



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 06:47 AM BST

PDB ID : 6VFW  
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 Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

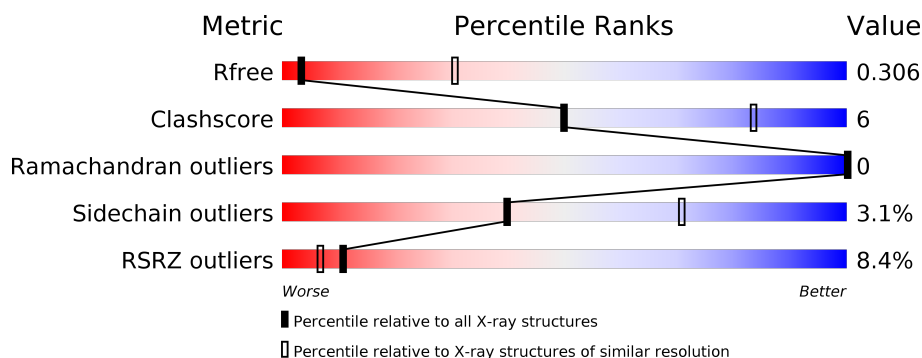
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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.





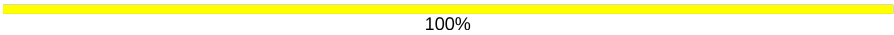
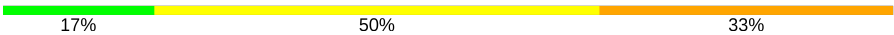
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	444	<div> <div>9%</div> <div>80% 15% 5%</div> </div>
1	B	444	<div> <div>7%</div> <div>80% 14% 5%</div> </div>
1	C	444	<div> <div>7%</div> <div>83% 13% .</div> </div>
1	D	444	<div> <div>6%</div> <div>82% 13% 5%</div> </div>
1	E	444	<div> <div>11%</div> <div>84% 11% 5%</div> </div>
2	F	6	<div> <div>50% 50%</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	6	 83%17%
2	H	6	 67%33%
2	I	6	 100%
2	J	6	 17%50%33%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FUC	I	6	-	-	-	X
4	MAN	C	510	-	-	-	X
4	MAN	E	510	-	-	-	X

## 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:

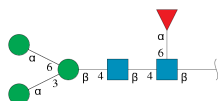
Chain	Residue	Modelled	Actual	Comment	Reference
A	439	HIS	-	expression tag	UNP Q9P2E7
A	440	HIS	-	expression tag	UNP Q9P2E7
A	441	HIS	-	expression tag	UNP Q9P2E7
A	442	HIS	-	expression tag	UNP Q9P2E7
A	443	HIS	-	expression tag	UNP Q9P2E7
A	444	HIS	-	expression tag	UNP Q9P2E7
B	439	HIS	-	expression tag	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 (three-letter code: CA) (formula: Ca).

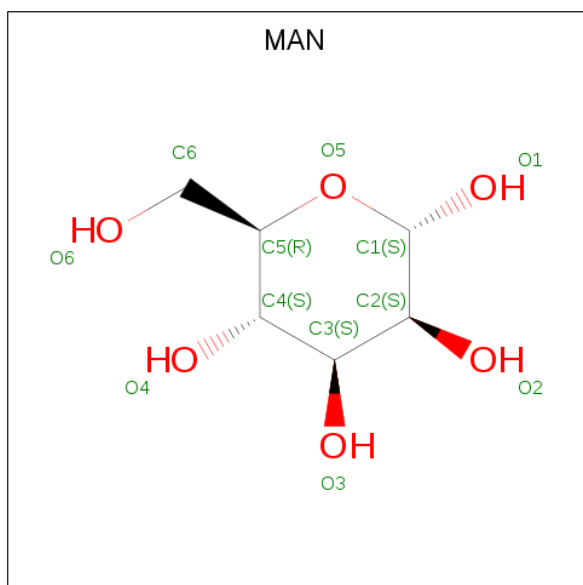
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	9	Total	Ca	0	0
			9	9		
3	A	9	Total	Ca	0	0
			9	9		
3	D	9	Total	Ca	0	0
			9	9		

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

- Molecule 4 is alpha-D-mannopyranose (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



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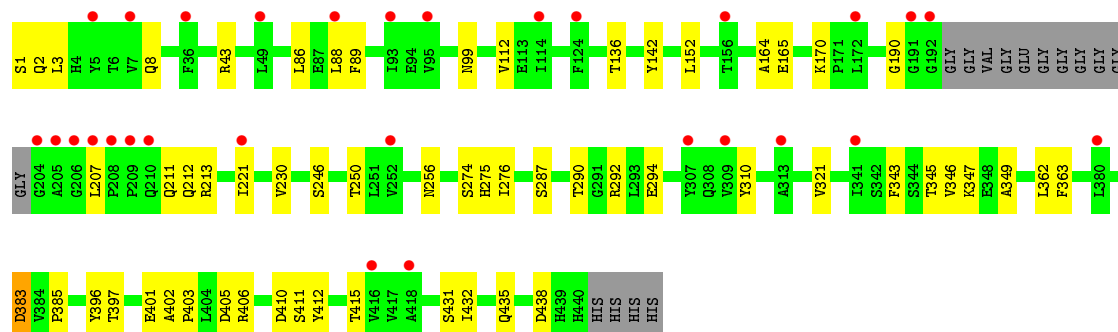
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	H	O	0	0
			22	6	11	5		

- Molecule 5 is water.

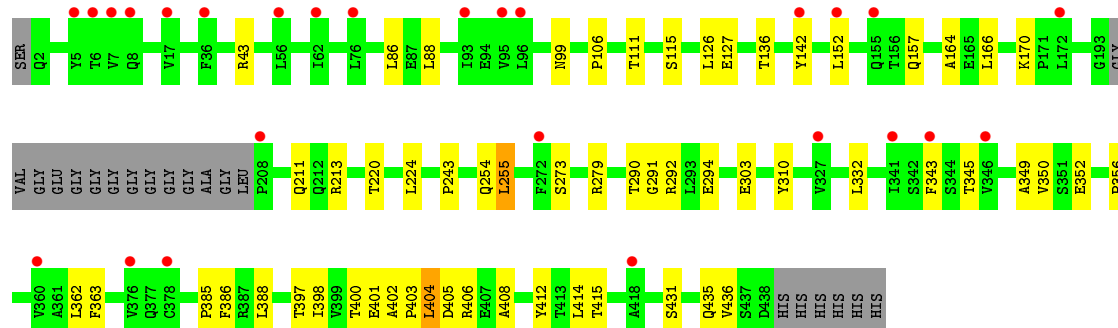
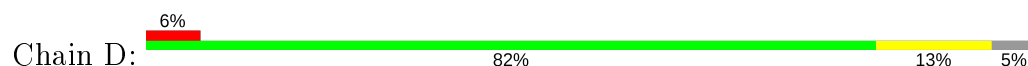
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	5	Total	O	0	0
			5	5		
5	B	5	Total	O	0	0
			5	5		
5	C	4	Total	O	0	0
			4	4		
5	D	4	Total	O	0	0
			4	4		
5	E	5	Total	O	0	0
			5	5		



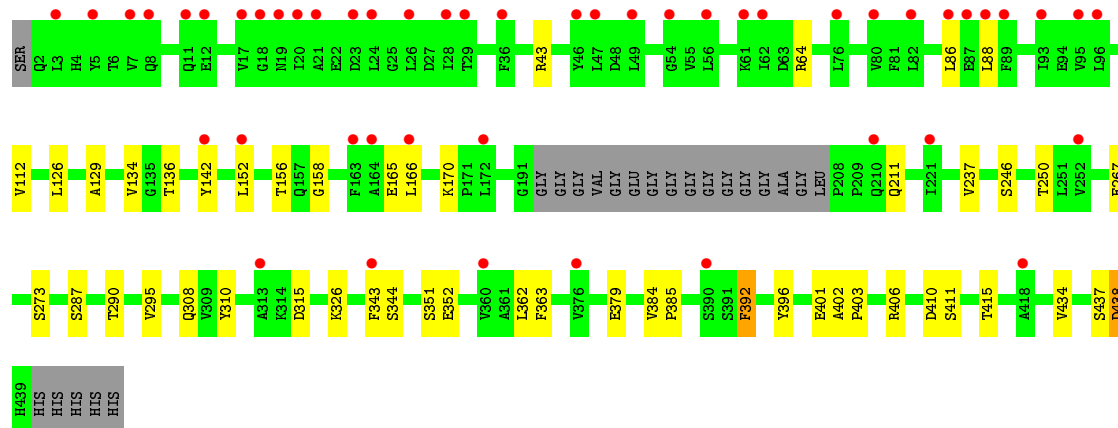
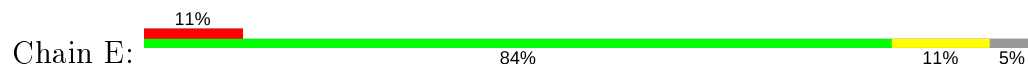




• Molecule 1: Protocadherin-10



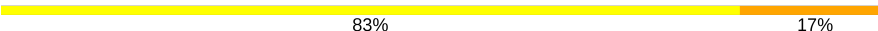
• Molecule 1: Protocadherin-10



• 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

Chain G:  83% 17%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
FUC6

• 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%

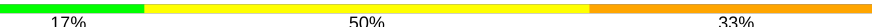
MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
FUC6

• 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 I:  100%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
FUC6

• 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 J:  17% 50% 33%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
FUC6

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	346.55Å 73.19Å 246.33Å 90.00° 132.06° 90.00°	Depositor
Resolution (Å)	19.99 – 3.60 39.82 – 3.60	Depositor EDS
% Data completeness (in resolution range)	93.4 (19.99-3.60) 77.5 (39.82-3.60)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.33 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.277 , 0.295 0.291 , 0.306	Depositor DCC
$R_{free}$ test set	1982 reflections (3.75%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	120.2	Xtriage
Anisotropy	0.669	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 171.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	32989	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

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

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

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	0.28	0/3343	0.50	0/4565
1	B	0.28	0/3342	0.50	0/4563
1	C	0.27	0/3370	0.49	0/4602
1	D	0.26	0/3335	0.49	0/4553
1	E	0.27	0/3338	0.50	0/4558
All	All	0.27	0/16728	0.50	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	50	0
1	C	3304	3152	3178	43	0
1	D	3270	3095	3147	32	0
1	E	3272	3128	3148	25	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	193	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.

