



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 02:43 AM BST

PDB ID : 3U7B
Title : A new crystal structure of a Fusarium oxysporum GH10 xylanase reveals the presence of an extended loop on top of the catalytic cleft
Authors : Dimarogona, M.; Topakas, E.; Christakopoulos, P.; Chrysina, E.D.
Deposited on : 2011-10-13
Resolution : 1.94 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

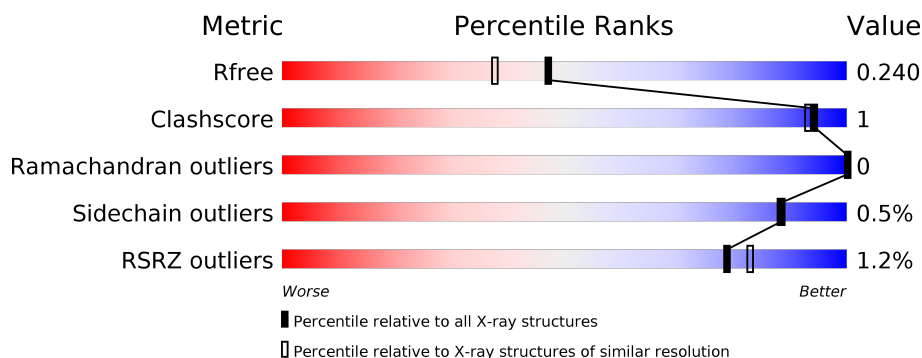
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 ≥ 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	327	<div> <div>2%</div> <div> <div></div> <div>96%</div> <div>•</div> </div> </div>
1	B	327	<div> <div>%</div> <div> <div></div> <div>97%</div> <div>•</div> </div> </div>
1	C	327	<div> <div>%</div> <div> <div></div> <div>94%</div> <div>5%</div> </div> </div>
1	D	327	<div> <div>%</div> <div> <div></div> <div>96%</div> <div>•</div> </div> </div>
1	E	327	<div> <div>2%</div> <div> <div></div> <div>97%</div> <div>•</div> </div> </div>
2	F	3	<div> <div></div> <div> <div>33%</div> <div>67%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	H	3	 <div>33% 67%</div>
3	G	5	 <div>60% 40%</div>
4	I	4	 <div>50% 50%</div>
4	J	4	 <div>50% 50%</div>

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:

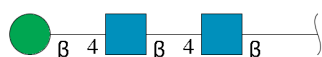
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EDO	A	409	-	-	X	-

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 ENDO-1,4-BETA-XYLANASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total 2550	C 1594	N 459	O 485	S 12	0	1	0
1	B	326	Total 2539	C 1588	N 455	O 484	S 12	0	1	0
1	C	326	Total 2545	C 1592	N 456	O 485	S 12	0	2	0
1	D	327	Total 2553	C 1596	N 459	O 486	S 12	0	2	0
1	E	326	Total 2539	C 1588	N 455	O 484	S 12	0	1	0

- 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
2	F	3	Total 39	C 22	N 2	O 15	0	0	0
2	H	3	Total 39	C 22	N 2	O 15	0	0	0

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



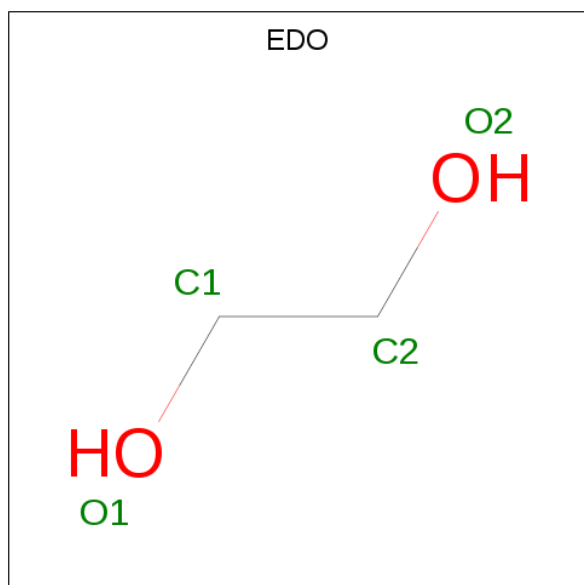
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	I	4	Total	C	N	O	0	0	0
			50	28	2	20			
4	J	4	Total	C	N	O	0	0	0
			50	28	2	20			

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



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

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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	E	1	Total 4	C 2	O 2	0	0

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	330	Total	O	0	0
			330	330		
6	B	440	Total	O	0	0
			440	440		
6	C	374	Total	O	0	0
			374	374		
6	D	404	Total	O	0	0
			404	404		
6	E	353	Total	O	0	0
			353	353		

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: ENDO-1,4-BETA-XYLANASE



- Molecule 1: ENDO-1,4-BETA-XYLANASE



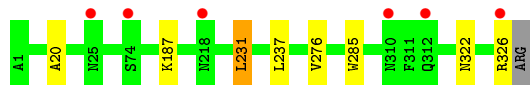
- Molecule 1: ENDO-1,4-BETA-XYLANASE



- Molecule 1: ENDO-1,4-BETA-XYLANASE



- Molecule 1: ENDO-1,4-BETA-XYLANASE



- 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:  33% 67%

MAG1
MAG2
BMA3

- 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:  33% 67%

MAG1
MAG2
BMA3

- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  60% 40%

MAG1
MAG2
BMA3
MAN4
MAN5

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

Chain I:  50% 50%

MAG1
MAG2
BMA3
MAN4

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

Chain J:  50% 50%

MAG1
MAG2
BMA3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	124.22Å 124.22Å 284.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.91 – 1.94 17.91 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.5 (17.91-1.94) 99.5 (17.91-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.33 (at 1.94Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.213 , 0.242 0.212 , 0.240	Depositor DCC
R_{free} test set	8169 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	15.3	Xtrriage
Anisotropy	0.031	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14970	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.91 % 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 5.4245e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: BMA, EDO, NAG, MAN

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	0.40	0/2609	0.51	0/3547
1	B	0.42	0/2598	0.54	0/3533
1	C	0.41	0/2607	0.52	0/3545
1	D	0.40	0/2615	0.52	0/3555
1	E	0.39	0/2598	0.51	0/3533
All	All	0.41	0/13027	0.52	0/17713

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	2550	0	2486	11	0
1	B	2539	0	2473	4	0
1	C	2545	0	2481	8	0
1	D	2553	0	2491	6	0
1	E	2539	0	2473	4	0
2	F	39	0	34	0	0
2	H	39	0	34	0	0
3	G	61	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	50	0	43	0	0
4	J	50	0	43	0	0
5	A	28	0	42	6	0
5	B	28	0	42	0	0
5	C	24	0	36	0	0
5	D	12	0	18	0	0
5	E	12	0	18	0	0
6	A	330	0	0	3	0
6	B	440	0	0	0	0
6	C	374	0	0	0	0
6	D	404	0	0	0	0
6	E	353	0	0	0	0
All	All	14970	0	12766	34	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 1.

