



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 21, 2023 – 08:31 AM JST

PDB ID : 7FE2
Title : Crystal structure of the mutant E494Q of GH92 alpha-1,2-mannosidase from *Enterococcus faecalis* ATCC 10100 in complex with alpha-1,2-mannobiose
Authors : Miyazaki, T.; Alonso-Gil, S.
Deposited on : 2021-07-19
Resolution : 1.75 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

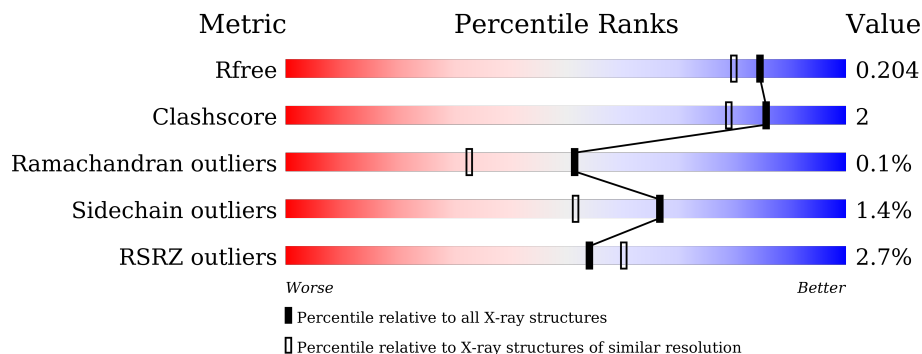
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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.




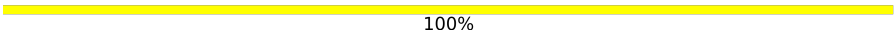
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	721	
1	B	721	
1	C	721	
1	D	721	
2	E	2	
2	F	2	

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Mol	Chain	Length	Quality of chain
2	G	2	 50% 50%
2	H	2	 100%

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 25083 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 Alpha-1,2-mannosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	712	5787	3716	946	1104	21	0	5	0
1	B	712	5773	3706	945	1101	21	0	2	0
1	C	712	5769	3703	945	1100	21	0	1	0
1	D	712	5769	3703	945	1100	21	0	1	0

There are 36 discrepancies between the modelled and reference sequences:

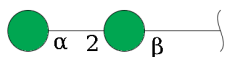
Chain	Residue	Modelled	Actual	Comment	Reference
A	494	GLN	GLU	engineered mutation	UNP A0A6N0WQ22
A	714	LEU	-	expression tag	UNP A0A6N0WQ22
A	715	GLU	-	expression tag	UNP A0A6N0WQ22
A	716	HIS	-	expression tag	UNP A0A6N0WQ22
A	717	HIS	-	expression tag	UNP A0A6N0WQ22
A	718	HIS	-	expression tag	UNP A0A6N0WQ22
A	719	HIS	-	expression tag	UNP A0A6N0WQ22
A	720	HIS	-	expression tag	UNP A0A6N0WQ22
A	721	HIS	-	expression tag	UNP A0A6N0WQ22
B	494	GLN	GLU	engineered mutation	UNP A0A6N0WQ22
B	714	LEU	-	expression tag	UNP A0A6N0WQ22
B	715	GLU	-	expression tag	UNP A0A6N0WQ22
B	716	HIS	-	expression tag	UNP A0A6N0WQ22
B	717	HIS	-	expression tag	UNP A0A6N0WQ22
B	718	HIS	-	expression tag	UNP A0A6N0WQ22
B	719	HIS	-	expression tag	UNP A0A6N0WQ22
B	720	HIS	-	expression tag	UNP A0A6N0WQ22
B	721	HIS	-	expression tag	UNP A0A6N0WQ22
C	494	GLN	GLU	engineered mutation	UNP A0A6N0WQ22
C	714	LEU	-	expression tag	UNP A0A6N0WQ22
C	715	GLU	-	expression tag	UNP A0A6N0WQ22

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Chain	Residue	Modelled	Actual	Comment	Reference
C	716	HIS	-	expression tag	UNP A0A6N0WQ22
C	717	HIS	-	expression tag	UNP A0A6N0WQ22
C	718	HIS	-	expression tag	UNP A0A6N0WQ22
C	719	HIS	-	expression tag	UNP A0A6N0WQ22
C	720	HIS	-	expression tag	UNP A0A6N0WQ22
C	721	HIS	-	expression tag	UNP A0A6N0WQ22
D	494	GLN	GLU	engineered mutation	UNP A0A6N0WQ22
D	714	LEU	-	expression tag	UNP A0A6N0WQ22
D	715	GLU	-	expression tag	UNP A0A6N0WQ22
D	716	HIS	-	expression tag	UNP A0A6N0WQ22
D	717	HIS	-	expression tag	UNP A0A6N0WQ22
D	718	HIS	-	expression tag	UNP A0A6N0WQ22
D	719	HIS	-	expression tag	UNP A0A6N0WQ22
D	720	HIS	-	expression tag	UNP A0A6N0WQ22
D	721	HIS	-	expression tag	UNP A0A6N0WQ22

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-beta-D-mannopyranos e.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			23	12	11			
2	F	2	Total	C	O	0	0	0
			23	12	11			
2	G	2	Total	C	O	0	0	0
			23	12	11			
2	H	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		
3	B	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		

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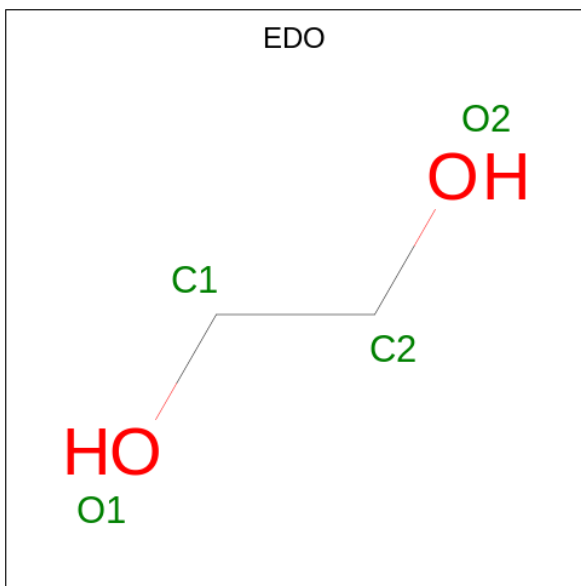
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Ca 1 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0