All (193) 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:OD1	1:A:383:ASP:N	2.19	0.75
1:A:409:GLY:O	1:A:435:GLN:NE2	2.21	0.74
1:A:234:ASP:OD1	1:A:238:TYR:OH	2.06	0.74
1:E:411:SER:HB2	1:E:434:VAL:O	1.87	0.73
1:D:292:ARG:NH1	1:D:294:GLU:OE2	2.22	0.73
1:E:438:ASP:N	1:E:438:ASP:OD1	2.20	0.72
1:D:385:PRO:O	1:D:401:GLU:HB3	1.88	0.72
1:D:352:GLU:O	1:D:404:LEU:HD11	1.90	0.72
1:D:386:PHE:CE1	1:D:400:THR:HG22	2.26	0.70
1:A:279:ARG:NH2	1:A:303:GLU:OE1	2.25	0.70
1:B:139:LEU:O	1:B:162:ARG:NH1	2.26	0.68
1:E:406:ARG:NH1	1:E:411:SER:O	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:406:ARG:HD3	1:E:410:ASP:OD2	1.94	0.68
1:B:402:ALA:HB1	1:B:403:PRO:HD2	1.78	0.65
1:C:406:ARG:HD2	1:C:412:TYR:CE1	2.31	0.65
1:A:392:PHE:HZ	1:C:1:SER:HB2	1.63	0.64
1:B:292:ARG:NH1	1:B:294:GLU:OE2	2.30	0.64
1:C:383:ASP:N	1:C:383:ASP:OD1	2.29	0.63
1:E:385:PRO:O	1:E:401:GLU:HB3	1.98	0.63
1:B:385:PRO:O	1:B:401:GLU:HB3	2.00	0.62
2:G:2:NAG:O3	2:G:2:NAG:H82	1.98	0.62
1:E:352:GLU:N	1:E:437:SER:O	2.34	0.61
1:A:234:ASP:OD1	1:A:234:ASP:N	2.30	0.61
1:C:287:SER:HG	1:C:290:THR:HG1	1.46	0.61
2:H:2:NAG:O7	2:H:2:NAG:C3	2.51	0.59
1:B:335:ASN:ND2	1:B:424:PRO:O	2.35	0.58
1:A:86:LEU:HD21	1:C:345:THR:HG21	1.86	0.58
1:B:352:GLU:HG3	1:B:437:SER:O	2.04	0.58
1:C:256:ASN:OD1	2:H:1:NAG:N2	2.36	0.58
1:B:231:PRO:HA	1:B:258:THR:O	2.04	0.57
1:A:393:LYS:HB3	1:B:169:GLU:HG3	1.86	0.57
1:A:402:ALA:HB1	1:A:403:PRO:HD2	1.86	0.57
1:C:385:PRO:O	1:C:401:GLU:HB3	2.05	0.57
1:C:276:ILE:HG22	1:C:310:TYR:H	1.70	0.56
1:B:438:ASP:O	1:B:439:HIS:ND1	2.37	0.56
1:A:392:PHE:CZ	1:C:1:SER:HB2	2.39	0.56
1:D:402:ALA:HB1	1:D:403:PRO:HD2	1.87	0.56
1:A:276:ILE:HD13	1:A:309:VAL:HA	1.88	0.56
1:D:388:LEU:HD11	1:D:398:ILE:HG12	1.88	0.55
1:B:169:GLU:OE1	1:B:170:LYS:HB3	2.06	0.55
1:A:357:GLY:N	1:A:400:THR:OG1	2.40	0.55
1:B:148:SER:O	1:B:169:GLU:OE1	2.25	0.55
1:E:343:PHE:CD1	1:E:363:PHE:HB3	2.42	0.54
1:A:169:GLU:OE1	1:A:170:LYS:HB2	2.08	0.54
1:E:287:SER:OG	1:E:290:THR:OG1	2.26	0.54
1:D:356:PRO:HA	1:D:400:THR:OG1	2.08	0.53
1:D:255:LEU:HD12	1:D:291:GLY:O	2.09	0.53
1:D:388:LEU:HD12	1:D:398:ILE:HG12	1.89	0.53
1:B:212:GLN:NE2	4:B:510:MAN:O3	2.40	0.53
1:C:406:ARG:HD3	1:C:410:ASP:CB	2.37	0.53
1:A:387:ARG:NE	1:A:401:GLU:HG3	2.24	0.52
1:D:126:LEU:HD11	1:D:166:LEU:HG	1.92	0.52
1:B:326:LYS:NZ	1:D:157:GLN:OE1	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:TYR:CD2	1:D:164:ALA:HB2	2.46	0.51
2:F:1:NAG:O3	2:F:2:NAG:H2	2.11	0.51
1:B:415:THR:HG23	1:B:431:SER:OG	2.10	0.51
1:E:344:SER:OG	1:E:362:LEU:HB2	2.10	0.51
1:C:415:THR:HG22	1:C:431:SER:HB3	1.93	0.51
1:E:129:ALA:N	1:E:142:TYR:OH	2.39	0.50
1:C:346:VAL:HG11	1:C:432:ILE:HD13	1.93	0.50
1:D:408:ALA:O	1:D:436:VAL:HB	2.12	0.50
2:J:1:NAG:O3	2:J:1:NAG:O7	2.24	0.50
1:D:352:GLU:O	1:D:404:LEU:CD1	2.59	0.49
1:A:148:SER:O	1:A:169:GLU:OE1	2.30	0.49
1:B:360:VAL:HG21	1:B:386:PHE:CE1	2.46	0.49
1:A:356:PRO:HA	1:A:400:THR:OG1	2.12	0.49
1:B:329:VAL:O	1:B:329:VAL:HG13	2.12	0.49
1:C:99:ASN:ND2	1:C:211:GLN:O	2.45	0.49
1:D:279:ARG:NE	1:D:303:GLU:OE2	2.46	0.49
1:B:326:LYS:HE2	1:B:328:LEU:HD13	1.94	0.49
1:A:164:ALA:O	1:C:275:HIS:NE2	2.46	0.49
1:D:352:GLU:O	1:D:404:LEU:CD2	2.56	0.48
2:F:2:NAG:O5	2:F:6:FUC:O2	2.29	0.48
1:A:287:SER:OG	1:A:290:THR:OG1	2.29	0.48
1:A:387:ARG:CZ	1:A:401:GLU:HG3	2.43	0.48
1:A:350:VAL:O	1:A:436:VAL:HA	2.14	0.48
1:A:380:LEU:HD12	1:A:415:THR:O	2.14	0.48
1:C:8:GLN:HG2	1:C:207:LEU:HD22	1.96	0.48
1:C:406:ARG:HD2	1:C:412:TYR:CD1	2.49	0.48
1:D:115:SER:HA	1:D:224:LEU:HB2	1.96	0.48
1:A:408:ALA:O	1:A:436:VAL:O	2.32	0.48
1:A:153:ASP:O	1:A:164:ALA:HA	2.14	0.47
1:A:393:LYS:HB3	1:B:169:GLU:CG	2.43	0.47
1:C:190:GLY:O	1:C:212:GLN:N	2.47	0.47
1:A:437:SER:OG	1:A:438:ASP:N	2.46	0.47
1:C:211:GLN:OE1	1:E:392:PHE:CE1	2.67	0.47
1:A:123:ARG:HA	1:A:166:LEU:O	2.13	0.47
1:B:308:GLN:HE22	1:D:157:GLN:HB3	1.79	0.47
1:A:386:PHE:O	1:A:387:ARG:NH1	2.42	0.47
1:E:402:ALA:HB1	1:E:403:PRO:CD	2.45	0.47
1:A:157:GLN:N	1:A:157:GLN:OE1	2.47	0.47
1:A:273:SER:HB3	1:A:310:TYR:HB3	1.97	0.46
1:B:405:ASP:HB2	1:B:412:TYR:OH	2.15	0.46
1:B:126:LEU:HD11	1:B:166:LEU:HG	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:276:ILE:HG22	1:C:310:TYR:HB2	1.97	0.46
1:B:114:ILE:HD12	1:B:221:ILE:CG2	2.45	0.46
1:E:308:GLN:N	1:E:308:GLN:OE1	2.48	0.46
1:A:418:ALA:O	1:A:427:SER:HA	2.16	0.46
1:C:347:LYS:CD	1:C:349:ALA:O	2.64	0.46
1:B:21:ALA:HB2	1:B:54:GLY:HA3	1.98	0.46
1:C:343:PHE:CD1	1:C:363:PHE:HB3	2.50	0.46
1:D:99:ASN:O	1:D:213:ARG:NH1	2.47	0.46
1:A:154:VAL:HG12	1:A:164:ALA:HB2	1.97	0.45
1:C:142:TYR:CD2	1:C:164:ALA:HB2	2.51	0.45
1:E:126:LEU:HD11	1:E:166:LEU:HG	1.98	0.45
1:B:179:VAL:HA	1:B:221:ILE:O	2.17	0.45
1:D:349:ALA:HA	1:D:435:GLN:O	2.16	0.45
1:D:343:PHE:CD1	1:D:363:PHE:HB3	2.52	0.45
1:E:246:SER:HB3	1:E:250:THR:HG21	1.99	0.45
1:B:386:PHE:CE1	1:B:400:THR:HG22	2.51	0.45
1:B:386:PHE:HE2	1:B:412:TYR:CD2	2.34	0.45
1:A:21:ALA:HB2	1:A:54:GLY:HA3	1.99	0.45
1:C:292:ARG:NH1	1:C:294:GLU:OE2	2.50	0.44
1:E:363:PHE:CZ	1:E:396:TYR:HB2	2.52	0.44
1:A:115:SER:HA	1:A:224:LEU:HB2	1.99	0.44
1:C:1:SER:OG	1:C:2:GLN:N	2.50	0.44
1:A:156:THR:OG1	1:A:162:ARG:HG2	2.17	0.44
1:A:378:CYS:SG	1:A:396:TYR:CZ	3.11	0.44
2:H:2:NAG:O3	2:H:2:NAG:O7	2.33	0.44
1:B:379:GLU:O	1:B:416:VAL:HG23	2.17	0.44
1:C:1:SER:HA	1:C:89:PHE:CD1	2.52	0.44
1:E:237:VAL:HA	1:E:326:LYS:O	2.17	0.44
1:B:267:GLU:O	1:B:315:ASP:HA	2.18	0.43
1:C:1:SER:HA	1:C:89:PHE:HD1	1.83	0.43
1:B:360:VAL:HG21	1:B:386:PHE:HE1	1.82	0.43
1:A:86:LEU:HD22	1:A:87:GLU:N	2.33	0.43
1:C:363:PHE:CZ	1:C:396:TYR:HB2	2.53	0.43
1:A:343:PHE:CD1	1:A:363:PHE:HB3	2.53	0.43
2:J:2:NAG:O3	2:J:5:MAN:H2	2.19	0.43
1:B:114:ILE:HD13	1:B:124:PHE:HE2	1.83	0.43
1:B:415:THR:HG22	1:B:430:LYS:C	2.39	0.43
1:B:405:ASP:O	1:B:406:ARG:HB2	2.19	0.43
1:A:386:PHE:HE2	1:A:412:TYR:CD1	2.37	0.42
1:A:26:LEU:HD13	1:A:82:LEU:HD21	2.01	0.42
1:D:350:VAL:O	1:D:436:VAL:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:GLU:HG3	1:C:274:SER:OG	2.20	0.42
1:B:86:LEU:HD11	1:D:345:THR:HG21	2.02	0.42
1:E:267:GLU:O	1:E:315:ASP:HA	2.19	0.42
1:D:362:LEU:HD22	1:D:397:THR:HG22	2.02	0.42
1:E:250:THR:HG22	1:E:295:VAL:HB	2.00	0.42
2:J:1:NAG:O3	2:J:2:NAG:O5	2.38	0.42
1:B:413:THR:HG22	1:B:433:GLN:HG2	2.01	0.42
1:C:432:ILE:O	1:C:432:ILE:HD12	2.20	0.42
1:D:414:LEU:O	1:D:431:SER:HA	2.18	0.42
1:A:381:LEU:HD11	1:A:417:VAL:HG21	2.01	0.42
1:B:415:THR:CG2	1:B:431:SER:OG	2.67	0.42
1:D:243:PRO:HA	1:D:332:LEU:HB2	2.02	0.42
1:A:276:ILE:HD11	1:A:280:ALA:CB	2.50	0.42
1:B:10:GLU:HG3	1:B:98:ILE:HD11	2.01	0.42
1:C:246:SER:HB3	1:C:250:THR:HG21	2.02	0.42
1:D:106:PRO:HG2	1:D:127:GLU:OE1	2.20	0.42
1:A:362:LEU:HD23	1:A:363:PHE:N	2.34	0.42
1:B:389:LYS:HG2	1:B:390:SER:N	2.35	0.41
1:D:254:GLN:NE2	1:D:290:THR:O	2.53	0.41
1:C:349:ALA:HA	1:C:435:GLN:O	2.20	0.41
1:E:273:SER:HB3	1:E:310:TYR:CB	2.50	0.41
1:A:393:LYS:HD3	1:B:169:GLU:HG2	2.01	0.41
1:B:415:THR:HA	1:B:430:LYS:O	2.19	0.41
1:E:156:THR:HG22	1:E:158:GLY:H	1.84	0.41
1:E:351:SER:HA	1:E:437:SER:O	2.20	0.41
1:C:112:VAL:CG1	1:C:221:ILE:HD13	2.51	0.41
1:C:99:ASN:O	1:C:213:ARG:NH1	2.48	0.41
1:A:392:PHE:HZ	1:C:1:SER:CB	2.32	0.41
1:B:140:ARG:NH2	1:B:212:GLN:OE1	2.48	0.41
1:B:307:TYR:HB2	1:B:329:VAL:CG1	2.50	0.41
1:B:352:GLU:HA	1:B:436:VAL:CG1	2.51	0.41
1:C:362:LEU:HD22	1:C:397:THR:HG22	2.03	0.41
1:C:415:THR:HG22	1:C:431:SER:CB	2.50	0.41
1:D:273:SER:HB3	1:D:310:TYR:CB	2.50	0.41
1:C:411:SER:CB	1:C:435:GLN:HA	2.51	0.41
1:E:402:ALA:HB1	1:E:403:PRO:HD2	2.03	0.41
2:H:2:NAG:H3	2:H:2:NAG:O7	2.19	0.41
1:B:402:ALA:HB1	1:B:403:PRO:CD	2.48	0.40
1:A:415:THR:HG22	1:A:431:SER:OG	2.21	0.40
1:B:388:LEU:CD1	1:B:398:ILE:HG12	2.50	0.40
1:B:418:ALA:O	1:B:427:SER:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:ASN:O	1:B:54:GLY:N	2.53	0.40
1:C:230:VAL:HG22	1:C:321:VAL:HB	2.03	0.40
1:C:362:LEU:CD2	1:C:397:THR:HG22	2.52	0.40
1:C:3:LEU:HA	1:C:3:LEU:HD23	1.97	0.40
1:E:352:GLU:HG3	1:E:437:SER:O	2.21	0.40
1:B:343:PHE:CD1	1:B:363:PHE:HB3	2.56	0.40
1:A:163:PHE:HB3	1:C:275:HIS:CD2	2.56	0.40
1:C:402:ALA:HB1	1:C:403:PRO:CD	2.51	0.40
1:D:111:THR:HG22	1:D:220:THR:HB	2.03	0.40
1:E:64:ARG:NH2	1:E:134:VAL:HG13	2.36	0.40
1:B:273:SER:HB3	1:B:310:TYR:HB3	2.04	0.40
1:B:308:GLN:HG2	1:B:328:LEU:CD1	2.52	0.40
1:B:416:VAL:O	1:B:429:SER:HA	2.22	0.40

