



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 7, 2024 – 10:13 am GMT

PDB ID : 6HH9
Title : Crystal structure of a two-domain esterase (CEX) active on acetylated man-
nans co-crystallized with mannopentaose
Authors : Michalak, L.; La Rosa, S.L.; Rohr, A.K.; Achmann, F.L.; Westereng, B.
Deposited on : 2018-08-27
Resolution : 2.40 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 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 : 1.8.4, 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

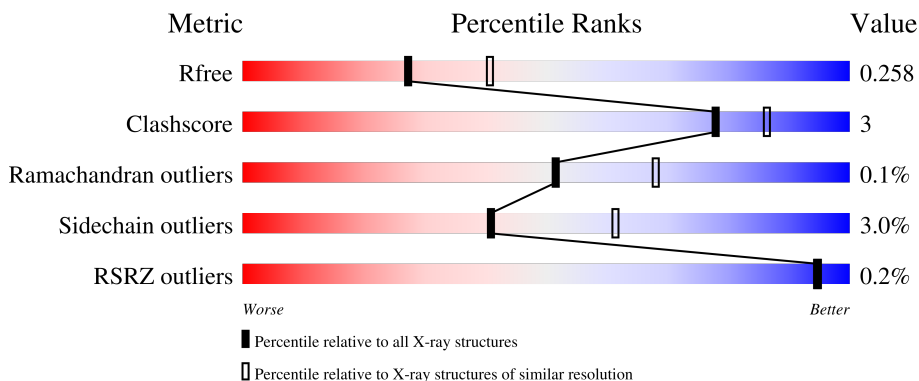
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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.



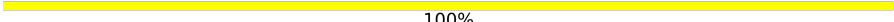
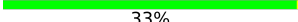
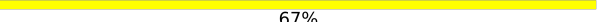
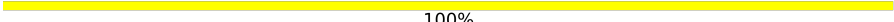
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	378	89% (green), 8% (yellow), 3% (orange), 2% (red), 2% (grey)
1	B	378	90% (green), 7% (yellow), 2% (orange), 1% (red), 1% (grey)
1	C	378	85% (green), 12% (yellow), 2% (orange), 1% (red), 1% (grey)
1	D	378	88% (green), 8% (yellow), 2% (orange), 1% (red), 1% (grey)
2	E	4	50% (green), 50% (yellow)

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

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 12202 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 GDSL-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	368	2901	1831	498	563	9	0	0	0
1	B	370	2921	1843	504	565	9	0	0	0
1	C	366	2885	1822	494	560	9	0	0	0
1	D	363	2861	1807	488	557	9	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	373	ALA	-	expression tag	UNP C7G6F8
A	374	HIS	-	expression tag	UNP C7G6F8
A	375	HIS	-	expression tag	UNP C7G6F8
A	376	HIS	-	expression tag	UNP C7G6F8
A	377	HIS	-	expression tag	UNP C7G6F8
A	378	HIS	-	expression tag	UNP C7G6F8
B	373	ALA	-	expression tag	UNP C7G6F8
B	374	HIS	-	expression tag	UNP C7G6F8
B	375	HIS	-	expression tag	UNP C7G6F8
B	376	HIS	-	expression tag	UNP C7G6F8
B	377	HIS	-	expression tag	UNP C7G6F8
B	378	HIS	-	expression tag	UNP C7G6F8
C	373	ALA	-	expression tag	UNP C7G6F8
C	374	HIS	-	expression tag	UNP C7G6F8
C	375	HIS	-	expression tag	UNP C7G6F8
C	376	HIS	-	expression tag	UNP C7G6F8
C	377	HIS	-	expression tag	UNP C7G6F8
C	378	HIS	-	expression tag	UNP C7G6F8
D	373	ALA	-	expression tag	UNP C7G6F8
D	374	HIS	-	expression tag	UNP C7G6F8
D	375	HIS	-	expression tag	UNP C7G6F8

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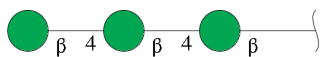
Chain	Residue	Modelled	Actual	Comment	Reference
D	376	HIS	-	expression tag	UNP C7G6F8
D	377	HIS	-	expression tag	UNP C7G6F8
D	378	HIS	-	expression tag	UNP C7G6F8

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	E	4	45	24	21	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
3	F	3	34	18	16	0	0	0
3	G	3	34	18	16	0	0	0
3	H	3	34	18	16	0	0	0


- Molecule 4 is water.

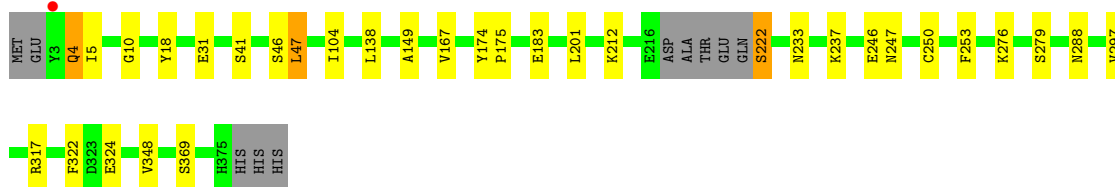
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	152	Total	O	0	0
			152	152		
4	B	149	Total	O	0	0
			149	149		
4	C	112	Total	O	0	0
			112	112		
4	D	74	Total	O	0	0
			74	74		

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.

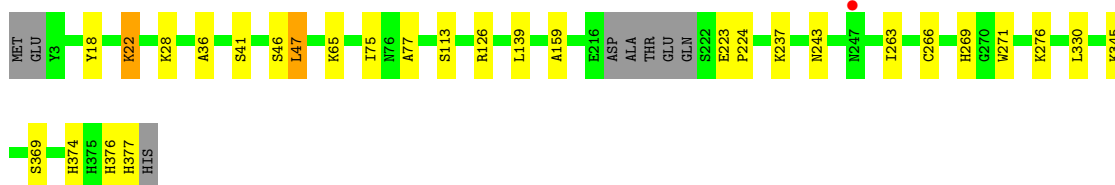
- Molecule 1: GDSL-like protein

Chain A:  89% 8% ..




