wwPDB X-ray Structure Validation Summary Report (i)

Oct 11, 2023 – 06:48 AM EDT

PDB ID	:	7N86
Title	:	Crystal Structure of Human Protocadherin-24 EC1-2 Form II
Authors	:	Modak, D.; Gray, M.E.; Sotomayor, M.
Deposited on	:	2021-06-13
Resolution	:	3.17 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 (i)) were used in the production of this report:

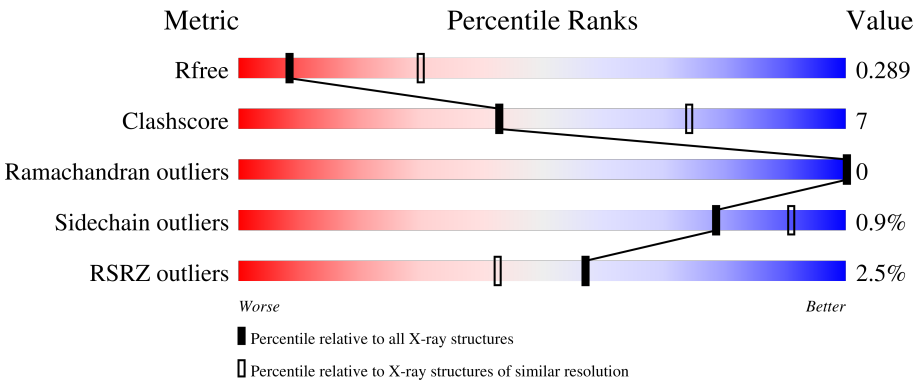
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.17 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	1467 (3.20-3.16)
Clashscore	141614	1599 (3.20-3.16)
Ramachandran outliers	138981	1574 (3.20-3.16)
Sidechain outliers	138945	1573 (3.20-3.16)
RSRZ outliers	127900	1423 (3.20-3.16)

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	238	% 77% 12% • 10%
1	B	238	3% 74% 15% • 11%
1	C	238	3% 71% 18% 12%
1	D	238	2% 72% 16% 12%
2	E	3	100%

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Mol	Chain	Length	Quality of chain
2	F	3	67% 33%
2	G	3	33% 67%
2	H	3	100%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 6720 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 Cadherin-related family member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	1648	1058	258	324	8	0	0	0
1	B	213	1636	1051	256	321	8	0	0	0
1	C	210	1604	1031	250	315	8	0	0	0
1	D	210	1612	1037	251	316	8	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	221	THR	-	expression tag	UNP Q9BYE9
A	222	VAL	-	expression tag	UNP Q9BYE9
A	223	PRO	-	expression tag	UNP Q9BYE9
A	224	ARG	-	expression tag	UNP Q9BYE9
A	225	ALA	-	expression tag	UNP Q9BYE9
A	226	ARG	-	expression tag	UNP Q9BYE9
A	227	ASP	-	expression tag	UNP Q9BYE9
A	228	PRO	-	expression tag	UNP Q9BYE9
A	229	PRO	-	expression tag	UNP Q9BYE9
A	230	VAL	-	expression tag	UNP Q9BYE9
A	231	GLY	-	expression tag	UNP Q9BYE9
A	232	GLY	-	expression tag	UNP Q9BYE9
A	233	HIS	-	expression tag	UNP Q9BYE9
A	234	HIS	-	expression tag	UNP Q9BYE9
A	235	HIS	-	expression tag	UNP Q9BYE9
A	236	HIS	-	expression tag	UNP Q9BYE9
A	237	HIS	-	expression tag	UNP Q9BYE9
A	238	HIS	-	expression tag	UNP Q9BYE9
B	221	THR	-	expression tag	UNP Q9BYE9
B	222	VAL	-	expression tag	UNP Q9BYE9
B	223	PRO	-	expression tag	UNP Q9BYE9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	224	ARG	-	expression tag	UNP Q9BYE9
B	225	ALA	-	expression tag	UNP Q9BYE9
B	226	ARG	-	expression tag	UNP Q9BYE9
B	227	ASP	-	expression tag	UNP Q9BYE9
B	228	PRO	-	expression tag	UNP Q9BYE9
B	229	PRO	-	expression tag	UNP Q9BYE9
B	230	VAL	-	expression tag	UNP Q9BYE9
B	231	GLY	-	expression tag	UNP Q9BYE9
B	232	GLY	-	expression tag	UNP Q9BYE9
B	233	HIS	-	expression tag	UNP Q9BYE9
B	234	HIS	-	expression tag	UNP Q9BYE9
B	235	HIS	-	expression tag	UNP Q9BYE9
B	236	HIS	-	expression tag	UNP Q9BYE9
B	237	HIS	-	expression tag	UNP Q9BYE9
B	238	HIS	-	expression tag	UNP Q9BYE9
C	221	THR	-	expression tag	UNP Q9BYE9
C	222	VAL	-	expression tag	UNP Q9BYE9
C	223	PRO	-	expression tag	UNP Q9BYE9
C	224	ARG	-	expression tag	UNP Q9BYE9
C	225	ALA	-	expression tag	UNP Q9BYE9
C	226	ARG	-	expression tag	UNP Q9BYE9
C	227	ASP	-	expression tag	UNP Q9BYE9
C	228	PRO	-	expression tag	UNP Q9BYE9
C	229	PRO	-	expression tag	UNP Q9BYE9
C	230	VAL	-	expression tag	UNP Q9BYE9
C	231	GLY	-	expression tag	UNP Q9BYE9
C	232	GLY	-	expression tag	UNP Q9BYE9
C	233	HIS	-	expression tag	UNP Q9BYE9
C	234	HIS	-	expression tag	UNP Q9BYE9
C	235	HIS	-	expression tag	UNP Q9BYE9
C	236	HIS	-	expression tag	UNP Q9BYE9
C	237	HIS	-	expression tag	UNP Q9BYE9
C	238	HIS	-	expression tag	UNP Q9BYE9
D	221	THR	-	expression tag	UNP Q9BYE9
D	222	VAL	-	expression tag	UNP Q9BYE9
D	223	PRO	-	expression tag	UNP Q9BYE9
D	224	ARG	-	expression tag	UNP Q9BYE9
D	225	ALA	-	expression tag	UNP Q9BYE9
D	226	ARG	-	expression tag	UNP Q9BYE9
D	227	ASP	-	expression tag	UNP Q9BYE9
D	228	PRO	-	expression tag	UNP Q9BYE9
D	229	PRO	-	expression tag	UNP Q9BYE9