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%)	362 (97%)	10 (3%)	44	73
1	B	372/381 (98%)	362 (97%)	10 (3%)	44	73
1	C	373/381 (98%)	363 (97%)	10 (3%)	44	73
1	D	371/381 (97%)	358 (96%)	13 (4%)	36	68
1	E	372/381 (98%)	358 (96%)	14 (4%)	33	66
All	All	1860/1905 (98%)	1803 (97%)	57 (3%)	40	71

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	ARG
1	A	86	LEU
1	A	88	LEU
1	A	110	LEU
1	A	112	VAL
1	A	136	THR
1	A	152	LEU
1	A	234	ASP
1	A	274	SER
1	A	383	ASP
1	B	43	ARG
1	B	86	LEU
1	B	88	LEU
1	B	112	VAL
1	B	136	THR
1	B	170	LYS
1	B	258	THR
1	B	412	TYR
1	B	415	THR
1	B	439	HIS
1	C	43	ARG
1	C	86	LEU
1	C	88	LEU

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Mol	Chain	Res	Type
1	C	136	THR
1	C	152	LEU
1	C	165	GLU
1	C	170	LYS
1	C	383	ASP
1	C	405	ASP
1	C	438	ASP
1	D	43	ARG
1	D	86	LEU
1	D	88	LEU
1	D	136	THR
1	D	152	LEU
1	D	170	LYS
1	D	211	GLN
1	D	255	LEU
1	D	404	LEU
1	D	405	ASP
1	D	406	ARG
1	D	412	TYR
1	D	415	THR
1	E	43	ARG
1	E	86	LEU
1	E	88	LEU
1	E	112	VAL
1	E	136	THR
1	E	152	LEU
1	E	165	GLU
1	E	170	LYS
1	E	211	GLN
1	E	379	GLU
1	E	384	VAL
1	E	392	PHE
1	E	415	THR
1	E	438	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	245	ASN
1	B	275	HIS
1	B	308	GLN
1	C	4	HIS

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Mol	Chain	Res	Type
1	C	41	ASN
1	C	245	ASN
1	D	254	GLN
1	D	377	GLN
1	E	2	GLN
1	E	435	GLN

### 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	1,2	14,14,15	0.70	1 (7%)	17,19,21	1.00	1 (5%)
2	NAG	F	2	2	14,14,15	1.28	1 (7%)	17,19,21	1.17	2 (11%)
2	BMA	F	3	2	11,11,12	1.14	1 (9%)	15,15,17	1.31	3 (20%)
2	MAN	F	4	2	11,11,12	1.12	1 (9%)	15,15,17	1.57	2 (13%)
2	MAN	F	5	2	11,11,12	1.33	2 (18%)	15,15,17	2.18	4 (26%)
2	FUC	F	6	2	10,10,11	1.17	1 (10%)	14,14,16	1.65	3 (21%)
2	NAG	G	1	1,2	14,14,15	0.97	1 (7%)	17,19,21	0.80	0
2	NAG	G	2	2	14,14,15	0.79	1 (7%)	17,19,21	0.87	1 (5%)
2	BMA	G	3	2	11,11,12	1.34	2 (18%)	15,15,17	0.85	0
2	MAN	G	4	2	11,11,12	0.96	1 (9%)	15,15,17	1.15	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MAN	G	5	2	11,11,12	0.86	1 (9%)	15,15,17	1.05	2 (13%)
2	FUC	G	6	2	10,10,11	0.71	0	14,14,16	1.82	4 (28%)
2	NAG	H	1	1,2	14,14,15	0.88	1 (7%)	17,19,21	0.53	0
2	NAG	H	2	2	14,14,15	0.34	0	17,19,21	0.77	1 (5%)
2	BMA	H	3	2	11,11,12	1.50	2 (18%)	15,15,17	1.03	0
2	MAN	H	4	2	11,11,12	1.20	2 (18%)	15,15,17	1.58	3 (20%)
2	MAN	H	5	2	11,11,12	0.90	1 (9%)	15,15,17	1.20	2 (13%)
2	FUC	H	6	2	10,10,11	1.07	1 (10%)	14,14,16	1.10	2 (14%)
2	NAG	I	1	1,2	14,14,15	0.57	1 (7%)	17,19,21	0.82	0
2	NAG	I	2	2	14,14,15	0.87	1 (7%)	17,19,21	0.87	1 (5%)
2	BMA	I	3	2	11,11,12	1.24	2 (18%)	15,15,17	1.41	3 (20%)
2	MAN	I	4	2	11,11,12	0.86	1 (9%)	15,15,17	1.22	2 (13%)
2	MAN	I	5	2	11,11,12	0.92	1 (9%)	15,15,17	1.49	2 (13%)
2	FUC	I	6	2	10,10,11	0.94	0	14,14,16	1.44	3 (21%)
2	NAG	J	1	1,2	14,14,15	0.39	0	17,19,21	0.64	0
2	NAG	J	2	2	14,14,15	0.28	0	17,19,21	0.94	1 (5%)
2	BMA	J	3	2	11,11,12	1.12	1 (9%)	15,15,17	1.17	1 (6%)
2	MAN	J	4	2	11,11,12	0.92	0	15,15,17	1.14	2 (13%)
2	MAN	J	5	2	11,11,12	0.97	1 (9%)	15,15,17	1.29	2 (13%)
2	FUC	J	6	2	10,10,11	0.75	0	14,14,16	0.99	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	1,2	-	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	1,2	-	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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	1,2	-	1/6/23/26	0/1/1/1
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	1,2	-	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	1,2	-	3/6/23/26	0/1/1/1
2	NAG	J	2	2	-	1/6/23/26	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

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	NAG	C1-C2	4.54	1.59	1.52
2	F	5	MAN	C1-C2	3.63	1.60	1.52
2	G	1	NAG	O5-C1	-3.49	1.38	1.43
2	H	4	MAN	C1-C2	3.17	1.59	1.52
2	F	4	MAN	C1-C2	3.14	1.59	1.52
2	H	1	NAG	O5-C1	-3.12	1.38	1.43
2	J	5	MAN	C1-C2	3.08	1.59	1.52
2	F	6	FUC	C1-C2	2.91	1.58	1.52
2	I	3	BMA	O5-C1	-2.80	1.39	1.43
2	I	2	NAG	O5-C1	-2.64	1.39	1.43
2	H	3	BMA	C1-C2	2.63	1.58	1.52
2	G	4	MAN	C1-C2	2.62	1.58	1.52
2	G	3	BMA	C1-C2	2.52	1.58	1.52
2	F	1	NAG	O5-C1	-2.37	1.39	1.43
2	H	3	BMA	C4-C3	2.34	1.58	1.52
2	H	5	MAN	C1-C2	2.32	1.57	1.52
2	I	3	BMA	C4-C5	2.28	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	6	FUC	C1-C2	2.23	1.57	1.52
2	F	5	MAN	O5-C1	2.20	1.47	1.43
2	G	3	BMA	C4-C5	2.15	1.57	1.53
2	F	3	BMA	C4-C5	2.15	1.57	1.53
2	G	2	NAG	C1-C2	2.14	1.55	1.52
2	I	4	MAN	C1-C2	2.12	1.57	1.52
2	H	4	MAN	O5-C5	2.10	1.47	1.43
2	G	5	MAN	C1-C2	2.07	1.56	1.52
2	I	1	NAG	O5-C1	-2.07	1.40	1.43
2	I	5	MAN	C1-C2	2.06	1.56	1.52
2	J	3	BMA	O3-C3	2.04	1.47	1.43