All (34) 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:300:GLY:H	5:A:409:EDO:H21	1.19	1.07
1:A:300:GLY:N	5:A:409:EDO:H21	2.00	0.69
1:A:300:GLY:H	5:A:409:EDO:C2	2.05	0.65
5:A:409:EDO:H22	6:A:1660:HOH:O	2.01	0.61
1:C:187:LYS:HG2	1:C:237:LEU:HD11	1.87	0.57
1:D:187:LYS:HG2	1:D:237:LEU:HD21	1.86	0.57
1:B:322:ASN:O	1:B:326:ARG:HG2	2.08	0.54
1:E:322:ASN:O	1:E:326:ARG:HG2	2.08	0.53
1:A:86:TRP:CE2	1:A:88:SER:HB3	2.45	0.51
1:A:326:ARG:NH1	6:A:1852:HOH:O	2.42	0.49
1:E:187:LYS:HG2	1:E:237:LEU:HD11	1.93	0.49
1:C:231:LEU:HB3	1:C:276:VAL:HG21	1.95	0.49
1:D:231:LEU:HB3	1:D:276:VAL:HG21	1.95	0.48
1:C:86:TRP:CE2	1:C:88:SER:HB3	2.51	0.46
1:B:53:ILE:HG21	1:B:115:VAL:CG2	2.46	0.46
1:C:99:TRP:CH2	1:C:107:VAL:HG21	2.51	0.45
1:C:247:ASP:HB2	1:C:304:ALA:HB1	1.99	0.44
1:B:86:TRP:CE2	1:B:88:SER:HB3	2.52	0.44
1:C:20:ALA:HB2	1:C:285:TRP:CE3	2.53	0.44
1:C:20:ALA:HA	1:C:43:THR:O	2.18	0.43
1:E:20:ALA:HB2	1:E:285:TRP:CE3	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:PRO:HB2	1:D:93:TRP:CD1	2.54	0.42
1:D:86:TRP:CE2	1:D:88:SER:HB3	2.54	0.42
1:B:111:HIS:O	1:B:115:VAL:HG23	2.19	0.42
1:D:294:VAL:HB	1:D:295:PRO:HD3	2.02	0.41
1:A:257:GLN:HG3	6:A:1465:HOH:O	2.20	0.41
1:A:249:ARG:HH12	5:A:401:EDO:H12	1.86	0.41
1:C:139:TYR:CE2	1:C:150:GLU:HG3	2.55	0.41
1:A:51:GLU:HA	1:A:91:PRO:HG3	2.03	0.41
1:D:111:HIS:O	1:D:115:VAL:HG12	2.21	0.41
1:A:86:TRP:CZ2	1:A:88:SER:HB3	2.56	0.40
1:A:299:PRO:HA	5:A:409:EDO:H21	2.03	0.40
1:E:231:LEU:HB3	1:E:276:VAL:HG21	2.04	0.40
1:A:99:TRP:CH2	1:A:107:VAL:HG21	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	326/327 (100%)	320 (98%)	6 (2%)	0	100	100
1	B	325/327 (99%)	320 (98%)	5 (2%)	0	100	100
1	C	326/327 (100%)	322 (99%)	4 (1%)	0	100	100
1	D	327/327 (100%)	321 (98%)	6 (2%)	0	100	100
1	E	325/327 (99%)	317 (98%)	8 (2%)	0	100	100
All	All	1629/1635 (100%)	1600 (98%)	29 (2%)	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	266/265 (100%)	264 (99%)	2 (1%)	81	78
1	B	265/265 (100%)	263 (99%)	2 (1%)	81	78
1	C	266/265 (100%)	264 (99%)	2 (1%)	81	78
1	D	267/265 (101%)	267 (100%)	0	100	100
1	E	265/265 (100%)	264 (100%)	1 (0%)	91	91
All	All	1329/1325 (100%)	1322 (100%)	7 (0%)	88	88

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	SER
1	A	231	LEU
1	B	231	LEU
1	B	278	ARG
1	C	278	ARG
1	C	326	ARG
1	E	231	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	217	GLN
1	B	67	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

19 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	0.56	0	17,19,21	0.69	0
2	NAG	F	2	2	14,14,15	0.46	0	17,19,21	0.95	1 (5%)
2	BMA	F	3	2	11,11,12	0.48	0	15,15,17	1.08	2 (13%)
3	NAG	G	1	1,3	14,14,15	0.54	0	17,19,21	0.76	0
3	NAG	G	2	3	14,14,15	0.51	0	17,19,21	0.96	1 (5%)
3	BMA	G	3	3	11,11,12	0.56	0	15,15,17	1.05	0
3	MAN	G	4	3	11,11,12	0.73	0	15,15,17	1.35	3 (20%)
3	MAN	G	5	3	11,11,12	0.59	0	15,15,17	0.80	0
2	NAG	H	1	1,2	14,14,15	0.57	0	17,19,21	0.73	0
2	NAG	H	2	2	14,14,15	0.45	0	17,19,21	0.96	1 (5%)
2	BMA	H	3	2	11,11,12	0.37	0	15,15,17	1.04	2 (13%)
4	NAG	I	1	1,4	14,14,15	0.51	0	17,19,21	1.05	1 (5%)
4	NAG	I	2	4	14,14,15	0.53	0	17,19,21	0.87	1 (5%)
4	BMA	I	3	4	11,11,12	0.38	0	15,15,17	0.70	0
4	MAN	I	4	4	11,11,12	0.68	0	15,15,17	0.92	0
4	NAG	J	1	1,4	14,14,15	0.59	0	17,19,21	0.84	0
4	NAG	J	2	4	14,14,15	0.50	0	17,19,21	0.74	1 (5%)
4	BMA	J	3	4	11,11,12	0.40	0	15,15,17	0.74	1 (6%)
4	MAN	J	4	4	11,11,12	0.59	0	15,15,17	0.72	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	-	0/6/23/26	0/1/1/1
2	BMA	F	3	2	-	2/2/19/22	0/1/1/1