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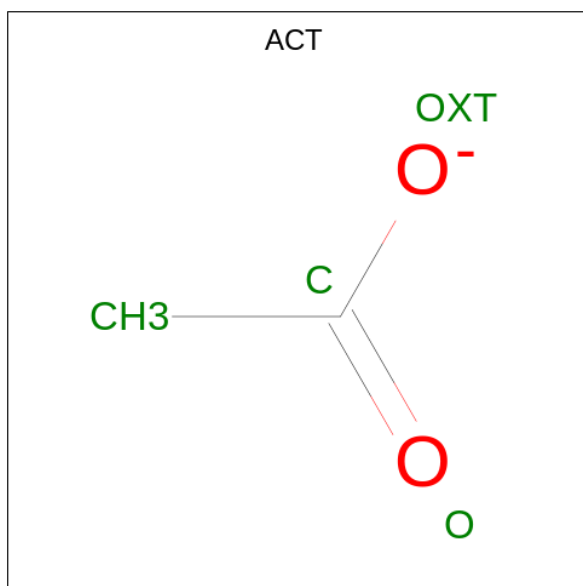
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	C	1	Total 4	C 2	O 2	0	0
5	D	1	Total 4	C 2	O 2	0	0
5	D	1	Total 4	C 2	O 2	0	0
5	D	1	Total 4	C 2	O 2	0	0
5	D	1	Total 4	C 2	O 2	0	0
5	D	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

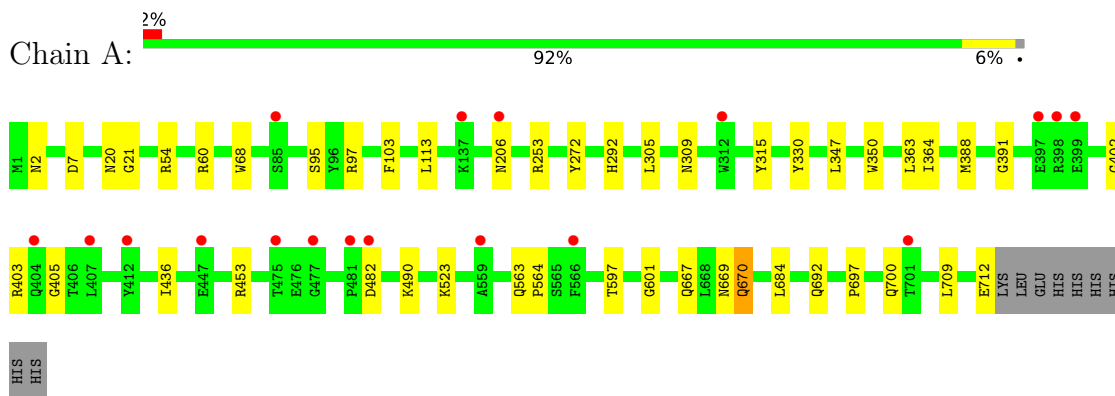
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	478	Total	O	0	0
			478	478		
7	B	421	Total	O	0	0
			421	421		
7	C	438	Total	O	0	0
			438	438		
7	D	436	Total	O	0	0
			436	436		

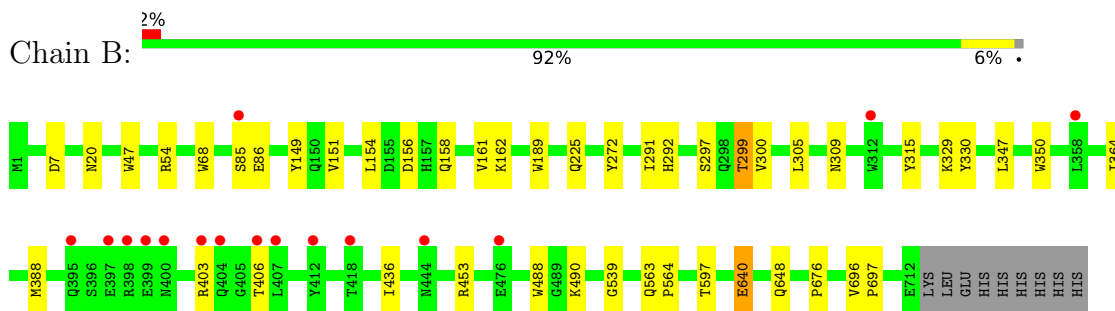
3 Residue-property plots [i](#)

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.

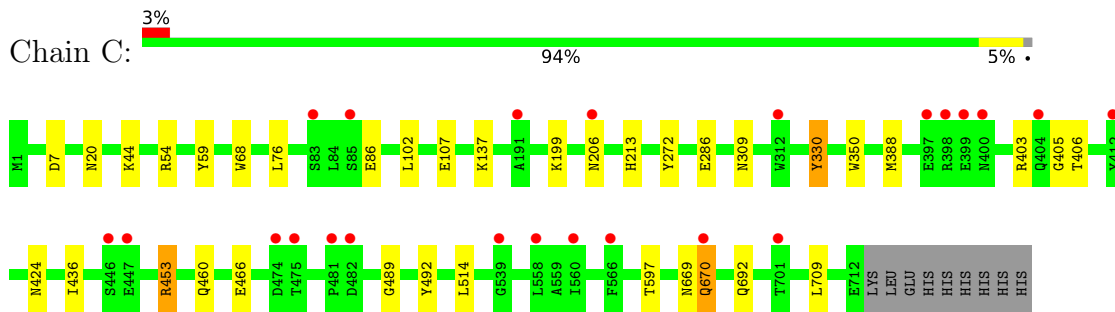
- Molecule 1: Alpha-1,2-mannosidase



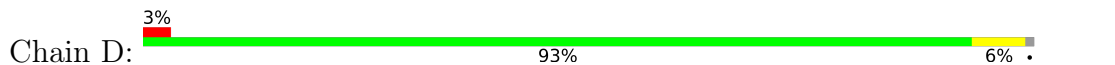
- Molecule 1: Alpha-1,2-mannosidase

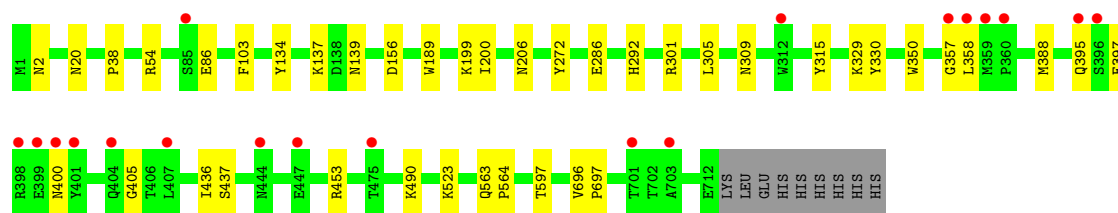


- Molecule 1: Alpha-1,2-mannosidase



- Molecule 1: Alpha-1,2-mannosidase





- Molecule 2: alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose

Chain E: 50% 50%

BNA1
MAN2

- Molecule 2: alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose

Chain F: 50% 50%

BNA1
MAN2

- Molecule 2: alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose

Chain G: 50% 50%

BNA1
MAN2

- Molecule 2: alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose

Chain H: 100%

BNA1
MAN2

4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	162.63Å 168.61Å 260.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.57 – 1.75 48.52 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.57-1.75) 99.6 (48.52-1.75)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 1.75Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.169 , 0.198 0.177 , 0.204	Depositor DCC
R_{free} test set	17508 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	21.9	Xtrriage
Anisotropy	0.004	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.033 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	25083	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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: NA, MAN, ACT, CA, EDO, 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	0.74	0/5974	0.84	2/8122 (0.0%)
1	B	0.72	0/5951	0.81	0/8091
1	C	0.72	0/5944	0.83	2/8081 (0.0%)
1	D	0.74	0/5944	0.83	1/8081 (0.0%)
All	All	0.73	0/23813	0.83	5/32375 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	330	TYR	CB-CG-CD1	6.69	125.01	121.00
1	A	60	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	D	301	ARG	CG-CD-NE	-6.29	98.58	111.80
1	A	253	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	C	453	ARG	NE-CZ-NH1	5.61	123.11	120.30