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	5	MAN	C1-O5-C5	6.00	120.33	112.19
2	F	4	MAN	C1-O5-C5	4.62	118.45	112.19
2	H	4	MAN	C1-O5-C5	4.41	118.16	112.19
2	I	5	MAN	C1-O5-C5	4.37	118.11	112.19
2	G	6	FUC	O5-C1-C2	4.13	117.14	110.77
2	F	5	MAN	C1-C2-C3	3.88	114.44	109.67
2	F	6	FUC	C1-C2-C3	3.88	114.44	109.67
2	G	6	FUC	C1-O5-C5	3.67	121.09	112.78
2	I	4	MAN	C1-O5-C5	3.42	116.83	112.19
2	F	6	FUC	C1-O5-C5	3.30	120.25	112.78
2	F	2	NAG	C1-O5-C5	-3.12	107.96	112.19
2	I	3	BMA	C1-O5-C5	3.11	116.41	112.19
2	H	5	MAN	C1-O5-C5	3.08	116.37	112.19
2	H	4	MAN	O2-C2-C3	-3.00	104.12	110.14
2	F	5	MAN	O5-C1-C2	2.97	115.35	110.77
2	J	5	MAN	C1-C2-C3	2.86	113.18	109.67
2	I	6	FUC	C1-C2-C3	2.84	113.16	109.67
2	J	3	BMA	O3-C3-C2	2.79	115.34	109.99
2	J	5	MAN	C1-O5-C5	2.77	115.95	112.19
2	F	3	BMA	O5-C5-C6	2.76	111.53	107.20
2	J	4	MAN	O2-C2-C3	-2.75	104.63	110.14
2	F	4	MAN	O2-C2-C3	-2.74	104.64	110.14
2	F	1	NAG	O4-C4-C5	-2.73	102.52	109.30
2	G	4	MAN	O2-C2-C3	-2.71	104.71	110.14
2	F	5	MAN	O2-C2-C3	-2.70	104.73	110.14
2	I	6	FUC	O5-C5-C4	2.68	114.34	109.52
2	G	4	MAN	C1-O5-C5	2.58	115.68	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	6	FUC	O5-C5-C4	2.53	114.06	109.52
2	G	5	MAN	O2-C2-C3	-2.49	105.15	110.14
2	I	4	MAN	O2-C2-C3	-2.47	105.18	110.14
2	H	2	NAG	C2-N2-C7	2.41	126.33	122.90
2	I	6	FUC	C1-O5-C5	2.40	118.22	112.78
2	F	6	FUC	O5-C1-C2	2.39	114.46	110.77
2	J	4	MAN	C1-O5-C5	2.36	115.39	112.19
2	H	5	MAN	O2-C2-C3	-2.34	105.46	110.14
2	G	6	FUC	C1-C2-C3	2.32	112.52	109.67
2	H	4	MAN	C1-C2-C3	2.32	112.51	109.67
2	F	3	BMA	O5-C1-C2	-2.31	107.20	110.77
2	I	3	BMA	C3-C4-C5	2.30	114.34	110.24
2	H	6	FUC	O5-C5-C4	2.25	113.56	109.52
2	I	5	MAN	O2-C2-C3	-2.23	105.67	110.14
2	G	5	MAN	C1-O5-C5	2.21	115.18	112.19
2	H	6	FUC	C1-O5-C5	2.16	117.67	112.78
2	F	2	NAG	O4-C4-C3	2.15	115.32	110.35
2	G	2	NAG	C2-N2-C7	2.12	125.92	122.90
2	I	3	BMA	O5-C5-C6	-2.08	103.94	107.20
2	J	2	NAG	C1-O5-C5	2.06	114.98	112.19
2	I	2	NAG	C1-O5-C5	-2.04	109.43	112.19
2	F	3	BMA	O6-C6-C5	-2.02	104.37	111.29

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
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
2	I	4	MAN	O5-C5-C6-O6
2	G	2	NAG	C4-C5-C6-O6
2	J	1	NAG	C1-C2-N2-C7
2	F	4	MAN	O5-C5-C6-O6
2	I	2	NAG	C8-C7-N2-C2
2	I	2	NAG	O7-C7-N2-C2
2	G	2	NAG	C8-C7-N2-C2
2	G	2	NAG	O7-C7-N2-C2
2	G	2	NAG	O5-C5-C6-O6
2	H	5	MAN	O5-C5-C6-O6
2	J	5	MAN	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
2	G	4	MAN	O5-C5-C6-O6
2	H	5	MAN	C4-C5-C6-O6
2	G	5	MAN	O5-C5-C6-O6
2	F	2	NAG	C1-C2-N2-C7
2	H	4	MAN	O5-C5-C6-O6
2	J	3	BMA	C4-C5-C6-O6
2	G	3	BMA	C4-C5-C6-O6
2	F	5	MAN	C4-C5-C6-O6
2	F	3	BMA	O5-C5-C6-O6
2	I	5	MAN	O5-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6
2	F	5	MAN	O5-C5-C6-O6
2	J	3	BMA	O5-C5-C6-O6
2	J	1	NAG	O5-C5-C6-O6
2	F	4	MAN	C4-C5-C6-O6
2	J	1	NAG	C3-C2-N2-C7
2	J	2	NAG	C3-C2-N2-C7
2	I	1	NAG	C4-C5-C6-O6
2	I	1	NAG	O5-C5-C6-O6
2	G	3	BMA	O5-C5-C6-O6

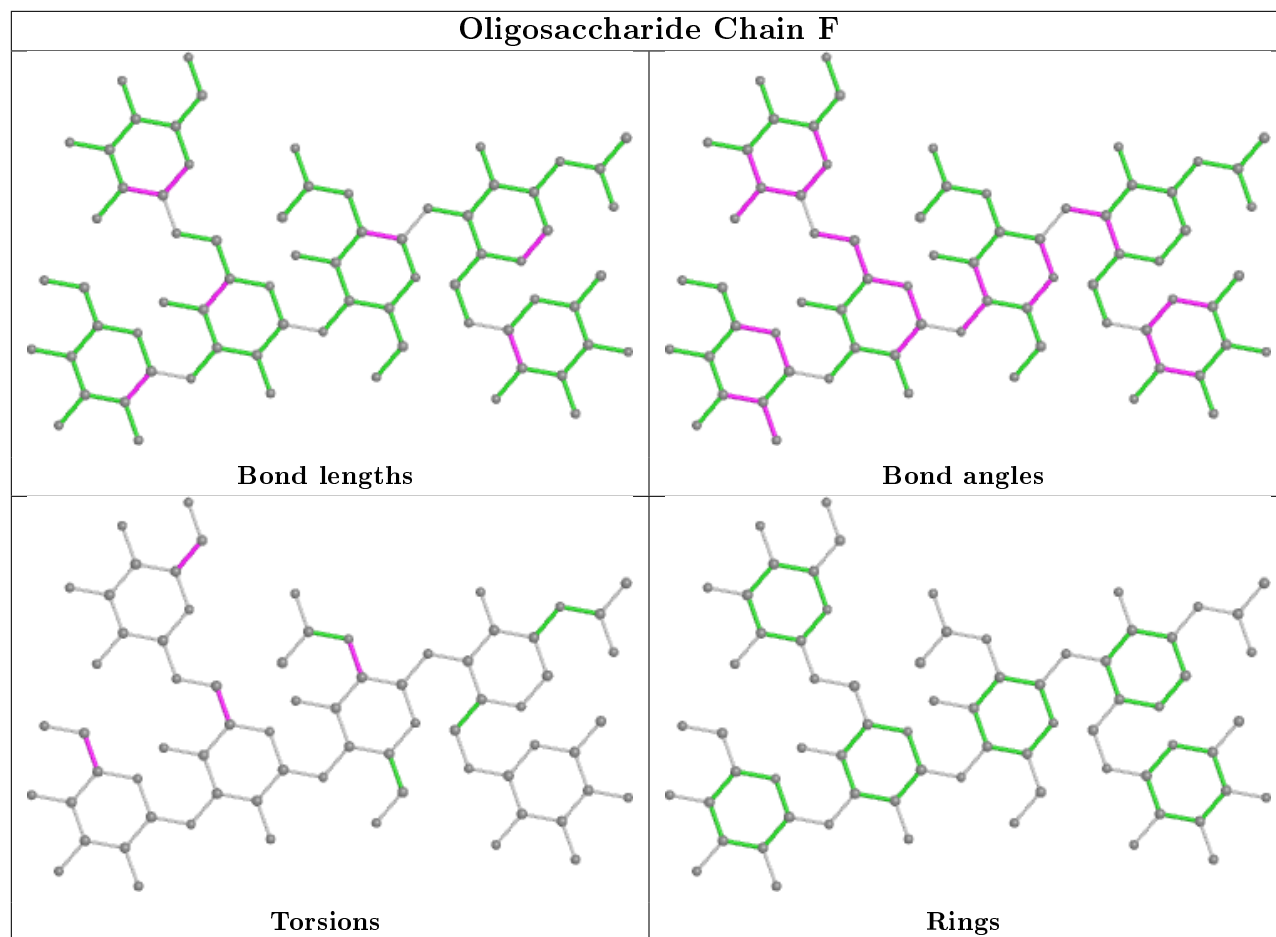
All (1) ring outliers are listed below:

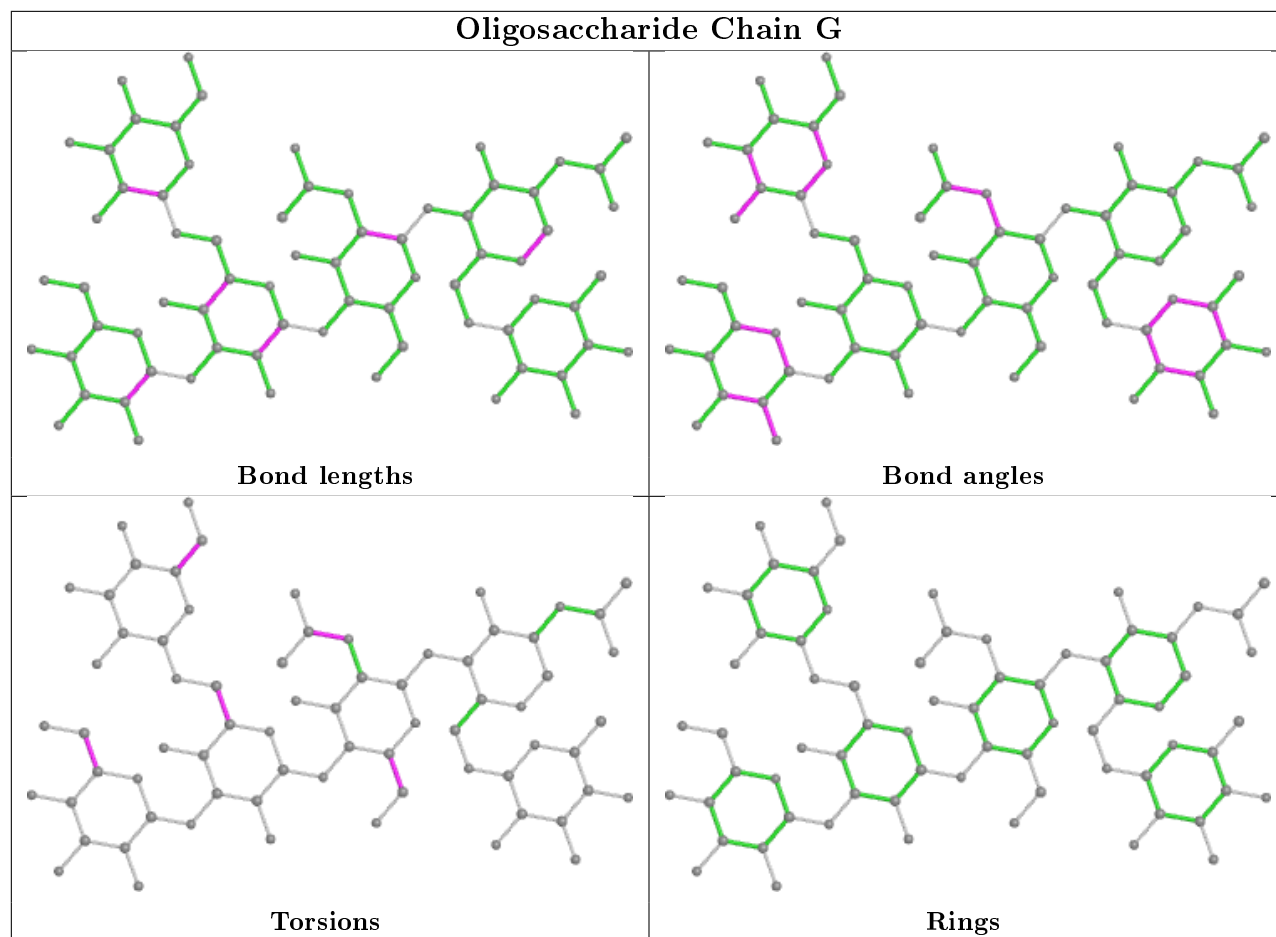
Mol	Chain	Res	Type	Atoms
2	I	5	MAN	C1-C2-C3-C4-C5-O5

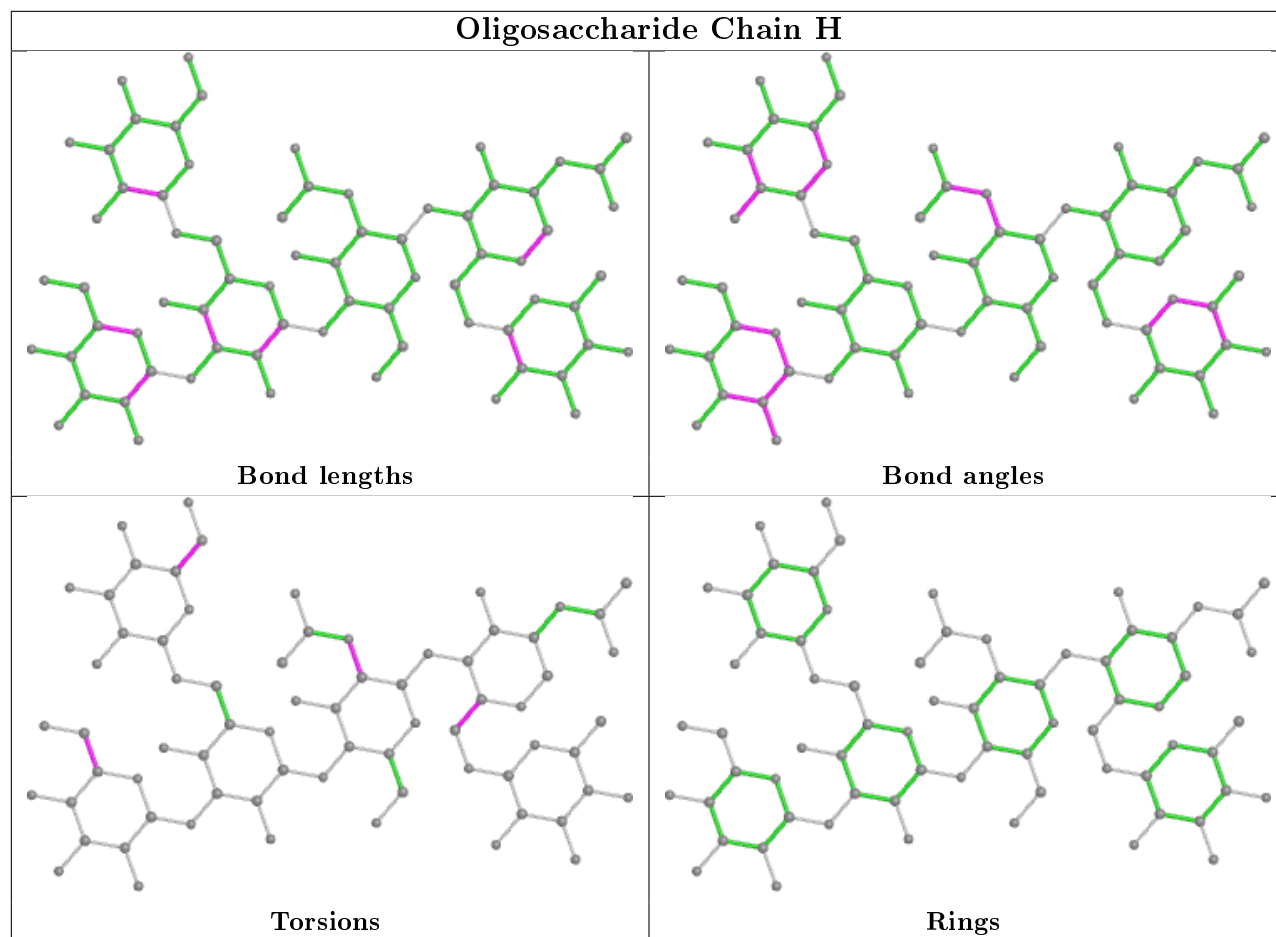
9 monomers are involved in 10 short contacts:

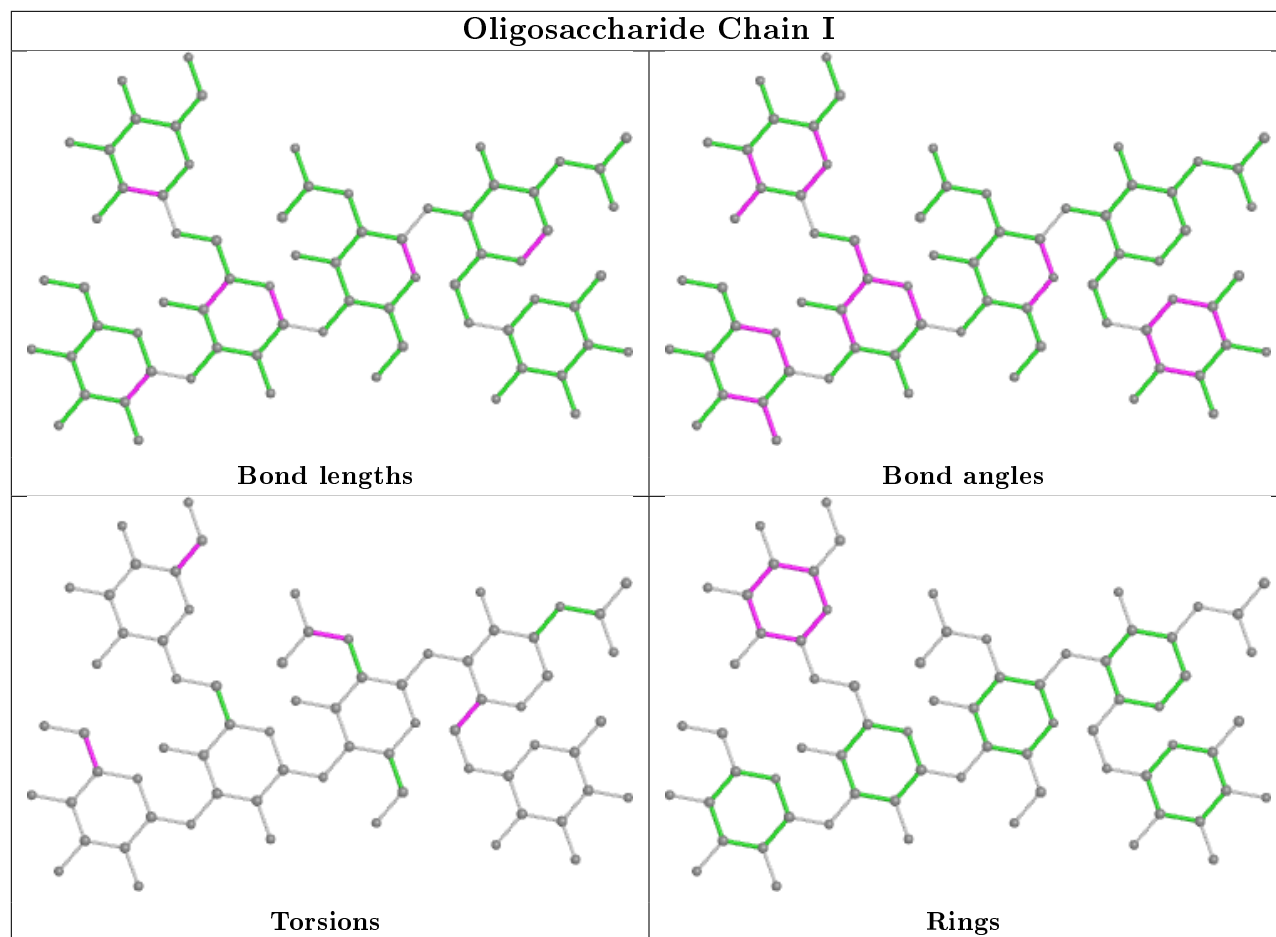
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	6	FUC	1	0
2	F	1	NAG	1	0
2	J	1	NAG	2	0
2	J	2	NAG	2	0
2	J	5	MAN	1	0
2	H	2	NAG	3	0
2	F	2	NAG	2	0
2	G	2	NAG	1	0
2	H	1	NAG	1	0