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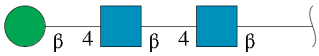
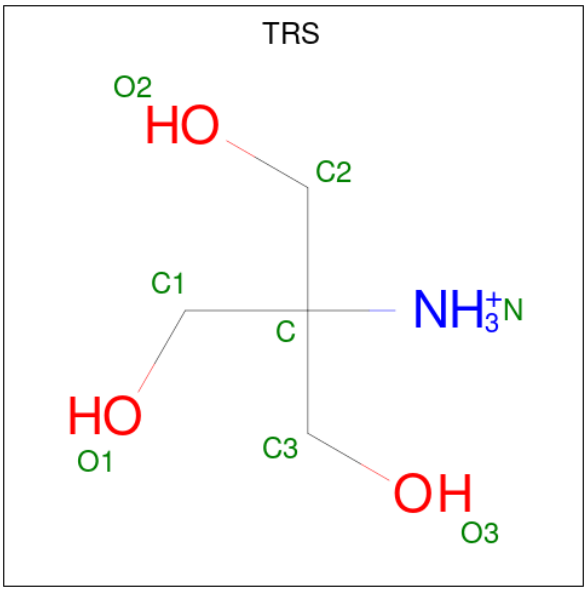
Chain	Residue	Modelled	Actual	Comment	Reference
D	230	VAL	-	expression tag	UNP Q9BYE9
D	231	GLY	-	expression tag	UNP Q9BYE9
D	232	GLY	-	expression tag	UNP Q9BYE9
D	233	HIS	-	expression tag	UNP Q9BYE9
D	234	HIS	-	expression tag	UNP Q9BYE9
D	235	HIS	-	expression tag	UNP Q9BYE9
D	236	HIS	-	expression tag	UNP Q9BYE9
D	237	HIS	-	expression tag	UNP Q9BYE9
D	238	HIS	-	expression tag	UNP Q9BYE9

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	3	39	22	2	15	0	0	0
			Total	C	N	O			
2	F	3	39	22	2	15	0	0	0
			Total	C	N	O			
2	G	3	39	22	2	15	0	0	0
			Total	C	N	O			
2	H	3	39	22	2	15	0	0	0

- Molecule 3 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
			Total	C	N	O		
3	A	1	8	4	1	3	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	A	3	3	3	0	0
4	B	3	3	3	0	0
4	C	4	4	4	0	0
4	D	4	4	4	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
5	A	1	1	1	0	0
5	B	1	1	1	0	0
5	C	3	3	3	0	0
5	D	1	1	1	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Na 1 1	0	0
6	B	1	Total Na 1 1	0	0

- Molecule 7 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total I 1 1	0	0

- Molecule 8 is water.

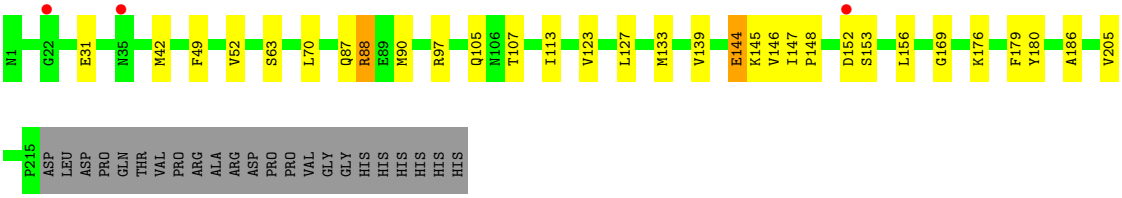
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	3	Total O 3 3	0	0
8	B	10	Total O 10 10	0	0
8	C	12	Total O 12 12	0	0
8	D	8	Total O 8 8	0	0

3 Residue-property plots (i)

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

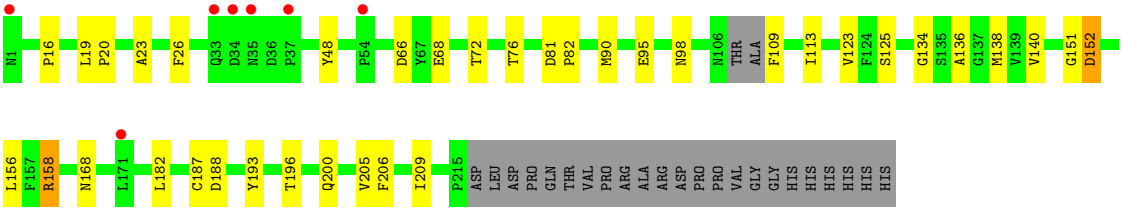
• Molecule 1: Cadherin-related family member 2