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	5787	0	5501	28	0
1	B	5773	0	5482	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	5769	0	5475	23	0
1	D	5769	0	5475	19	0
2	E	23	0	19	1	0
2	F	23	0	19	1	0
2	G	23	0	19	1	0
2	H	23	0	19	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	32	0	48	1	0
5	B	24	0	36	3	0
5	C	24	0	36	1	0
5	D	24	0	36	2	0
6	A	4	0	3	1	0
6	B	4	0	3	0	0
7	A	478	0	0	11	0
7	B	421	0	0	3	0
7	C	438	0	0	9	0
7	D	436	0	0	6	0
All	All	25083	0	22171	98	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 2.

The worst 5 of 98 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:213:HIS:HD2	7:C:949:HOH:O	1.44	1.00
1:A:692[A]:GLN:HG2	7:A:917:HOH:O	1.85	0.76
1:B:297:SER:O	1:B:299[A]:THR:HG22	1.90	0.72
1:D:86:GLU:HB3	7:D:1258:HOH:O	1.92	0.68
1:C:86:GLU:HB3	7:C:1266:HOH:O	1.97	0.64

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	715/721 (99%)	696 (97%)	18 (2%)	1 (0%)	51	33
1	B	712/721 (99%)	691 (97%)	20 (3%)	1 (0%)	51	33
1	C	711/721 (99%)	691 (97%)	20 (3%)	0	100	100
1	D	711/721 (99%)	689 (97%)	21 (3%)	1 (0%)	51	33
All	All	2849/2884 (99%)	2767 (97%)	79 (3%)	3 (0%)	51	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	490	LYS
1	D	490	LYS
1	B	490	LYS

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	632/636 (99%)	622 (98%)	10 (2%)	62	45
1	B	629/636 (99%)	620 (99%)	9 (1%)	67	52
1	C	628/636 (99%)	620 (99%)	8 (1%)	69	54
1	D	628/636 (99%)	619 (99%)	9 (1%)	67	52
All	All	2517/2544 (99%)	2481 (99%)	36 (1%)	67	52

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	272	TYR
1	D	523	LYS
1	D	309	ASN
1	D	350	TRP
1	B	299[B]	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	213	HIS
1	C	648	GLN
1	D	590	GLN
1	D	158	GLN
1	D	395	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](#)

8 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	BMA	E	1	2	12,12,12	0.58	0	17,17,17	0.90	1 (5%)
2	MAN	E	2	2,3	11,11,12	1.10	0	15,15,17	3.33	9 (60%)
2	BMA	F	1	2	12,12,12	0.89	1 (8%)	17,17,17	1.63	4 (23%)
2	MAN	F	2	2,3	11,11,12	1.51	3 (27%)	15,15,17	3.77	10 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BMA	G	1	2	12,12,12	0.78	0	17,17,17	1.41	2 (11%)
2	MAN	G	2	2,3	11,11,12	1.27	2 (18%)	15,15,17	3.47	10 (66%)
2	BMA	H	1	2	12,12,12	0.86	0	17,17,17	1.62	4 (23%)
2	MAN	H	2	2,3	11,11,12	1.88	4 (36%)	15,15,17	4.52	9 (60%)

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	BMA	E	1	2	-	2/2/22/22	0/1/1/1
2	MAN	E	2	2,3	-	0/2/19/22	0/1/1/1
2	BMA	F	1	2	-	0/2/22/22	0/1/1/1
2	MAN	F	2	2,3	-	0/2/19/22	0/1/1/1
2	BMA	G	1	2	-	0/2/22/22	0/1/1/1
2	MAN	G	2	2,3	-	0/2/19/22	0/1/1/1
2	BMA	H	1	2	-	2/2/22/22	0/1/1/1
2	MAN	H	2	2,3	-	0/2/19/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	2	MAN	C1-C2	3.28	1.59	1.52
2	H	2	MAN	O3-C3	3.12	1.50	1.43
2	F	2	MAN	C1-C2	2.85	1.58	1.52
2	F	2	MAN	O2-C2	2.75	1.49	1.43
2	H	2	MAN	O2-C2	2.58	1.48	1.43

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	2	MAN	C1-O5-C5	8.66	123.92	112.19
2	H	2	MAN	C1-C2-C3	8.04	119.55	109.67
2	H	2	MAN	O2-C2-C3	-7.87	94.37	110.14
2	F	2	MAN	O5-C1-C2	7.47	122.30	110.77
2	H	2	MAN	O3-C3-C2	-7.32	95.98	109.99

There are no chirality outliers.

All (4) torsion outliers are listed below:

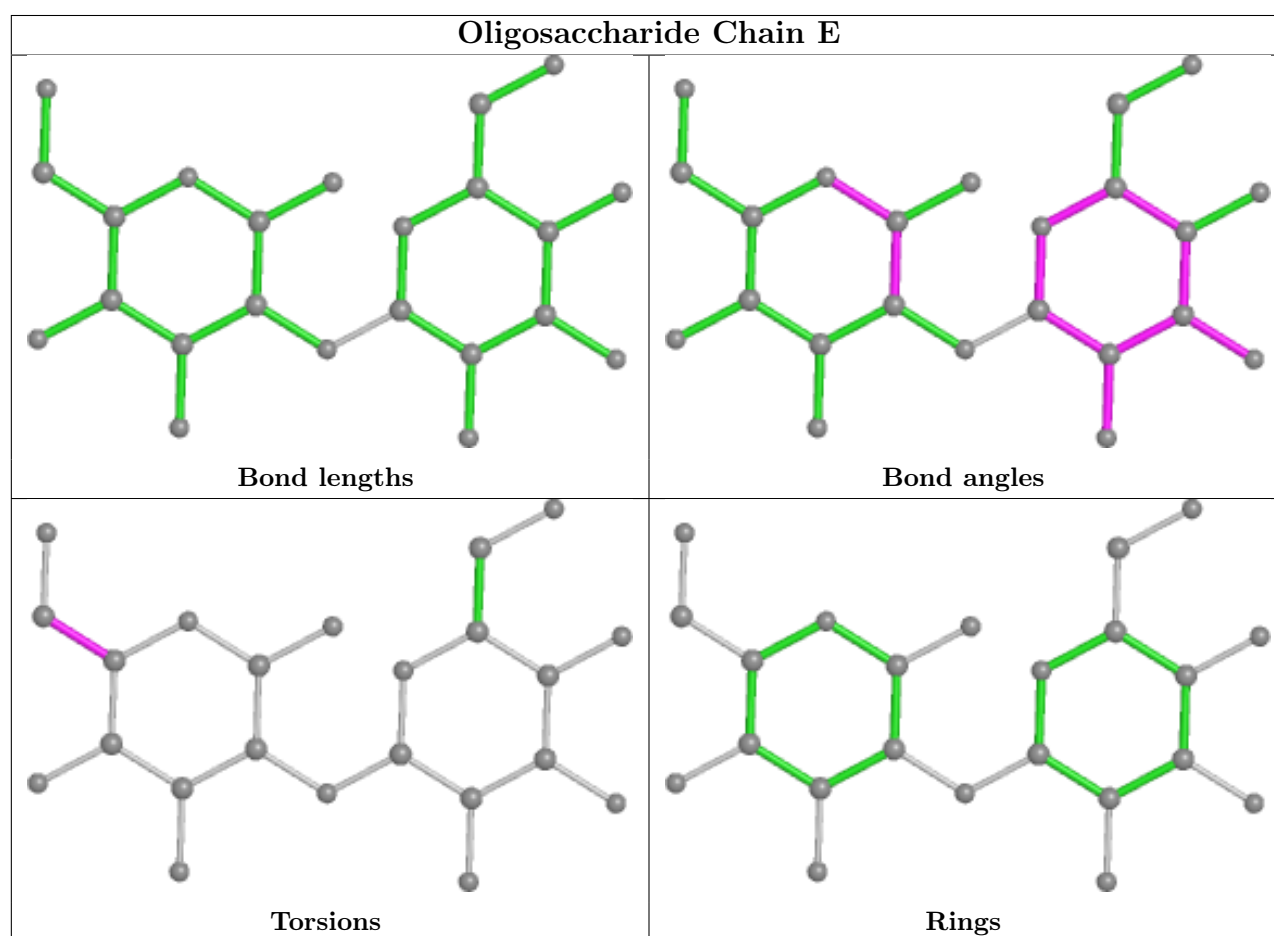
Mol	Chain	Res	Type	Atoms
2	H	1	BMA	C4-C5-C6-O6
2	E	1	BMA	C4-C5-C6-O6
2	E	1	BMA	O5-C5-C6-O6
2	H	1	BMA	O5-C5-C6-O6

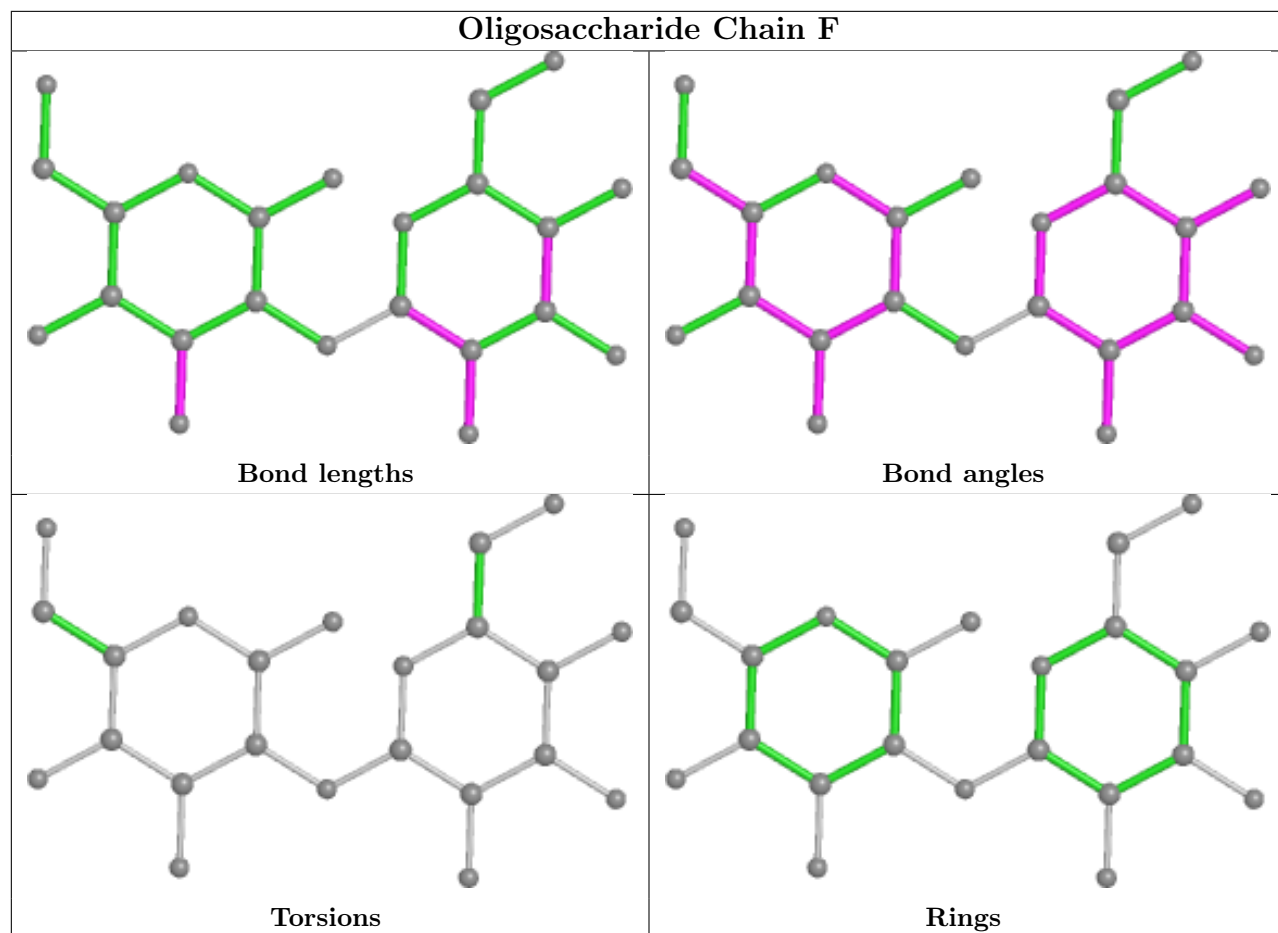
There are no ring outliers.

