



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 02:31 PM BST

PDB ID : 3S5Y
Title : Pharmacological Chaperoning in Human alpha-Galactosidase
Authors : Guce, A.I.; Clark, N.E.; Garman, S.C.
Deposited on : 2011-05-23
Resolution : 2.10 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
buster-report : 1.1.7 (2018)
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

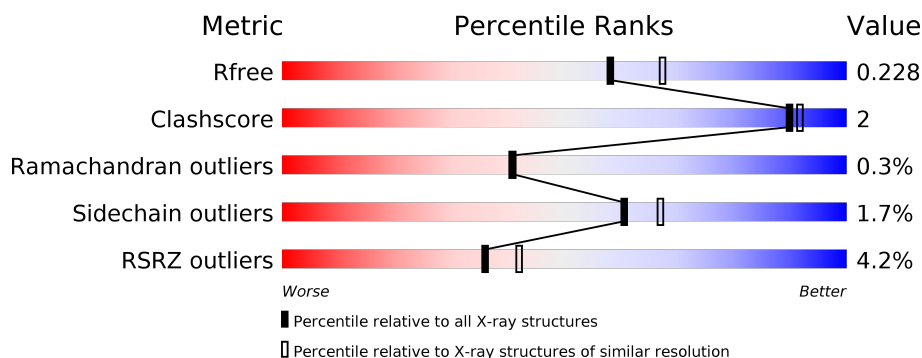
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	398	<div> <div>5%</div> <div> <div></div> <div>93%</div> <div>5%</div> </div> </div>
1	B	398	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>8%</div> </div> </div>
2	C	7	<div> <div>29%</div> <div>71%</div> </div>
3	D	5	<div> <div>20%</div> <div>80%</div> </div>
4	E	3	<div> <div>100%</div> </div>
5	F	5	<div> <div>40%</div> <div>60%</div> </div>

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Mol	Chain	Length	Quality of chain
6	G	4	

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
11	ACY	B	842	-	-	-	X
2	NAG	C	2	-	-	-	X
2	MAN	C	5	-	-	-	X
3	FUC	D	5	-	-	-	X
9	NAG	B	639	-	-	-	X

2 Entry composition [i](#)

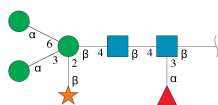
There are 12 unique types of molecules in this entry. The entry contains 7134 atoms, of which 0 are hydrogens and 0 are deuteriums.

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-galactosidase A.

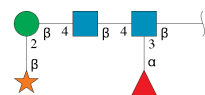
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	4	0
			3141	1999	538	575	29			
1	B	391	Total	C	N	O	S	0	4	0
			3150	2004	540	577	29			

- Molecule 2 is an oligosaccharide called beta-D-xylopyranose-(1-2)-[alpha-D-mannopyranose-(1-3)][alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose.



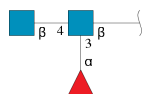
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			80	45	2	33			

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



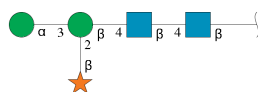
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	5	Total	C	N	O	0	0	0
			58	33	2	23			

- Molecule 4 is an oligosaccharide called alpha-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose.



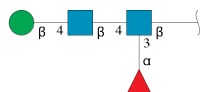
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 5 is an oligosaccharide called beta-D-xylopyranose-(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.



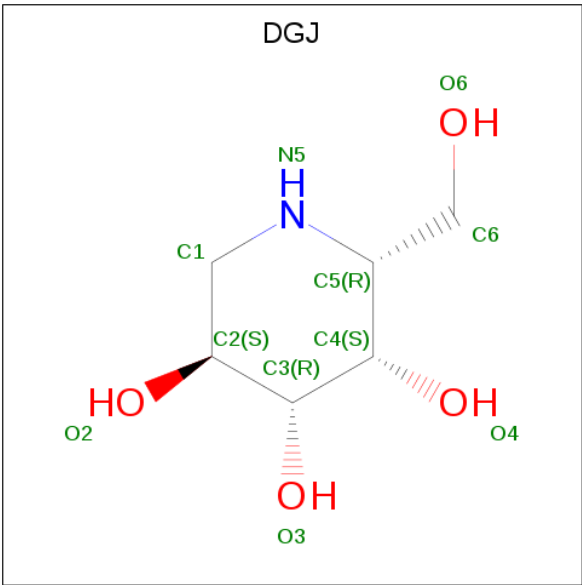
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	F	5	Total	C	N	O	0	0	0
			59	33	2	24			

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose.



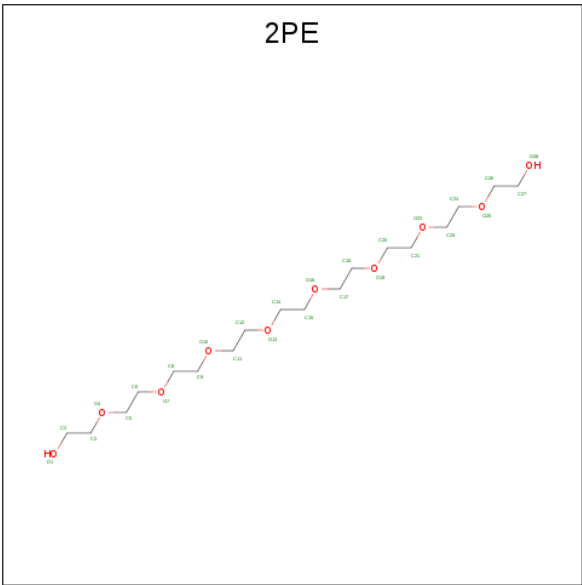
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	G	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 7 is (2R,3S,4R,5S)-2-(hydroxymethyl)piperidine-3,4,5-triol (three-letter code: DGJ) (formula: C₆H₁₃NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			11	6	1	4		
7	B	1	Total	C	N	O	0	0
			11	6	1	4		

- Molecule 8 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: C₁₈H₃₈O₁₀).