Chain A:



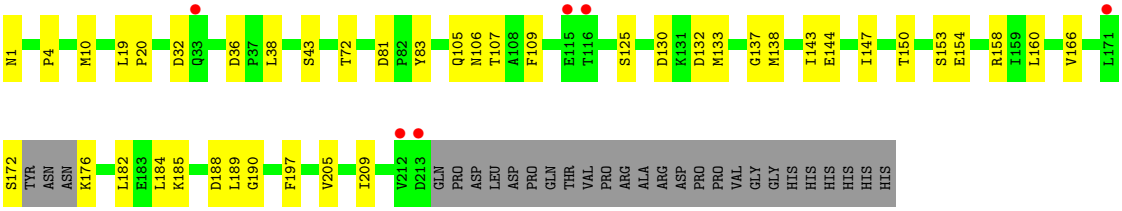
• Molecule 1: Cadherin-related family member 2

Chain B:



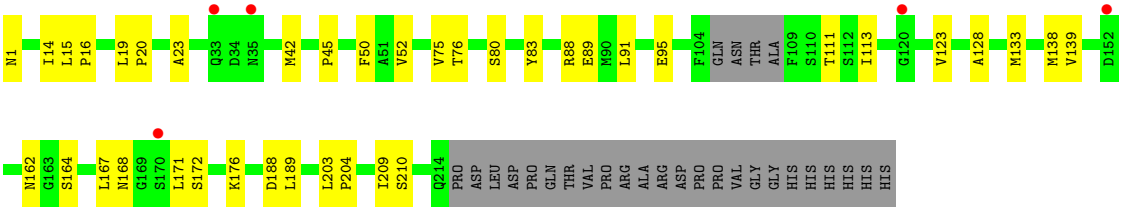
• Molecule 1: Cadherin-related family member 2

Chain C:



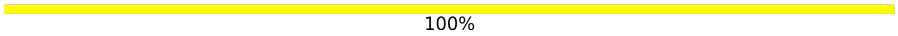
• Molecule 1: Cadherin-related family member 2

Chain D:



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

Chain E:

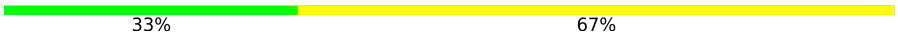


• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:

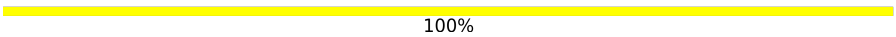
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



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

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	63.90Å 86.64Å 104.89Å 90.00° 103.46° 90.00°	Depositor
Resolution (Å)	49.15 – 3.17 49.10 – 3.17	Depositor EDS
% Data completeness (in resolution range)	95.2 (49.15-3.17) 95.2 (49.10-3.17)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.64 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.213 , 0.290 0.216 , 0.289	Depositor DCC
R_{free} test set	862 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å^2)	43.9	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 35.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	6720	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.20 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.1532e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NA, BMA, CL, NAG, TRS, IOD

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	0.93	1/1684 (0.1%)	1.12	4/2299 (0.2%)
1	B	0.92	1/1671 (0.1%)	1.06	2/2279 (0.1%)
1	C	0.93	1/1637 (0.1%)	1.08	2/2232 (0.1%)
1	D	0.98	3/1646 (0.2%)	1.10	1/2244 (0.0%)
All	All	0.94	6/6638 (0.1%)	1.09	9/9054 (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
1	A	0	1
1	C	0	1
All	All	0	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	210	SER	CA-CB	-5.54	1.44	1.52
1	A	144	GLU	CD-OE2	-5.52	1.19	1.25
1	D	45	PRO	N-CD	-5.41	1.40	1.47
1	B	125	SER	CA-CB	-5.18	1.45	1.52
1	D	89	GLU	C-O	5.11	1.33	1.23

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	179	PHE	CB-CA-C	-8.66	93.08	110.40
1	A	179	PHE	CB-CG-CD2	-7.15	115.80	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	88	ARG	NE-CZ-NH2	5.88	123.24	120.30
1	D	88	ARG	NE-CZ-NH2	5.73	123.16	120.30
1	B	158	ARG	NE-CZ-NH1	-5.72	117.44	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	147	ILE	Peptide
1	C	147	ILE	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	1648	0	1621	20	0
1	B	1636	0	1608	22	0
1	C	1604	0	1584	27	0
1	D	1612	0	1587	28	0
2	E	39	0	34	0	0
2	F	39	0	34	0	0
2	G	39	0	34	0	0
2	H	39	0	34	0	0
3	A	8	0	12	5	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	3	0	0	0	0
5	D	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	B	1	0	0	0	0
8	A	3	0	0	0	0
8	B	10	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	C	12	0	0	0	0
8	D	8	0	0	1	0
All	All	6720	0	6548	90	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 90 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:176:LYS:HG2	3:A:301:TRS:H31	1.42	1.00
1:A:156:LEU:HD12	1:A:169:GLY:HA3	1.57	0.86
1:C:1:ASN:HD22	1:C:83:TYR:HB2	1.50	0.77
1:C:1:ASN:ND2	1:C:83:TYR:HB2	2.07	0.69
1:C:172:SER:C	1:C:176:LYS:HD3	2.12	0.69