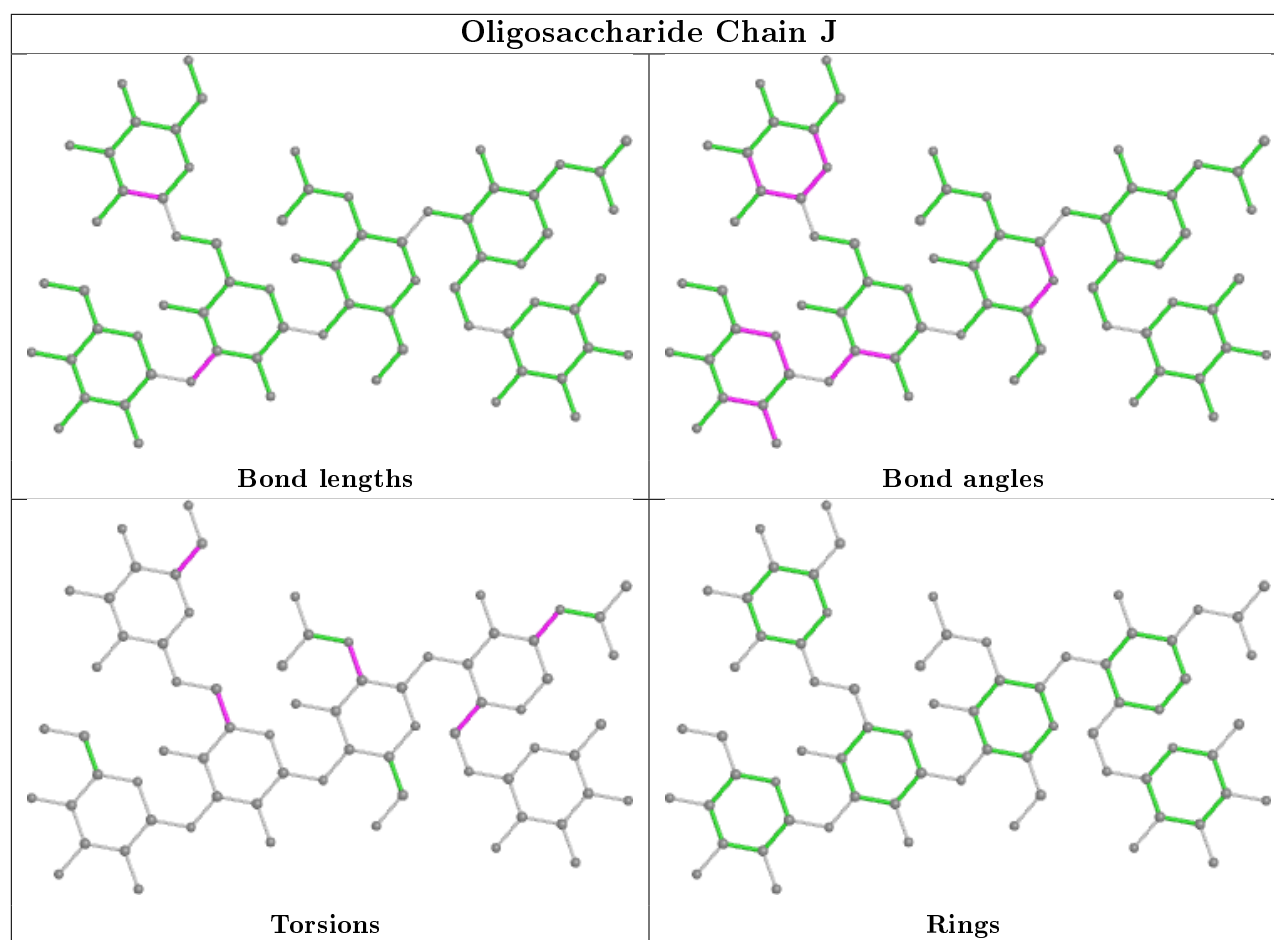
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











## 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	E	511	1	11,11,12	0.80	0	15,15,17	1.00	2 (13%)
4	MAN	B	511	1	11,11,12	0.80	1 (9%)	15,15,17	0.97	2 (13%)
4	MAN	C	511	1	11,11,12	0.91	1 (9%)	15,15,17	0.97	2 (13%)
4	MAN	A	511	1	11,11,12	0.72	0	15,15,17	1.03	2 (13%)
4	MAN	E	510	1	11,11,12	0.79	0	15,15,17	1.13	2 (13%)
4	MAN	C	510	1	11,11,12	0.77	0	15,15,17	1.12	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	0.65	0	15,15,17	1.13	2 (13%)
4	MAN	D	510	1	11,11,12	0.68	0	15,15,17	1.09	2 (13%)
4	MAN	B	510	1	11,11,12	0.65	0	15,15,17	1.08	2 (13%)
4	MAN	D	511	1	11,11,12	0.81	1 (9%)	15,15,17	0.98	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	E	511	1	-	2/2/19/22	0/1/1/1
4	MAN	B	511	1	-	2/2/19/22	0/1/1/1
4	MAN	C	511	1	-	2/2/19/22	0/1/1/1
4	MAN	A	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	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	D	510	1	-	0/2/19/22	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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	511	MAN	O5-C1	-2.41	1.39	1.43
4	B	511	MAN	O5-C1	-2.21	1.40	1.43
4	D	511	MAN	O5-C1	-2.13	1.40	1.43

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	510	MAN	C1-O5-C5	2.92	116.16	112.19
4	C	510	MAN	C1-O5-C5	2.86	116.06	112.19
4	E	510	MAN	C1-O5-C5	2.76	115.93	112.19
4	D	510	MAN	C1-O5-C5	2.74	115.90	112.19
4	B	510	MAN	C1-O5-C5	2.59	115.70	112.19
4	A	511	MAN	C1-O5-C5	2.59	115.70	112.19
4	E	511	MAN	C1-O5-C5	2.42	115.47	112.19
4	C	510	MAN	O2-C2-C3	-2.39	105.34	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	510	MAN	O2-C2-C3	-2.35	105.44	110.14
4	C	511	MAN	O2-C2-C3	-2.33	105.47	110.14
4	D	510	MAN	O2-C2-C3	-2.32	105.48	110.14
4	D	511	MAN	O2-C2-C3	-2.32	105.48	110.14
4	A	510	MAN	O2-C2-C3	-2.29	105.55	110.14
4	A	511	MAN	O2-C2-C3	-2.29	105.56	110.14
4	B	510	MAN	O2-C2-C3	-2.28	105.56	110.14
4	D	511	MAN	C1-O5-C5	2.28	115.28	112.19
4	E	511	MAN	O2-C2-C3	-2.27	105.60	110.14
4	B	511	MAN	O2-C2-C3	-2.24	105.64	110.14
4	B	511	MAN	C1-O5-C5	2.23	115.21	112.19
4	C	511	MAN	C1-O5-C5	2.11	115.05	112.19

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	511	MAN	O5-C5-C6-O6
4	E	511	MAN	O5-C5-C6-O6
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	B	511	MAN	C4-C5-C6-O6
4	D	511	MAN	C4-C5-C6-O6
4	E	511	MAN	C4-C5-C6-O6
4	A	511	MAN	C4-C5-C6-O6
4	C	511	MAN	C4-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

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	423/444 (95%)	0.32	41 (9%) <b>7</b> <b>4</b>	162, 220, 377, 463	0
1	B	423/444 (95%)	0.18	33 (7%) <b>13</b> <b>8</b>	173, 220, 376, 461	0
1	C	429/444 (96%)	0.09	29 (6%) <b>17</b> <b>10</b>	179, 232, 287, 362	0
1	D	423/444 (95%)	0.12	26 (6%) <b>21</b> <b>12</b>	187, 238, 306, 375	0
1	E	422/444 (95%)	0.25	49 (11%) <b>4</b> <b>3</b>	173, 239, 345, 398	0
All	All	2120/2220 (95%)	0.19	178 (8%) <b>11</b> <b>7</b>	162, 230, 350, 463	0

All (178) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	46	TYR	8.8
1	B	49	LEU	8.6
1	A	88	LEU	8.5
1	D	8	GLN	7.6
1	B	62	ILE	7.6
1	C	207	LEU	7.1
1	B	8	GLN	6.8
1	C	205	ALA	6.8
1	A	87	GLU	6.6
1	A	62	ILE	6.4
1	D	7	VAL	6.4
1	C	204	GLY	6.0
1	B	47	LEU	5.9
1	C	209	PRO	5.8
1	C	210	GLN	5.7
1	E	62	ILE	5.7
1	E	3	LEU	5.6
1	D	96	LEU	5.5
1	A	96	LEU	5.4
1	D	208	PRO	5.2

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Mol	Chain	Res	Type	RSRZ
1	D	5	TYR	5.2
1	E	20	ILE	5.2
1	B	46	TYR	5.1
1	D	95	VAL	4.9
1	E	88	LEU	4.9
1	E	93	ILE	4.9
1	A	7	VAL	4.8
1	C	206	GLY	4.8
1	A	93	ILE	4.7
1	A	49	LEU	4.7
1	A	5	TYR	4.6
1	A	17	VAL	4.6
1	B	26	LEU	4.6
1	C	208	PRO	4.6
1	E	95	VAL	4.4
1	E	26	LEU	4.4
1	A	8	GLN	4.4
1	A	20	ILE	4.3
1	A	47	LEU	4.3
1	E	28	ILE	4.3
1	B	7	VAL	4.3
1	A	86	LEU	4.2
1	D	62	ILE	4.2
1	E	56	LEU	4.2
1	A	80	VAL	4.1
1	A	26	LEU	4.0
1	A	61	LYS	4.0
1	D	36	PHE	3.9
1	A	89	PHE	3.9
1	A	52	GLU	3.9
1	B	11	GLN	3.8
1	A	48	ASP	3.8
1	A	24	LEU	3.8
1	B	95	VAL	3.7
1	B	96	LEU	3.7
1	C	341	ILE	3.7
1	A	95	VAL	3.7
1	A	11	GLN	3.6
1	A	81	PHE	3.6
1	E	89	PHE	3.6
1	C	114	ILE	3.5
1	A	56	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	11	GLN	3.5
1	E	49	LEU	3.5
1	B	391	SER	3.5
1	D	142	TYR	3.5
1	C	221	ILE	3.4
1	C	93	ILE	3.4
1	E	17	VAL	3.4
1	D	93	ILE	3.4
1	A	12	GLU	3.3
1	D	343	PHE	3.2
1	C	95	VAL	3.2
1	A	82	LEU	3.2
1	E	46	TYR	3.2
1	B	142	TYR	3.1
1	C	380	LEU	3.1
1	E	164	ALA	3.1
1	C	416	VAL	3.1
1	D	341	ILE	3.1
1	E	142	TYR	3.0
1	A	391	SER	3.0
1	B	360	VAL	3.0
1	E	36	PHE	3.0
1	E	24	LEU	3.0
1	C	418	ALA	3.0
1	E	376	VAL	3.0
1	A	6	THR	2.9
1	B	52	GLU	2.9
1	C	307	TYR	2.9
1	D	346	VAL	2.9
1	E	80	VAL	2.9
1	E	96	LEU	2.9
1	C	192	GLY	2.8
1	A	38	THR	2.8
1	C	36	PHE	2.8
1	D	172	LEU	2.8
1	B	88	LEU	2.8
1	E	54	GLY	2.8
1	E	47	LEU	2.8
1	A	84	ASN	2.8
1	C	191	GLY	2.7
1	D	378	CYS	2.7
1	A	36	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	82	LEU	2.7
1	D	17	VAL	2.6
1	B	48	ASP	2.6
1	E	21	ALA	2.6
1	C	172	LEU	2.6
1	D	56	LEU	2.6
1	B	36	PHE	2.6
1	A	37	GLN	2.5
1	D	272	PHE	2.5
1	E	360	VAL	2.5
1	E	172	LEU	2.5
1	B	51	LEU	2.5
1	D	6	THR	2.5
1	C	88	LEU	2.5
1	C	252	VAL	2.5
1	A	83	GLU	2.4
1	C	124	PHE	2.4
1	C	5	TYR	2.4
1	E	8	GLN	2.4
1	E	343	PHE	2.4
1	E	86	LEU	2.4
1	B	76	LEU	2.4
1	E	5	TYR	2.4
1	B	20	ILE	2.4
1	B	82	LEU	2.3
1	A	139	LEU	2.3
1	D	152	LEU	2.3
1	B	60	GLU	2.3
1	B	341	ILE	2.3
1	A	3	LEU	2.3
1	B	50	ASN	2.3
1	E	163	PHE	2.3
1	E	76	LEU	2.3
1	E	166	LEU	2.3
1	A	58	VAL	2.3
1	D	76	LEU	2.3
1	E	252	VAL	2.3
1	B	394	ASN	2.2
1	E	23	ASP	2.2
1	A	390	SER	2.2
1	B	61	LYS	2.2
1	D	155	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	87	GLU	2.2
1	B	361	ALA	2.2
1	E	19	ASN	2.2
1	E	418	ALA	2.1
1	E	29	THR	2.1
1	B	86	LEU	2.1
1	D	376	VAL	2.1
1	A	272	PHE	2.1
1	E	18	GLY	2.1
1	E	313	ALA	2.1
1	E	210	GLN	2.1
1	E	61	LYS	2.1
1	B	24	LEU	2.1
1	D	360	VAL	2.1
1	C	309	VAL	2.1
1	C	156	THR	2.1
1	B	398	ILE	2.1
1	E	221	ILE	2.1
1	E	152	LEU	2.1
1	B	37	GLN	2.0
1	C	7	VAL	2.0
1	A	124	PHE	2.0
1	C	313	ALA	2.0
1	B	58	VAL	2.0
1	E	7	VAL	2.0
1	A	393	LYS	2.0
1	E	12	GLU	2.0
1	D	418	ALA	2.0
1	D	327	VAL	2.0
1	E	390	SER	2.0
1	B	390	SER	2.0
1	C	49	LEU	2.0

