



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 03:05 AM UTC

PDB ID : 6VFW / pdb_00006vfw
Title : Crystal structure of human delta protocadherin 10 EC1-EC4
Authors : Harrison, O.J.; Brasch, J.; Shapiro, L.
Deposited on : 2020-01-06
Resolution : 3.60 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

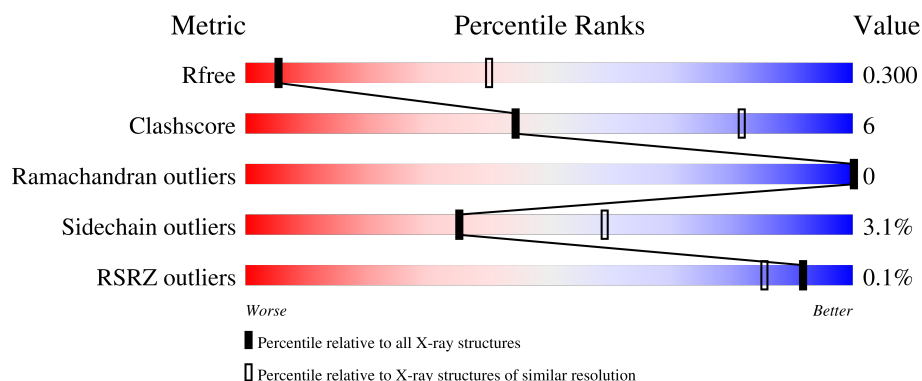
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

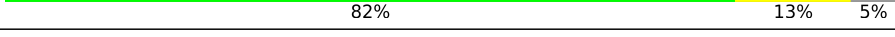
The reported resolution of this entry is 3.60 Å.

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}	180053	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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 $\leq 5\%$. 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	444	
1	B	444	
1	C	444	
1	D	444	
1	E	444	

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Mol	Chain	Length	Quality of chain
2	F	6	50%50%
2	G	6	83%17%
2	H	6	67%33%
2	I	6	17%83%
2	J	6	17%50%33%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 32989 atoms, of which 16057 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 Protocadherin-10.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	423	Total	C	H	N	O	S	0	0	0
			6412	2048	3135	550	675	4			
1	B	423	Total	C	H	N	O	S	0	0	0
			6408	2047	3132	550	675	4			
1	C	429	Total	C	H	N	O	S	0	0	0
			6456	2064	3152	556	680	4			
1	D	423	Total	C	H	N	O	S	0	0	0
			6365	2043	3095	548	675	4			
1	E	422	Total	C	H	N	O	S	0	0	0
			6400	2045	3128	549	674	4			

There are 30 discrepancies between the modelled and reference sequences:

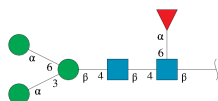
Chain	Residue	Modelled	Actual	Comment	Reference
A	439	HIS	-	expression tag	UNP Q9P2E7
A	440	HIS	-	expression tag	UNP Q9P2E7
A	441	HIS	-	expression tag	UNP Q9P2E7
A	442	HIS	-	expression tag	UNP Q9P2E7
A	443	HIS	-	expression tag	UNP Q9P2E7
A	444	HIS	-	expression tag	UNP Q9P2E7
B	439	HIS	-	expression tag	UNP Q9P2E7
B	440	HIS	-	expression tag	UNP Q9P2E7
B	441	HIS	-	expression tag	UNP Q9P2E7
B	442	HIS	-	expression tag	UNP Q9P2E7
B	443	HIS	-	expression tag	UNP Q9P2E7
B	444	HIS	-	expression tag	UNP Q9P2E7
C	439	HIS	-	expression tag	UNP Q9P2E7
C	440	HIS	-	expression tag	UNP Q9P2E7
C	441	HIS	-	expression tag	UNP Q9P2E7
C	442	HIS	-	expression tag	UNP Q9P2E7
C	443	HIS	-	expression tag	UNP Q9P2E7
C	444	HIS	-	expression tag	UNP Q9P2E7
D	439	HIS	-	expression tag	UNP Q9P2E7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	440	HIS	-	expression tag	UNP Q9P2E7
D	441	HIS	-	expression tag	UNP Q9P2E7
D	442	HIS	-	expression tag	UNP Q9P2E7
D	443	HIS	-	expression tag	UNP Q9P2E7
D	444	HIS	-	expression tag	UNP Q9P2E7
E	439	HIS	-	expression tag	UNP Q9P2E7
E	440	HIS	-	expression tag	UNP Q9P2E7
E	441	HIS	-	expression tag	UNP Q9P2E7
E	442	HIS	-	expression tag	UNP Q9P2E7
E	443	HIS	-	expression tag	UNP Q9P2E7
E	444	HIS	-	expression tag	UNP Q9P2E7

- Molecule 2 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
2	F	6	Total 130	C 40	H 59	N 2	O 29	0	0	0
2	G	6	Total 134	C 40	H 63	N 2	O 29	0	0	0
2	H	6	Total 134	C 40	H 63	N 2	O 29	0	0	0
2	I	6	Total 131	C 40	H 60	N 2	O 29	0	0	0
2	J	6	Total 131	C 40	H 60	N 2	O 29	0	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

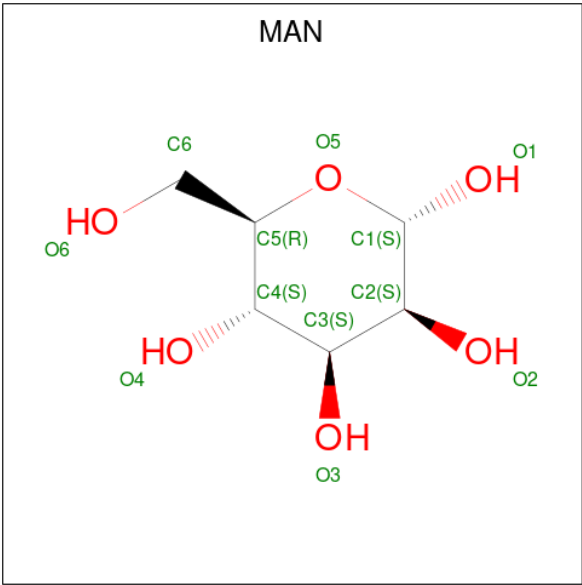
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	Ca	0	0
			9	9		
3	B	9	Total	Ca	0	0
			9	9		
3	C	9	Total	Ca	0	0
			9	9		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	9	Total	Ca		0	0
			9	9			
3	E	9	Total	Ca		0	0
			9	9			

- Molecule 4 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			22	6	11	5		
4	A	1	Total	C	H	O	0	0
			22	6	11	5		
4	B	1	Total	C	H	O	0	0
			22	6	11	5		
4	B	1	Total	C	H	O	0	0
			22	6	11	5		
4	C	1	Total	C	H	O	0	0
			22	6	11	5		
4	C	1	Total	C	H	O	0	0
			22	6	11	5		
4	D	1	Total	C	H	O	0	0
			22	6	11	5		
4	D	1	Total	C	H	O	0	0
			22	6	11	5		
4	E	1	Total	C	H	O	0	0
			22	6	11	5		

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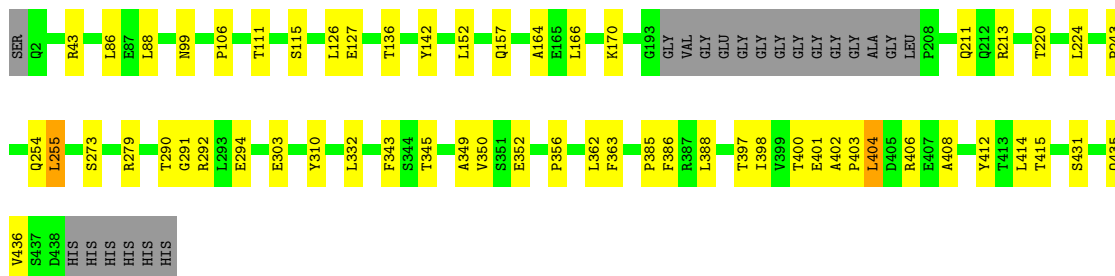
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	H	O	0	0
			22	6	11	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	5	Total	O	0	0
			5	5		
5	B	5	Total	O	0	0
			5	5		
5	C	4	Total	O	0	0
			4	4		
5	D	4	Total	O	0	0
			4	4		
5	E	5	Total	O	0	0
			5	5		