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	213/238 (90%)	201 (94%)	12 (6%)	0	100	100
1	B	209/238 (88%)	199 (95%)	10 (5%)	0	100	100
1	C	206/238 (87%)	194 (94%)	12 (6%)	0	100	100
1	D	206/238 (87%)	198 (96%)	8 (4%)	0	100	100
All	All	834/952 (88%)	792 (95%)	42 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	187/207 (90%)	184 (98%)	3 (2%)	62	83
1	B	186/207 (90%)	185 (100%)	1 (0%)	88	95
1	C	182/207 (88%)	180 (99%)	2 (1%)	73	88
1	D	183/207 (88%)	182 (100%)	1 (0%)	88	95
All	All	738/828 (89%)	731 (99%)	7 (1%)	78	91

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	156	LEU
1	C	43	SER
1	D	80	SER
1	C	125	SER
1	A	144	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	114	ASN
1	D	168	ASN
1	C	35	ASN
1	C	195	ASN
1	D	33	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

12 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	E	1	1,2	14,14,15	0.68	0	17,19,21	0.85	1 (5%)
2	NAG	E	2	2	14,14,15	0.85	0	17,19,21	1.20	2 (11%)
2	BMA	E	3	2	11,11,12	0.39	0	15,15,17	1.30	1 (6%)
2	NAG	F	1	1,2	14,14,15	0.56	0	17,19,21	1.39	3 (17%)
2	NAG	F	2	2	14,14,15	0.79	0	17,19,21	0.99	0
2	BMA	F	3	2	11,11,12	0.61	0	15,15,17	1.00	0
2	NAG	G	1	1,2	14,14,15	0.60	0	17,19,21	1.34	2 (11%)
2	NAG	G	2	2	14,14,15	0.59	0	17,19,21	1.08	0
2	BMA	G	3	2	11,11,12	0.60	0	15,15,17	1.36	2 (13%)
2	NAG	H	1	1,2	14,14,15	0.82	1 (7%)	17,19,21	1.15	2 (11%)
2	NAG	H	2	2	14,14,15	0.91	1 (7%)	17,19,21	1.47	2 (11%)
2	BMA	H	3	2	11,11,12	0.22	0	15,15,17	1.08	1 (6%)

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	E	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	E	2	2	-	1/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	BMA	F	3	2	-	0/2/19/22	0/1/1/1
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	2/2/19/22	1/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1
2	BMA	H	3	2	-	1/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1	NAG	O5-C1	-2.56	1.39	1.43
2	H	2	NAG	C2-N2	-2.33	1.42	1.46

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	2	NAG	O5-C1-C2	-3.06	106.45	111.29
2	H	3	BMA	C1-O5-C5	2.91	116.14	112.19
2	G	3	BMA	C1-O5-C5	2.67	115.81	112.19
2	G	3	BMA	O5-C1-C2	2.65	114.86	110.77
2	F	1	NAG	C4-C3-C2	2.59	114.82	111.02

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	3	BMA	O5-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6
2	H	2	NAG	O5-C5-C6-O6
2	H	1	NAG	C4-C5-C6-O6
2	F	2	NAG	O5-C5-C6-O6

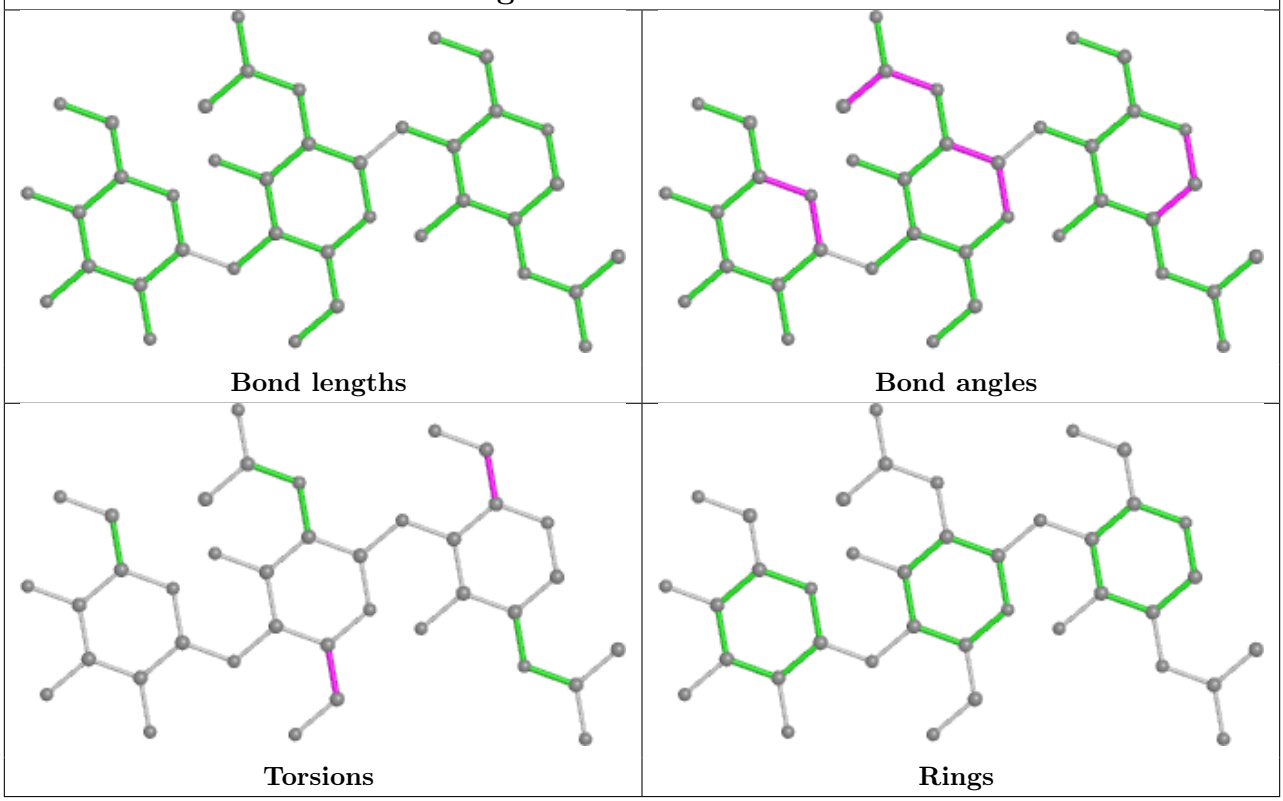
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	3	BMA	C1-C2-C3-C4-C5-O5

