7	CB-CG-CD	-3.09	104.28	112.91
3	M	98[A]	DV7	OH1-CZ1-OH2	-2.41	113.37	116.44

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	M	98[A]	DV7	CE2-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
3	Y	98[A]	DV7	CE2-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Y	98[B]	DV7	2	0

5.5 Carbohydrates (i)

21 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	D	1[A]	1	14,14,15	0.47	0	17,19,21	2.19	7 (41%)
4	NAG	D	1[B]	1,4	14,14,15	0.85	0	17,19,21	2.17	3 (17%)
4	NAG	D	2[B]	4	14,14,15	0.49	0	17,19,21	1.46	4 (23%)
4	BMA	D	3[B]	4	11,11,12	0.41	0	15,15,17	1.33	2 (13%)
4	MAN	D	4[B]	4	11,11,12	0.38	0	15,15,17	1.36	3 (20%)
4	MAN	D	5[B]	4	11,11,12	0.41	0	15,15,17	1.45	2 (13%)
4	MAN	D	6[B]	4	11,11,12	0.32	0	15,15,17	1.22	2 (13%)
4	NAG	E	1[A]	1	14,14,15	0.46	0	17,19,21	2.28	5 (29%)
4	NAG	E	1[B]	1,4	14,14,15	0.68	0	17,19,21	2.18	4 (23%)
4	NAG	E	2[B]	4	14,14,15	0.46	0	17,19,21	1.22	2 (11%)
4	BMA	E	3[B]	4	11,11,12	0.41	0	15,15,17	0.78	0
4	MAN	E	4[B]	4	11,11,12	0.41	0	15,15,17	1.28	1 (6%)
4	MAN	E	5[B]	4	11,11,12	0.30	0	15,15,17	1.71	3 (20%)
4	MAN	E	6[B]	4	11,11,12	0.51	0	15,15,17	1.82	2 (13%)
4	NAG	F	1[A]	1	14,14,15	0.60	0	17,19,21	1.91	7 (41%)
4	NAG	F	1[B]	1,4	14,14,15	0.62	0	17,19,21	1.92	4 (23%)
4	NAG	F	2[B]	4	14,14,15	0.44	0	17,19,21	1.49	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	BMA	F	3[B]	4	11,11,12	0.34	0	15,15,17	1.56	4 (26%)
4	MAN	F	4[B]	4	11,11,12	0.34	0	15,15,17	1.18	1 (6%)
4	MAN	F	5[B]	4	11,11,12	0.33	0	15,15,17	1.46	3 (20%)
4	MAN	F	6[B]	4	11,11,12	0.63	0	15,15,17	1.81	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
4	NAG	D	1[A]	1	-	1/6/23/26	0/1/1/1
4	NAG	D	1[B]	1,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2[B]	4	-	2/6/23/26	0/1/1/1
4	BMA	D	3[B]	4	-	0/2/19/22	0/1/1/1
4	MAN	D	4[B]	4	-	1/2/19/22	0/1/1/1
4	MAN	D	5[B]	4	-	0/2/19/22	0/1/1/1
4	MAN	D	6[B]	4	-	2/2/19/22	0/1/1/1
4	NAG	E	1[A]	1	-	1/6/23/26	0/1/1/1
4	NAG	E	1[B]	1,4	-	1/6/23/26	0/1/1/1
4	NAG	E	2[B]	4	-	1/6/23/26	0/1/1/1
4	BMA	E	3[B]	4	-	0/2/19/22	0/1/1/1
4	MAN	E	4[B]	4	-	0/2/19/22	0/1/1/1
4	MAN	E	5[B]	4	-	0/2/19/22	0/1/1/1
4	MAN	E	6[B]	4	-	0/2/19/22	0/1/1/1
4	NAG	F	1[A]	1	-	0/6/23/26	0/1/1/1
4	NAG	F	1[B]	1,4	-	1/6/23/26	0/1/1/1
4	NAG	F	2[B]	4	-	2/6/23/26	0/1/1/1
4	BMA	F	3[B]	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4[B]	4	-	0/2/19/22	0/1/1/1
4	MAN	F	5[B]	4	-	2/2/19/22	0/1/1/1
4	MAN	F	6[B]	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1[B]	NAG	C1-O5-C5	7.71	122.64	112.19
4	D	1[B]	NAG	C1-O5-C5	5.91	120.20	112.19
4	F	1[B]	NAG	C1-O5-C5	5.77	120.01	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	F	6[B]	MAN	O5-C5-C6	4.97	114.99	107.20
4	E	6[B]	MAN	O5-C5-C6	4.90	114.88	107.20