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

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

## 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

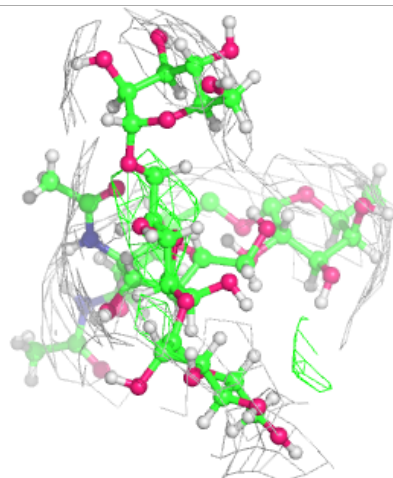
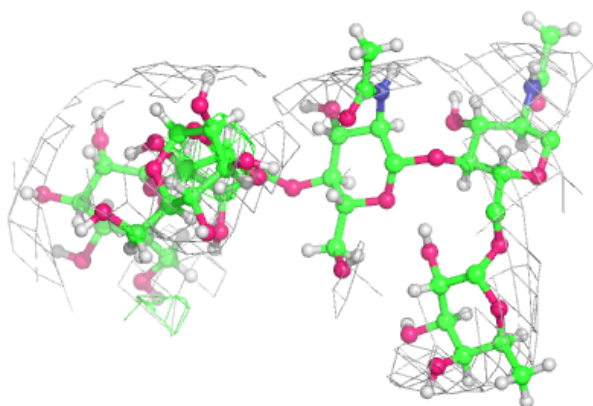
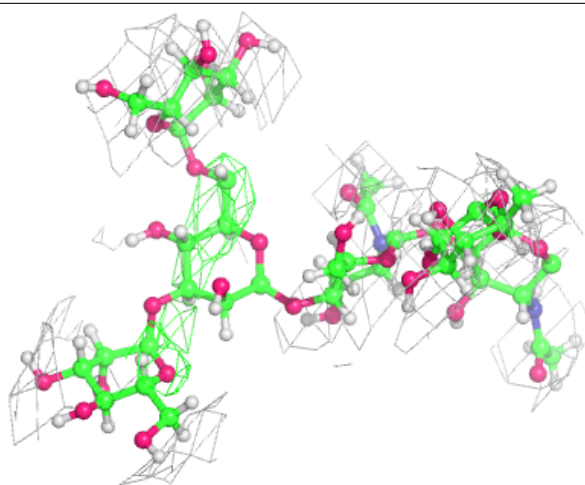
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	BMA	H	3	11/12	0.36	0.18	428,455,555,593	0
2	MAN	H	4	11/12	0.40	0.17	411,474,516,568	0
2	MAN	J	4	11/12	0.63	0.18	357,379,448,466	0
2	FUC	J	6	10/11	0.69	0.33	300,336,390,403	0
2	FUC	I	6	10/11	0.70	0.42	370,430,486,516	0
2	MAN	I	4	11/12	0.76	0.20	351,385,448,462	0
2	BMA	F	3	11/12	0.77	0.06	357,397,469,476	0
2	BMA	I	3	11/12	0.79	0.12	380,412,494,504	0
2	FUC	G	6	10/11	0.80	0.20	363,410,484,492	0
2	MAN	G	5	11/12	0.81	0.16	272,368,441,487	0
2	NAG	H	2	14/15	0.82	0.15	381,422,502,506	0
2	MAN	F	5	11/12	0.82	0.18	350,381,431,458	0
2	MAN	I	5	11/12	0.82	0.12	388,425,490,508	0
2	NAG	I	1	14/15	0.82	0.14	305,357,429,441	0
2	NAG	I	2	14/15	0.83	0.10	281,353,442,450	0
2	MAN	G	4	11/12	0.83	0.16	361,426,495,562	0
2	MAN	H	5	11/12	0.84	0.36	378,430,509,516	0
2	BMA	G	3	11/12	0.85	0.15	321,350,420,420	0
2	MAN	F	4	11/12	0.86	0.10	361,414,473,521	0
2	NAG	J	2	14/15	0.88	0.11	351,380,466,466	0
2	NAG	G	1	14/15	0.88	0.13	285,304,357,400	0
2	NAG	H	1	14/15	0.89	0.22	363,413,496,560	0
2	BMA	J	3	11/12	0.89	0.06	290,348,409,426	0
2	FUC	H	6	10/11	0.91	0.12	329,374,449,449	0
2	MAN	J	5	11/12	0.92	0.08	342,409,451,491	0
2	NAG	F	1	14/15	0.92	0.12	247,283,348,351	0
2	NAG	G	2	14/15	0.94	0.14	276,340,451,451	0
2	NAG	F	2	14/15	0.94	0.11	305,389,476,540	0
2	NAG	J	1	14/15	0.95	0.13	242,325,404,426	0
2	FUC	F	6	10/11	0.96	0.12	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.



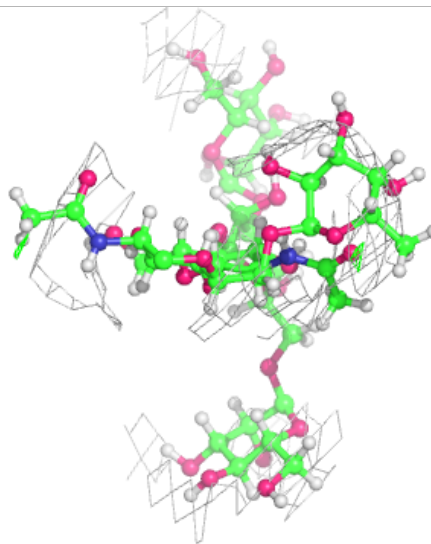
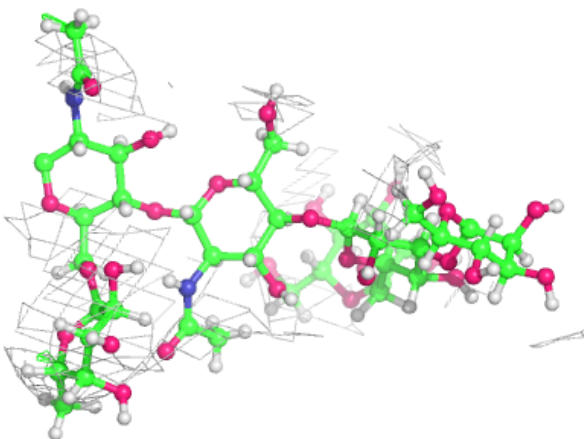
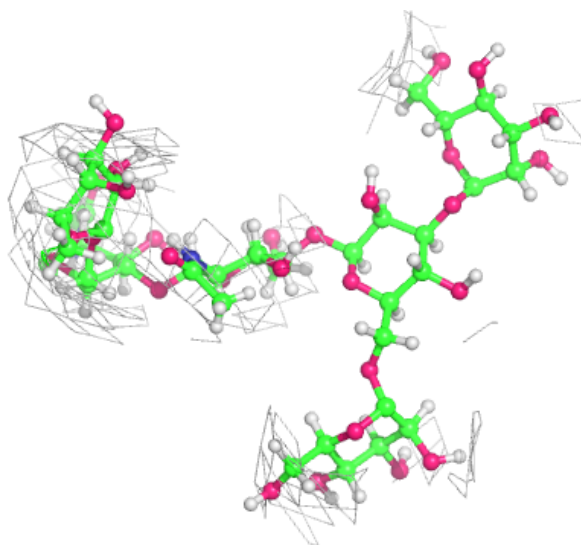
**Electron density around Chain F:**

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



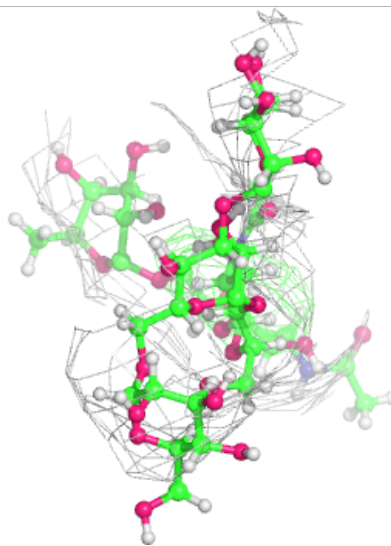
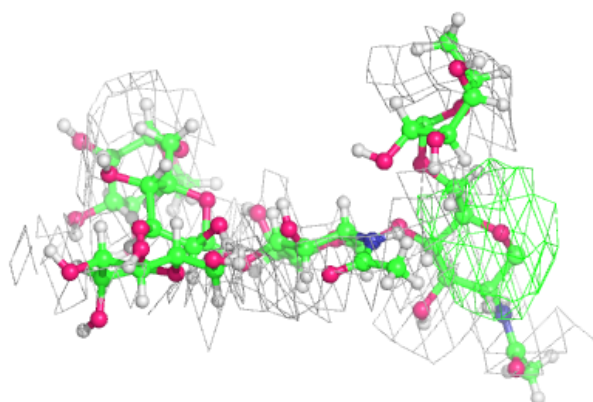
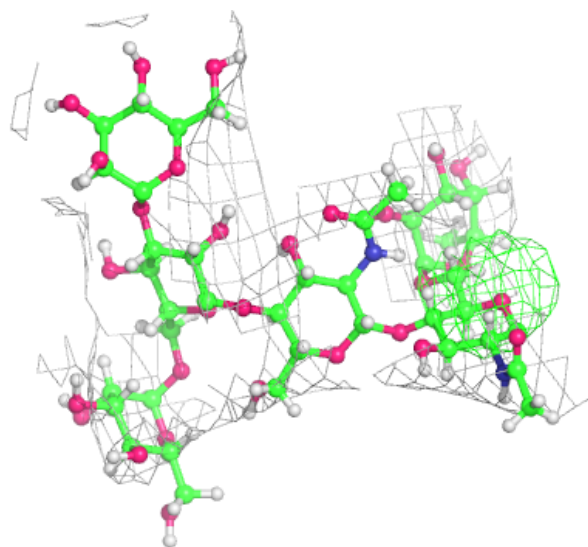
**Electron density around Chain G:**