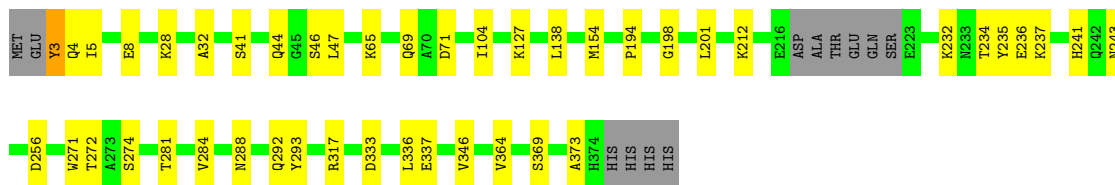
- Molecule 1: GDSL-like protein

Chain B:  90% 7% ..



- Molecule 1: GDSL-like protein

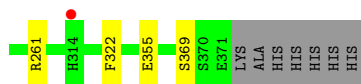
Chain C:  85% 12% .



- Molecule 1: GDSL-like protein

Chain D:  88% 8% .





- Molecule 2: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose



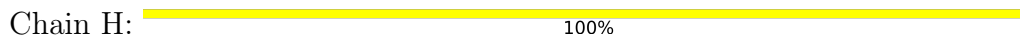
- Molecule 3: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.48Å 136.69Å 85.41Å 90.00° 113.86° 90.00°	Depositor
Resolution (Å)	47.84 – 2.40 47.79 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.6 (47.84-2.40) 98.7 (47.79-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.181 , 0.253 0.187 , 0.258	Depositor DCC
R_{free} test set	3029 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	42.1	Xtrriage
Anisotropy	0.222	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12202	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.46	0/2967	0.64	0/4027
1	B	0.46	0/2989	0.64	0/4057
1	C	0.45	0/2950	0.63	0/4004
1	D	0.42	0/2925	0.60	0/3971
All	All	0.45	0/11831	0.63	0/16059

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	D	0	2
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	317	ARG	Sidechain
1	D	126	ARG	Sidechain
1	D	261	ARG	Sidechain

5.2 Too-close contacts

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	2901	0	2808	18	0
1	B	2921	0	2822	17	0
1	C	2885	0	2796	23	0
1	D	2861	0	2771	10	0
2	E	45	0	39	0	0
3	F	34	0	30	0	0
3	G	34	0	30	0	0
3	H	34	0	30	0	0
4	A	152	0	0	0	0
4	B	149	0	0	4	0
4	C	112	0	0	4	0
4	D	74	0	0	0	0
All	All	12202	0	11326	66	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 3.