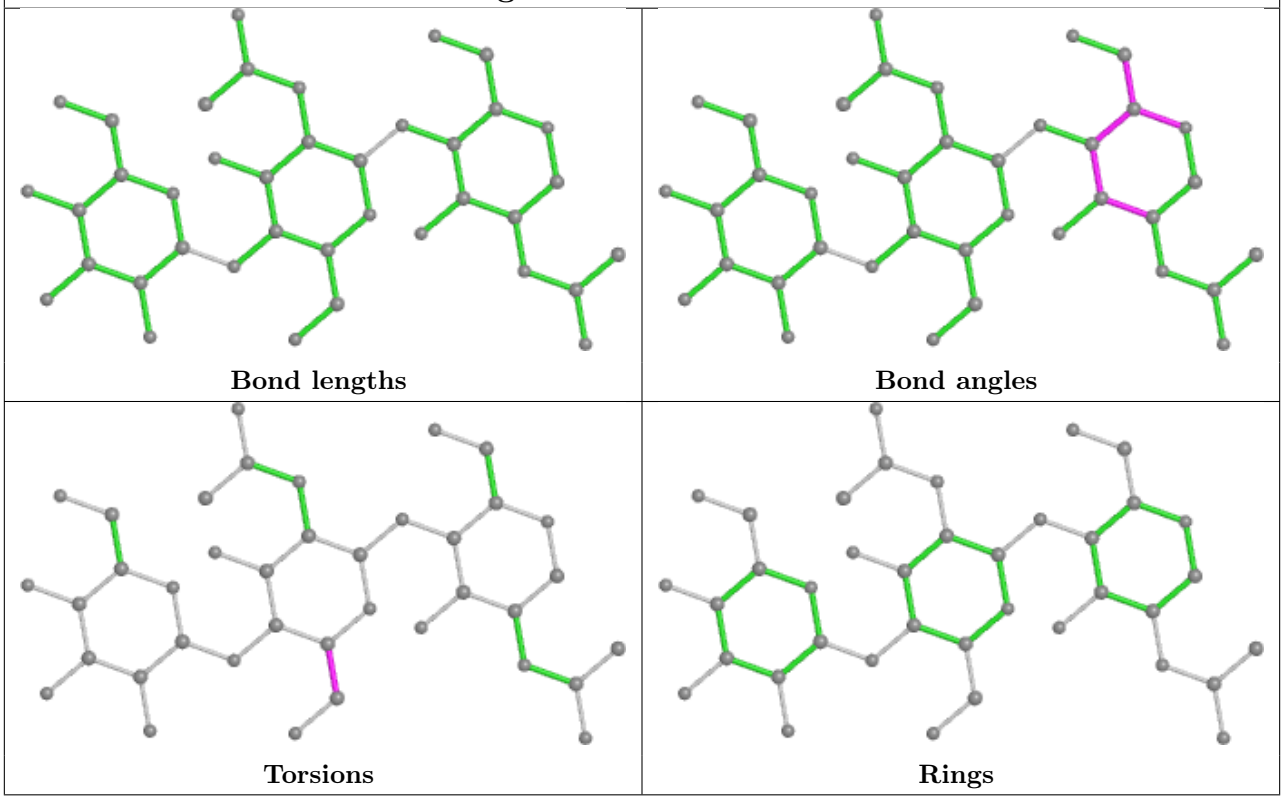
No monomer is involved in short contacts.