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

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	2	NAG	C1-O5-C5	3.39	116.78	112.19
2	F	2	NAG	C1-O5-C5	3.18	116.49	112.19
3	G	4	MAN	C1-C2-C3	2.98	113.33	109.67
3	G	4	MAN	C2-C3-C4	2.82	115.78	110.89
4	I	2	NAG	C1-O5-C5	2.78	115.96	112.19
3	G	2	NAG	C1-O5-C5	2.48	115.56	112.19
3	G	4	MAN	C3-C4-C5	2.45	114.62	110.24
4	I	1	NAG	C1-O5-C5	2.37	115.40	112.19
2	F	3	BMA	O5-C5-C6	2.30	110.80	107.20
2	F	3	BMA	C1-O5-C5	2.21	115.19	112.19
2	H	3	BMA	C1-O5-C5	2.17	115.13	112.19
4	J	3	BMA	O5-C5-C6	2.05	110.41	107.20
2	H	3	BMA	O5-C5-C6	2.05	110.41	107.20
4	J	2	NAG	C1-O5-C5	2.00	114.91	112.19

There are no chirality outliers.

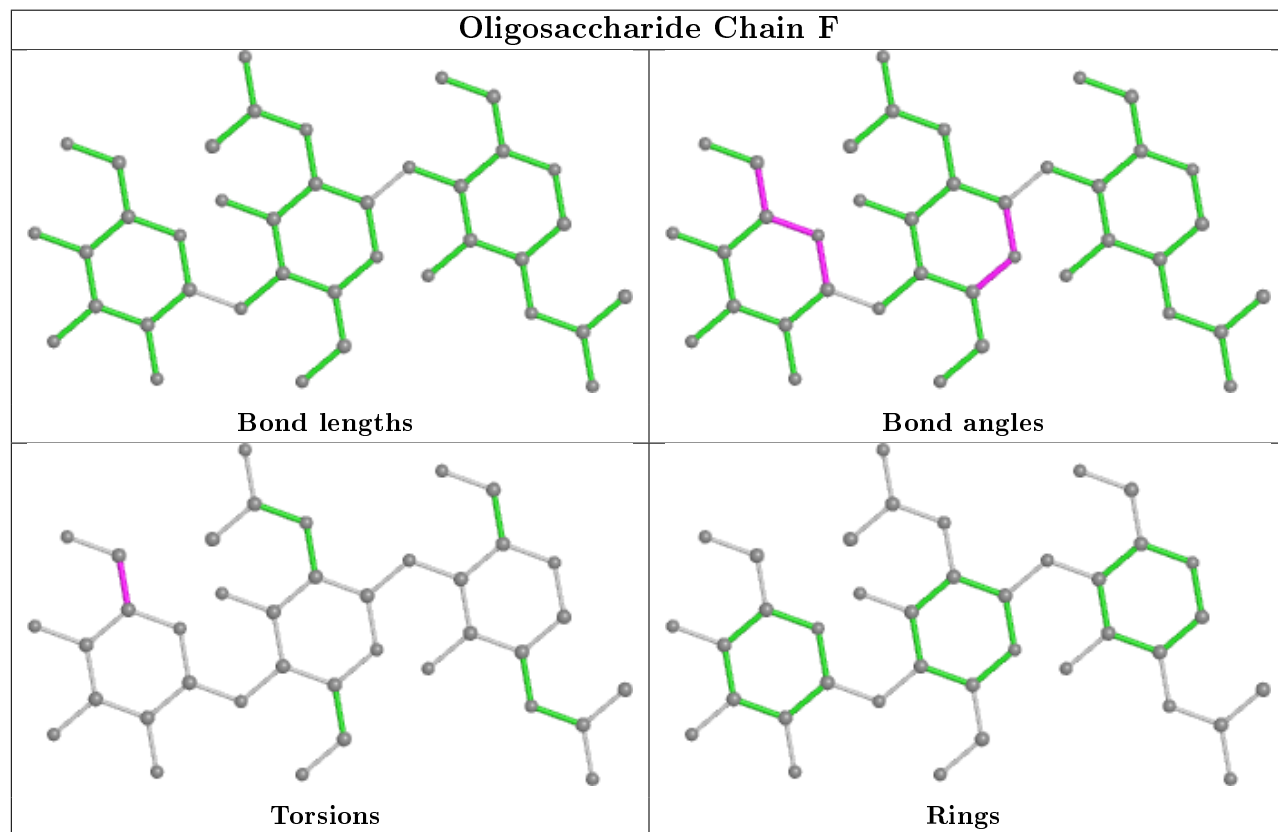
All (9) torsion outliers are listed below:

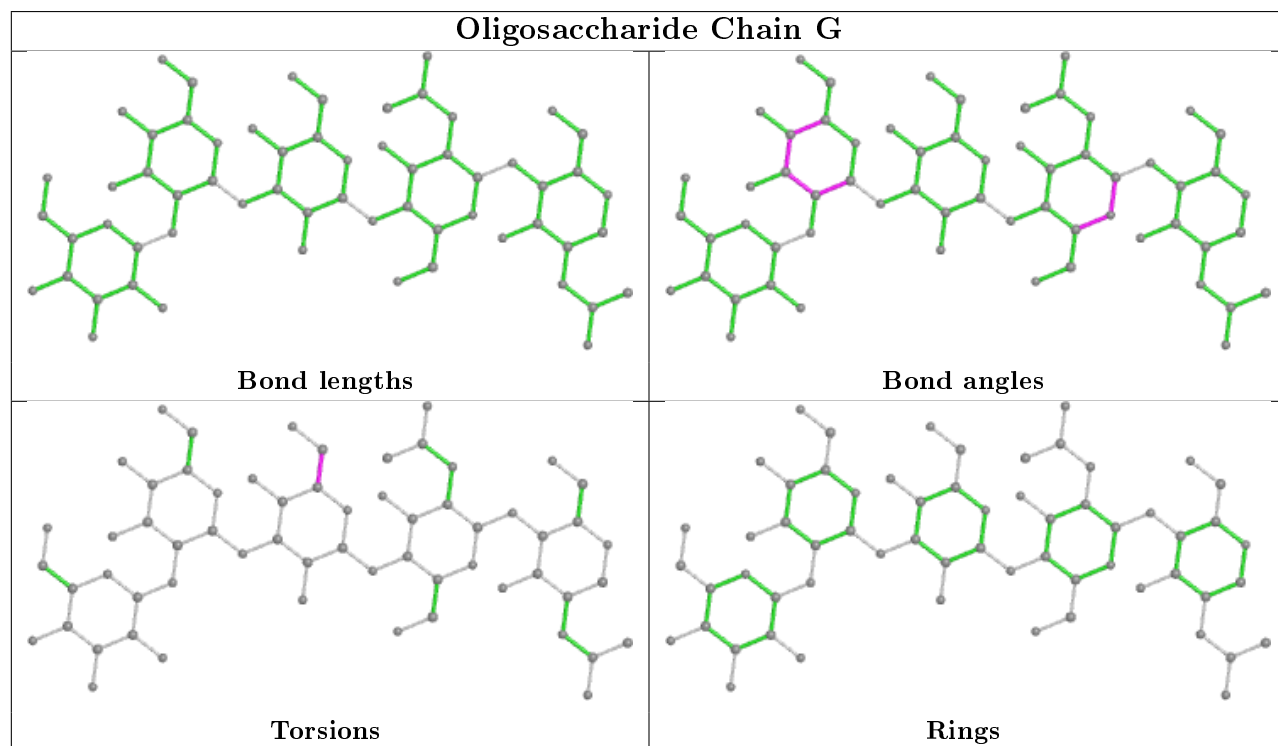
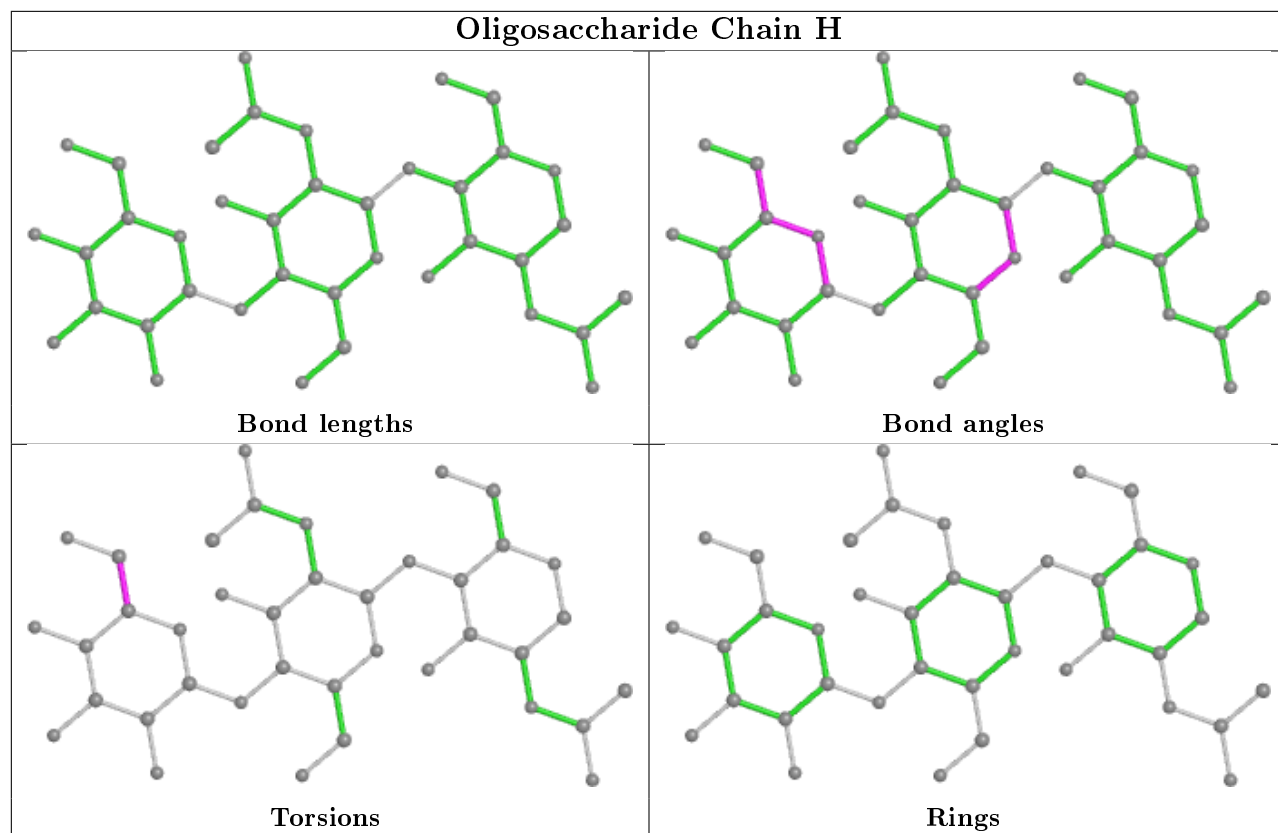
Mol	Chain	Res	Type	Atoms
2	F	3	BMA	O5-C5-C6-O6
2	F	3	BMA	C4-C5-C6-O6
2	H	3	BMA	O5-C5-C6-O6
2	H	3	BMA	C4-C5-C6-O6
3	G	3	BMA	C4-C5-C6-O6
4	J	3	BMA	C4-C5-C6-O6
3	G	3	BMA	O5-C5-C6-O6
4	I	3	BMA	C4-C5-C6-O6
4	J	3	BMA	O5-C5-C6-O6