All (66) 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:B:126:ARG:HH22	1:B:374:HIS:CD2	1.99	0.80
1:B:276:LYS:HD2	4:B:631:HOH:O	1.94	0.67
1:D:10:GLY:O	1:D:167:VAL:HA	1.98	0.63
1:A:246:GLU:O	1:A:247:ASN:HB2	2.00	0.61
1:C:243:ASN:ND2	1:C:256:ASP:O	2.33	0.61
1:A:31:GLU:OE2	1:B:269:HIS:HE1	1.85	0.59
1:A:18:TYR:CD1	1:A:222:SER:HB3	2.38	0.59
1:C:237:LYS:O	1:C:369:SER:HA	2.03	0.58
1:C:234:THR:O	1:C:288:ASN:ND2	2.37	0.58
1:B:377:HIS:O	4:B:501:HOH:O	2.17	0.58
1:C:3:TYR:HB2	4:C:517:HOH:O	2.03	0.58
1:C:5:ILE:HD12	1:C:201:LEU:HD11	1.89	0.55
1:A:288:ASN:HB2	1:A:369:SER:HB2	1.89	0.53
1:B:46:SER:HB3	1:B:47:LEU:HD13	1.91	0.53
1:B:139:LEU:HD12	1:B:159:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:127:LYS:NZ	1:C:236:GLU:O	2.41	0.53
1:C:235:TYR:OH	1:C:337:GLU:OE2	2.18	0.53
1:B:126:ARG:HH22	1:B:374:HIS:HD2	1.56	0.52
1:A:10:GLY:O	1:A:167:VAL:HA	2.10	0.52
1:B:377:HIS:C	4:B:590:HOH:O	2.47	0.52
1:C:281:THR:HA	1:C:346:VAL:O	2.10	0.51
1:B:269:HIS:HD2	4:B:561:HOH:O	1.93	0.51
1:A:322:PHE:CZ	1:A:324:GLU:HB2	2.46	0.50
1:B:77:ALA:HA	1:B:263:ILE:HD11	1.94	0.50
1:C:154:MET:HE1	4:C:580:HOH:O	2.12	0.50
1:C:8:GLU:HB2	4:C:593:HOH:O	2.12	0.49
1:B:18:TYR:CE1	1:B:22:LYS:HE3	2.47	0.49
1:B:126:ARG:NH2	1:B:374:HIS:CD2	2.77	0.49
1:D:139:LEU:HD12	1:D:159:ALA:HB2	1.95	0.49
1:A:4:GLN:O	1:A:4:GLN:HG2	2.13	0.48
1:A:5:ILE:CD1	1:A:201:LEU:HD11	2.43	0.48
1:A:237:LYS:O	1:A:369:SER:HA	2.14	0.48
1:B:223:GLU:HG3	1:B:224:PRO:HD2	1.96	0.47
1:A:246:GLU:O	1:A:247:ASN:CB	2.62	0.47
1:D:34:ASN:ND2	1:D:99:GLU:O	2.38	0.47
1:D:211:ASP:O	1:D:215:THR:HG23	2.15	0.46
1:A:250:CYS:HB3	1:A:253:PHE:O	2.16	0.46
1:B:237:LYS:O	1:B:369:SER:HA	2.16	0.46
1:C:243:ASN:HA	1:C:271:TRP:CZ2	2.51	0.46
1:C:288:ASN:HA	1:C:336:LEU:O	2.16	0.45
1:D:237:LYS:O	1:D:369:SER:HA	2.17	0.45
1:C:44:GLN:NE2	4:C:506:HOH:O	2.50	0.43
1:A:149:ALA:HB2	1:D:149:ALA:HB2	2.01	0.43
1:C:293:TYR:OH	1:C:333:ASP:OD2	2.27	0.43
1:C:194:PRO:HB3	1:C:198:GLY:HA3	1.99	0.43
1:C:46:SER:HA	1:C:47:LEU:HA	1.82	0.43
1:C:104:ILE:HA	1:C:138:LEU:O	2.18	0.43
1:D:5:ILE:CD1	1:D:201:LEU:HD11	2.49	0.43
1:C:235:TYR:HA	1:C:369:SER:HB3	2.01	0.43
1:C:32:ALA:HA	1:C:71:ASP:O	2.19	0.43
1:A:5:ILE:HD12	1:A:201:LEU:HD11	2.00	0.42
1:A:46:SER:HA	1:A:47:LEU:HA	1.76	0.42
1:A:233:ASN:CG	1:A:233:ASN:O	2.57	0.42
1:C:292:GLN:HB3	1:C:364:VAL:HB	2.01	0.41
1:D:4:GLN:HE21	1:D:4:GLN:N	2.18	0.41
1:B:243:ASN:HA	1:B:271:TRP:CZ2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:THR:CB	1:C:288:ASN:HD21	2.33	0.41
1:A:104:ILE:HA	1:A:138:LEU:O	2.21	0.41
1:A:279:SER:HA	1:A:348:VAL:O	2.20	0.41
1:D:209:PHE:O	1:D:213:VAL:HG23	2.21	0.41
1:A:174:TYR:N	1:A:175:PRO:CD	2.84	0.41
1:C:4:GLN:O	1:C:4:GLN:CG	2.69	0.41
1:B:266:CYS:HB2	1:B:330:LEU:HD22	2.04	0.40
1:C:241:HIS:CD2	1:C:284:VAL:HG22	2.56	0.40
1:B:36:ALA:HA	1:B:75:ILE:O	2.21	0.40
1:D:14:ARG:NH2	1:D:216:GLU:OE1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	364/378 (96%)	354 (97%)	10 (3%)	0	100	100
1	B	366/378 (97%)	352 (96%)	13 (4%)	1 (0%)	41	55
1	C	362/378 (96%)	340 (94%)	21 (6%)	1 (0%)	41	55
1	D	359/378 (95%)	332 (92%)	27 (8%)	0	100	100
All	All	1451/1512 (96%)	1378 (95%)	71 (5%)	2 (0%)	51	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	376	HIS
1	C	373	ALA

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	314/323 (97%)	306 (98%)	8 (2%)	47 67
1	B	316/323 (98%)	309 (98%)	7 (2%)	52 71
1	C	312/323 (97%)	302 (97%)	10 (3%)	39 59
1	D	310/323 (96%)	297 (96%)	13 (4%)	30 47
All	All	1252/1292 (97%)	1214 (97%)	38 (3%)	41 61

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	41	SER
1	A	47	LEU
1	A	183	GLU
1	A	212	LYS
1	A	222	SER
1	A	276	LYS
1	A	297	VAL
1	B	22	LYS
1	B	28	LYS
1	B	41	SER
1	B	47	LEU
1	B	65	LYS
1	B	113	SER
1	B	345	LYS
1	C	3	TYR
1	C	28	LYS
1	C	41	SER
1	C	65	LYS
1	C	69	GLN
1	C	212	LYS
1	C	232	LYS
1	C	272	THR
1	C	274	SER

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Mol	Chain	Res	Type
1	C	317	ARG
1	D	4	GLN
1	D	28	LYS
1	D	44	GLN
1	D	47	LEU
1	D	54	CYS
1	D	55	TYR
1	D	65	LYS
1	D	71	ASP
1	D	73	THR
1	D	212	LYS
1	D	247	ASN
1	D	322	PHE
1	D	355	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	9	ASN
1	B	269	HIS
1	B	374	HIS
1	C	241	HIS
1	C	242	GLN
1	C	374	HIS
1	D	4	GLN
1	D	241	HIS

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](#)

13 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	0.59	0	17,17,17	0.97	0
2	BMA	E	2	2	11,11,12	0.42	0	15,15,17	0.86	0
2	BMA	E	3	2	11,11,12	0.65	0	15,15,17	1.04	1 (6%)
2	BMA	E	4	2	11,11,12	0.63	0	15,15,17	1.44	2 (13%)
3	BMA	F	1	3	12,12,12	1.10	0	17,17,17	0.90	1 (5%)
3	BMA	F	2	3	11,11,12	0.93	0	15,15,17	1.49	2 (13%)
3	BMA	F	3	3	11,11,12	0.96	0	15,15,17	2.24	4 (26%)
3	BMA	G	1	3	12,12,12	0.98	0	17,17,17	0.95	0
3	BMA	G	2	3	11,11,12	0.93	0	15,15,17	1.59	3 (20%)
3	BMA	G	3	3	11,11,12	0.88	0	15,15,17	1.71	2 (13%)
3	BMA	H	1	3	12,12,12	0.83	0	17,17,17	0.99	1 (5%)
3	BMA	H	2	3	11,11,12	1.00	1 (9%)	15,15,17	1.95	3 (20%)
3	BMA	H	3	3	11,11,12	0.87	0	15,15,17	1.78	3 (20%)