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	5[B]	MAN	O5-C5-C6-O6
4	F	5[B]	MAN	C4-C5-C6-O6
4	D	1[B]	NAG	C8-C7-N2-C2
4	D	1[B]	NAG	O7-C7-N2-C2
4	D	6[B]	MAN	C4-C5-C6-O6

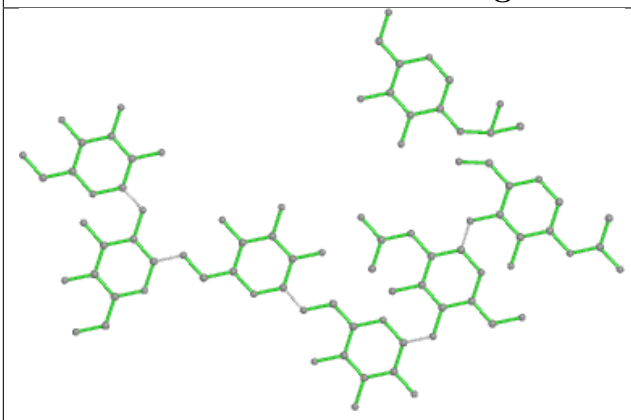
There are no ring outliers.

9 monomers are involved in 8 short contacts:

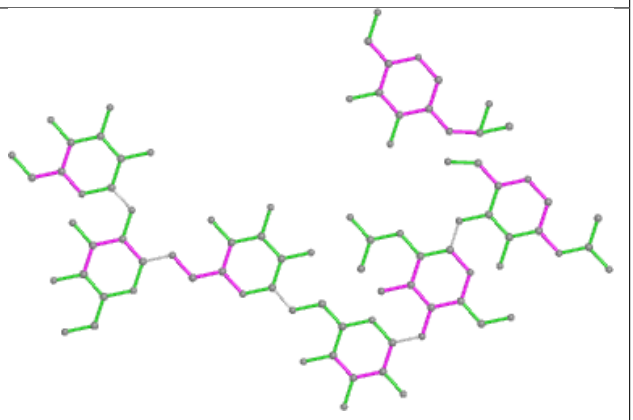
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	3[B]	BMA	2	0
4	F	1[A]	NAG	1	0
4	F	4[B]	MAN	1	0
4	D	1[B]	NAG	1	0
4	E	2[B]	NAG	1	0
4	E	3[B]	BMA	1	0
4	D	2[B]	NAG	3	0
4	D	3[B]	BMA	1	0
4	F	2[B]	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