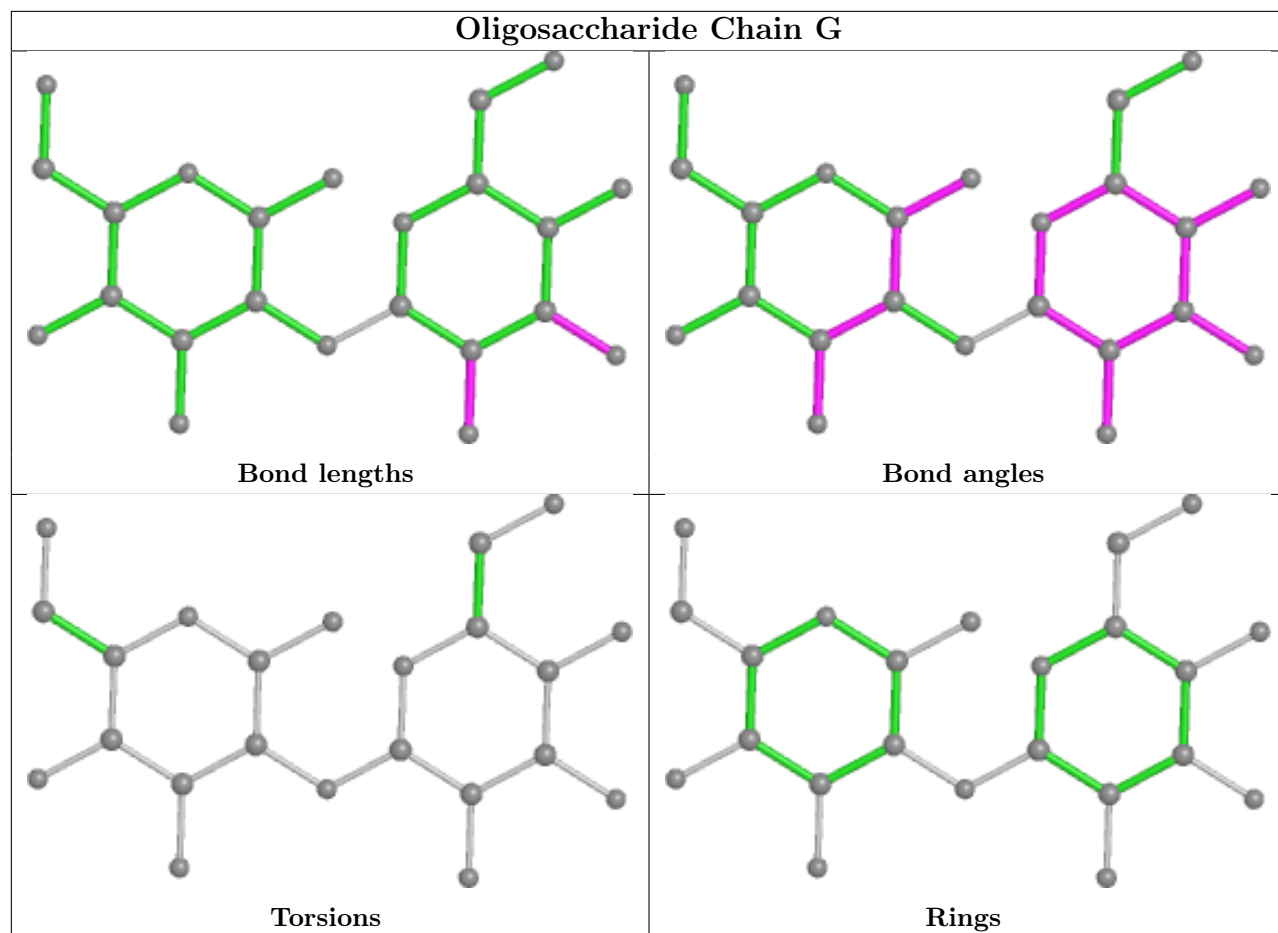
3 monomers are involved in 3 short contacts:

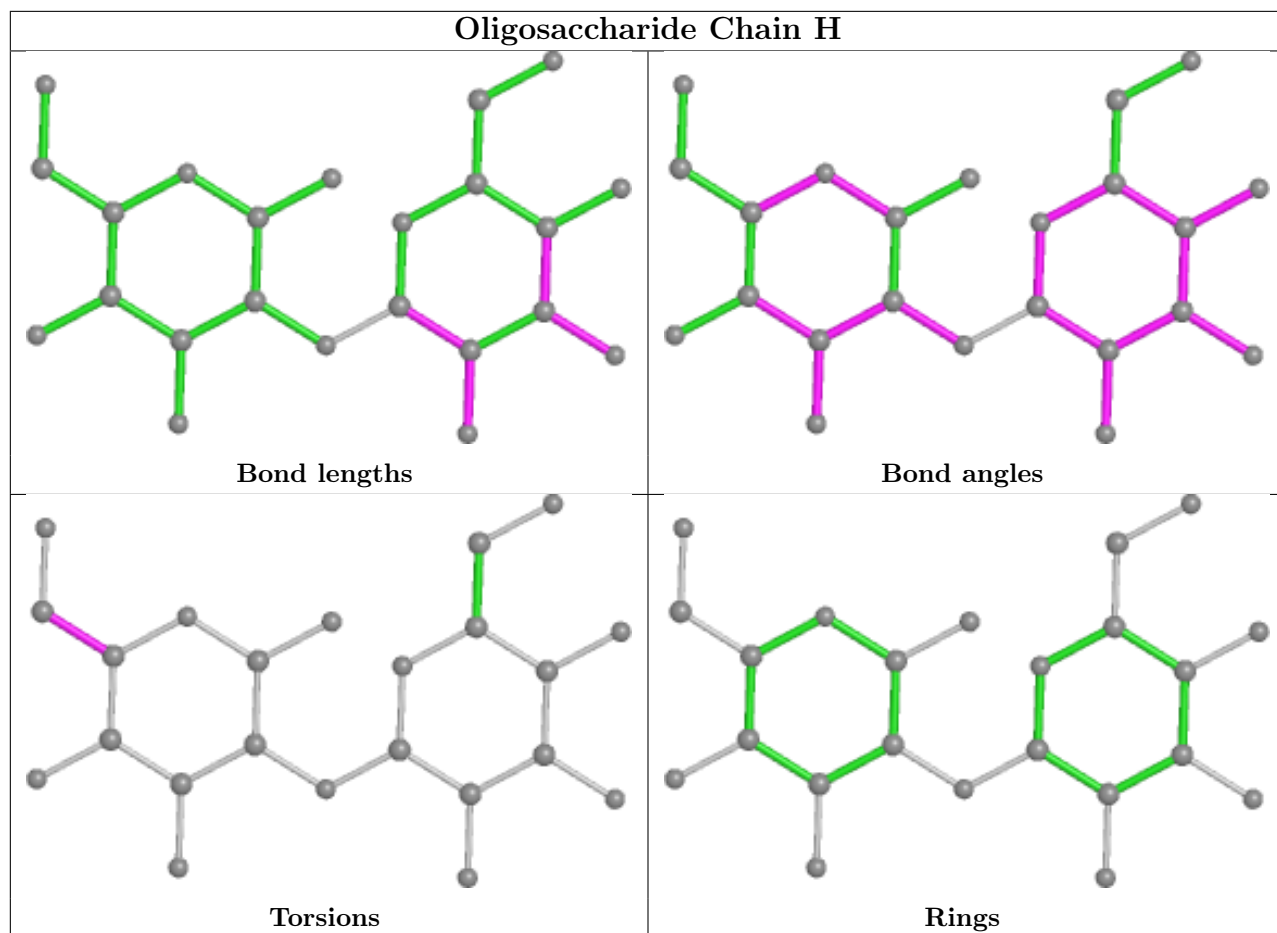
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	BMA	1	0
2	F	1	BMA	1	0
2	G	1	BMA	1	0