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	-	0/2/22/22	0/1/1/1
2	BMA	E	2	2	-	0/2/19/22	0/1/1/1
2	BMA	E	3	2	-	2/2/19/22	0/1/1/1
2	BMA	E	4	2	-	2/2/19/22	0/1/1/1
3	BMA	F	1	3	-	0/2/22/22	0/1/1/1
3	BMA	F	2	3	-	1/2/19/22	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	BMA	G	1	3	-	0/2/22/22	0/1/1/1
3	BMA	G	2	3	-	0/2/19/22	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
3	BMA	H	1	3	-	0/2/22/22	0/1/1/1
3	BMA	H	2	3	-	2/2/19/22	0/1/1/1

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	2	BMA	C2-C3	2.04	1.55	1.52

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	3	BMA	C1-O5-C5	6.70	121.27	112.19
3	H	2	BMA	C1-C2-C3	5.13	115.97	109.67
3	G	3	BMA	C1-O5-C5	4.83	118.74	112.19
3	H	3	BMA	C1-O5-C5	4.33	118.06	112.19
2	E	4	BMA	C1-C2-C3	3.94	114.50	109.67
3	G	2	BMA	C1-C2-C3	3.61	114.10	109.67
3	H	2	BMA	C2-C3-C4	3.39	116.76	110.89
3	H	3	BMA	C1-C2-C3	3.36	113.79	109.67
3	H	3	BMA	C2-C3-C4	3.32	116.64	110.89
3	F	2	BMA	O2-C2-C1	3.27	115.84	109.15
3	F	3	BMA	C1-C2-C3	3.21	113.61	109.67
3	H	2	BMA	C1-O5-C5	2.91	116.13	112.19
3	G	2	BMA	O5-C5-C6	2.71	111.46	107.20
3	G	3	BMA	O5-C5-C6	2.65	111.36	107.20
3	G	2	BMA	C1-O5-C5	2.62	115.75	112.19
3	H	1	BMA	C4-C3-C2	2.53	115.24	110.82
3	F	3	BMA	O5-C5-C6	-2.51	103.27	107.20
2	E	3	BMA	O2-C2-C1	2.23	113.72	109.15
3	F	3	BMA	C2-C3-C4	2.21	114.73	110.89
3	F	1	BMA	C4-C3-C2	2.15	114.57	110.82
3	F	2	BMA	C1-O5-C5	2.11	115.05	112.19
2	E	4	BMA	O5-C5-C4	2.10	115.93	110.83

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	3	BMA	C4-C5-C6-O6
3	H	3	BMA	O5-C5-C6-O6
3	H	2	BMA	C4-C5-C6-O6
2	E	4	BMA	C4-C5-C6-O6