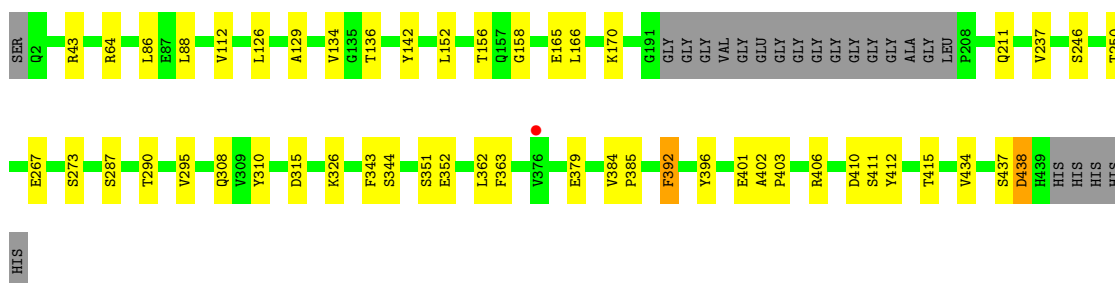
- Molecule 1: Protocadherin-10

Chain D:  82% 13% 5%



- Molecule 1: Protocadherin-10

Chain E:  84% 11% 5%



- Molecule 2: 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 F:  50% 50%

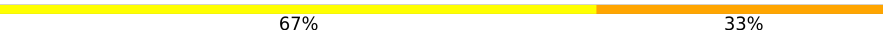


- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  83% 17%



- Molecule 2: 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

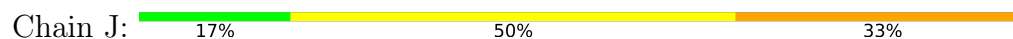
Chain H:  67% 33%



- Molecule 2: 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



- Molecule 2: 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



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	346.55Å 73.19Å 246.33Å 90.00° 132.06° 90.00°	Depositor
Resolution (Å)	19.99 – 3.60 19.99 – 3.60	Depositor EDS
% Data completeness (in resolution range)	93.4 (19.99-3.60) 76.8 (19.99-3.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.33 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.277 , 0.295 0.284 , 0.300	Depositor DCC
R_{free} test set	1982 reflections (3.75%)	wwPDB-VP
Wilson B-factor (Å ²)	120.2	Xtriage
Anisotropy	0.669	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 160.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	32989	wwPDB-VP
Average B, all atoms (Å ²)	270.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, FUC, NAG, MAN, BMA

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	0.18	0/3343	0.40	0/4565
1	B	0.18	0/3342	0.41	0/4563
1	C	0.16	0/3370	0.37	0/4602
1	D	0.16	0/3335	0.38	0/4553
1	E	0.16	0/3338	0.38	0/4558
All	All	0.17	0/16728	0.39	0/22841

There are no bond length outliers.

There are no bond angle outliers.

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	3277	3135	3150	48	0
1	B	3276	3132	3151	51	0
1	C	3304	3152	3178	46	0
1	D	3270	3095	3147	32	0
1	E	3272	3128	3148	26	0
2	F	71	59	61	2	0
2	G	71	63	61	1	0
2	H	71	63	61	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	71	60	61	0	0
2	J	71	60	61	3	0
3	A	9	0	0	0	0
3	B	9	0	0	0	0
3	C	9	0	0	0	0
3	D	9	0	0	0	0
3	E	9	0	0	0	0
4	A	22	22	20	0	0
4	B	22	22	20	1	0
4	C	22	22	20	0	0
4	D	22	22	20	0	0
4	E	22	22	20	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	4	0	0	0	0
5	D	4	0	0	0	0
5	E	5	0	0	0	0
All	All	16932	16057	16179	198	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 6.

The worst 5 of 198 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:387:ARG:HG2	1:A:401:GLU:HB2	1.62	0.82
1:D:388:LEU:CD1	1:D:398:ILE:HG12	2.12	0.79
1:C:406:ARG:HD3	1:C:410:ASP:HB3	1.65	0.79
1:D:352:GLU:O	1:D:404:LEU:HD21	1.84	0.77
1:A:383:ASP:N	1:A:383:ASP:OD1	2.19	0.75

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	419/444 (94%)	404 (96%)	15 (4%)	0	100	100
1	B	419/444 (94%)	406 (97%)	13 (3%)	0	100	100
1	C	425/444 (96%)	405 (95%)	20 (5%)	0	100	100
1	D	419/444 (94%)	409 (98%)	10 (2%)	0	100	100
1	E	418/444 (94%)	403 (96%)	15 (4%)	0	100	100
All	All	2100/2220 (95%)	2027 (96%)	73 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	372/381 (98%)	361 (97%)	11 (3%)	36	59
1	B	372/381 (98%)	362 (97%)	10 (3%)	39	61
1	C	373/381 (98%)	362 (97%)	11 (3%)	37	60
1	D	371/381 (97%)	359 (97%)	12 (3%)	34	58
1	E	372/381 (98%)	358 (96%)	14 (4%)	29	55
All	All	1860/1905 (98%)	1802 (97%)	58 (3%)	35	59

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	170	LYS
1	E	392	PHE
1	D	136	THR
1	E	384	VAL
1	E	152	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	59	ASN
1	D	275	HIS
1	E	77	HIS
1	D	254	GLN
1	D	324	HIS