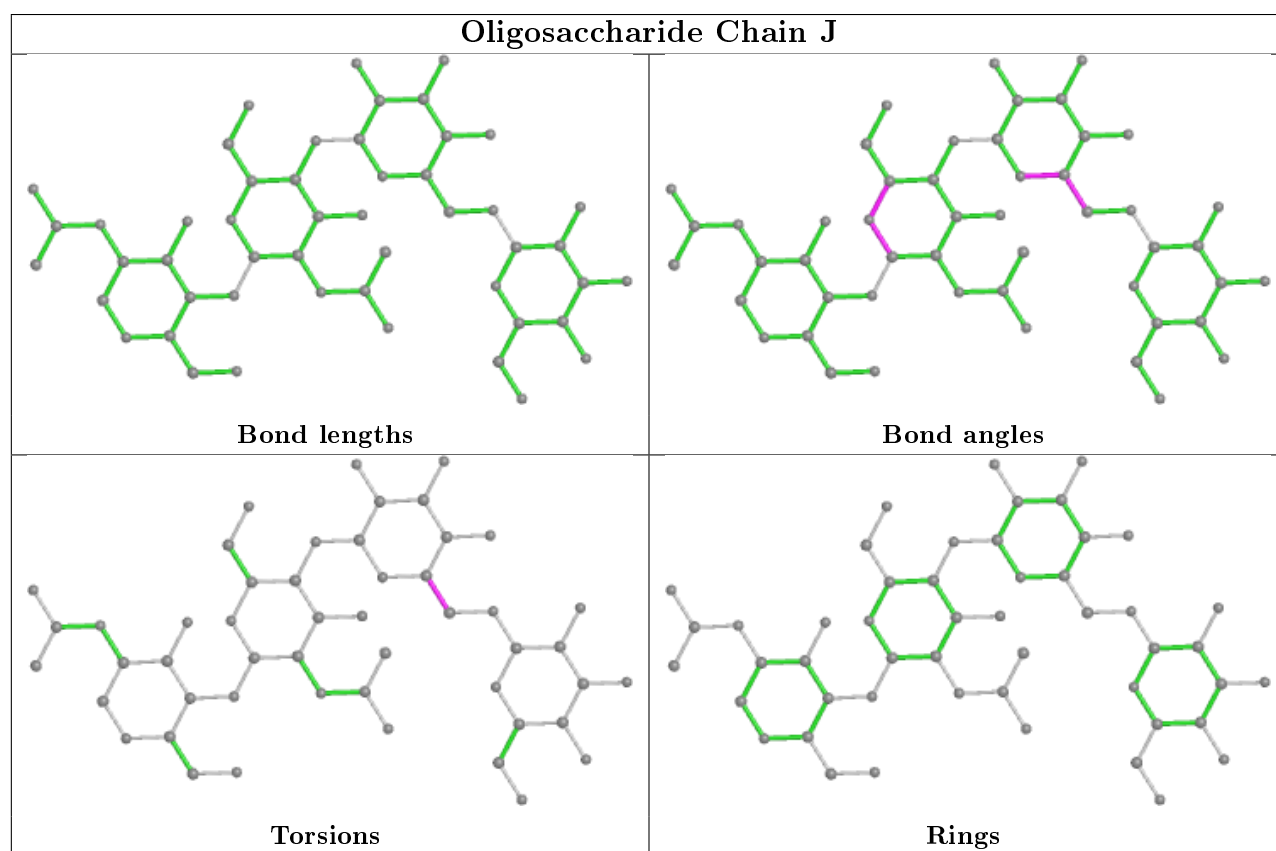
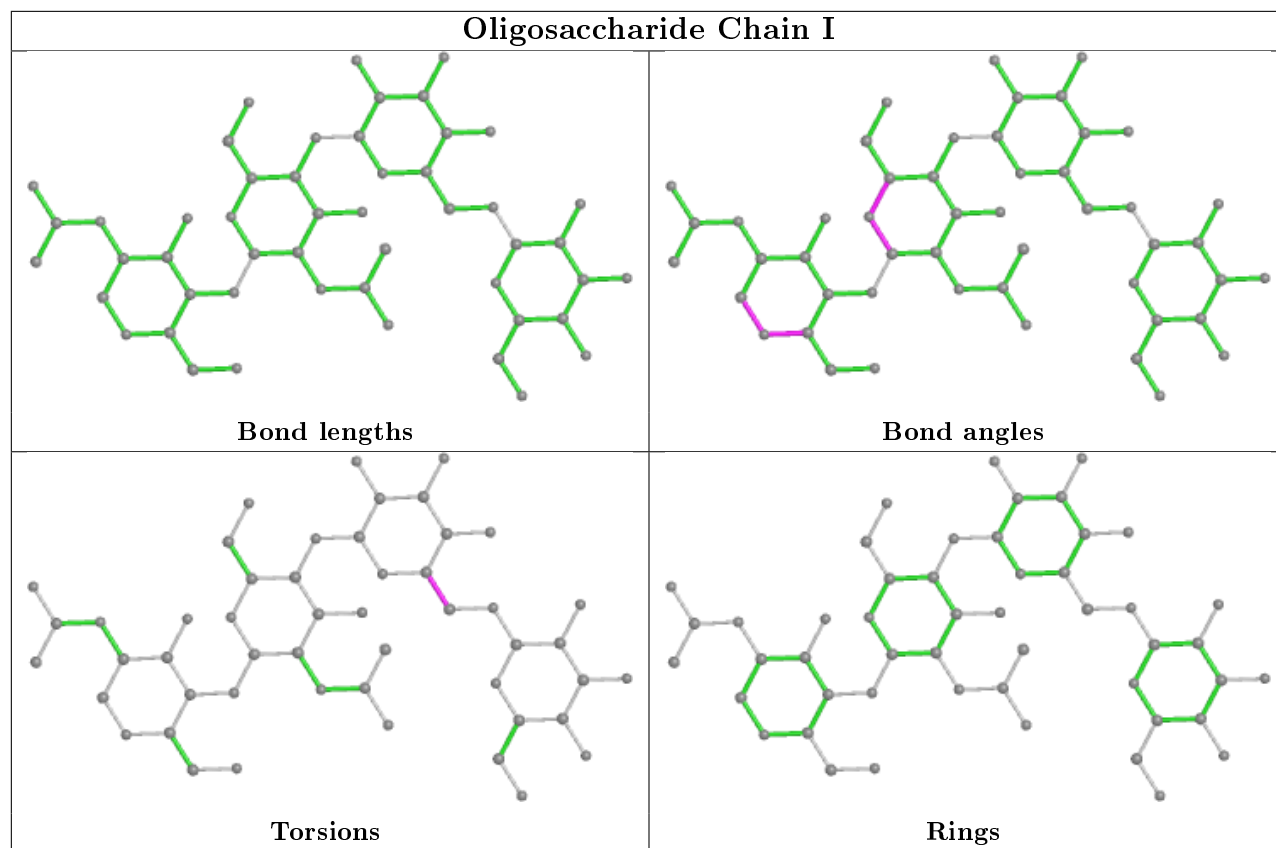
There are no ring outliers.

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.