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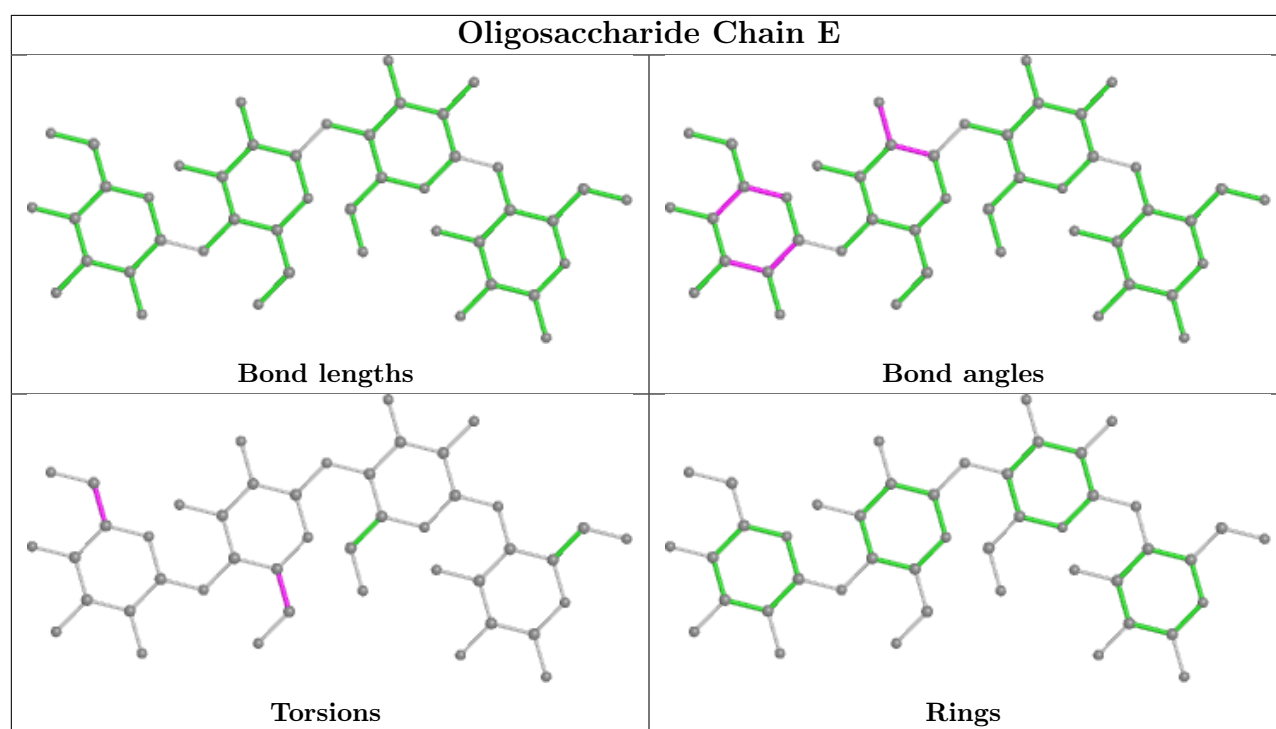
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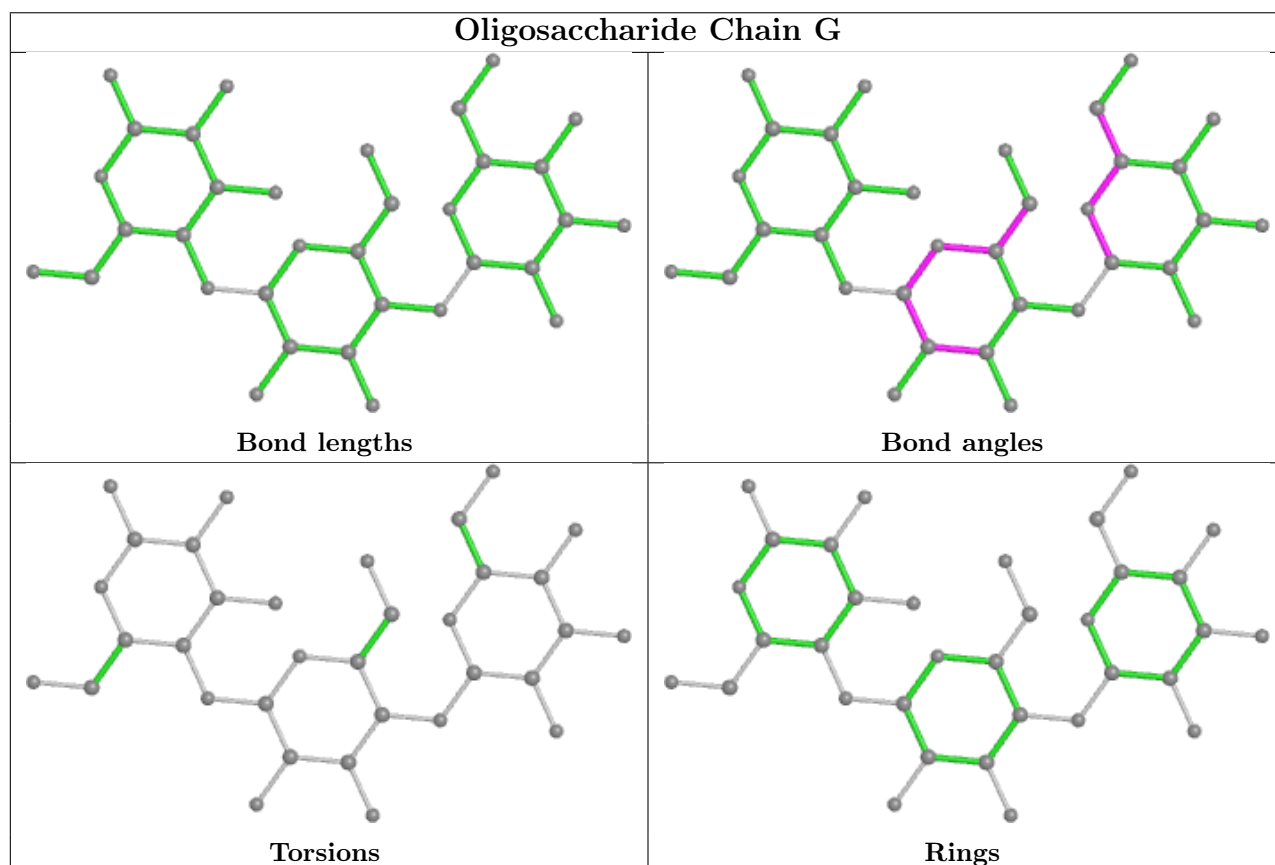
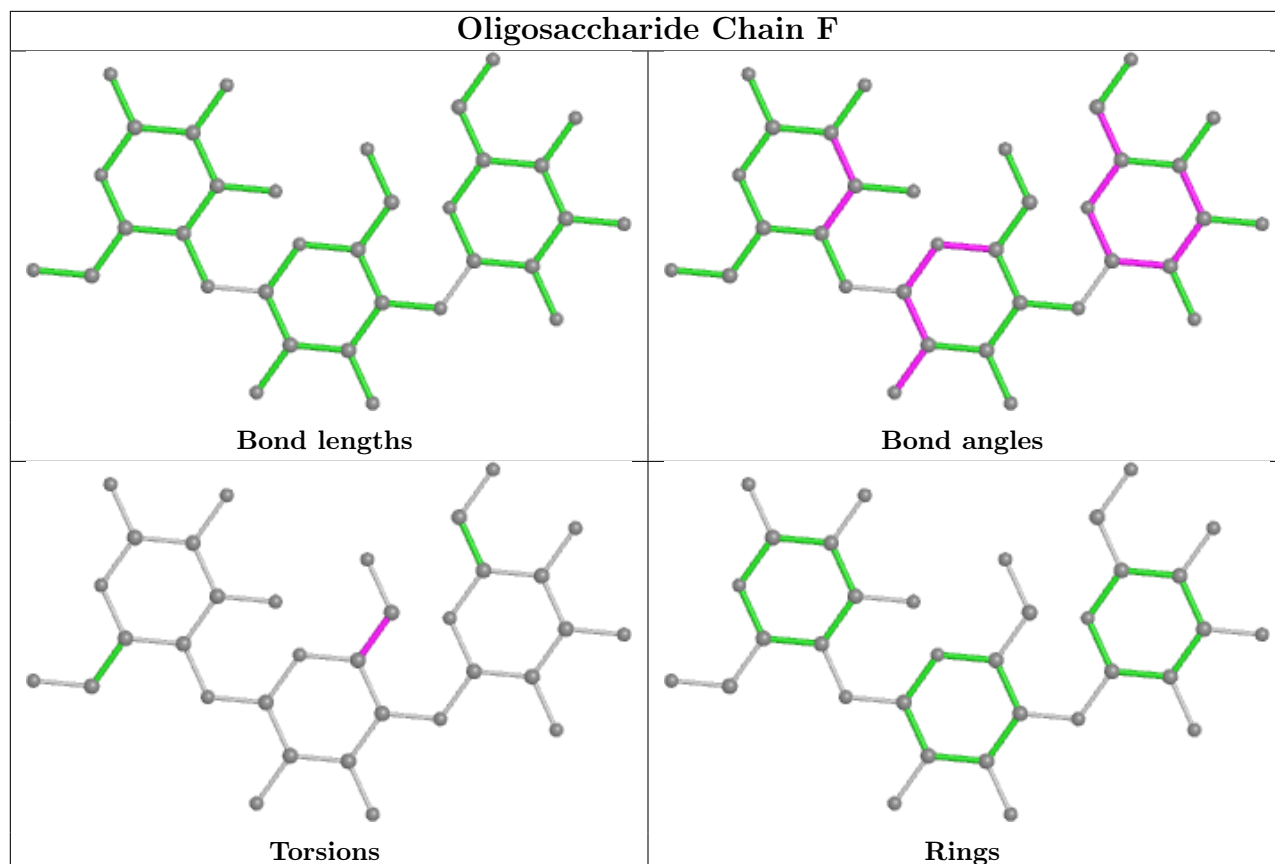
Mol	Chain	Res	Type	Atoms
2	E	4	BMA	O5-C5-C6-O6
3	H	2	BMA	O5-C5-C6-O6
2	E	3	BMA	C4-C5-C6-O6
2	E	3	BMA	O5-C5-C6-O6
3	F	2	BMA	O5-C5-C6-O6