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 36 ligands modelled in this entry, 8 are monoatomic - leaving 28 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	$\# Z > 2$
5	EDO	B	809	-	3,3,3	0.28	0	2,2,2	0.42	0
5	EDO	A	808	-	3,3,3	0.28	0	2,2,2	0.33	0
5	EDO	A	807	-	3,3,3	0.13	0	2,2,2	0.32	0
5	EDO	D	808	-	3,3,3	0.20	0	2,2,2	0.22	0
5	EDO	A	803	-	3,3,3	0.07	0	2,2,2	0.30	0
5	EDO	A	804	-	3,3,3	0.06	0	2,2,2	0.11	0
5	EDO	D	803	-	3,3,3	0.40	0	2,2,2	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	B	807	-	3,3,3	0.30	0	2,2,2	0.13	0
6	ACT	B	806	-	3,3,3	0.91	0	3,3,3	0.89	0
5	EDO	B	808	-	3,3,3	0.20	0	2,2,2	0.45	0
6	ACT	A	805	-	3,3,3	1.00	0	3,3,3	0.90	0
5	EDO	C	806	-	3,3,3	0.14	0	2,2,2	0.07	0
5	EDO	A	806	-	3,3,3	0.46	0	2,2,2	0.59	0
5	EDO	A	810	-	3,3,3	0.45	0	2,2,2	0.87	0
5	EDO	B	803	-	3,3,3	0.09	0	2,2,2	0.04	0
5	EDO	C	807	-	3,3,3	0.31	0	2,2,2	0.22	0
5	EDO	C	808	-	3,3,3	0.20	0	2,2,2	0.21	0
5	EDO	C	804	-	3,3,3	0.19	0	2,2,2	0.25	0
5	EDO	D	804	-	3,3,3	0.08	0	2,2,2	0.15	0
5	EDO	B	804	-	3,3,3	0.26	0	2,2,2	0.44	0
5	EDO	B	805	-	3,3,3	0.13	0	2,2,2	0.26	0
5	EDO	A	809	-	3,3,3	0.15	0	2,2,2	0.35	0
5	EDO	D	807	-	3,3,3	0.18	0	2,2,2	0.19	0
5	EDO	C	805	-	3,3,3	0.16	0	2,2,2	0.16	0
5	EDO	A	811	-	3,3,3	0.21	0	2,2,2	0.19	0
5	EDO	D	805	-	3,3,3	0.12	0	2,2,2	0.39	0
5	EDO	D	806	-	3,3,3	0.23	0	2,2,2	0.54	0
5	EDO	C	803	-	3,3,3	0.31	0	2,2,2	0.61	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	809	-	-	0/1/1/1	-
5	EDO	A	808	-	-	0/1/1/1	-
5	EDO	A	807	-	-	0/1/1/1	-
5	EDO	D	808	-	-	0/1/1/1	-
5	EDO	A	803	-	-	1/1/1/1	-
5	EDO	A	804	-	-	0/1/1/1	-
5	EDO	D	803	-	-	1/1/1/1	-
5	EDO	B	807	-	-	0/1/1/1	-
5	EDO	B	808	-	-	1/1/1/1	-
5	EDO	C	806	-	-	0/1/1/1	-
5	EDO	A	806	-	-	1/1/1/1	-
5	EDO	A	810	-	-	1/1/1/1	-
5	EDO	B	803	-	-	0/1/1/1	-
5	EDO	C	807	-	-	0/1/1/1	-
5	EDO	C	808	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	C	804	-	-	0/1/1/1	-
5	EDO	D	804	-	-	0/1/1/1	-
5	EDO	B	804	-	-	1/1/1/1	-
5	EDO	B	805	-	-	1/1/1/1	-
5	EDO	A	809	-	-	0/1/1/1	-
5	EDO	D	807	-	-	0/1/1/1	-
5	EDO	C	805	-	-	1/1/1/1	-
5	EDO	A	811	-	-	1/1/1/1	-
5	EDO	D	805	-	-	0/1/1/1	-
5	EDO	D	806	-	-	1/1/1/1	-
5	EDO	C	803	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	806	EDO	O1-C1-C2-O2
5	B	808	EDO	O1-C1-C2-O2
5	C	808	EDO	O1-C1-C2-O2
5	D	803	EDO	O1-C1-C2-O2
5	A	803	EDO	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	809	EDO	1	0
5	A	808	EDO	1	0
5	B	808	EDO	1	0
6	A	805	ACT	1	0
5	B	804	EDO	1	0
5	D	806	EDO	2	0
5	C	803	EDO	1	0

5.7 Other polymers [i](#)

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 [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	712/721 (98%)	-0.14	18 (2%) 57 63	16, 23, 42, 82	0
1	B	712/721 (98%)	-0.21	16 (2%) 62 69	17, 25, 49, 104	0
1	C	712/721 (98%)	-0.09	23 (3%) 47 54	17, 25, 46, 78	0
1	D	712/721 (98%)	-0.16	19 (2%) 54 60	17, 25, 46, 106	0
All	All	2848/2884 (98%)	-0.15	76 (2%) 54 60	16, 24, 46, 106	0

The worst 5 of 76 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	404	GLN	7.4
1	D	400	ASN	6.8
1	D	358	LEU	5.7
1	B	398	ARG	5.6
1	B	404	GLN	5.6

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.