5.6 Ligand geometry

26 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	EDO	A	403	-	3,3,3	0.42	0	2,2,2	0.40	0
5	EDO	C	414	-	3,3,3	0.49	0	2,2,2	0.27	0
5	EDO	E	406	-	3,3,3	0.52	0	2,2,2	0.10	0
5	EDO	D	402	-	3,3,3	0.51	0	2,2,2	0.30	0
5	EDO	C	400	-	3,3,3	0.50	0	2,2,2	0.34	0
5	EDO	A	413	-	3,3,3	0.48	0	2,2,2	0.15	0
5	EDO	B	401	-	3,3,3	0.40	0	2,2,2	0.53	0
5	EDO	B	404	-	3,3,3	0.46	0	2,2,2	0.36	0
5	EDO	E	407	-	3,3,3	0.45	0	2,2,2	0.34	0
5	EDO	E	410	-	3,3,3	0.50	0	2,2,2	0.24	0
5	EDO	C	401	-	3,3,3	0.47	0	2,2,2	0.33	0
5	EDO	D	408	-	3,3,3	0.43	0	2,2,2	0.42	0
5	EDO	B	402	-	3,3,3	0.46	0	2,2,2	0.17	0
5	EDO	C	411	-	3,3,3	0.50	0	2,2,2	0.33	0
5	EDO	C	406	-	3,3,3	0.53	0	2,2,2	0.18	0
5	EDO	B	403	-	3,3,3	0.45	0	2,2,2	0.34	0
5	EDO	A	409	-	3,3,3	0.46	0	2,2,2	0.24	0
5	EDO	B	400	-	3,3,3	0.51	0	2,2,2	0.30	0
5	EDO	A	400	-	3,3,3	0.45	0	2,2,2	0.30	0
5	EDO	A	404	-	3,3,3	0.49	0	2,2,2	0.22	0
5	EDO	B	405	-	3,3,3	0.47	0	2,2,2	0.28	0
5	EDO	A	402	-	3,3,3	0.49	0	2,2,2	0.03	0
5	EDO	D	401	-	3,3,3	0.42	0	2,2,2	0.46	0
5	EDO	A	401	-	3,3,3	0.46	0	2,2,2	0.37	0
5	EDO	C	412	-	3,3,3	0.44	0	2,2,2	0.38	0
5	EDO	B	407	-	3,3,3	0.43	0	2,2,2	0.41	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
5	EDO	A	403	-	-	0/1/1/1	-
5	EDO	C	414	-	-	0/1/1/1	-
5	EDO	E	406	-	-	1/1/1/1	-
5	EDO	D	402	-	-	0/1/1/1	-
5	EDO	C	400	-	-	0/1/1/1	-
5	EDO	A	413	-	-	1/1/1/1	-
5	EDO	B	401	-	-	1/1/1/1	-
5	EDO	B	404	-	-	1/1/1/1	-
5	EDO	E	407	-	-	1/1/1/1	-
5	EDO	E	410	-	-	1/1/1/1	-
5	EDO	C	401	-	-	1/1/1/1	-
5	EDO	D	408	-	-	0/1/1/1	-
5	EDO	B	402	-	-	1/1/1/1	-
5	EDO	C	411	-	-	0/1/1/1	-
5	EDO	C	406	-	-	1/1/1/1	-
5	EDO	B	403	-	-	1/1/1/1	-
5	EDO	A	409	-	-	0/1/1/1	-
5	EDO	B	400	-	-	0/1/1/1	-
5	EDO	A	400	-	-	0/1/1/1	-
5	EDO	A	404	-	-	1/1/1/1	-
5	EDO	B	405	-	-	1/1/1/1	-
5	EDO	A	402	-	-	1/1/1/1	-
5	EDO	D	401	-	-	1/1/1/1	-
5	EDO	A	401	-	-	0/1/1/1	-
5	EDO	C	412	-	-	0/1/1/1	-
5	EDO	B	407	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	404	EDO	O1-C1-C2-O2
5	A	402	EDO	O1-C1-C2-O2
5	B	407	EDO	O1-C1-C2-O2
5	C	401	EDO	O1-C1-C2-O2
5	A	404	EDO	O1-C1-C2-O2
5	E	407	EDO	O1-C1-C2-O2
5	B	403	EDO	O1-C1-C2-O2
5	A	413	EDO	O1-C1-C2-O2
5	D	401	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
5	E	406	EDO	O1-C1-C2-O2
5	B	401	EDO	O1-C1-C2-O2
5	B	405	EDO	O1-C1-C2-O2
5	E	410	EDO	O1-C1-C2-O2
5	B	402	EDO	O1-C1-C2-O2
5	C	406	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	409	EDO	5	0
5	A	401	EDO	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	327/327 (100%)	0.13	6 (1%) 68 74	8, 17, 24, 33	0
1	B	326/327 (99%)	-0.35	2 (0%) 89 92	5, 10, 15, 26	0
1	C	326/327 (99%)	-0.18	2 (0%) 89 92	7, 13, 19, 29	0
1	D	327/327 (100%)	-0.12	4 (1%) 79 83	7, 14, 20, 33	0
1	E	326/327 (99%)	0.15	6 (1%) 68 74	11, 17, 24, 36	0
All	All	1632/1635 (99%)	-0.07	20 (1%) 79 83	5, 14, 23, 36	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	327	ARG	5.1
1	A	1	ALA	5.0
1	E	326	ARG	4.9
1	D	327	ARG	4.7
1	D	98	ASN	3.6
1	D	1	ALA	3.5
1	C	326	ARG	3.5
1	D	326	ARG	3.3
1	C	1	ALA	3.2
1	A	326	ARG	3.1
1	E	310	ASN	3.1
1	A	257	GLN	2.9
1	B	1	ALA	2.8
1	B	326	ARG	2.6
1	E	218	ASN	2.4
1	A	146	ARG	2.4
1	E	25	ASN	2.3
1	E	312	GLN	2.2
1	E	74	SER	2.1
1	A	141	ASP	2.0