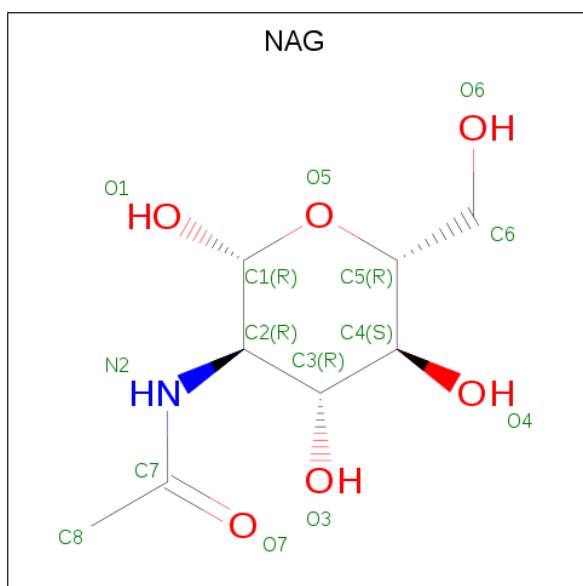
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			10	6	4		
8	B	1	Total	C	O	0	0
			16	10	6		

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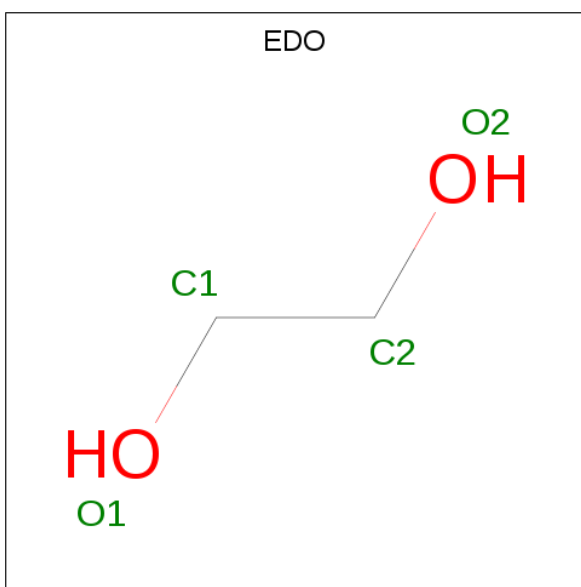
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			28	18	10		
8	B	1	Total	C	O	0	0
			7	4	3		
8	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



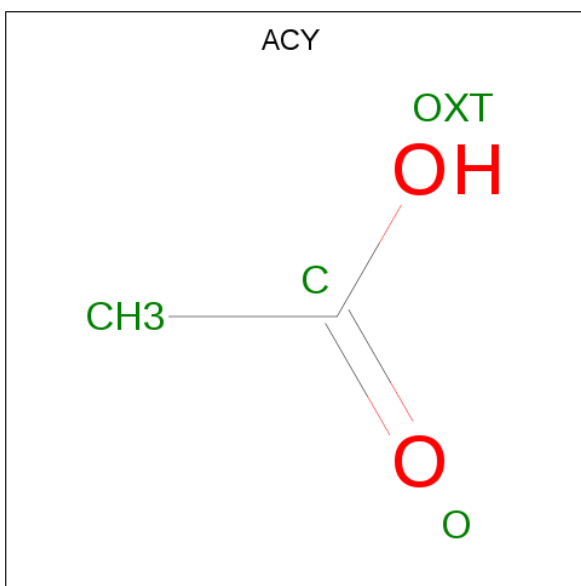
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 11 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



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

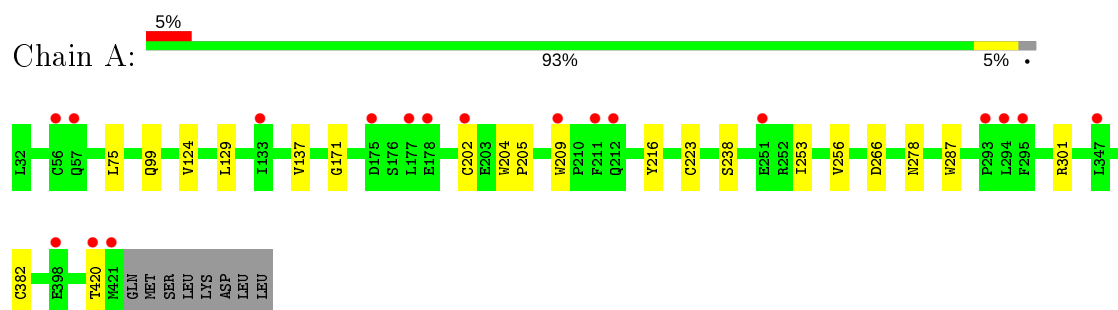
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	235	Total 235	O 235	0	0
12	B	205	Total 205	O 205	0	0