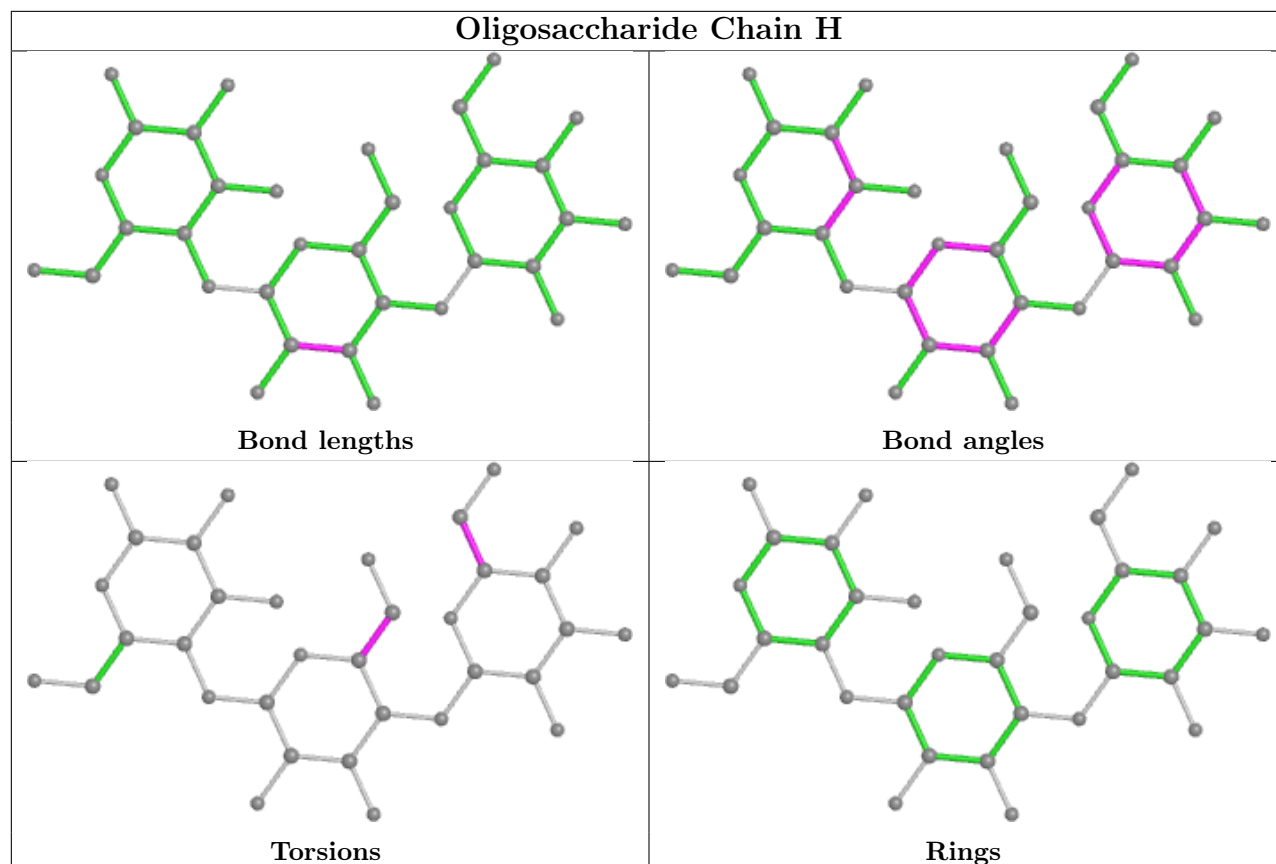
There are no ring outliers.

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 [i](#)

There are no ligands in this entry.

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	368/378 (97%)	-0.62	1 (0%) 94 93	32, 41, 60, 101	0
1	B	370/378 (97%)	-0.63	1 (0%) 94 93	29, 43, 64, 87	0
1	C	366/378 (96%)	-0.37	0 100 100	30, 52, 91, 119	0
1	D	363/378 (96%)	-0.32	1 (0%) 94 93	37, 62, 90, 124	0
All	All	1467/1512 (97%)	-0.49	3 (0%) 95 94	29, 47, 84, 124	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	314	HIS	3.8
1	B	247	ASN	3.1
1	A	3	TYR	2.2

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.