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

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

6.3 Carbohydrates ⓘ

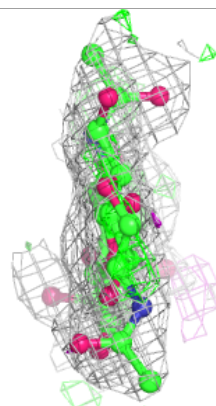
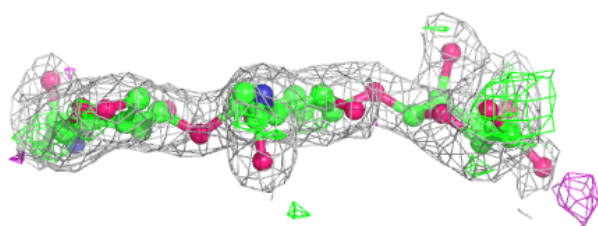
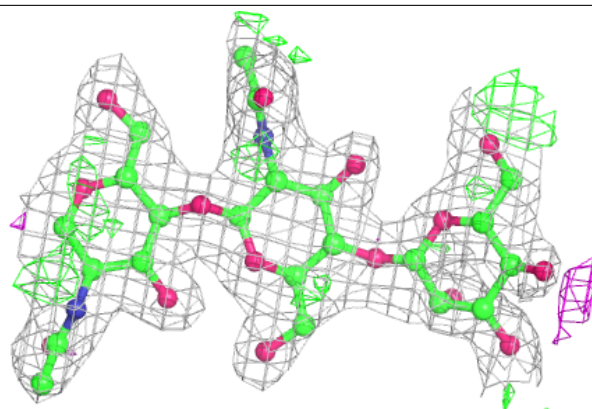
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BMA	F	3	11/12	0.60	0.29	37,38,39,39	0
3	MAN	G	4	11/12	0.64	0.34	40,42,42,43	0
3	BMA	G	3	11/12	0.65	0.23	31,33,34,36	0
4	MAN	I	4	11/12	0.68	0.30	40,41,43,43	0
4	MAN	J	4	11/12	0.80	0.30	42,44,45,45	0
3	MAN	G	5	11/12	0.83	0.38	40,40,40,41	0
2	NAG	F	2	14/15	0.86	0.15	33,33,35,36	0
2	BMA	H	3	11/12	0.87	0.20	25,26,27,27	0
2	NAG	F	1	14/15	0.87	0.14	28,30,32,32	0
4	BMA	J	3	11/12	0.88	0.21	33,34,36,39	0
4	BMA	I	3	11/12	0.90	0.20	29,30,32,35	0
4	NAG	J	2	14/15	0.92	0.15	23,24,27,28	0
2	NAG	H	2	14/15	0.93	0.11	23,24,25,25	0
4	NAG	I	1	14/15	0.94	0.09	23,23,24,24	0
3	NAG	G	2	14/15	0.94	0.11	21,23,24,27	0
4	NAG	I	2	14/15	0.94	0.11	25,26,27,27	0
4	NAG	J	1	14/15	0.95	0.12	17,18,20,21	0
2	NAG	H	1	14/15	0.95	0.09	22,22,23,24	0
3	NAG	G	1	14/15	0.96	0.10	17,19,21,22	0

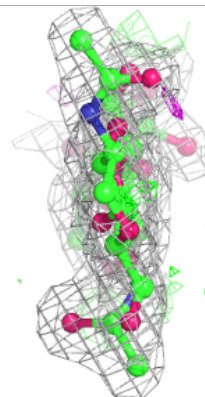
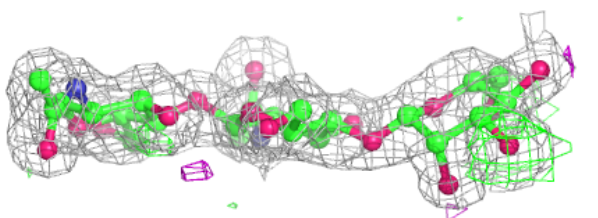
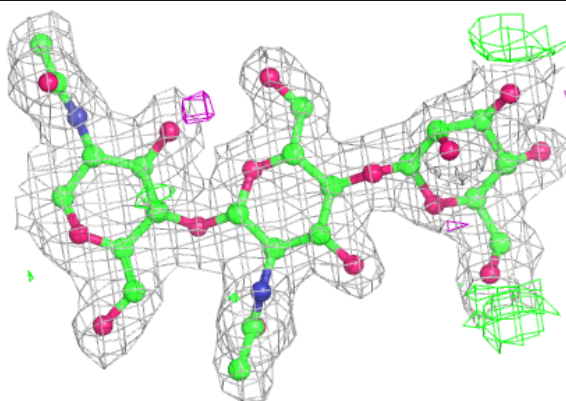
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

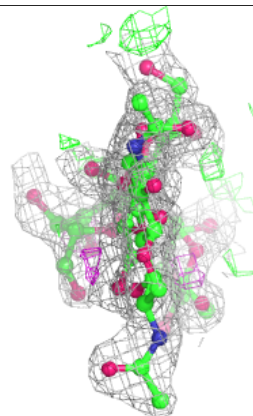
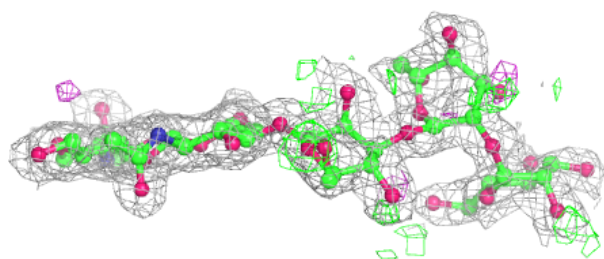
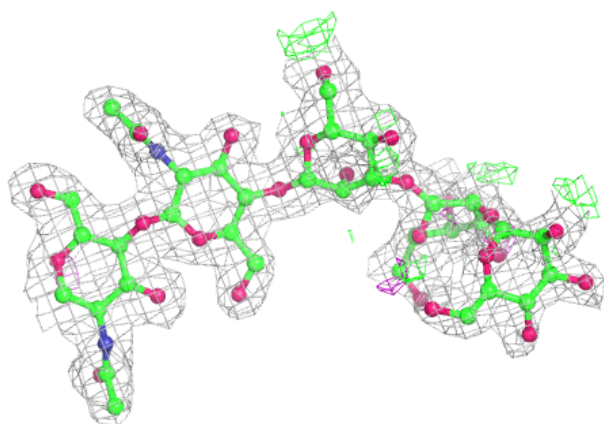
**Electron density around Chain H:**