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

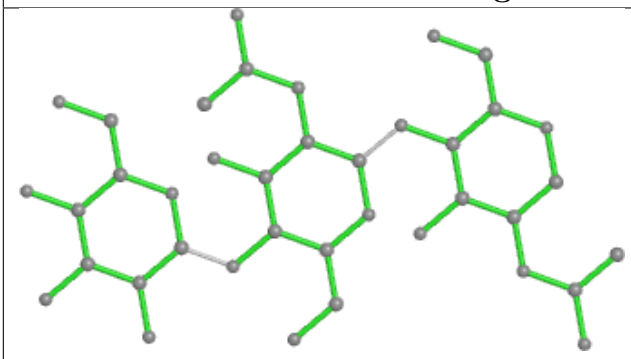
Oligosaccharide Chain E



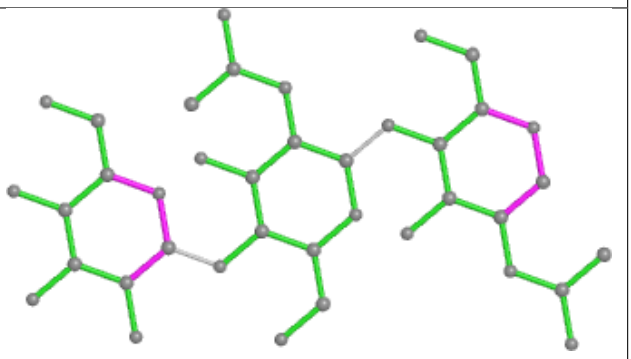
Oligosaccharide Chain F



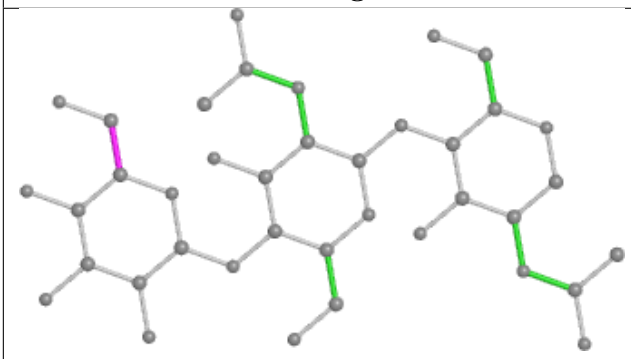
Oligosaccharide Chain G



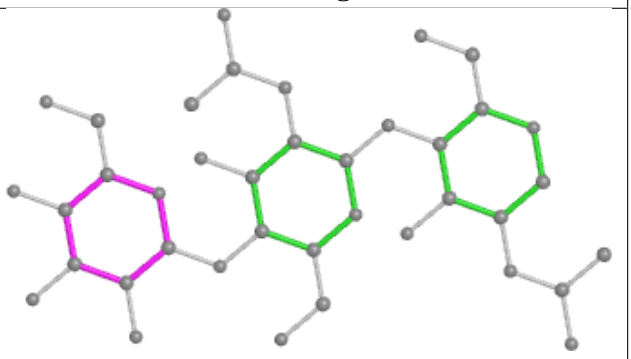
Bond lengths



Bond angles

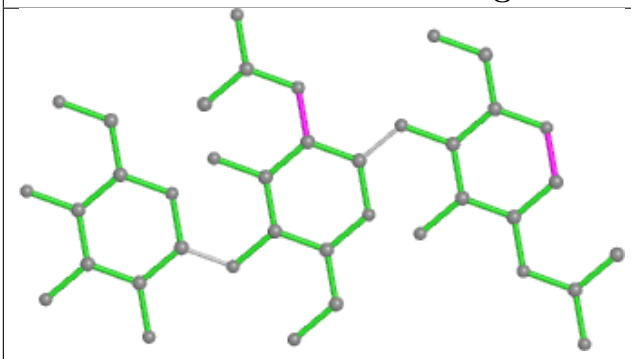


Torsions

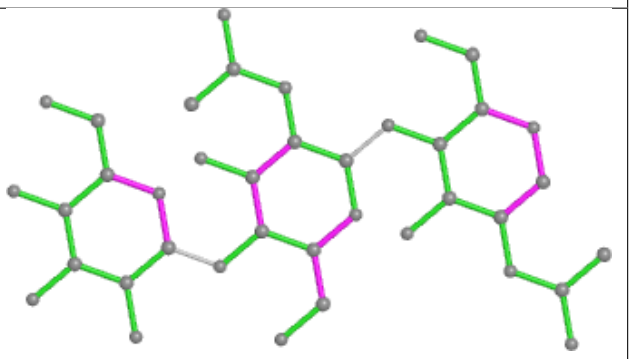


Rings

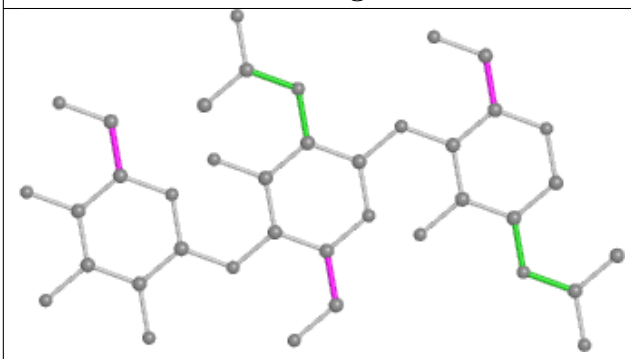
Oligosaccharide Chain H



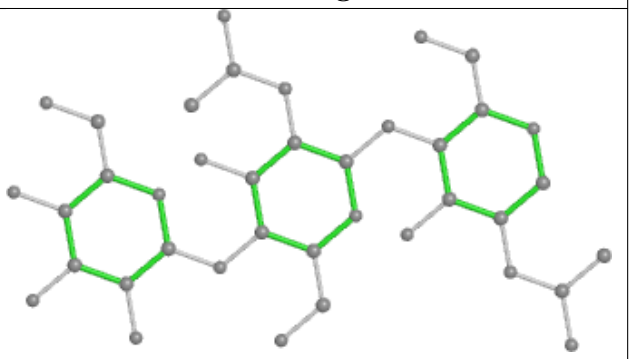
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 24 ligands modelled in this entry, 23 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
3	TRS	A	301	-	7,7,7	0.09	0	9,9,9	0.73	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
3	TRS	A	301	-	-	2/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	TRS	N-C-C1-O1
3	A	301	TRS	C3-C-C1-O1