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 ⓘ

30 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	$\# Z > 2$
2	NAG	F	1	2,1	14,14,15	0.66	1 (7%)	17,19,21	1.00	1 (5%)
2	NAG	F	2	2	14,14,15	1.39	1 (7%)	17,19,21	1.16	2 (11%)
2	BMA	F	3	2	11,11,12	1.13	1 (9%)	15,15,17	1.11	1 (6%)
2	MAN	F	4	2	11,11,12	1.08	1 (9%)	15,15,17	1.52	2 (13%)
2	MAN	F	5	2	11,11,12	1.28	2 (18%)	15,15,17	2.03	3 (20%)
2	FUC	F	6	2	10,10,11	1.12	1 (10%)	14,14,16	1.44	2 (14%)
2	NAG	G	1	2,1	14,14,15	0.92	1 (7%)	17,19,21	0.80	0
2	NAG	G	2	2	14,14,15	0.81	1 (7%)	17,19,21	0.90	1 (5%)
2	BMA	G	3	2	11,11,12	1.30	2 (18%)	15,15,17	0.78	0
2	MAN	G	4	2	11,11,12	0.93	1 (9%)	15,15,17	1.10	2 (13%)
2	MAN	G	5	2	11,11,12	0.83	0	15,15,17	1.01	2 (13%)
2	FUC	G	6	2	10,10,11	0.69	0	14,14,16	1.53	3 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	H	1	2,1	14,14,15	0.84	1 (7%)	17,19,21	0.54	0
2	NAG	H	2	2	14,14,15	0.34	0	17,19,21	0.80	1 (5%)
2	BMA	H	3	2	11,11,12	1.46	2 (18%)	15,15,17	0.93	0
2	MAN	H	4	2	11,11,12	1.18	2 (18%)	15,15,17	1.54	2 (13%)
2	MAN	H	5	2	11,11,12	0.88	1 (9%)	15,15,17	1.16	2 (13%)
2	FUC	H	6	2	10,10,11	1.08	2 (20%)	14,14,16	1.04	1 (7%)
2	NAG	I	1	2,1	14,14,15	0.54	0	17,19,21	0.83	0
2	NAG	I	2	2	14,14,15	0.86	1 (7%)	17,19,21	0.88	1 (5%)
2	BMA	I	3	2	11,11,12	1.20	2 (18%)	15,15,17	1.37	2 (13%)
2	MAN	I	4	2	11,11,12	0.84	1 (9%)	15,15,17	1.20	2 (13%)
2	MAN	I	5	2	11,11,12	0.90	0	15,15,17	1.44	2 (13%)
2	FUC	I	6	2	10,10,11	0.94	0	14,14,16	1.34	3 (21%)
2	NAG	J	1	2,1	14,14,15	0.38	0	17,19,21	0.65	0
2	NAG	J	2	2	14,14,15	0.29	0	17,19,21	0.96	1 (5%)
2	BMA	J	3	2	11,11,12	1.10	0	15,15,17	1.05	1 (6%)
2	MAN	J	4	2	11,11,12	0.92	0	15,15,17	1.07	2 (13%)
2	MAN	J	5	2	11,11,12	0.94	1 (9%)	15,15,17	1.19	2 (13%)
2	FUC	J	6	2	10,10,11	0.74	0	14,14,16	0.87	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
2	NAG	F	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	1/6/23/26	0/1/1/1
2	BMA	F	3	2	-	1/2/19/22	0/1/1/1
2	MAN	F	4	2	-	2/2/19/22	0/1/1/1
2	MAN	F	5	2	-	2/2/19/22	0/1/1/1
2	FUC	F	6	2	-	-	0/1/1/1
2	NAG	G	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	4/6/23/26	0/1/1/1
2	BMA	G	3	2	-	2/2/19/22	0/1/1/1
2	MAN	G	4	2	-	2/2/19/22	0/1/1/1
2	MAN	G	5	2	-	1/2/19/22	0/1/1/1
2	FUC	G	6	2	-	-	0/1/1/1
2	NAG	H	1	2,1	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	H	2	2	-	1/6/23/26	0/1/1/1
2	BMA	H	3	2	-	0/2/19/22	0/1/1/1
2	MAN	H	4	2	-	1/2/19/22	0/1/1/1
2	MAN	H	5	2	-	2/2/19/22	0/1/1/1
2	FUC	H	6	2	-	-	0/1/1/1
2	NAG	I	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
2	BMA	I	3	2	-	0/2/19/22	0/1/1/1
2	MAN	I	4	2	-	2/2/19/22	0/1/1/1
2	MAN	I	5	2	-	1/2/19/22	1/1/1/1
2	FUC	I	6	2	-	-	0/1/1/1
2	NAG	J	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	J	2	2	-	2/6/23/26	0/1/1/1
2	BMA	J	3	2	-	2/2/19/22	0/1/1/1
2	MAN	J	4	2	-	0/2/19/22	0/1/1/1
2	MAN	J	5	2	-	2/2/19/22	0/1/1/1
2	FUC	J	6	2	-	-	0/1/1/1

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	NAG	C1-C2	4.98	1.59	1.52
2	F	5	MAN	C1-C2	3.47	1.60	1.52
2	G	1	NAG	O5-C1	-3.31	1.38	1.43
2	H	4	MAN	C1-C2	3.03	1.59	1.52
2	F	4	MAN	C1-C2	2.99	1.59	1.52

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	5	MAN	C1-O5-C5	6.07	120.33	112.19
2	F	4	MAN	C1-O5-C5	4.68	118.45	112.19
2	H	4	MAN	C1-O5-C5	4.46	118.16	112.19
2	I	5	MAN	C1-O5-C5	4.42	118.11	112.19
2	I	4	MAN	C1-O5-C5	3.47	116.83	112.19

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	2	NAG	C1-C2-N2-C7
2	H	2	NAG	C3-C2-N2-C7
2	J	5	MAN	C4-C5-C6-O6
2	G	4	MAN	C4-C5-C6-O6
2	I	4	MAN	C4-C5-C6-O6

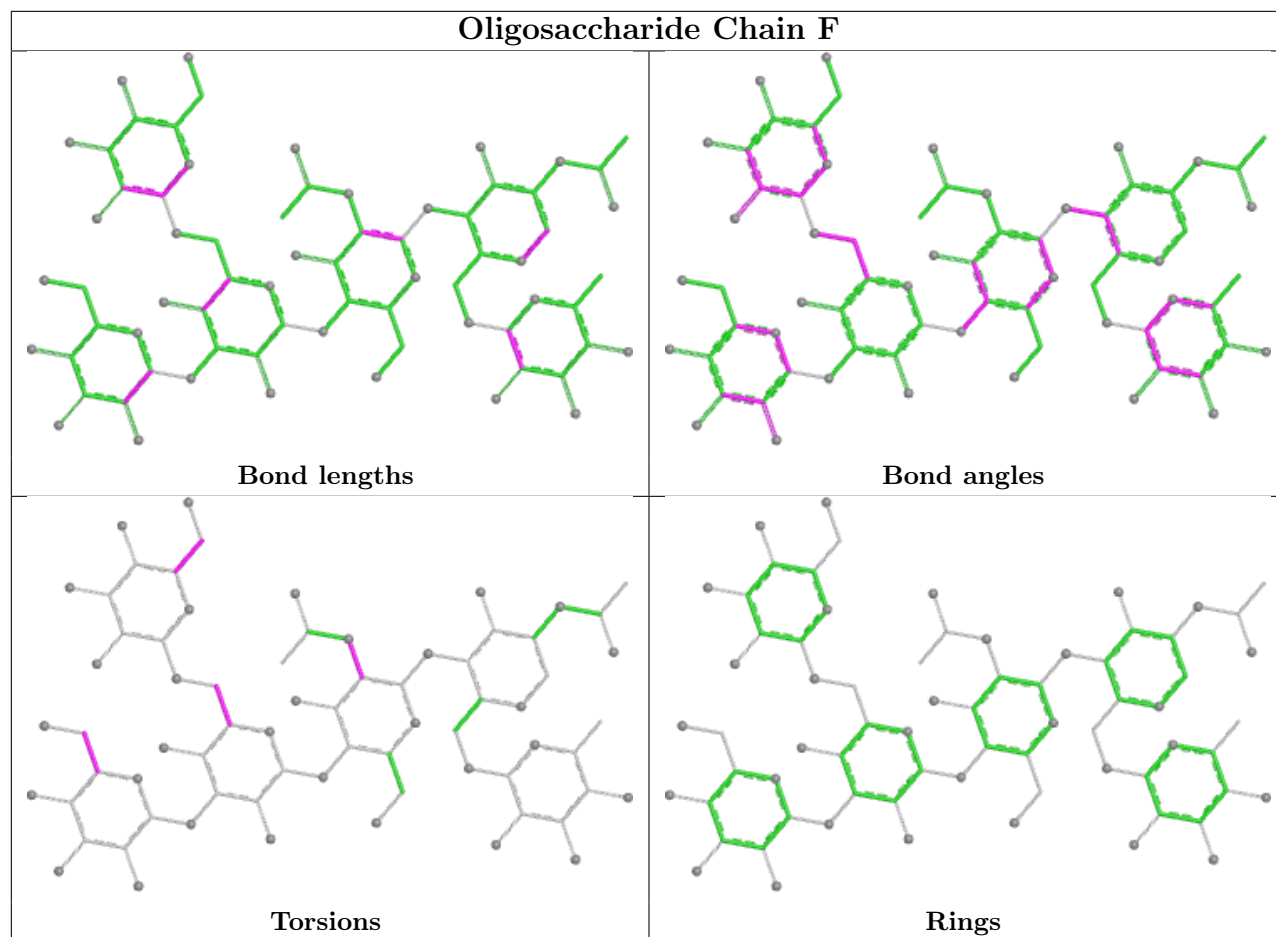
All (1) ring outliers are listed below:

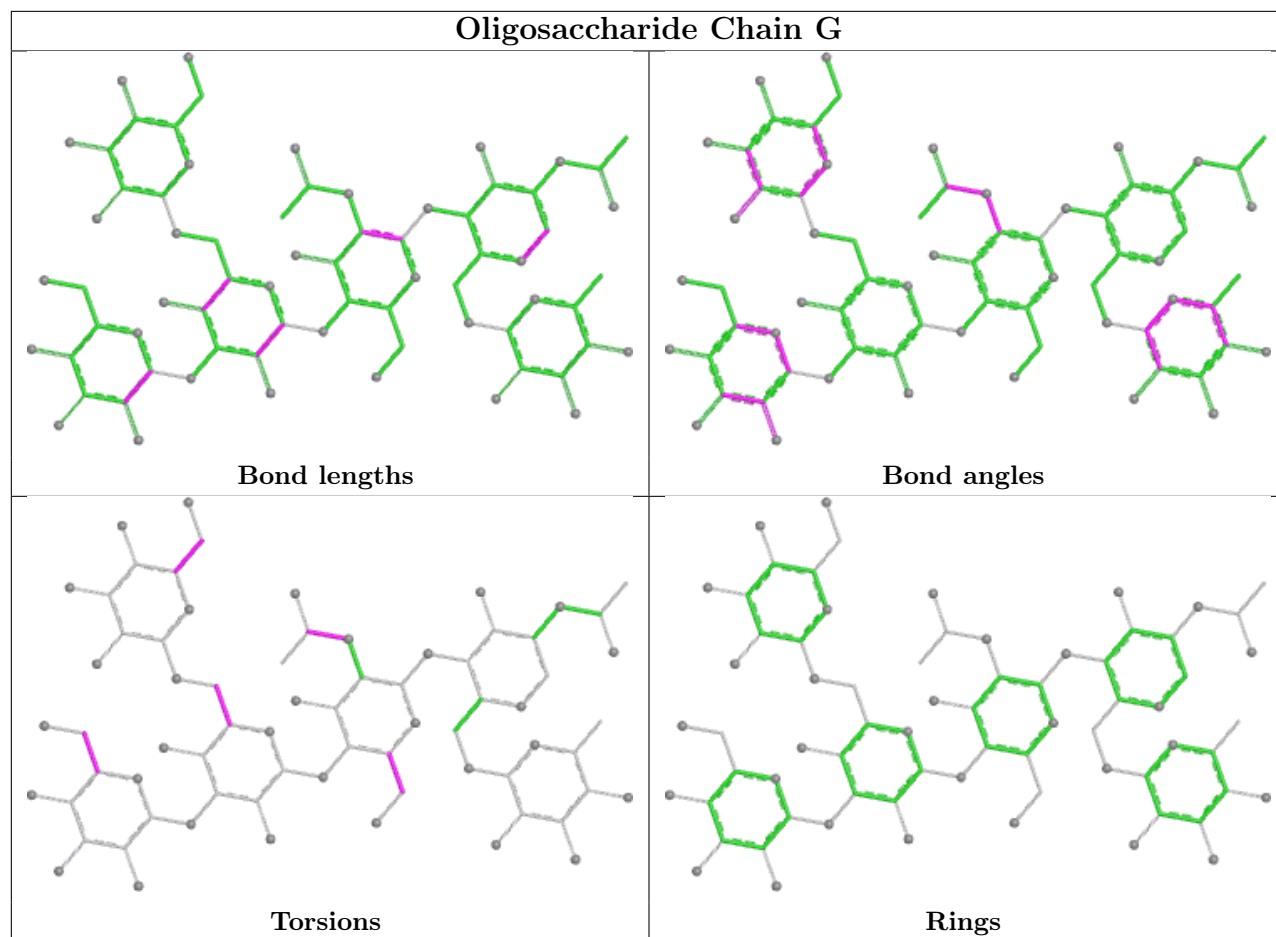
Mol	Chain	Res	Type	Atoms
2	I	5	MAN	C1-C2-C3-C4-C5-O5

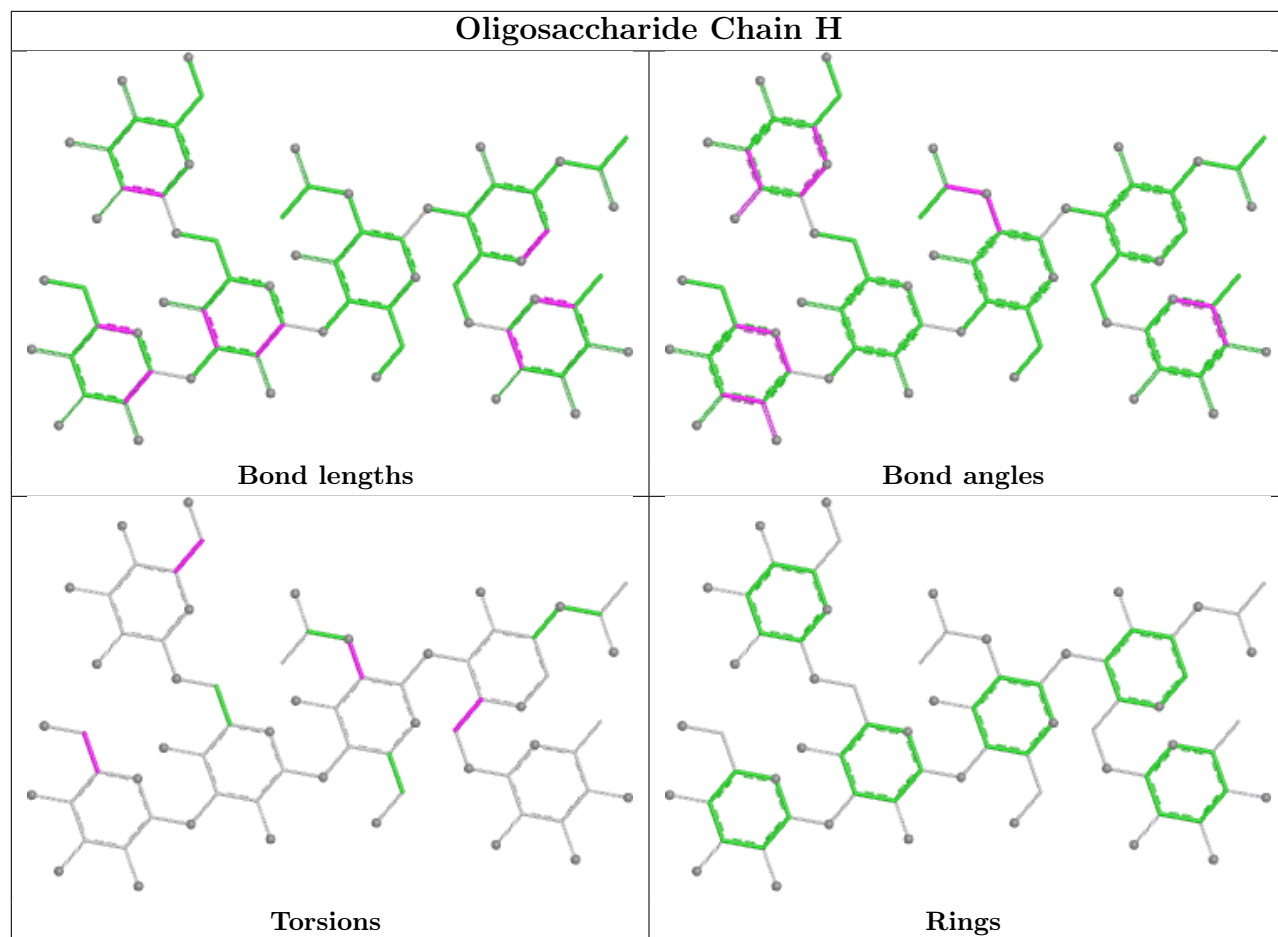
9 monomers are involved in 10 short contacts:

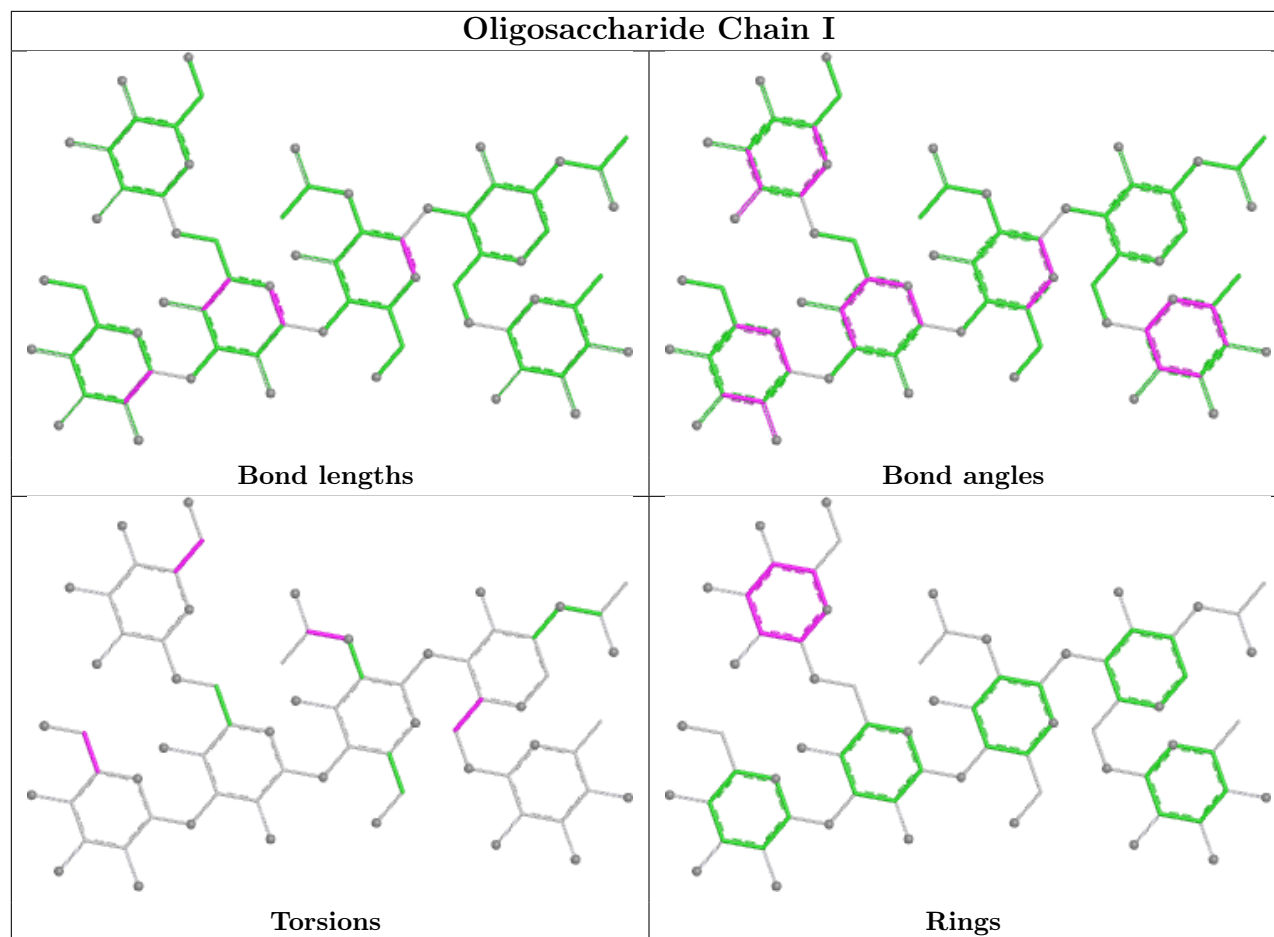
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	6	FUC	1	0
2	H	2	NAG	3	0
2	J	5	MAN	1	0
2	J	1	NAG	2	0
2	G	2	NAG	1	0
2	H	1	NAG	1	0
2	J	2	NAG	2	0
2	F	2	NAG	2	0
2	F	1	NAG	1	0

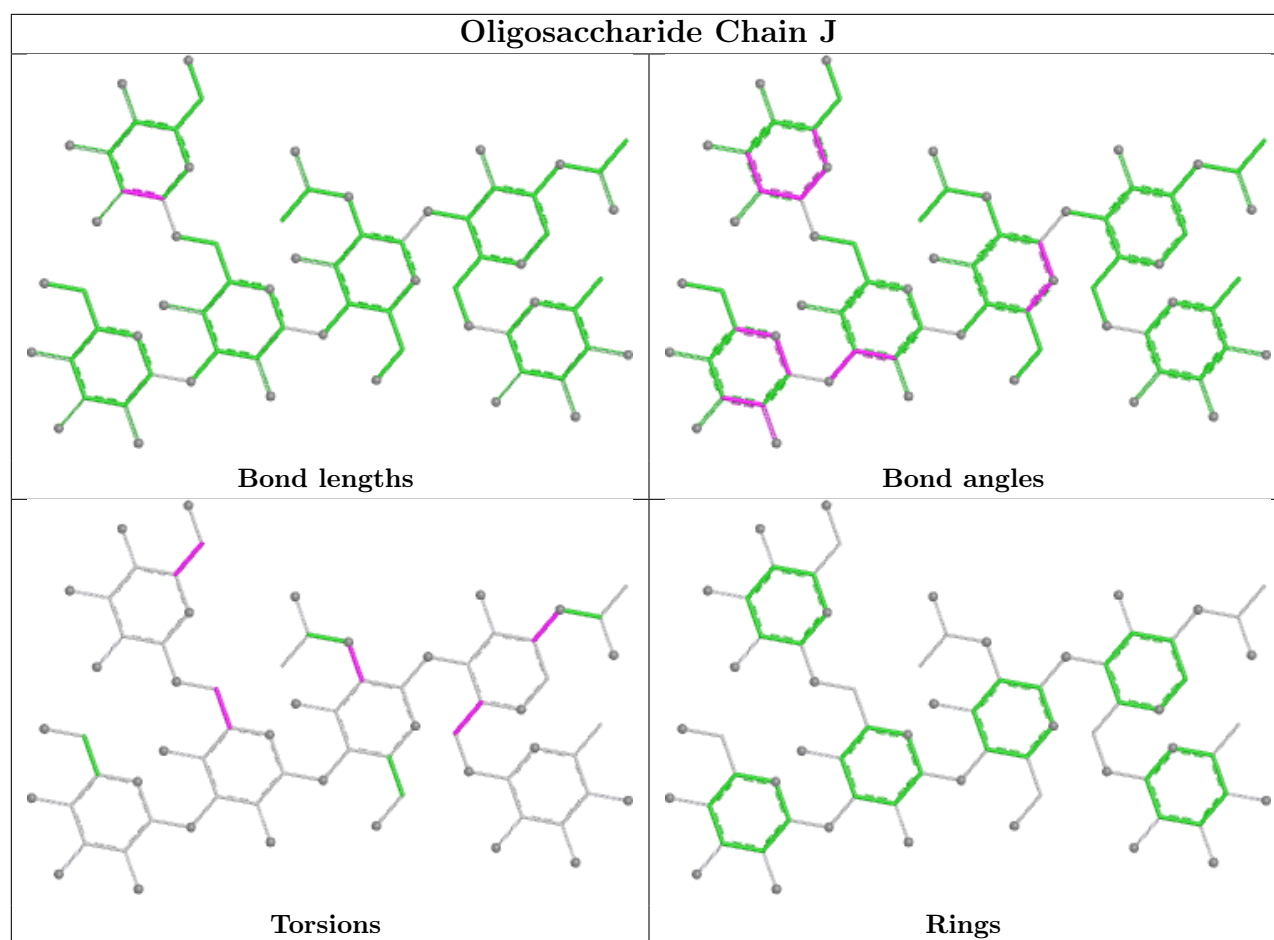
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 55 ligands modelled in this entry, 45 are monoatomic - leaving 10 for Mogul analysis.