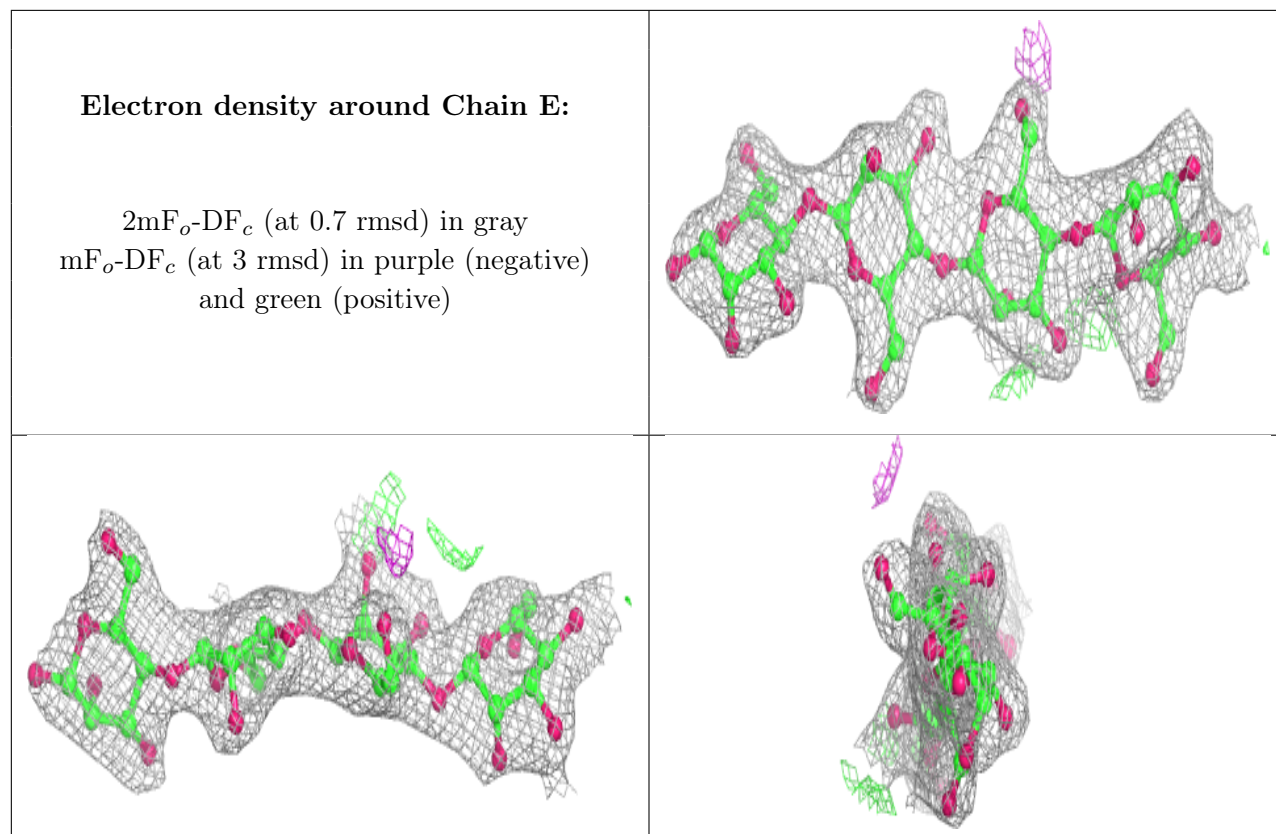
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BMA	F	3	11/12	0.78	0.22	71,83,87,89	0
3	BMA	H	3	11/12	0.84	0.19	70,80,90,91	0
3	BMA	G	1	12/12	0.88	0.12	51,56,61,61	0
3	BMA	F	1	12/12	0.90	0.15	59,72,75,77	0

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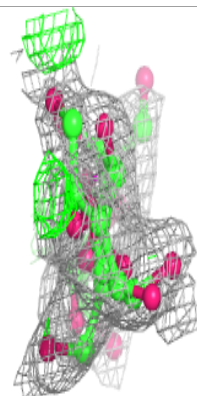
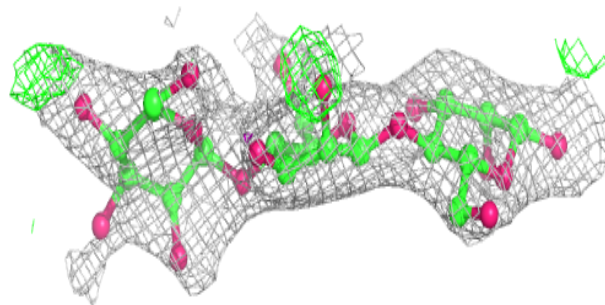
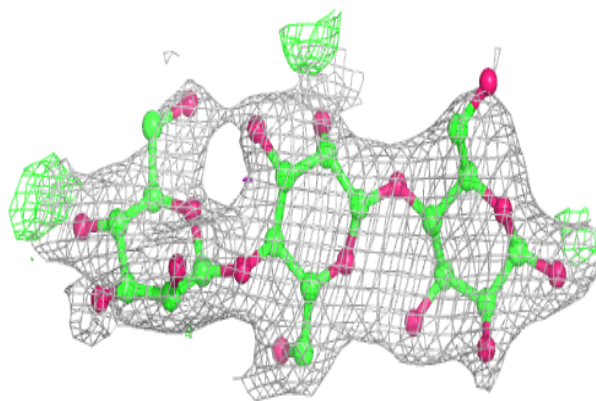
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	BMA	H	1	12/12	0.92	0.15	70,78,85,85	0
3	BMA	G	3	11/12	0.93	0.12	47,56,63,64	0
2	BMA	E	1	12/12	0.93	0.11	59,65,70,73	0
3	BMA	F	2	11/12	0.93	0.15	59,67,73,76	0
3	BMA	H	2	11/12	0.94	0.17	73,75,82,88	0
3	BMA	G	2	11/12	0.95	0.10	50,55,60,60	0
2	BMA	E	4	11/12	0.96	0.11	44,48,52,53	0
2	BMA	E	2	11/12	0.97	0.09	46,52,55,55	0
2	BMA	E	3	11/12	0.97	0.09	42,48,50,51	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.