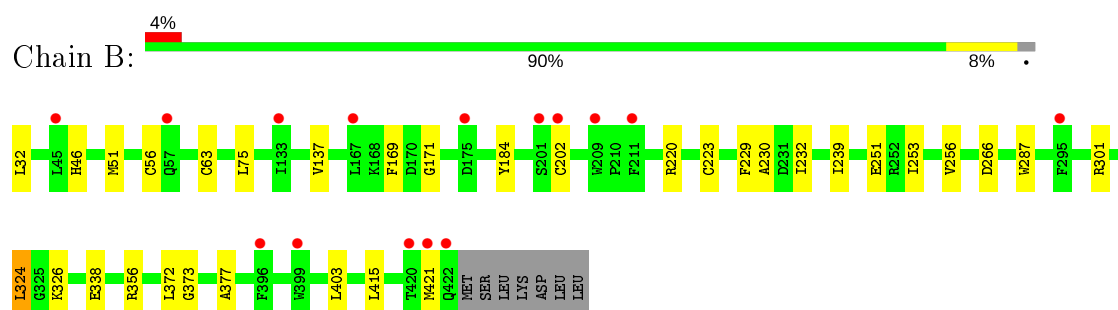
3 Residue-property plots [i](#)

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

- Molecule 1: Alpha-galactosidase A



- Molecule 1: Alpha-galactosidase A



- Molecule 2: beta-D-xylopyranose-(1-2)-[alpha-D-mannopyranose-(1-3)][alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: beta-D-xylopyranose-(1-2)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: α -L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

NAG1
FUC2
NAG3

- Molecule 5: beta-D-xylopyranose-(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 F:  40% 60%

NAG1
NAG2
BNA3
XYP4
MAN5

- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  50% 50%

NAG1
NAG2
BNA3
FUC4



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	136.81Å 182.63Å 47.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.44 – 2.10 30.44 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.5 (30.44-2.10) 94.5 (30.44-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.194 , 0.230 0.191 , 0.228	Depositor DCC
R_{free} test set	3360 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7134	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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: XYP, BMA, NAG, DGJ, EDO, 2PE, FUC, ACY, 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	0.36	0/3238	0.54	0/4396
1	B	0.37	0/3247	0.55	0/4408
All	All	0.36	0/6485	0.54	0/8804

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

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	3141	0	3004	9	0
1	B	3150	0	3012	15	0
2	C	80	0	60	0	0
3	D	58	0	42	0	0
4	E	38	0	34	0	0
5	F	59	0	42	0	0
6	G	49	0	43	0	0
7	A	11	0	13	0	0
7	B	11	0	13	0	0
8	A	10	0	13	0	0
8	B	61	0	81	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	B	14	0	13	0	0
10	B	4	0	6	0	0
11	B	8	0	6	0	0
12	A	235	0	0	2	0
12	B	205	0	0	0	0
All	All	7134	0	6382	24	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.

All (24) 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:403:LEU:HD21	1:B:415:LEU:CD1	2.31	0.61
1:B:75:LEU:HD11	1:B:301:ARG:HG2	1.83	0.61
1:B:338:GLU:OE2	1:B:356:ARG:NH1	2.39	0.56
1:B:137:VAL:HG12	1:B:171:GLY:HA2	1.93	0.51
1:A:278:ASN:ND2	12:A:1183:HOH:O	2.37	0.50
1:B:202[B]:CYS:SG	1:B:223:CYS:SG	3.03	0.48
1:A:253:ILE:O	1:A:256:VAL:HG12	2.13	0.48
1:A:216:TYR:HB3	1:A:256:VAL:HG21	1.96	0.47
1:B:229:PHE:HB3	8:B:812:2PE:H52	1.96	0.46
1:B:56[B]:CYS:HB3	1:B:63:CYS:SG	2.56	0.46
1:A:202[B]:CYS:SG	1:A:223:CYS:SG	3.08	0.46
1:A:204:TRP:HB3	1:A:205:PRO:HD3	1.98	0.45
1:A:137:VAL:HG12	1:A:171:GLY:HA2	1.99	0.44
1:B:184:TYR:CE1	1:B:202[B]:CYS:HB2	2.53	0.44
1:B:324:LEU:HD22	1:B:326:LYS:HG3	1.99	0.43
1:A:382:CYS:HA	1:A:420:THR:HG22	2.00	0.43
1:A:124:VAL:HG13	1:A:129:LEU:HB2	2.01	0.43
12:A:1414:HOH:O	1:B:51:MET:HE2	2.19	0.43
1:B:373:GLY:HA3	1:B:377:ALA:HB2	2.01	0.43
1:B:232:ILE:HD11	1:B:239:ILE:HD13	2.00	0.42
1:A:75:LEU:HD11	1:A:301:ARG:HG2	2.02	0.41
1:B:230:ALA:HB3	8:B:812:2PE:H32	2.04	0.40
1:B:253:ILE:O	1:B:256:VAL:HG22	2.20	0.40
1:B:32:LEU:N	1:B:220:ARG:O	2.55	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	392/398 (98%)	383 (98%)	8 (2%)	1 (0%)	41	41
1	B	393/398 (99%)	381 (97%)	11 (3%)	1 (0%)	41	41
All	All	785/796 (99%)	764 (97%)	19 (2%)	2 (0%)	41	41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ASP
1	B	266	ASP