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

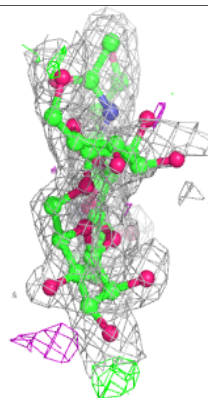
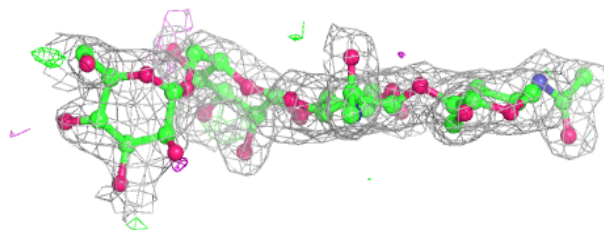
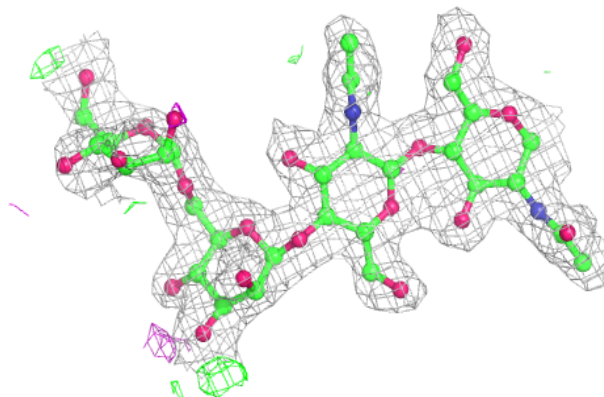


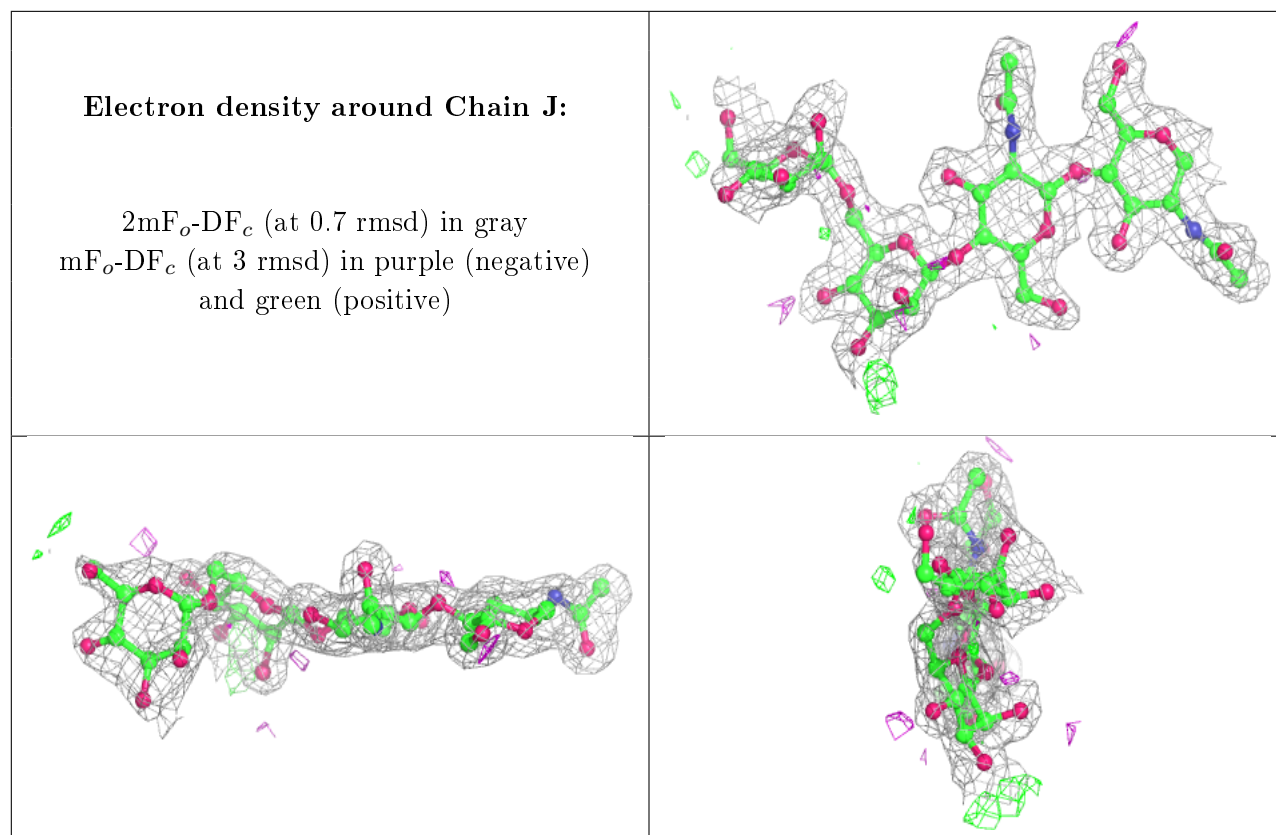
Electron density around Chain G:

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

**Electron density around Chain I:**

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





6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	A	404	4/4	0.53	0.35	44,44,44,45	0
5	EDO	C	401	4/4	0.74	0.21	39,40,40,40	0
5	EDO	E	407	4/4	0.75	0.36	46,47,47,47	0
5	EDO	A	409	4/4	0.79	0.23	27,28,28,30	0
5	EDO	B	407	4/4	0.79	0.32	35,36,36,37	0
5	EDO	B	403	4/4	0.81	0.20	40,40,40,40	0
5	EDO	B	405	4/4	0.83	0.24	46,46,47,47	0
5	EDO	B	404	4/4	0.84	0.18	21,23,25,27	0
5	EDO	C	414	4/4	0.86	0.18	31,32,32,33	0
5	EDO	B	401	4/4	0.86	0.18	19,20,20,21	0
5	EDO	C	412	4/4	0.87	0.16	46,46,46,46	0
5	EDO	A	403	4/4	0.88	0.31	46,46,46,46	0
5	EDO	D	401	4/4	0.88	0.18	34,35,35,35	0
5	EDO	A	401	4/4	0.89	0.12	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	E	406	4/4	0.90	0.18	21,23,23,24	0
5	EDO	C	406	4/4	0.90	0.18	16,18,18,19	0
5	EDO	D	402	4/4	0.92	0.15	16,16,17,17	0
5	EDO	A	402	4/4	0.93	0.15	21,21,22,23	0
5	EDO	A	413	4/4	0.94	0.13	18,20,20,20	0
5	EDO	B	402	4/4	0.94	0.11	17,17,18,19	0
5	EDO	E	410	4/4	0.94	0.14	26,26,27,27	0
5	EDO	B	400	4/4	0.95	0.11	15,17,17,17	0
5	EDO	A	400	4/4	0.96	0.10	20,20,20,20	0
5	EDO	C	411	4/4	0.96	0.11	18,18,18,19	0
5	EDO	C	400	4/4	0.97	0.08	14,14,14,14	0
5	EDO	D	408	4/4	0.97	0.10	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.