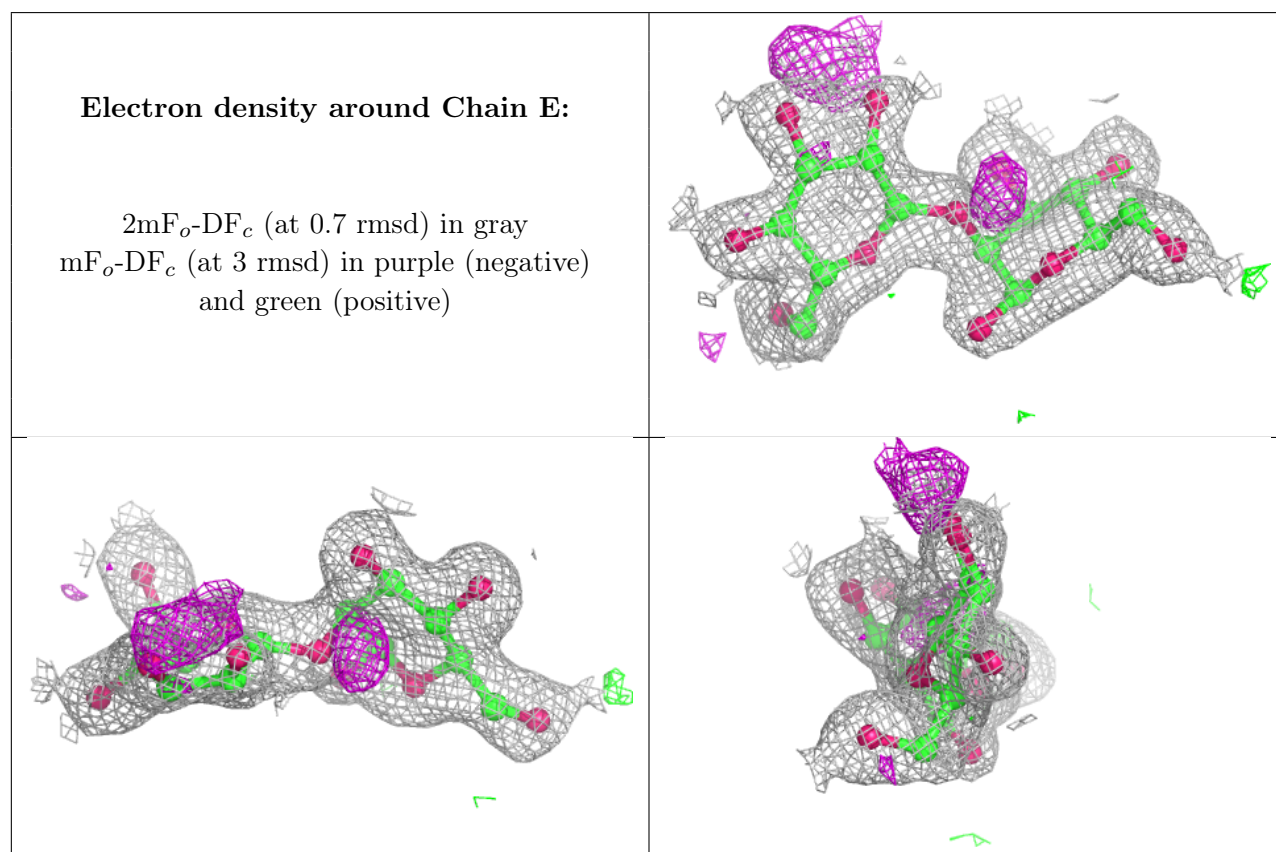
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MAN	H	2	11/12	0.84	0.18	30,45,53,53	0
2	MAN	G	2	11/12	0.89	0.11	26,38,44,45	0

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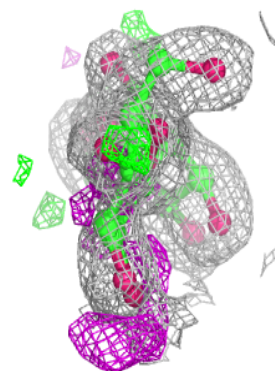
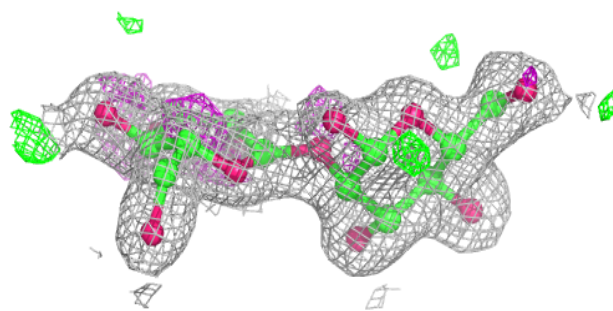
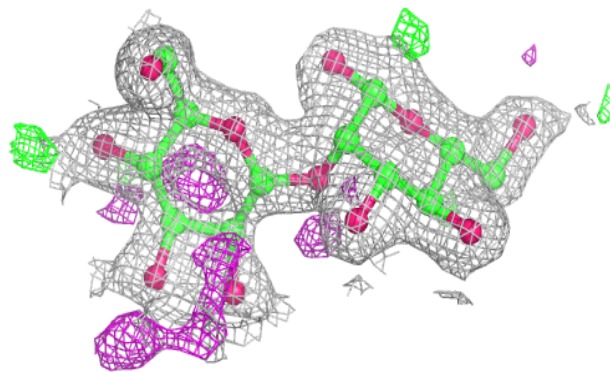
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MAN	F	2	11/12	0.89	0.13	32,38,44,45	0
2	MAN	E	2	11/12	0.91	0.14	25,32,41,44	0
2	BMA	G	1	12/12	0.92	0.10	26,38,44,46	0
2	BMA	F	1	12/12	0.93	0.10	27,39,42,43	0
2	BMA	H	1	12/12	0.94	0.14	31,47,50,55	0
2	BMA	E	1	12/12	0.94	0.11	22,36,40,41	0

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.

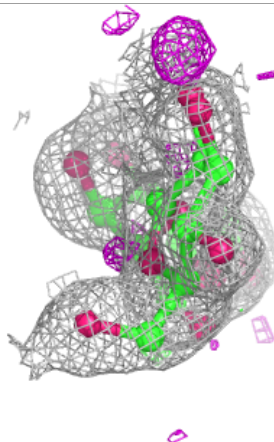
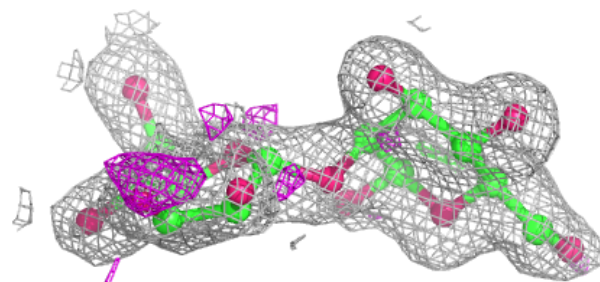
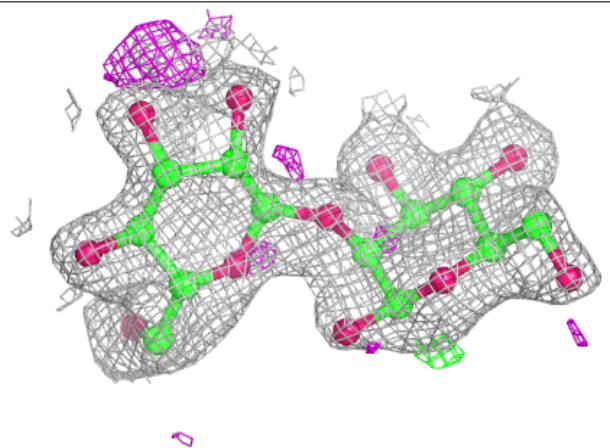