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	MAN	B	511	1	11,11,12	0.77	1 (9%)	15,15,17	0.93	2 (13%)
4	MAN	B	510	1	11,11,12	0.62	0	15,15,17	1.01	2 (13%)
4	MAN	D	511	1	11,11,12	0.78	1 (9%)	15,15,17	0.95	2 (13%)
4	MAN	E	510	1	11,11,12	0.77	0	15,15,17	1.08	2 (13%)
4	MAN	C	511	1	11,11,12	0.87	1 (9%)	15,15,17	0.93	2 (13%)
4	MAN	D	510	1	11,11,12	0.66	0	15,15,17	1.04	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	A	510	1	11,11,12	0.64	0	15,15,17	1.08	2 (13%)
4	MAN	A	511	1	11,11,12	0.70	0	15,15,17	0.99	2 (13%)
4	MAN	C	510	1	11,11,12	0.75	0	15,15,17	1.08	2 (13%)
4	MAN	E	511	1	11,11,12	0.77	0	15,15,17	0.97	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	MAN	B	511	1	-	2/2/19/22	0/1/1/1
4	MAN	B	510	1	-	0/2/19/22	0/1/1/1
4	MAN	D	511	1	-	2/2/19/22	0/1/1/1
4	MAN	E	510	1	-	0/2/19/22	0/1/1/1
4	MAN	C	511	1	-	2/2/19/22	0/1/1/1
4	MAN	D	510	1	-	0/2/19/22	0/1/1/1
4	MAN	A	510	1	-	0/2/19/22	0/1/1/1
4	MAN	A	511	1	-	2/2/19/22	0/1/1/1
4	MAN	C	510	1	-	0/2/19/22	0/1/1/1
4	MAN	E	511	1	-	2/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	511	MAN	O5-C1	-2.28	1.39	1.43
4	B	511	MAN	O5-C1	-2.09	1.40	1.43
4	D	511	MAN	O5-C1	-2.01	1.40	1.43

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	510	MAN	C1-O5-C5	2.96	116.15	112.19
4	C	510	MAN	C1-O5-C5	2.89	116.06	112.19
4	E	510	MAN	C1-O5-C5	2.79	115.93	112.19
4	D	510	MAN	C1-O5-C5	2.77	115.90	112.19
4	B	510	MAN	C1-O5-C5	2.63	115.70	112.19

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	511	MAN	O5-C5-C6-O6
4	B	511	MAN	O5-C5-C6-O6
4	C	511	MAN	O5-C5-C6-O6
4	D	511	MAN	O5-C5-C6-O6
4	E	511	MAN	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	510	MAN	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 [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, 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	423/444 (95%)	-0.55	0 100 100	180, 241, 410, 510	0
1	B	423/444 (95%)	-0.60	1 (0%) 91 80	187, 241, 409, 507	0
1	C	429/444 (96%)	-0.65	0 100 100	195, 254, 315, 391	0
1	D	423/444 (95%)	-0.62	0 100 100	204, 261, 333, 413	0
1	E	422/444 (95%)	-0.67	1 (0%) 91 80	189, 260, 379, 434	0
All	All	2120/2220 (95%)	-0.62	2 (0%) 92 85	180, 253, 385, 510	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	62	ILE	2.8
1	E	376	VAL	2.6

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, 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
2	MAN	J	5	11/12	0.13	0.08	342,409,451,491	0
2	BMA	J	3	11/12	0.23	0.09	290,348,409,426	0
2	NAG	H	2	14/15	0.30	0.12	381,422,502,506	0

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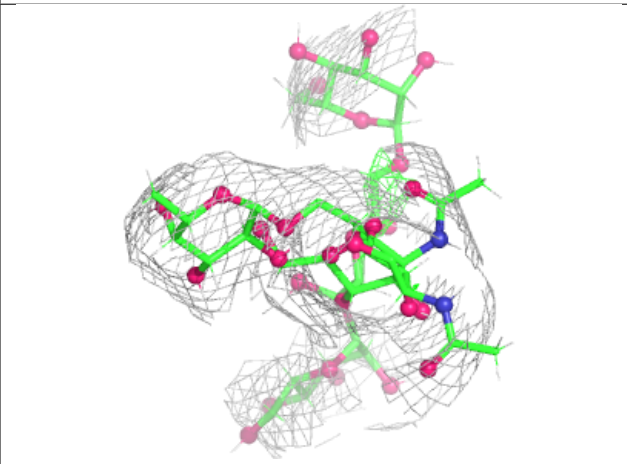
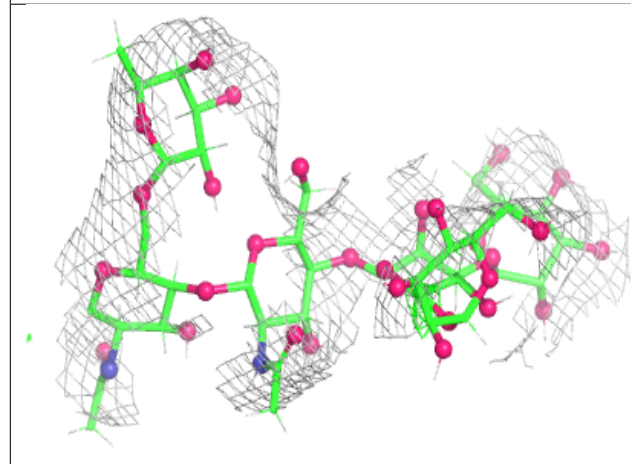
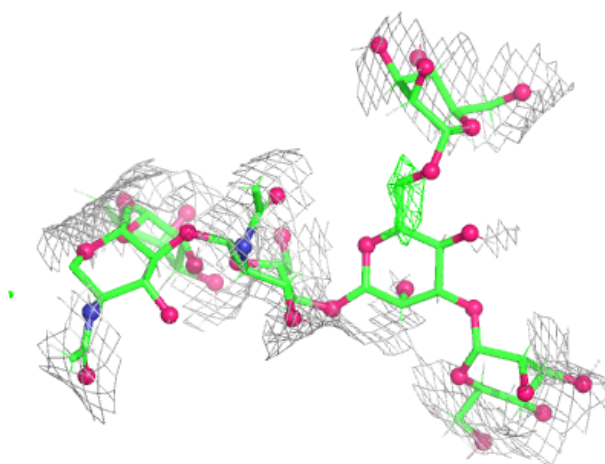
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MAN	H	5	11/12	0.34	0.11	378,430,509,516	0
2	MAN	I	4	11/12	0.34	0.08	351,385,448,462	0
2	MAN	H	4	11/12	0.35	0.07	411,474,516,568	0
2	FUC	J	6	10/11	0.38	0.15	300,336,390,403	0
2	MAN	F	5	11/12	0.41	0.07	350,381,431,458	0
2	BMA	H	3	11/12	0.41	0.09	428,455,555,593	0
2	FUC	G	6	10/11	0.43	0.14	363,410,484,492	0
2	MAN	F	4	11/12	0.52	0.07	361,414,473,521	0
2	BMA	F	3	11/12	0.54	0.06	357,397,469,476	0
2	MAN	I	5	11/12	0.57	0.08	388,425,490,508	0
2	NAG	F	2	14/15	0.60	0.07	305,389,476,540	0
2	BMA	G	3	11/12	0.65	0.05	321,350,420,420	0
2	MAN	G	4	11/12	0.66	0.07	361,426,495,562	0
2	MAN	G	5	11/12	0.66	0.06	272,368,441,487	0
2	NAG	G	1	14/15	0.72	0.09	285,304,357,400	0
2	NAG	G	2	14/15	0.76	0.07	276,340,451,451	0
2	BMA	I	3	11/12	0.76	0.05	380,412,494,504	0
2	NAG	J	2	14/15	0.76	0.08	351,380,466,466	0
2	NAG	I	2	14/15	0.78	0.06	281,353,442,450	0
2	FUC	I	6	10/11	0.83	0.08	370,430,486,516	0
2	FUC	H	6	10/11	0.87	0.08	329,374,449,449	0
2	NAG	H	1	14/15	0.87	0.11	363,413,496,560	0
2	NAG	I	1	14/15	0.88	0.10	305,357,429,441	0
2	NAG	J	1	14/15	0.89	0.07	242,325,404,426	0
2	MAN	J	4	11/12	0.91	0.09	357,379,448,466	0
2	NAG	F	1	14/15	0.92	0.06	247,283,348,351	0
2	FUC	F	6	10/11	0.92	0.06	265,299,352,359	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.