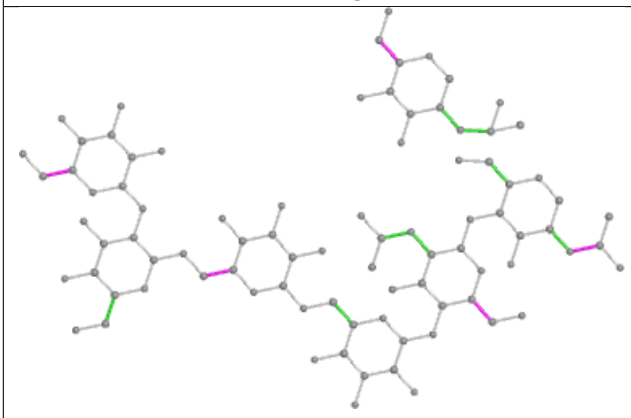
Oligosaccharide Chain D



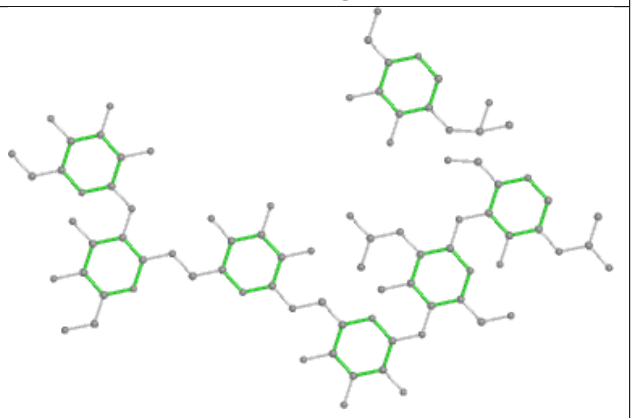
Bond lengths



Bond angles

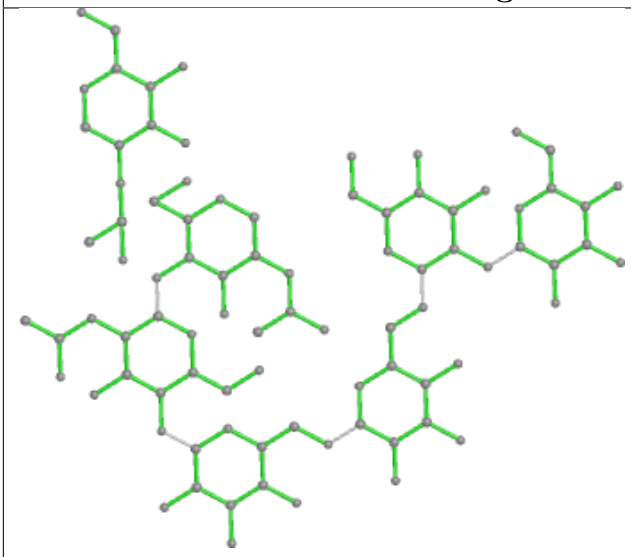


Torsions

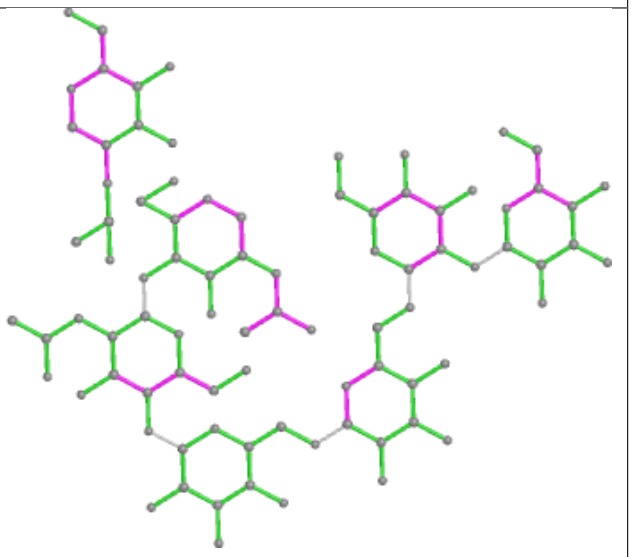