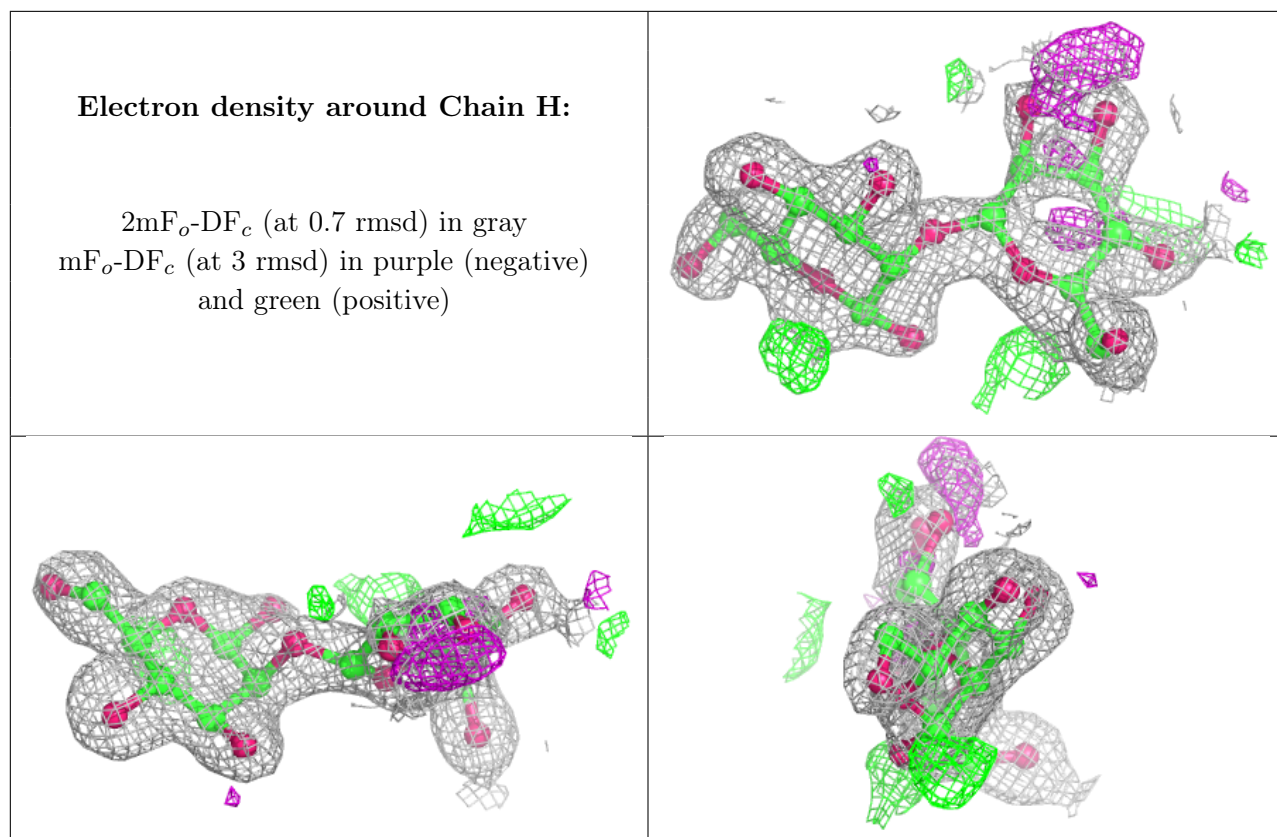
Electron density around Chain F:

$2mF_o-DF_c$ (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)





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
5	EDO	C	807	4/4	0.74	0.15	41,43,45,49	0
5	EDO	D	803	4/4	0.76	0.15	34,35,37,37	0
5	EDO	A	808	4/4	0.84	0.17	40,43,44,46	0
5	EDO	B	805	4/4	0.88	0.21	47,50,51,52	0
5	EDO	D	805	4/4	0.88	0.21	41,42,45,46	0
5	EDO	A	807	4/4	0.89	0.21	39,45,46,47	0
5	EDO	B	809	4/4	0.89	0.13	40,42,45,48	0
5	EDO	C	805	4/4	0.89	0.16	40,46,48,54	0
5	EDO	B	807	4/4	0.90	0.13	31,39,40,42	0
5	EDO	A	810	4/4	0.91	0.13	34,40,43,44	0
5	EDO	A	811	4/4	0.91	0.15	41,43,44,47	0
5	EDO	C	806	4/4	0.91	0.13	34,35,35,37	0
5	EDO	A	804	4/4	0.92	0.13	35,37,37,41	0
5	EDO	C	808	4/4	0.92	0.13	44,48,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	D	807	4/4	0.92	0.16	36,44,44,48	0
5	EDO	D	804	4/4	0.93	0.19	39,41,43,44	0
5	EDO	A	809	4/4	0.93	0.20	39,42,44,44	0
5	EDO	D	806	4/4	0.93	0.10	29,40,40,44	0
5	EDO	B	808	4/4	0.93	0.12	34,37,40,43	0
5	EDO	B	803	4/4	0.94	0.17	32,32,33,36	0
5	EDO	A	806	4/4	0.94	0.14	39,40,41,44	0
5	EDO	C	804	4/4	0.94	0.11	37,38,38,39	0
5	EDO	A	803	4/4	0.94	0.09	33,39,44,46	0
5	EDO	D	808	4/4	0.94	0.13	41,43,43,52	0
5	EDO	C	803	4/4	0.95	0.13	41,41,42,46	0
5	EDO	B	804	4/4	0.95	0.14	36,40,46,47	0
6	ACT	A	805	4/4	0.95	0.12	31,33,34,36	0
3	CA	C	801	1/1	0.96	0.06	32,32,32,32	0
4	NA	B	802	1/1	0.97	0.16	29,29,29,29	0
3	CA	D	801	1/1	0.97	0.06	35,35,35,35	0
6	ACT	B	806	4/4	0.97	0.08	32,34,37,39	0
3	CA	A	801	1/1	0.98	0.05	29,29,29,29	0
4	NA	D	802	1/1	0.98	0.04	32,32,32,32	0
3	CA	B	801	1/1	0.98	0.04	32,32,32,32	0
4	NA	C	802	1/1	0.99	0.05	27,27,27,27	0
4	NA	A	802	1/1	0.99	0.04	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.