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



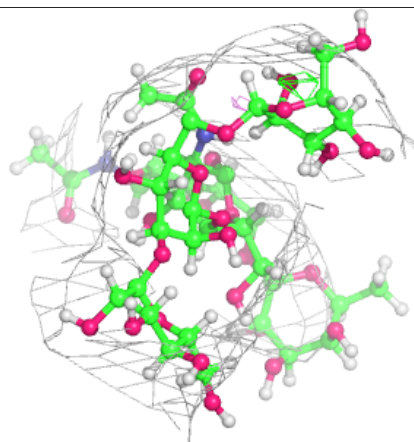
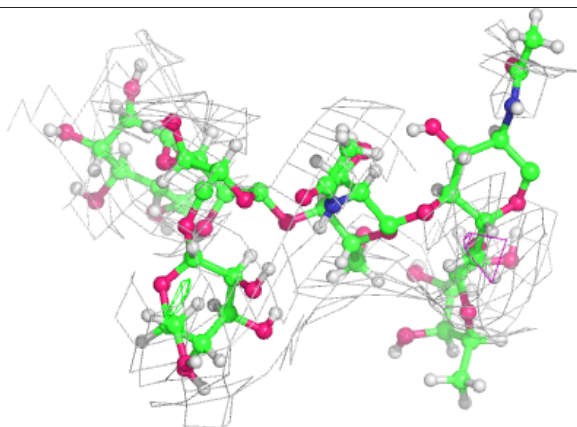
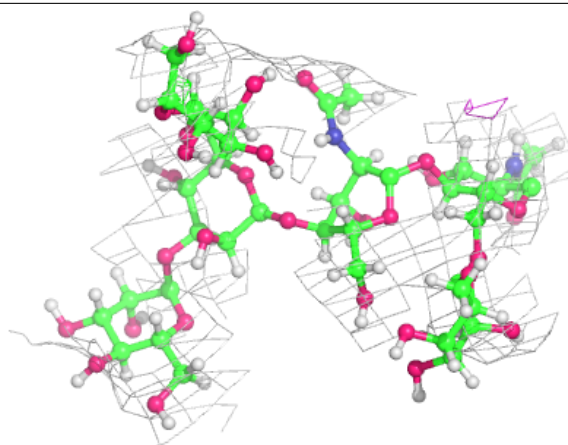
**Electron density around Chain H:**

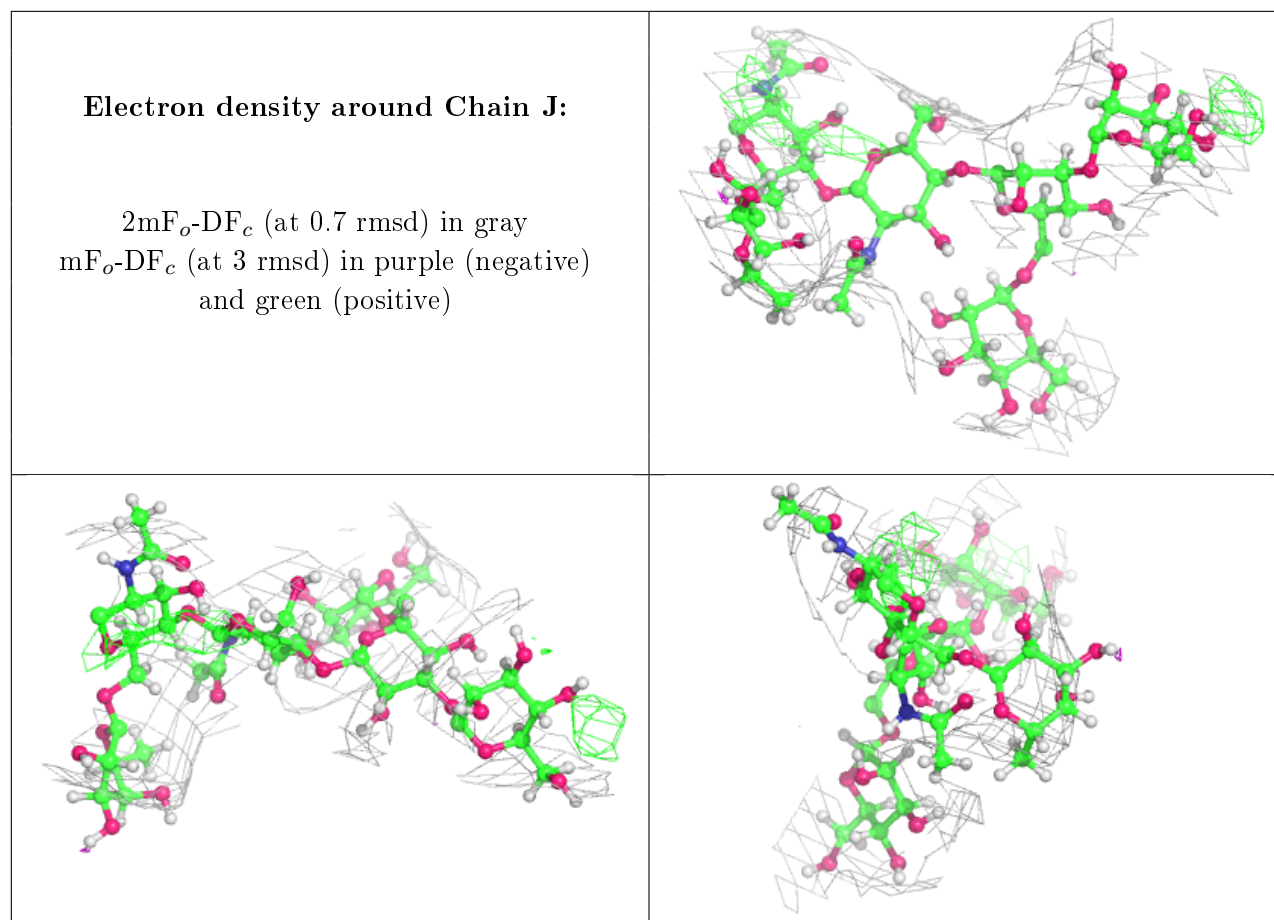
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	CA	C	501	1/1	0.40	0.19	277,277,277,277	0
4	MAN	D	510	11/12	0.62	0.35	298,325,384,391	0
3	CA	E	503	1/1	0.63	0.14	277,277,277,277	0
3	CA	A	501	1/1	0.63	0.24	475,475,475,475	0
3	CA	C	505	1/1	0.67	0.21	203,203,203,203	0
4	MAN	D	511	11/12	0.67	0.36	302,322,385,387	0
4	MAN	C	511	11/12	0.69	0.33	293,324,381,388	0
4	MAN	C	510	11/12	0.75	0.46	295,328,387,394	0
3	CA	E	502	1/1	0.76	0.16	258,258,258,258	0
3	CA	B	502	1/1	0.76	0.13	269,269,269,269	0
4	MAN	E	511	11/12	0.79	0.32	455,564,628,754	0
4	MAN	E	510	11/12	0.79	0.52	325,354,414,425	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CA	D	508	1/1	0.81	0.17	207,207,207,207	0
3	CA	B	501	1/1	0.81	0.13	553,553,553,553	0
3	CA	A	508	1/1	0.82	0.28	203,203,203,203	0
4	MAN	A	511	11/12	0.82	0.18	318,357,422,428	0
3	CA	D	506	1/1	0.85	0.24	203,203,203,203	0
4	MAN	B	511	11/12	0.85	0.18	283,315,374,379	0
4	MAN	B	510	11/12	0.85	0.25	252,311,373,375	0
4	MAN	A	510	11/12	0.86	0.19	283,307,356,368	0
3	CA	A	509	1/1	0.89	0.20	203,203,203,203	0
3	CA	A	502	1/1	0.89	0.12	254,254,254,254	0
3	CA	A	506	1/1	0.91	0.24	203,203,203,203	0
3	CA	B	505	1/1	0.91	0.25	219,219,219,219	0
3	CA	E	505	1/1	0.92	0.28	231,231,231,231	0
3	CA	D	501	1/1	0.92	0.24	277,277,277,277	0
3	CA	B	507	1/1	0.93	0.30	297,297,297,297	0
3	CA	D	507	1/1	0.93	0.17	206,206,206,206	0
3	CA	A	503	1/1	0.93	0.16	225,225,225,225	0
3	CA	C	509	1/1	0.93	0.22	205,205,205,205	0
3	CA	A	505	1/1	0.94	0.23	203,203,203,203	0
3	CA	E	506	1/1	0.94	0.25	203,203,203,203	0
3	CA	D	503	1/1	0.94	0.13	227,227,227,227	0
3	CA	C	503	1/1	0.95	0.14	208,208,208,208	0
3	CA	B	509	1/1	0.96	0.19	211,211,211,211	0
3	CA	D	504	1/1	0.96	0.20	223,223,223,223	0
3	CA	D	505	1/1	0.96	0.21	203,203,203,203	0
3	CA	C	508	1/1	0.96	0.22	217,217,217,217	0
3	CA	D	502	1/1	0.96	0.16	231,231,231,231	0
3	CA	C	506	1/1	0.96	0.20	203,203,203,203	0
3	CA	E	504	1/1	0.96	0.23	243,243,243,243	0
3	CA	E	507	1/1	0.96	0.21	218,218,218,218	0
3	CA	B	508	1/1	0.97	0.25	203,203,203,203	0
3	CA	A	507	1/1	0.97	0.28	203,203,203,203	0
3	CA	E	508	1/1	0.97	0.18	203,203,203,203	0
3	CA	E	501	1/1	0.97	0.27	333,333,333,333	0
3	CA	B	503	1/1	0.97	0.08	272,272,272,272	0
3	CA	B	504	1/1	0.98	0.18	219,219,219,219	0
3	CA	D	509	1/1	0.98	0.11	223,223,223,223	0
3	CA	E	509	1/1	0.98	0.16	224,224,224,224	0
3	CA	C	502	1/1	0.98	0.18	219,219,219,219	0
3	CA	A	504	1/1	0.99	0.20	203,203,203,203	0
3	CA	B	506	1/1	0.99	0.25	203,203,203,203	0
3	CA	C	507	1/1	0.99	0.22	203,203,203,203	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CA	C	504	1/1	0.99	0.19	254,254,254,254	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.