Rings

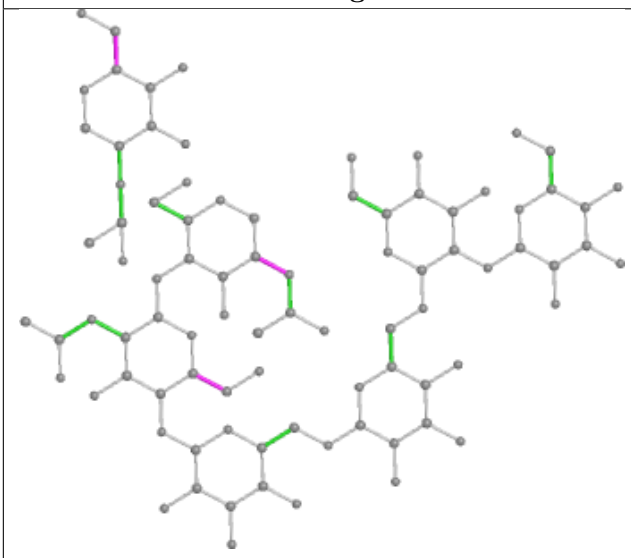
Oligosaccharide Chain E



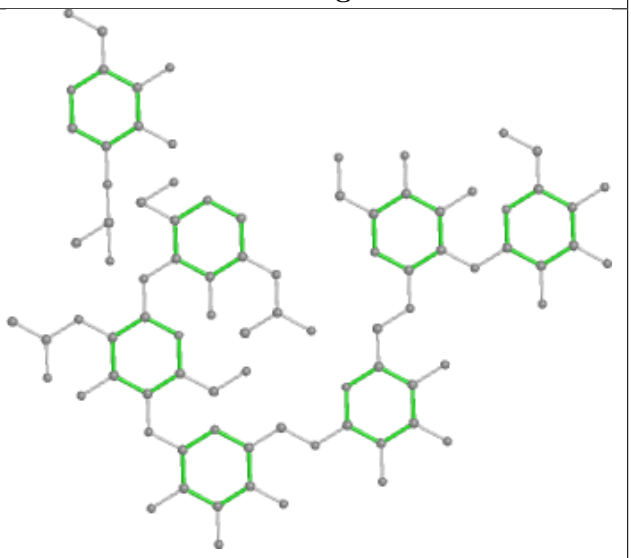
Bond lengths



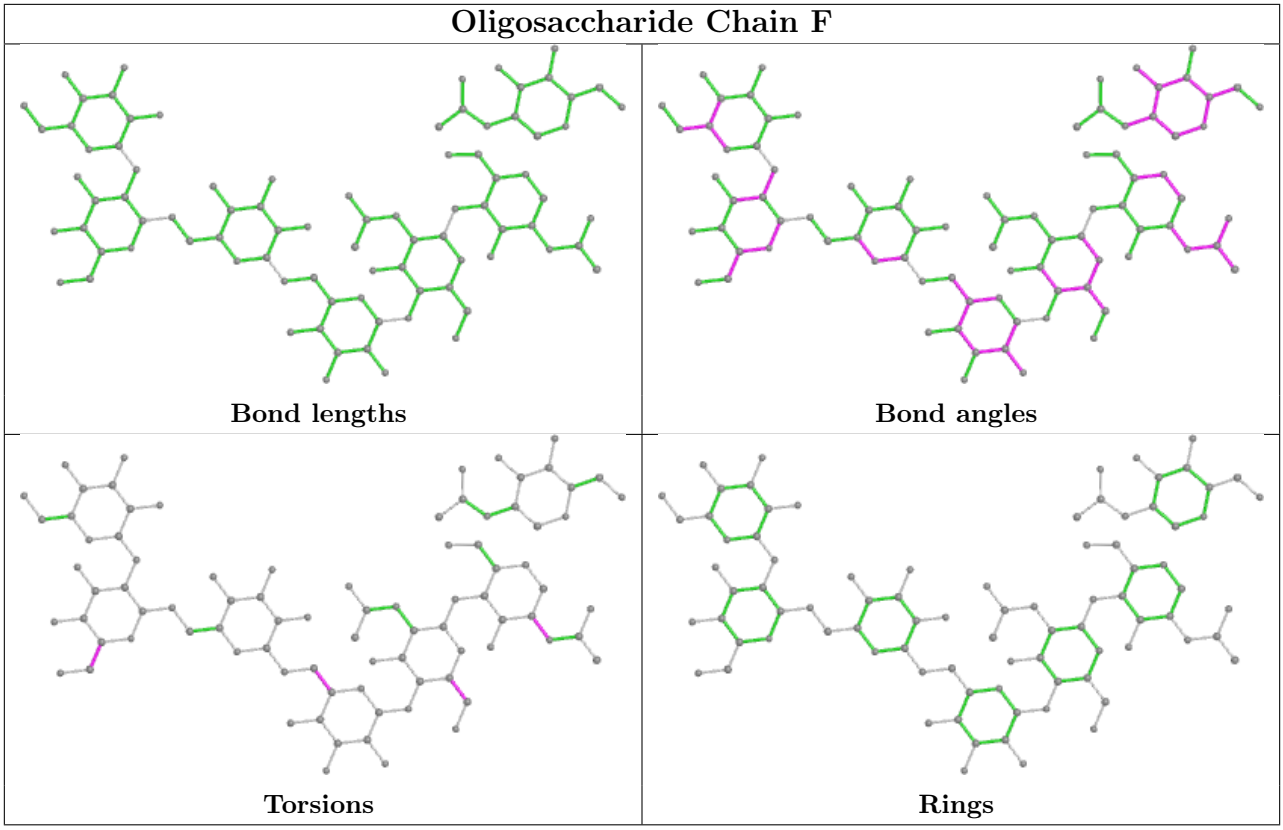
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