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	335/339 (99%)	331 (99%)	4 (1%)	71	77
1	B	336/339 (99%)	329 (98%)	7 (2%)	53	59
All	All	671/678 (99%)	660 (98%)	11 (2%)	60	69

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	GLN
1	A	209	TRP
1	A	238	SER
1	A	287	TRP

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Mol	Chain	Res	Type
1	B	46	HIS
1	B	169	PHE
1	B	251	GLU
1	B	287	TRP
1	B	324	LEU
1	B	372	LEU
1	B	421	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	228	ASN
1	A	330	GLN
1	A	379	ASN
1	B	179	ASN
1	B	221	GLN
1	B	228	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

24 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	C	1	1,2	14,14,15	0.62	0	17,19,21	0.87	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	2	2	14,14,15	0.58	0	17,19,21	1.13	1 (5%)
2	BMA	C	3	2	11,11,12	0.50	0	15,15,17	0.87	1 (6%)
2	XYP	C	4	2	9,9,10	1.27	1 (11%)	10,12,14	0.78	0
2	MAN	C	5	2	11,11,12	0.59	0	15,15,17	0.92	1 (6%)
2	MAN	C	6	2	11,11,12	0.55	0	15,15,17	1.39	3 (20%)
2	FUC	C	7	2	10,10,11	0.57	0	14,14,16	0.72	0
3	NAG	D	1	1,3	14,14,15	0.48	0	17,19,21	1.15	2 (11%)
3	NAG	D	2	3	14,14,15	0.51	0	17,19,21	0.79	0
3	BMA	D	3	3	11,11,12	0.42	0	15,15,17	1.23	2 (13%)
3	XYP	D	4	3	9,9,10	1.36	1 (11%)	10,12,14	1.15	1 (10%)
3	FUC	D	5	3	10,10,11	0.62	0	14,14,16	1.56	2 (14%)
4	NAG	E	1	1,4	14,14,15	0.58	0	17,19,21	0.69	0
4	FUC	E	2	4	10,10,11	0.60	0	14,14,16	0.60	0
4	NAG	E	3	4	14,14,15	0.52	0	17,19,21	0.76	0
5	NAG	F	1	1,5	14,14,15	0.61	0	17,19,21	1.09	1 (5%)
5	NAG	F	2	5	14,14,15	0.53	0	17,19,21	1.02	1 (5%)
5	BMA	F	3	5	11,11,12	0.34	0	15,15,17	0.90	0
5	XYP	F	4	5	9,9,10	1.35	1 (11%)	10,12,14	0.86	0
5	MAN	F	5	5	11,11,12	0.57	0	15,15,17	0.69	0
6	NAG	G	1	1,6	14,14,15	0.54	0	17,19,21	0.67	0
6	NAG	G	2	6	14,14,15	0.53	0	17,19,21	1.02	1 (5%)
6	BMA	G	3	6	11,11,12	0.30	0	15,15,17	0.69	0
6	FUC	G	4	6	10,10,11	0.58	0	14,14,16	0.76	1 (7%)

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	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1
2	XYP	C	4	2	-	-	0/1/1/1
2	MAN	C	5	2	-	0/2/19/22	0/1/1/1
2	MAN	C	6	2	-	2/2/19/22	0/1/1/1
2	FUC	C	7	2	-	-	0/1/1/1
3	NAG	D	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	D	2	3	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	D	3	3	-	1/2/19/22	0/1/1/1
3	XYP	D	4	3	-	-	0/1/1/1
3	FUC	D	5	3	-	-	0/1/1/1
4	NAG	E	1	1,4	-	0/6/23/26	0/1/1/1
4	FUC	E	2	4	-	-	0/1/1/1
4	NAG	E	3	4	-	0/6/23/26	0/1/1/1
5	NAG	F	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	F	2	5	-	1/6/23/26	0/1/1/1
5	BMA	F	3	5	-	0/2/19/22	0/1/1/1
5	XYP	F	4	5	-	-	0/1/1/1
5	MAN	F	5	5	-	2/2/19/22	0/1/1/1
6	NAG	G	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	G	2	6	-	2/6/23/26	0/1/1/1
6	BMA	G	3	6	-	2/2/19/22	0/1/1/1
6	FUC	G	4	6	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	4	XYP	O5-C1	-3.67	1.35	1.42
3	D	4	XYP	O5-C1	-3.65	1.35	1.42
2	C	4	XYP	O5-C1	-3.39	1.36	1.42

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	5	FUC	C1-C2-C3	4.91	115.70	109.67
5	F	1	NAG	C1-O5-C5	3.69	117.20	112.19
2	C	6	MAN	C1-C2-C3	3.33	113.76	109.67
3	D	1	NAG	C1-O5-C5	3.18	116.49	112.19
2	C	2	NAG	C4-C3-C2	3.06	115.50	111.02
2	C	6	MAN	C1-O5-C5	3.02	116.29	112.19
3	D	4	XYP	C5-C4-C3	2.96	113.30	109.67
5	F	2	NAG	C1-O5-C5	2.61	115.72	112.19
3	D	3	BMA	C3-C4-C5	2.49	114.68	110.24
2	C	5	MAN	C1-C2-C3	2.48	112.71	109.67
3	D	3	BMA	O5-C1-C2	-2.45	106.98	110.77
2	C	3	BMA	O5-C5-C6	2.31	110.82	107.20
6	G	2	NAG	C1-C2-N2	-2.25	106.64	110.49
2	C	6	MAN	O5-C5-C6	2.20	110.66	107.20
6	G	4	FUC	C1-C2-C3	2.13	112.29	109.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	5	FUC	C1-O5-C5	2.06	117.44	112.78
3	D	1	NAG	C1-C2-N2	-2.01	107.05	110.49

There are no chirality outliers.