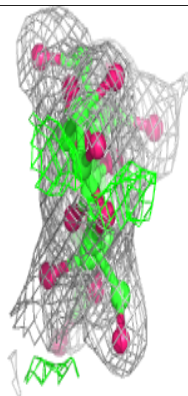
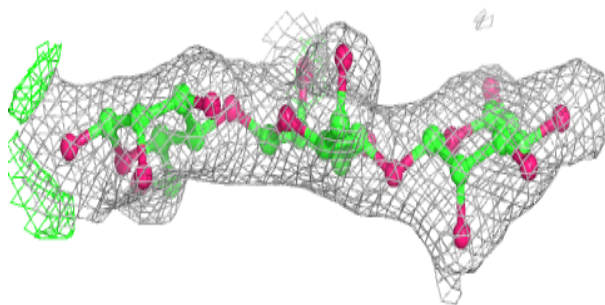
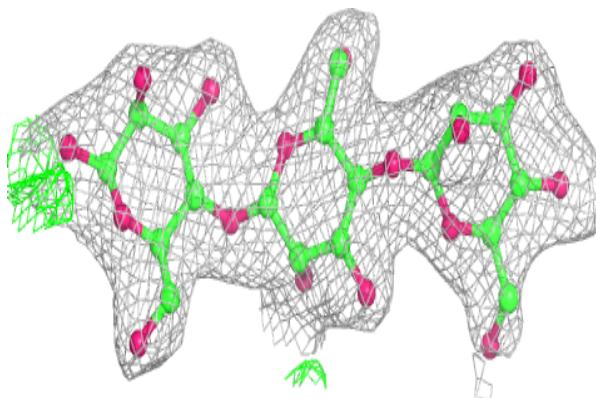


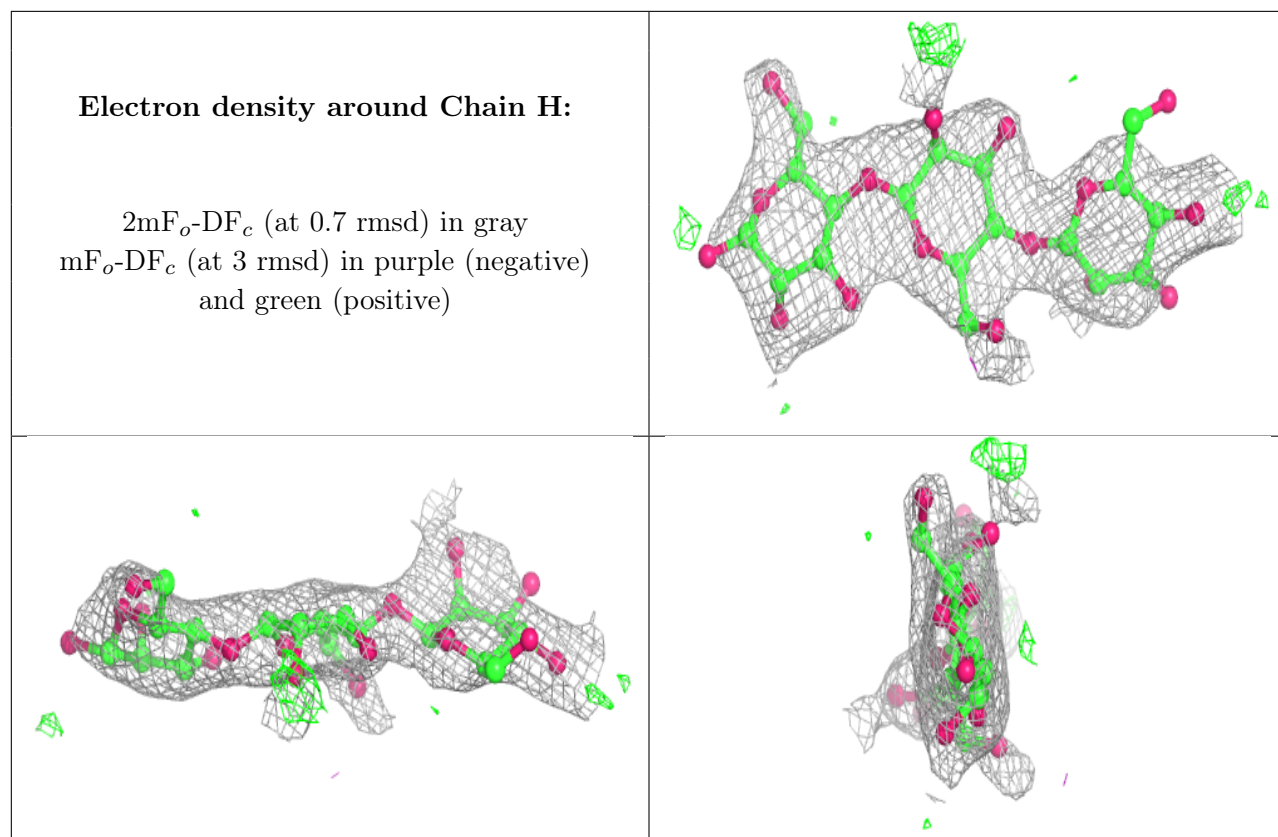
Electron density around Chain F:

$2mF_o-DF_c$ (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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.