35 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	$\#\|Z\| > 2$
7	TMO	Y	305	-	4,4,4	6.26	1 (25%)	6,6,6	0.23	0
7	TMO	C	309	-	4,4,4	5.94	1 (25%)	6,6,6	0.30	0
7	TMO	K	304	-	4,4,4	6.24	1 (25%)	6,6,6	0.16	0
7	TMO	L	305	-	4,4,4	6.13	1 (25%)	6,6,6	0.25	0
7	TMO	L	302	-	4,4,4	6.28	1 (25%)	6,6,6	0.17	0
5	PEG	Y	303	-	6,6,6	0.48	0	5,5,5	0.58	0
5	PEG	L	301	-	6,6,6	0.48	0	5,5,5	0.36	0
7	TMO	K	301	-	4,4,4	6.53	1 (25%)	6,6,6	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	TMO	M	304	-	4,4,4	6.32	1 (25%)	6,6,6	0.19	0
7	TMO	Y	304	-	4,4,4	6.34	1 (25%)	6,6,6	0.22	0
7	TMO	B	308	-	4,4,4	6.23	1 (25%)	6,6,6	0.32	0
6	TRS	A	308	-	7,7,7	0.40	0	9,9,9	0.50	0
5	PEG	B	307	-	6,6,6	0.56	0	5,5,5	0.39	0
6	TRS	A	309	-	7,7,7	0.47	0	9,9,9	0.38	0
7	TMO	L	304	-	4,4,4	6.33	1 (25%)	6,6,6	0.17	0
7	TMO	M	301	-	4,4,4	6.36	1 (25%)	6,6,6	0.20	0
8	ETE	M	305	-	9,9,13	0.54	0	8,8,12	0.35	0
7	TMO	M	302	-	4,4,4	6.31	1 (25%)	6,6,6	0.23	0
7	TMO	H	301	-	4,4,4	5.92	1 (25%)	6,6,6	0.26	0
5	PEG	C	307	-	6,6,6	0.48	0	5,5,5	0.17	0
7	TMO	M	303	-	4,4,4	6.14	1 (25%)	6,6,6	0.21	0
5	PEG	C	308	-	6,6,6	0.51	0	5,5,5	0.39	0
5	PEG	Y	302	-	6,6,6	0.61	0	5,5,5	0.35	0
7	TMO	K	303	-	4,4,4	6.40	1 (25%)	6,6,6	0.15	0
7	TMO	X	301	-	4,4,4	6.33	1 (25%)	6,6,6	0.19	0
7	TMO	K	302	-	4,4,4	6.24	1 (25%)	6,6,6	0.21	0
8	ETE	B	309	-	13,13,13	0.57	0	12,12,12	0.66	0
7	TMO	L	303	-	4,4,4	6.29	1 (25%)	6,6,6	0.24	0
9	1PE	C	310	-	15,15,15	0.50	0	14,14,14	0.37	0
7	TMO	A	310	-	4,4,4	6.32	1 (25%)	6,6,6	0.22	0
7	TMO	X	302	-	4,4,4	6.42	1 (25%)	6,6,6	0.16	0
5	PEG	A	307	-	6,6,6	0.46	0	5,5,5	0.51	0
5	PEG	Y	301	-	6,6,6	0.48	0	5,5,5	0.25	0
7	TMO	H	302	-	4,4,4	6.32	1 (25%)	6,6,6	0.18	0
8	ETE	A	311	-	12,12,13	0.61	0	11,11,12	0.75	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	TRS	A	308	-	-	3/9/9/9	-
5	PEG	C	308	-	-	1/4/4/4	-
5	PEG	B	307	-	-	2/4/4/4	-
5	PEG	Y	302	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	1PE	C	310	-	-	9/13/13/13	-
5	PEG	A	307	-	-	3/4/4/4	-
6	TRS	A	309	-	-	7/9/9/9	-
5	PEG	Y	301	-	-	1/4/4/4	-
5	PEG	Y	303	-	-	1/4/4/4	-
5	PEG	L	301	-	-	2/4/4/4	-
8	ETE	M	305	-	-	3/7/7/11	-
8	ETE	B	309	-	-	7/11/11/11	-
5	PEG	C	307	-	-	2/4/4/4	-
8	ETE	A	311	-	-	7/10/10/11	-

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	301	TMO	OAE-NAC	-13.05	1.24	1.42
7	X	302	TMO	OAE-NAC	-12.79	1.25	1.42
7	K	303	TMO	OAE-NAC	-12.74	1.25	1.42
7	M	301	TMO	OAE-NAC	-12.69	1.25	1.42
7	L	304	TMO	OAE-NAC	-12.65	1.25	1.42

There are no bond angle outliers.

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	308	TRS	C2-C-C1-O1
6	A	309	TRS	C1-C-C2-O2
6	A	309	TRS	C3-C-C2-O2
6	A	309	TRS	N-C-C2-O2
8	A	311	ETE	C14-C24-OH4-C13

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	Y	304	TMO	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95^{th} 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	137/146 (93%)	-0.29	0 100 100	14, 22, 44, 56	0
1	B	137/146 (93%)	-0.37	0 100 100	15, 23, 39, 66	0
1	C	139/146 (95%)	-0.26	1 (0%) 87 86	15, 23, 45, 64	1 (0%)
2	H	212/226 (93%)	-0.06	8 (3%) 40 35	20, 43, 63, 74	0
2	K	213/226 (94%)	-0.57	2 (0%) 84 82	18, 35, 53, 75	0
2	X	211/226 (93%)	-0.15	7 (3%) 46 40	19, 39, 63, 76	0
3	L	214/218 (98%)	-0.28	8 (3%) 41 36	15, 27, 76, 86	0
3	M	215/218 (98%)	-0.50	5 (2%) 60 56	15, 25, 58, 68	0
3	Y	215/218 (98%)	-0.37	7 (3%) 46 40	16, 27, 64, 78	0
All	All	1693/1770 (95%)	-0.32	38 (2%) 62 58	14, 29, 62, 86	1 (0%)