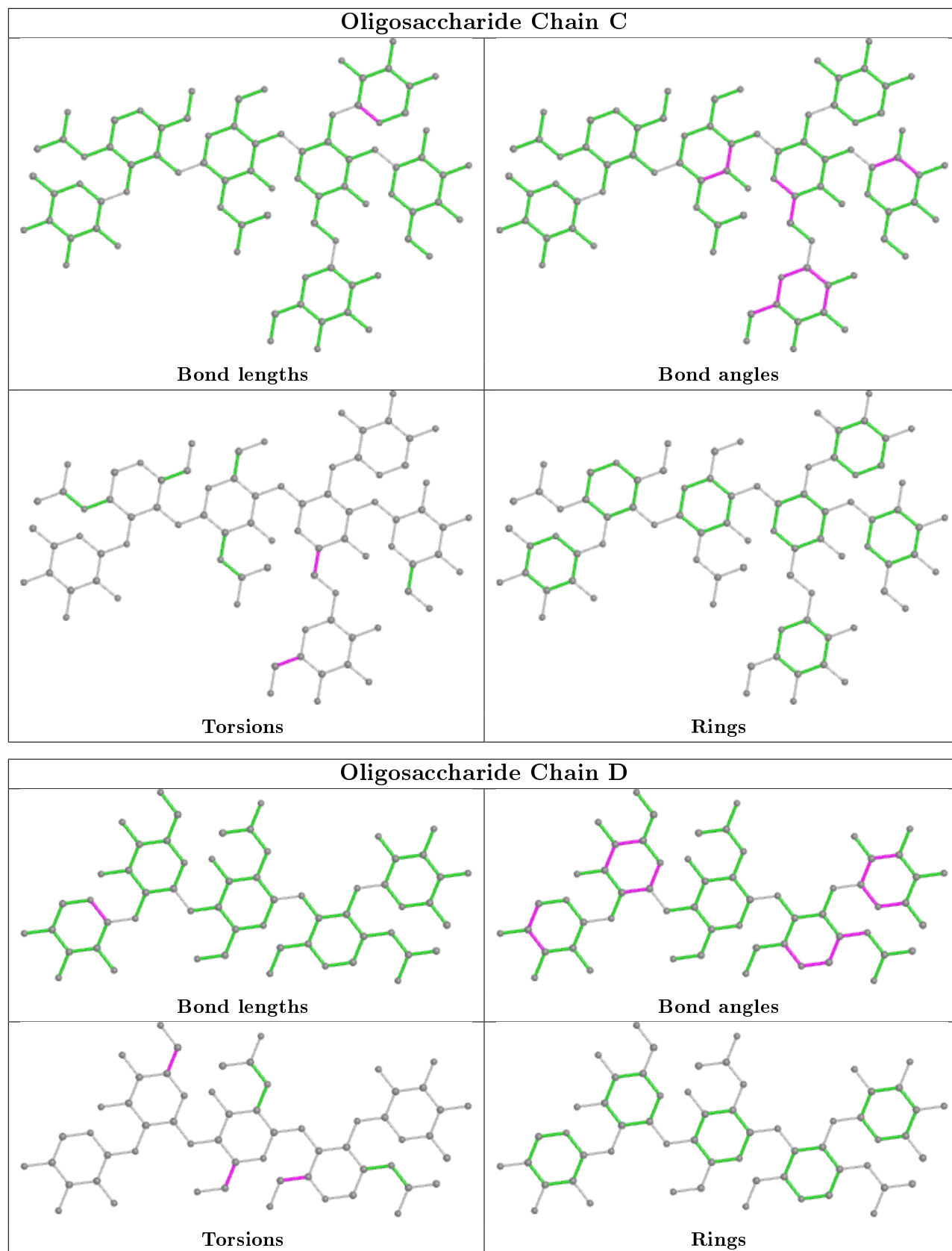
All (15) torsion outliers are listed below:

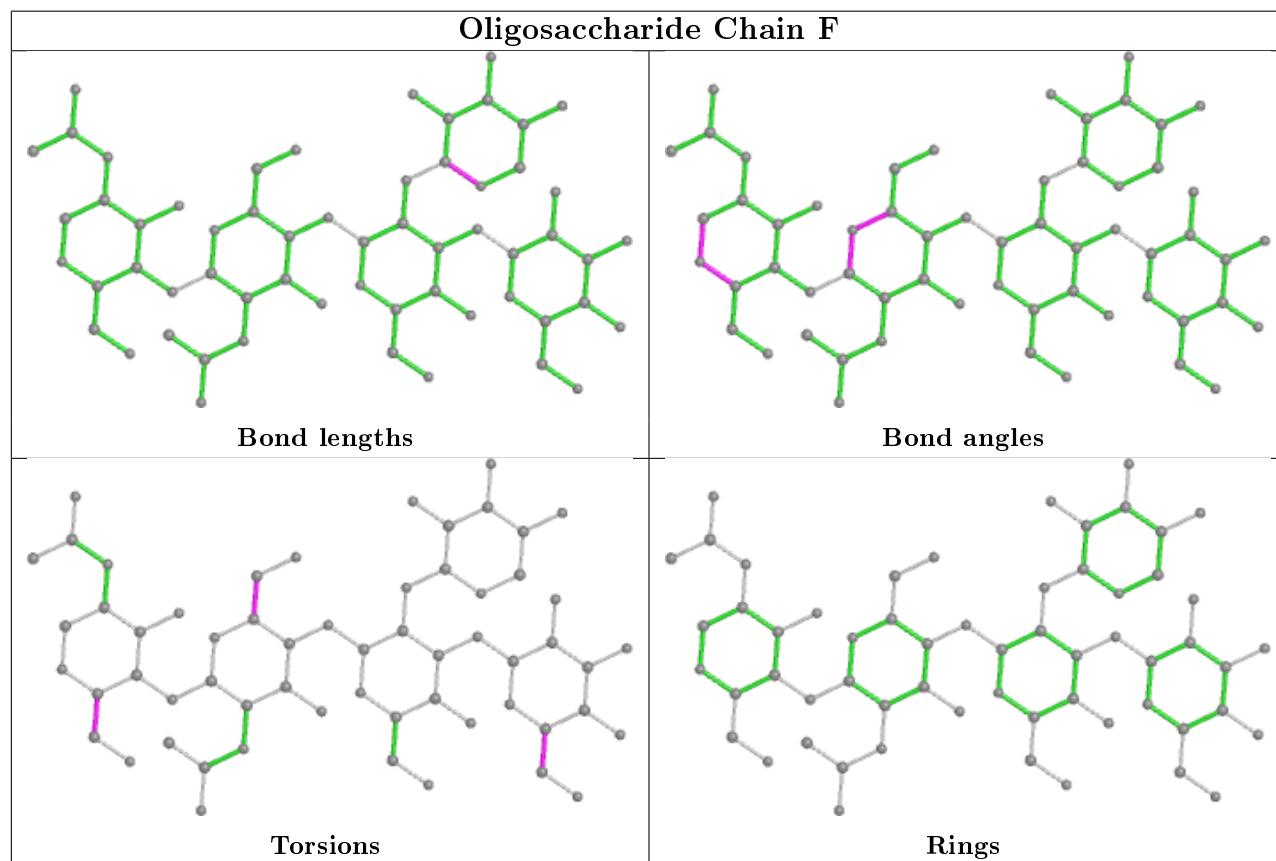
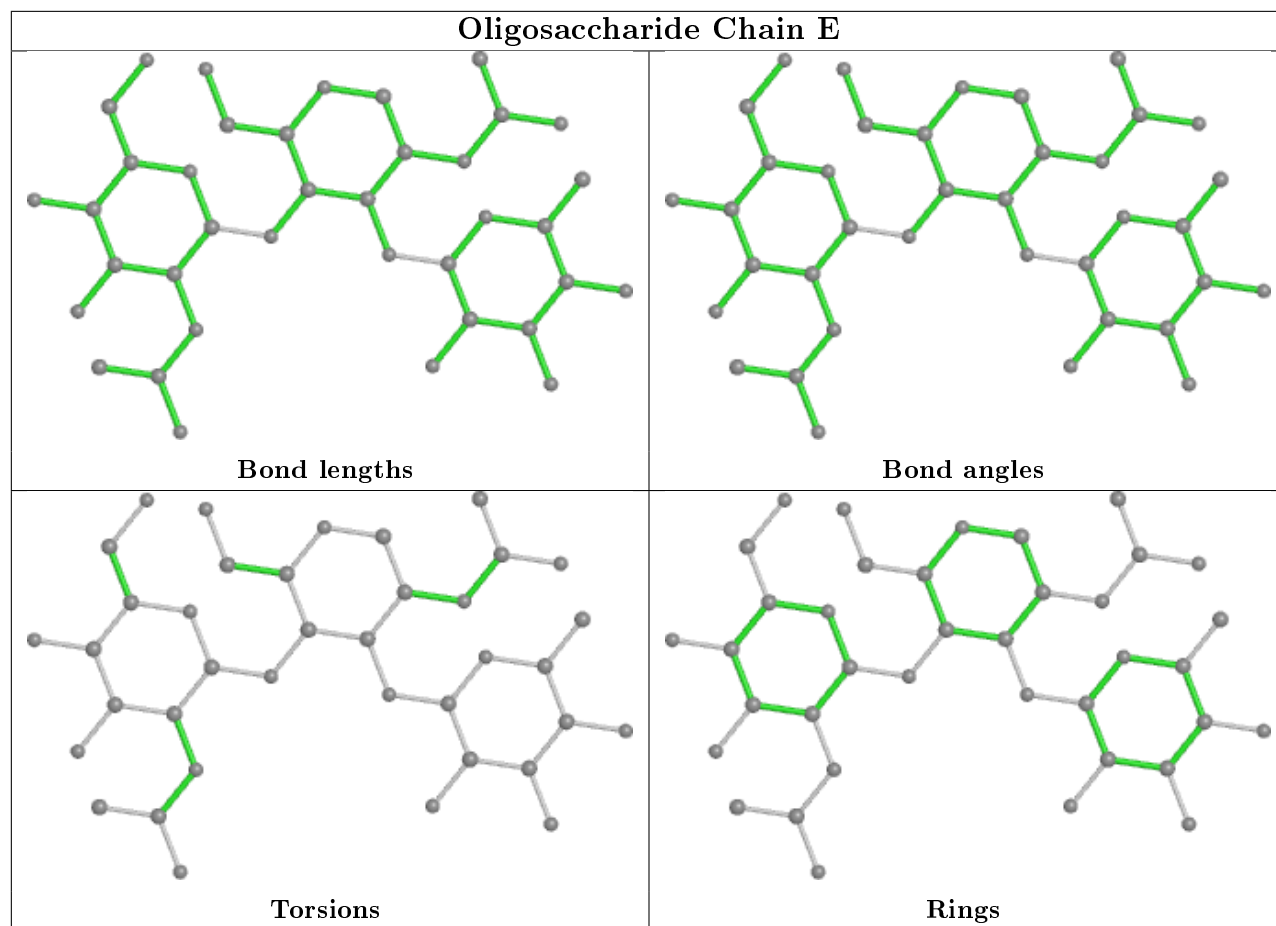
Mol	Chain	Res	Type	Atoms
2	C	3	BMA	O5-C5-C6-O6
6	G	3	BMA	O5-C5-C6-O6
2	C	3	BMA	C4-C5-C6-O6
6	G	3	BMA	C4-C5-C6-O6
2	C	6	MAN	O5-C5-C6-O6
5	F	5	MAN	C4-C5-C6-O6
6	G	2	NAG	O5-C5-C6-O6
6	G	2	NAG	C4-C5-C6-O6
5	F	5	MAN	O5-C5-C6-O6
5	F	2	NAG	O5-C5-C6-O6
2	C	6	MAN	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6
5	F	1	NAG	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6