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	TRS	5	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	215/238 (90%)	-0.26	3 (1%)	75	63	21, 40, 71, 102	0
1	B	213/238 (89%)	-0.12	7 (3%)	46	30	17, 41, 74, 106	0
1	C	210/238 (88%)	-0.13	6 (2%)	51	35	22, 41, 73, 132	0
1	D	210/238 (88%)	-0.17	5 (2%)	59	44	17, 37, 76, 130	0
All	All	848/952 (89%)	-0.17	21 (2%)	57	43	17, 40, 75, 132	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	22	GLY	3.6
1	B	34	ASP	3.2
1	C	33	GLN	3.2
1	C	116	THR	3.2
1	D	35	ASN	3.1

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	BMA	G	3	11/12	0.48	0.35	69,93,109,113	0
2	BMA	E	3	11/12	0.82	0.16	48,70,86,95	0

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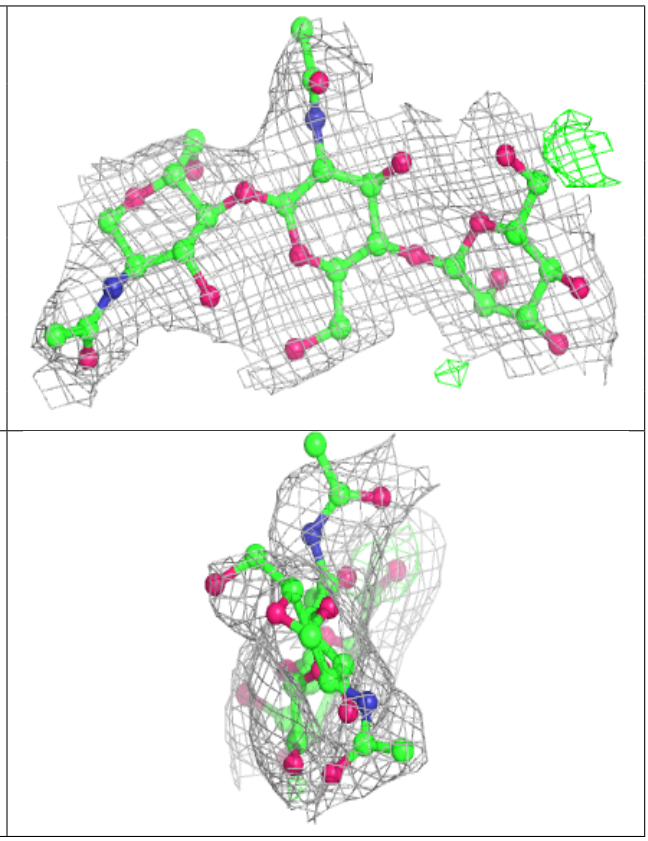
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	BMA	F	3	11/12	0.83	0.25	59,70,80,94	0
2	BMA	H	3	11/12	0.84	0.24	60,77,88,89	0
2	NAG	H	1	14/15	0.92	0.15	30,36,51,67	0
2	NAG	F	2	14/15	0.92	0.28	42,49,59,63	0
2	NAG	F	1	14/15	0.93	0.27	41,49,59,61	0
2	NAG	G	2	14/15	0.94	0.28	37,42,52,78	0
2	NAG	H	2	14/15	0.94	0.29	33,48,55,57	0
2	NAG	E	2	14/15	0.94	0.14	38,43,58,64	0
2	NAG	G	1	14/15	0.95	0.14	25,32,38,39	0
2	NAG	E	1	14/15	0.95	0.18	30,35,46,53	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.

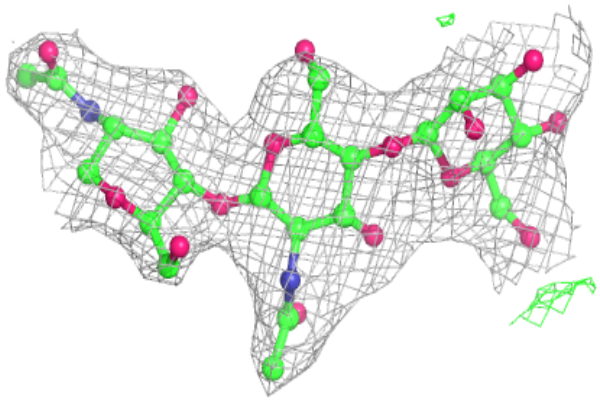
Electron density around Chain E:

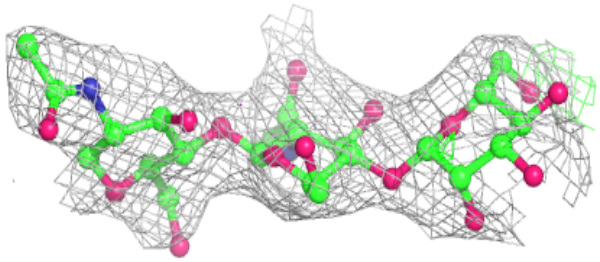
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

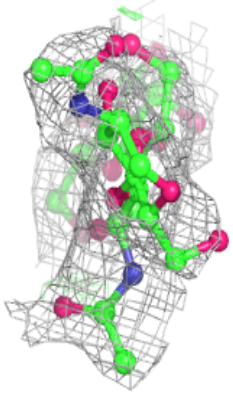


Electron density around Chain F:

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

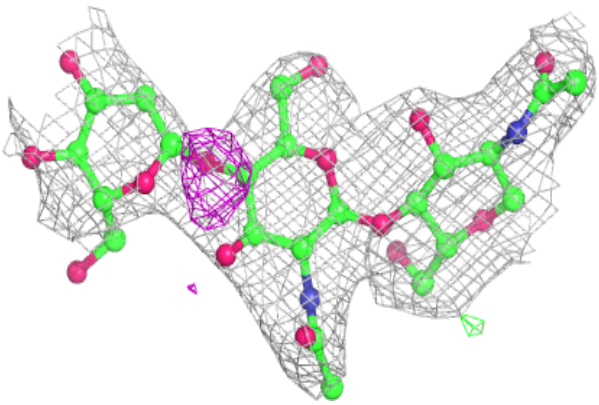


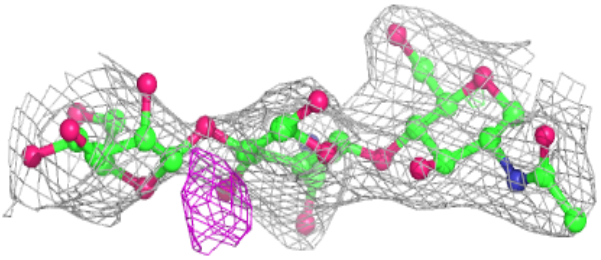


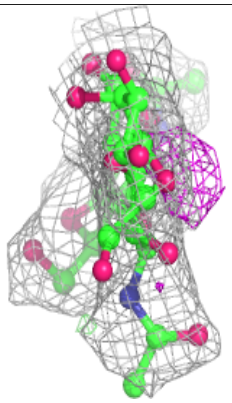


Electron density around Chain G:

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

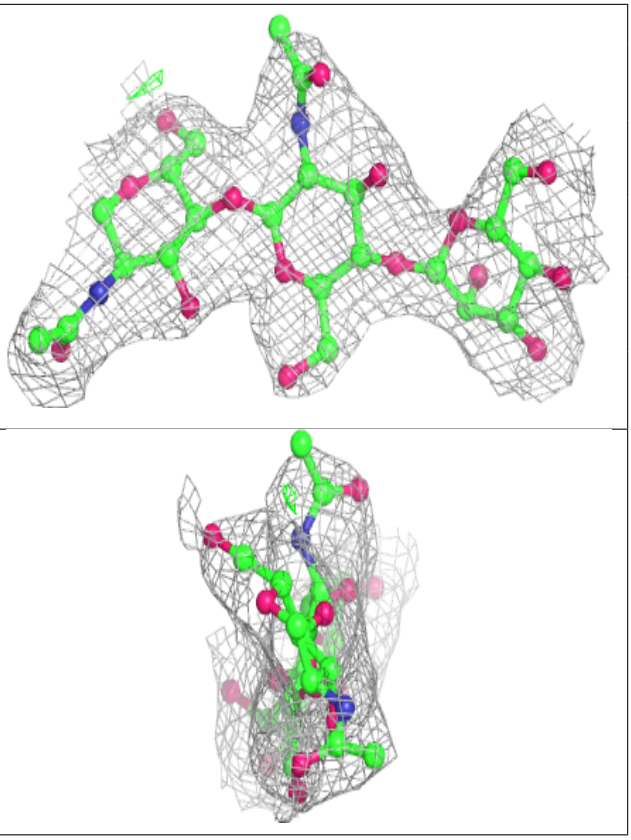






Electron density around Chain H:

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



6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	TRS	A	301	8/8	0.87	0.26	20,25,30,32	0
5	CL	C	305	1/1	0.95	0.10	46,46,46,46	0
4	CA	D	301	1/1	0.96	0.04	54,54,54,54	0
4	CA	B	301	1/1	0.97	0.09	63,63,63,63	0
4	CA	C	301	1/1	0.97	0.05	56,56,56,56	0
5	CL	C	306	1/1	0.97	0.08	14,14,14,14	0
5	CL	C	307	1/1	0.97	0.10	1,1,1,1	0
4	CA	B	302	1/1	0.98	0.07	27,27,27,27	0
4	CA	D	302	1/1	0.98	0.04	54,54,54,54	0
4	CA	D	304	1/1	0.98	0.06	23,23,23,23	0
5	CL	B	305	1/1	0.98	0.11	6,6,6,6	0
4	CA	A	303	1/1	0.98	0.07	33,33,33,33	0
4	CA	C	302	1/1	0.98	0.06	55,55,55,55	0
4	CA	C	304	1/1	0.98	0.07	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	NA	A	306	1/1	0.98	0.08	19,19,19,19	0
6	NA	B	306	1/1	0.98	0.12	37,37,37,37	0
4	CA	B	303	1/1	0.99	0.05	25,25,25,25	0
4	CA	A	302	1/1	0.99	0.06	36,36,36,36	0
4	CA	A	304	1/1	0.99	0.12	24,24,24,24	0
4	CA	D	303	1/1	0.99	0.07	26,26,26,26	0
4	CA	C	303	1/1	0.99	0.16	35,35,35,35	0
5	CL	A	305	1/1	0.99	0.11	12,12,12,12	0
7	IOD	B	304	1/1	0.99	0.04	73,73,73,73	0
5	CL	D	305	1/1	1.00	0.07	13,13,13,13	0

6.5 Other polymers (i)

There are no such residues in this entry.