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	134	THR	7.6
2	K	138	GLY	4.6
3	Y	129	LEU	3.9
3	Y	188	ALA	3.5
2	H	42	GLY	3.4

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

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^{th} 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
3	DV7	Y	98[A]	18/19	0.92	0.19	23,37,42,45	15
3	DV7	Y	98[B]	18/19	0.92	0.19	23,33,35,38	15
3	DV7	M	98[A]	18/19	0.94	0.13	23,35,39,43	13
3	DV7	L	98[A]	18/19	0.95	0.13	23,32,36,38	13

6.3 Carbohydrates (i)

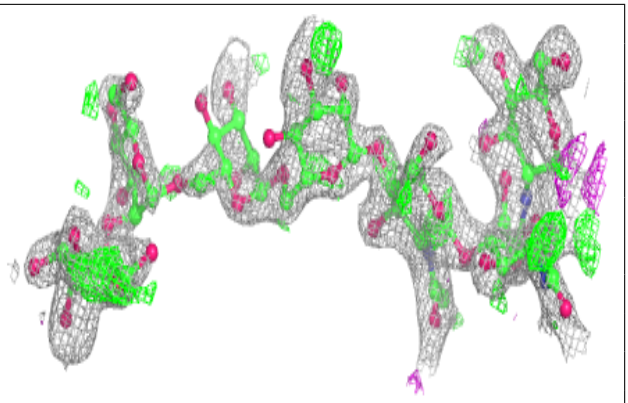
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

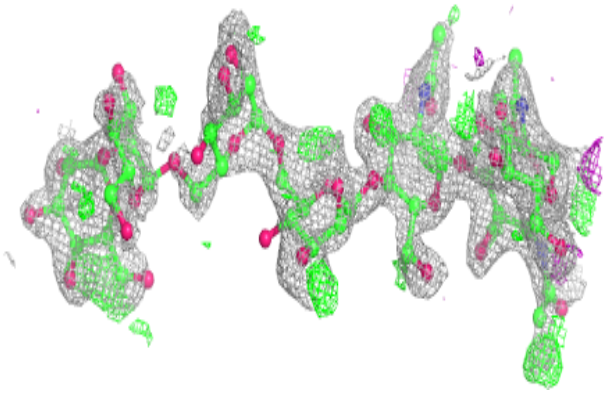
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MAN	D	4[B]	11/12	0.51	0.28	44,47,50,51	11
4	MAN	E	4[B]	11/12	0.55	0.17	60,68,75,76	11
4	BMA	E	3[B]	11/12	0.62	0.19	47,52,56,58	11
4	MAN	E	5[B]	11/12	0.64	0.31	72,80,91,92	11
4	MAN	D	5[B]	11/12	0.66	0.28	49,53,55,58	11
4	MAN	F	5[B]	11/12	0.67	0.23	37,41,45,47	11
4	MAN	E	6[B]	11/12	0.71	0.22	60,72,78,81	11
4	BMA	D	3[B]	11/12	0.71	0.18	39,41,43,43	11
4	MAN	F	4[B]	11/12	0.75	0.15	36,38,44,48	11
4	NAG	D	2[B]	14/15	0.76	0.17	36,37,38,39	14
4	BMA	F	3[B]	11/12	0.78	0.12	35,37,41,43	11
4	NAG	E	2[B]	14/15	0.79	0.17	37,40,45,46	14
4	NAG	F	2[B]	14/15	0.80	0.16	33,35,37,38	14
4	NAG	D	1[B]	14/15	0.85	0.17	36,37,39,40	14
4	NAG	D	1[A]	14/15	0.85	0.17	37,39,40,40	14
4	NAG	F	1[A]	14/15	0.85	0.15	36,40,45,45	14
4	NAG	F	1[B]	14/15	0.85	0.15	32,34,38,40	14
4	NAG	E	1[B]	14/15	0.87	0.14	29,31,38,38	14
4	NAG	E	1[A]	14/15	0.87	0.14	32,35,39,40	14
4	MAN	D	6[B]	11/12	0.89	0.15	43,49,53,54	11
4	MAN	F	6[B]	11/12	0.90	0.12	32,33,35,35	11