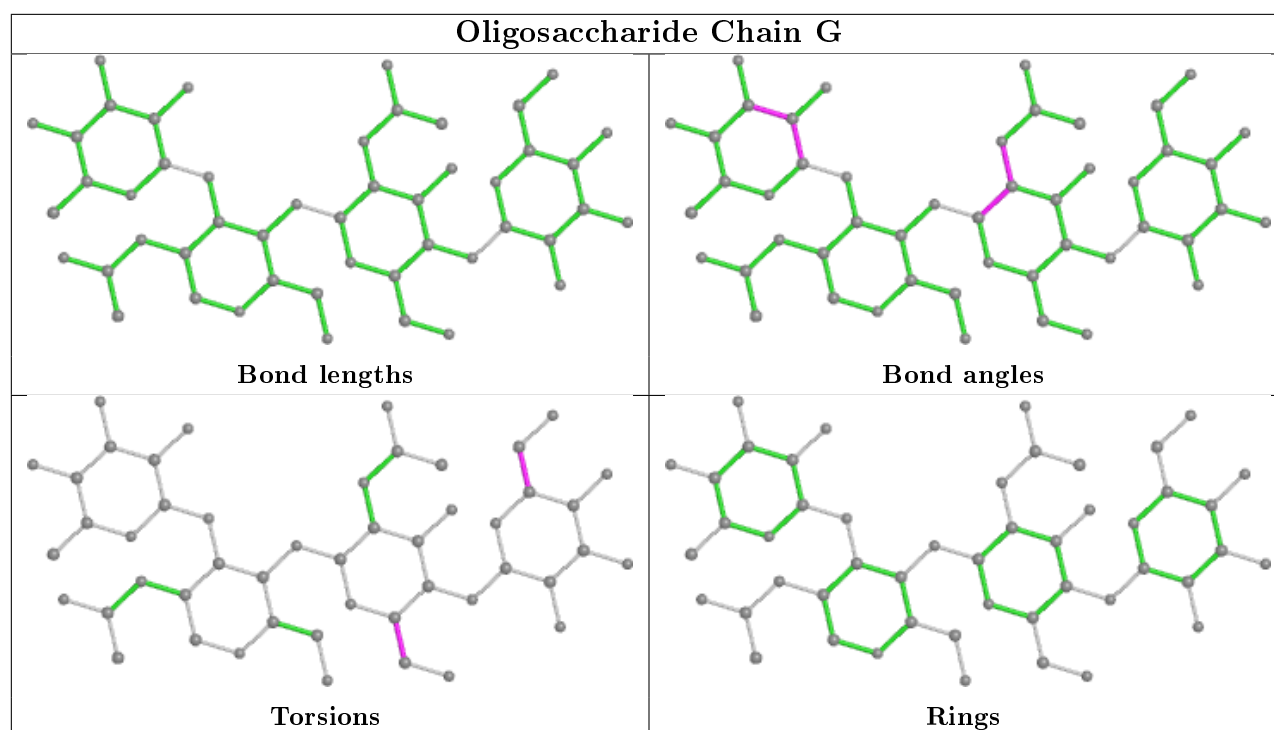
There are no ring outliers.