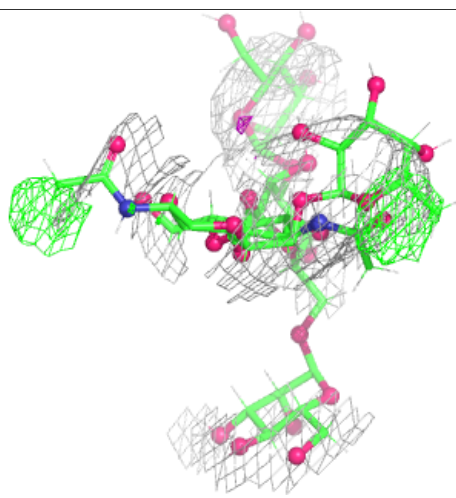
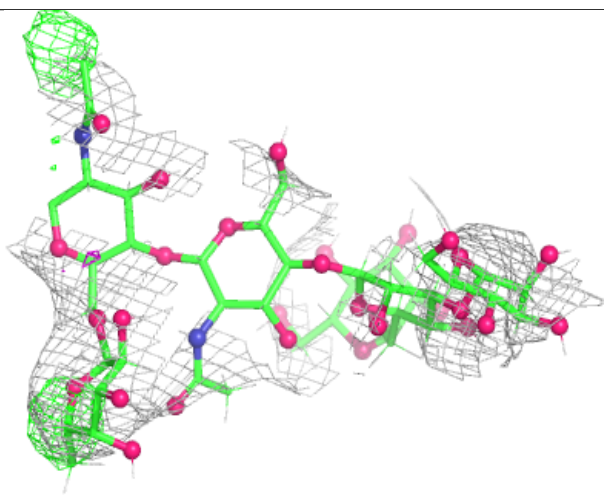
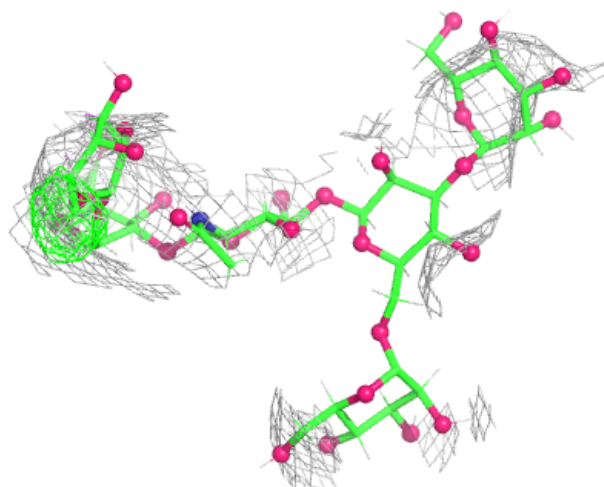
Electron density around Chain F:

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



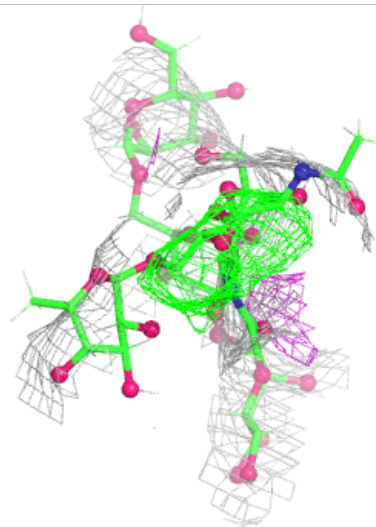
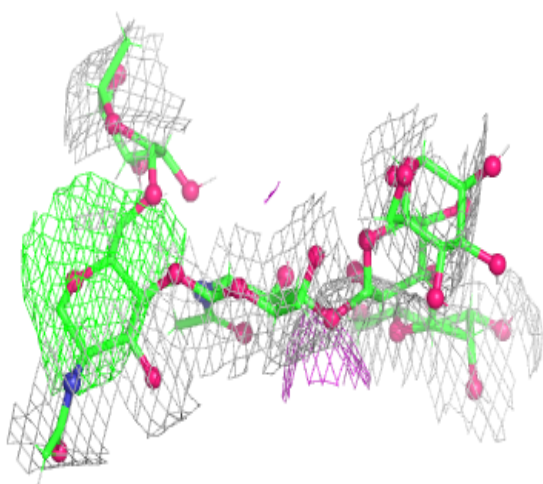
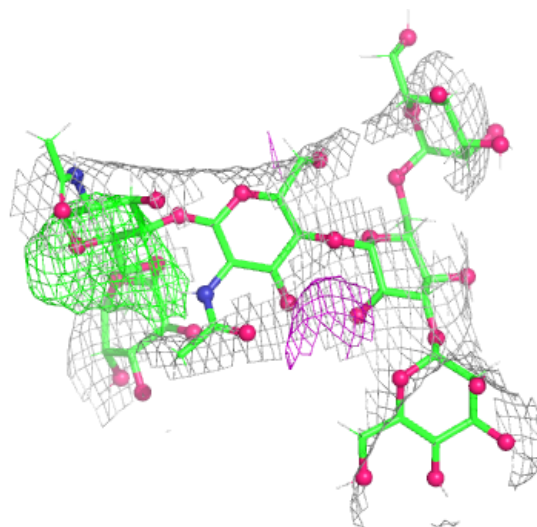
Electron density around Chain G:

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



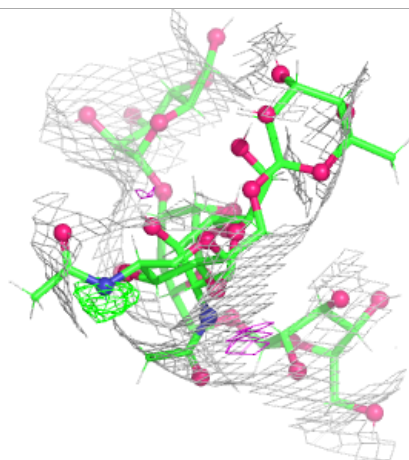
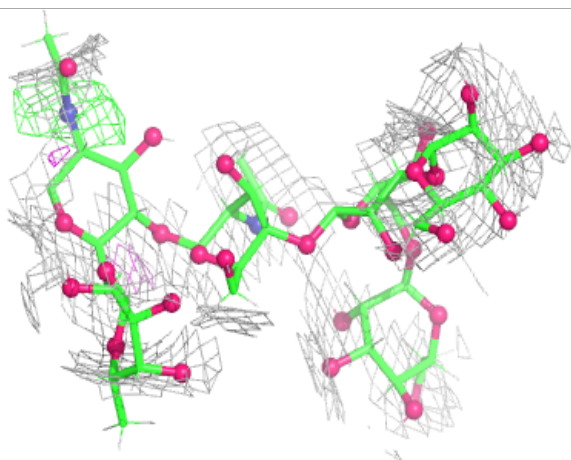
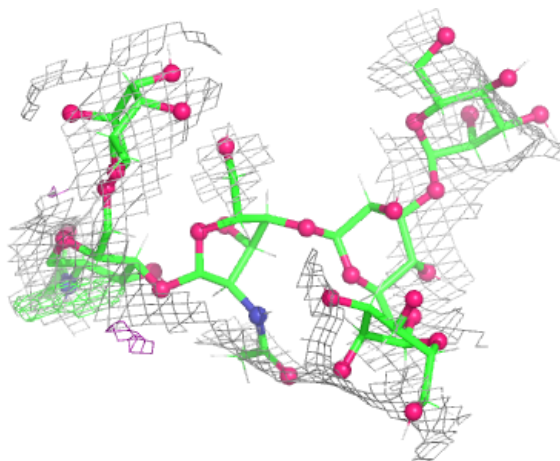
Electron density around Chain H:

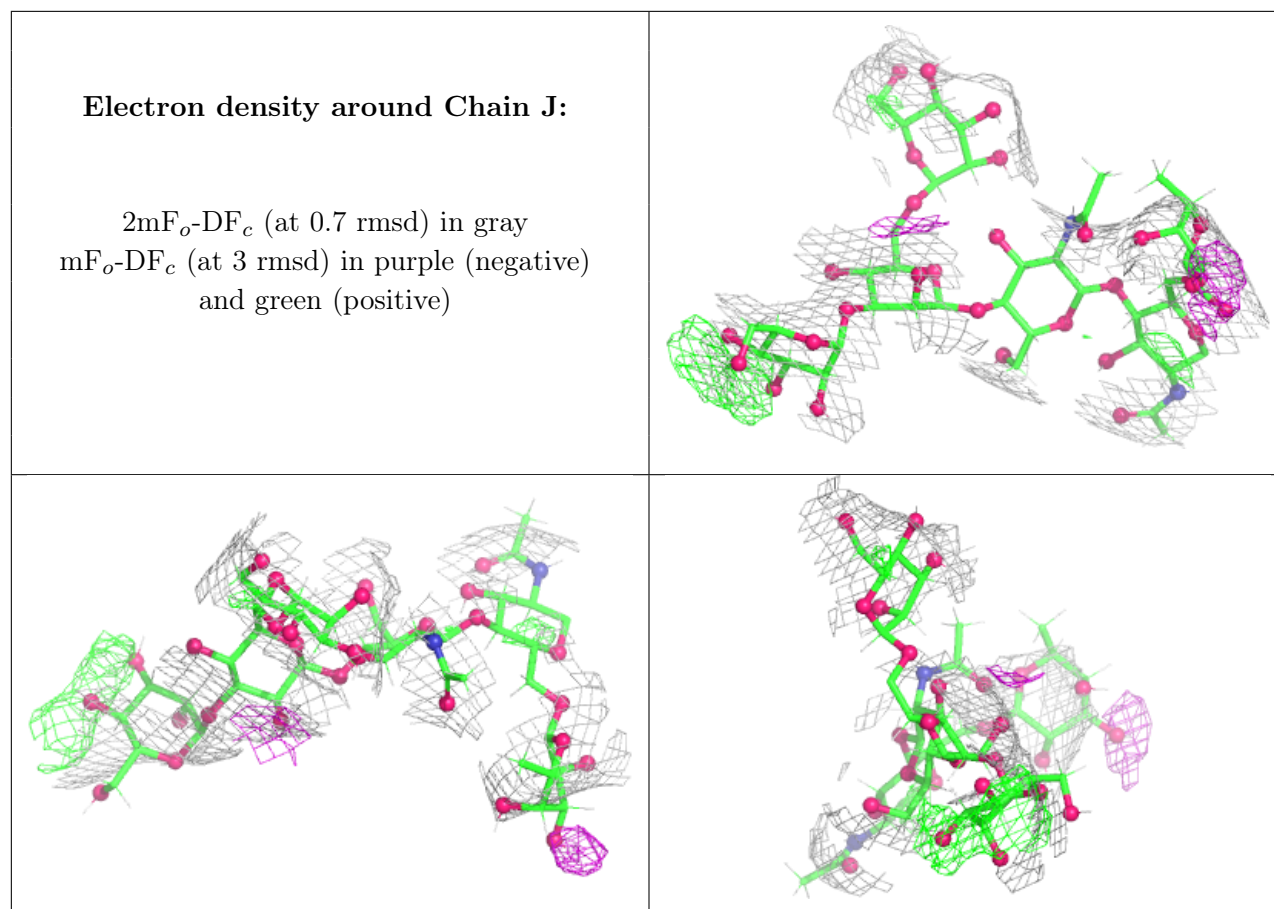
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain I:

$2mF_o-DF_c$ (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, 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
3	CA	B	501	1/1	0.48	0.14	553,553,553,553	0
3	CA	A	501	1/1	0.52	0.17	475,475,475,475	0
4	MAN	D	510	11/12	0.57	0.12	298,325,384,391	0
4	MAN	A	511	11/12	0.59	0.12	318,357,422,428	0
4	MAN	A	510	11/12	0.67	0.10	283,307,356,368	0
4	MAN	C	511	11/12	0.71	0.06	293,324,381,388	0
3	CA	C	501	1/1	0.71	0.09	277,277,277,277	0
4	MAN	E	510	11/12	0.72	0.07	325,354,414,425	0
4	MAN	E	511	11/12	0.72	0.20	455,564,628,754	0
4	MAN	B	511	11/12	0.75	0.09	283,315,374,379	0
3	CA	E	501	1/1	0.81	0.17	333,333,333,333	0
4	MAN	B	510	11/12	0.82	0.09	252,311,373,375	0
4	MAN	C	510	11/12	0.85	0.10	295,328,387,394	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MAN	D	511	11/12	0.85	0.10	302,322,385,387	0
3	CA	D	501	1/1	0.86	0.13	277,277,277,277	0
3	CA	B	507	1/1	0.91	0.14	297,297,297,297	0
3	CA	A	502	1/1	0.92	0.04	254,254,254,254	0
3	CA	B	502	1/1	0.92	0.04	269,269,269,269	0
3	CA	C	503	1/1	0.94	0.03	208,208,208,208	0
3	CA	C	505	1/1	0.95	0.03	203,203,203,203	0
3	CA	E	503	1/1	0.95	0.04	277,277,277,277	0
3	CA	D	503	1/1	0.95	0.04	227,227,227,227	0
3	CA	C	508	1/1	0.96	0.06	217,217,217,217	0
3	CA	E	502	1/1	0.96	0.03	258,258,258,258	0
3	CA	D	504	1/1	0.96	0.05	223,223,223,223	0
3	CA	E	504	1/1	0.96	0.03	243,243,243,243	0
3	CA	E	506	1/1	0.96	0.03	203,203,203,203	0
3	CA	B	505	1/1	0.97	0.05	219,219,219,219	0
3	CA	A	506	1/1	0.97	0.07	203,203,203,203	0
3	CA	B	503	1/1	0.97	0.02	272,272,272,272	0
3	CA	B	504	1/1	0.97	0.03	219,219,219,219	0
3	CA	C	504	1/1	0.97	0.02	254,254,254,254	0
3	CA	E	508	1/1	0.97	0.04	203,203,203,203	0
3	CA	D	507	1/1	0.97	0.03	206,206,206,206	0
3	CA	D	508	1/1	0.97	0.05	207,207,207,207	0
3	CA	A	508	1/1	0.98	0.08	203,203,203,203	0
3	CA	B	506	1/1	0.98	0.04	203,203,203,203	0
3	CA	D	506	1/1	0.98	0.07	203,203,203,203	0
3	CA	A	509	1/1	0.98	0.05	203,203,203,203	0
3	CA	B	509	1/1	0.98	0.03	211,211,211,211	0
3	CA	E	509	1/1	0.98	0.11	224,224,224,224	0
3	CA	D	509	1/1	0.98	0.04	223,223,223,223	0
3	CA	A	505	1/1	0.98	0.03	203,203,203,203	0
3	CA	C	507	1/1	0.99	0.04	203,203,203,203	0
3	CA	C	502	1/1	0.99	0.05	219,219,219,219	0
3	CA	C	509	1/1	0.99	0.06	205,205,205,205	0
3	CA	B	508	1/1	0.99	0.07	203,203,203,203	0
3	CA	D	502	1/1	0.99	0.05	231,231,231,231	0
3	CA	A	507	1/1	0.99	0.09	203,203,203,203	0
3	CA	A	503	1/1	0.99	0.04	225,225,225,225	0
3	CA	E	505	1/1	0.99	0.02	231,231,231,231	0
3	CA	D	505	1/1	0.99	0.04	203,203,203,203	0
3	CA	E	507	1/1	0.99	0.04	218,218,218,218	0
3	CA	C	506	1/1	0.99	0.02	203,203,203,203	0
3	CA	A	504	1/1	1.00	0.01	203,203,203,203	0

6.5 Other polymers [i](#)

There are no such residues in this entry.