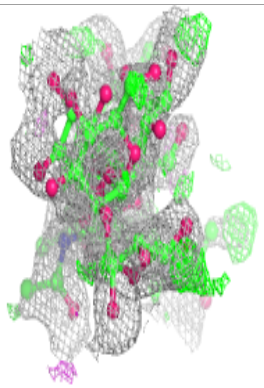
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain D:

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

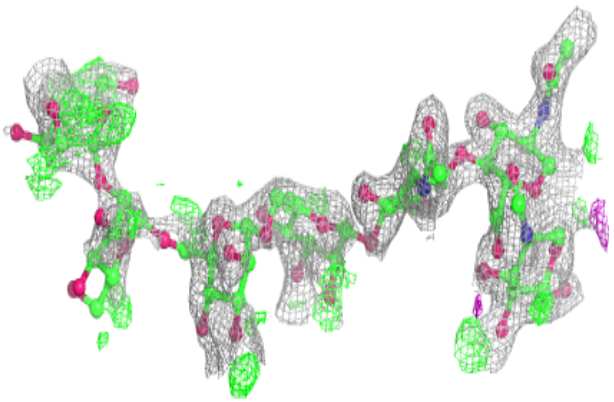


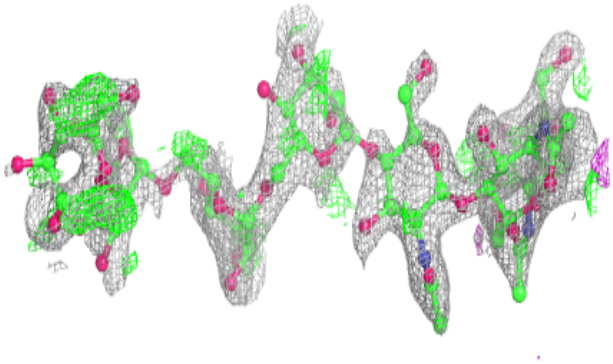


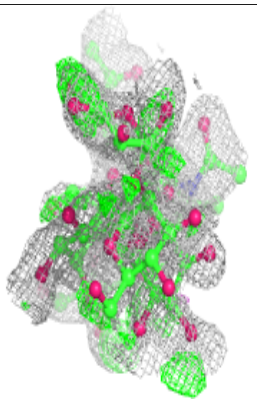


Electron density around Chain E:

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

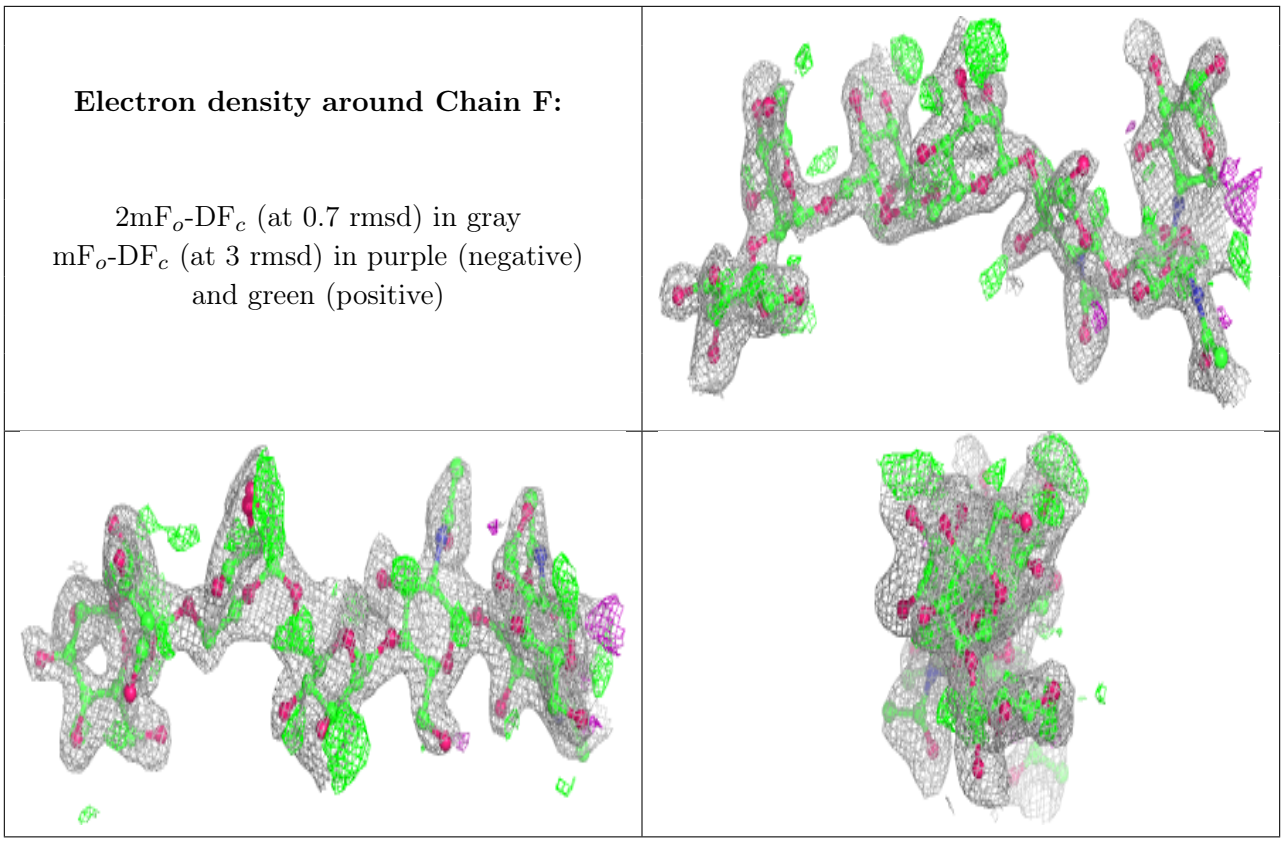






Electron density around Chain F:

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



6.4 Ligands

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^{th} 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
6	TRS	A	309	8/8	0.52	0.28	79,84,86,87	0
5	PEG	C	308	7/7	0.71	0.19	58,60,63,64	0
7	TMO	K	304	5/5	0.71	0.18	65,65,69,71	0
8	ETE	B	309	14/14	0.71	0.20	62,64,68,71	0
5	PEG	Y	302	7/7	0.72	0.16	59,66,67,71	0
7	TMO	M	303	5/5	0.72	0.21	68,70,73,74	0
5	PEG	B	307	7/7	0.72	0.15	57,61,64,64	0
5	PEG	L	301	7/7	0.73	0.16	47,49,50,55	0
5	PEG	C	307	7/7	0.73	0.22	64,64,67,70	0
7	TMO	L	304	5/5	0.75	0.20	74,75,76,77	0
6	TRS	A	308	8/8	0.76	0.24	57,61,63,67	0
8	ETE	A	311	13/14	0.76	0.23	53,62,65,66	0
5	PEG	A	307	7/7	0.76	0.13	59,61,63,63	0
9	1PE	C	310	16/16	0.76	0.22	63,72,76,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	ETE	M	305	10/14	0.79	0.15	58,60,64,64	0
5	PEG	Y	303	7/7	0.80	0.13	64,66,68,69	0
7	TMO	X	302	5/5	0.80	0.23	68,70,73,74	0
7	TMO	K	303	5/5	0.81	0.22	64,67,68,72	0
7	TMO	H	302	5/5	0.81	0.20	61,62,65,67	0
5	PEG	Y	301	7/7	0.83	0.12	48,50,55,56	0
7	TMO	Y	305	5/5	0.83	0.14	63,64,66,67	0
7	TMO	A	310	5/5	0.86	0.16	47,53,55,60	0
7	TMO	M	302	5/5	0.87	0.14	62,65,66,67	0
7	TMO	H	301	5/5	0.91	0.13	50,50,53,54	0
7	TMO	L	305	5/5	0.91	0.17	71,73,74,75	0
7	TMO	M	304	5/5	0.91	0.16	50,52,53,57	0
7	TMO	L	303	5/5	0.92	0.17	64,65,67,69	0
7	TMO	X	301	5/5	0.93	0.11	44,46,47,47	0
7	TMO	B	308	5/5	0.94	0.12	60,60,61,62	0
7	TMO	C	309	5/5	0.95	0.12	49,50,52,53	0
7	TMO	K	301	5/5	0.95	0.11	41,42,43,45	0
7	TMO	K	302	5/5	0.96	0.28	67,68,69,69	0
7	TMO	M	301	5/5	0.97	0.09	40,41,42,42	0
7	TMO	Y	304	5/5	0.98	0.12	46,46,47,51	0
7	TMO	L	302	5/5	0.98	0.12	40,41,42,43	0

6.5 Other polymers (i)

There are no such residues in this entry.