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](#)

11 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	$\# Z > 2$
9	NAG	B	639	1	14,14,15	0.54	0	17,19,21	1.04	1 (5%)
7	DGJ	A	801	-	11,11,11	0.78	0	13,15,15	1.63	1 (7%)
8	2PE	B	812	-	6,6,27	0.55	0	5,5,26	0.23	0
10	EDO	B	814	-	3,3,3	0.44	0	2,2,2	0.26	0
8	2PE	B	815	-	9,9,27	0.49	0	8,8,26	0.25	0
8	2PE	A	813	-	9,9,27	0.47	0	8,8,26	0.15	0
11	ACY	B	842	-	1,3,3	1.73	0	0,3,3	0.00	-
11	ACY	B	843	-	1,3,3	1.63	0	0,3,3	0.00	-
8	2PE	B	810	-	15,15,27	0.47	0	14,14,26	0.23	0
8	2PE	B	811	-	27,27,27	0.49	0	26,26,26	0.17	0
7	DGJ	B	802	-	11,11,11	0.73	0	13,15,15	1.57	1 (7%)

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
9	NAG	B	639	1	-	0/6/23/26	0/1/1/1
7	DGJ	A	801	-	-	0/2/19/19	0/1/1/1
8	2PE	B	812	-	-	2/4/4/25	-
10	EDO	B	814	-	-	1/1/1/1	-
8	2PE	B	815	-	-	2/7/7/25	-
8	2PE	A	813	-	-	3/7/7/25	-
8	2PE	B	810	-	-	4/13/13/25	-
8	2PE	B	811	-	-	9/25/25/25	-
7	DGJ	B	802	-	-	0/2/19/19	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	802	DGJ	C1-N5-C5	5.06	120.56	109.61
7	A	801	DGJ	C1-N5-C5	4.98	120.39	109.61
9	B	639	NAG	O5-C1-C2	-3.15	106.32	111.29

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	815	2PE	O4-C5-C6-O7
8	B	810	2PE	O7-C8-C9-O10
8	B	811	2PE	O19-C20-C21-O22
8	B	812	2PE	O4-C5-C6-O7
8	B	811	2PE	O1-C2-C3-O4
8	B	811	2PE	O25-C26-C27-O28
8	B	811	2PE	O22-C23-C24-O25
10	B	814	EDO	O1-C1-C2-O2
8	B	810	2PE	C11-C12-O13-C14
8	B	811	2PE	C6-C5-O4-C3
8	B	811	2PE	C18-C17-O16-C15
8	B	811	2PE	C9-C8-O7-C6
8	A	813	2PE	C9-C8-O7-C6
8	B	810	2PE	C9-C8-O7-C6

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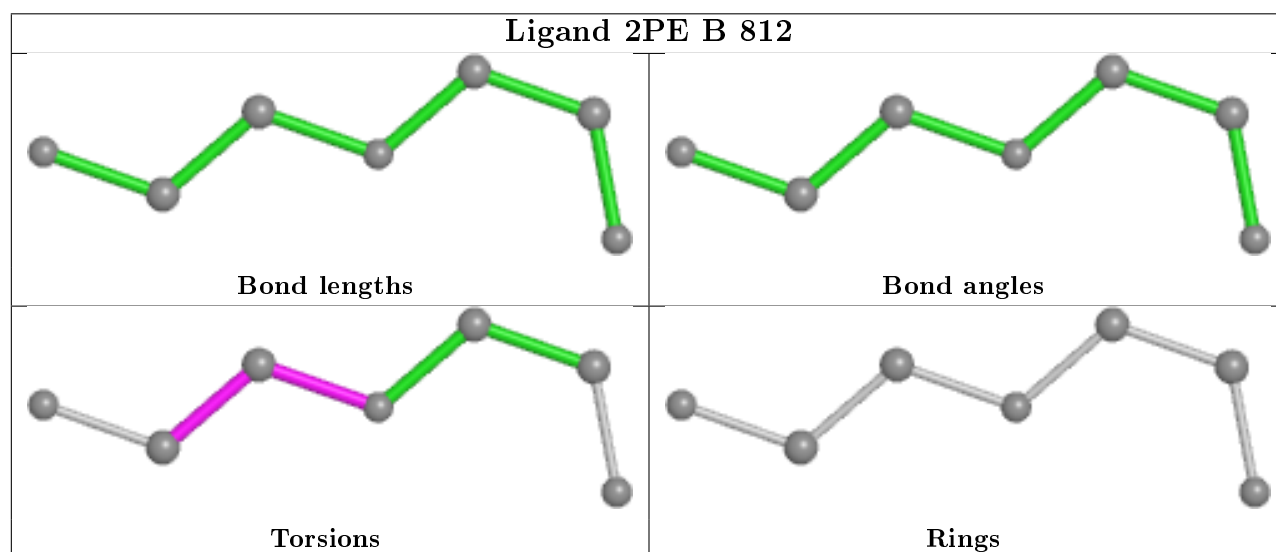
Mol	Chain	Res	Type	Atoms
8	B	811	2PE	C27-C26-O25-C24
8	B	811	2PE	O16-C17-C18-O19
8	B	810	2PE	C12-C11-O10-C9
8	B	812	2PE	C6-C5-O4-C3
8	B	815	2PE	O7-C8-C9-O10
8	A	813	2PE	C2-C3-O4-C5
8	A	813	2PE	C5-C6-O7-C8

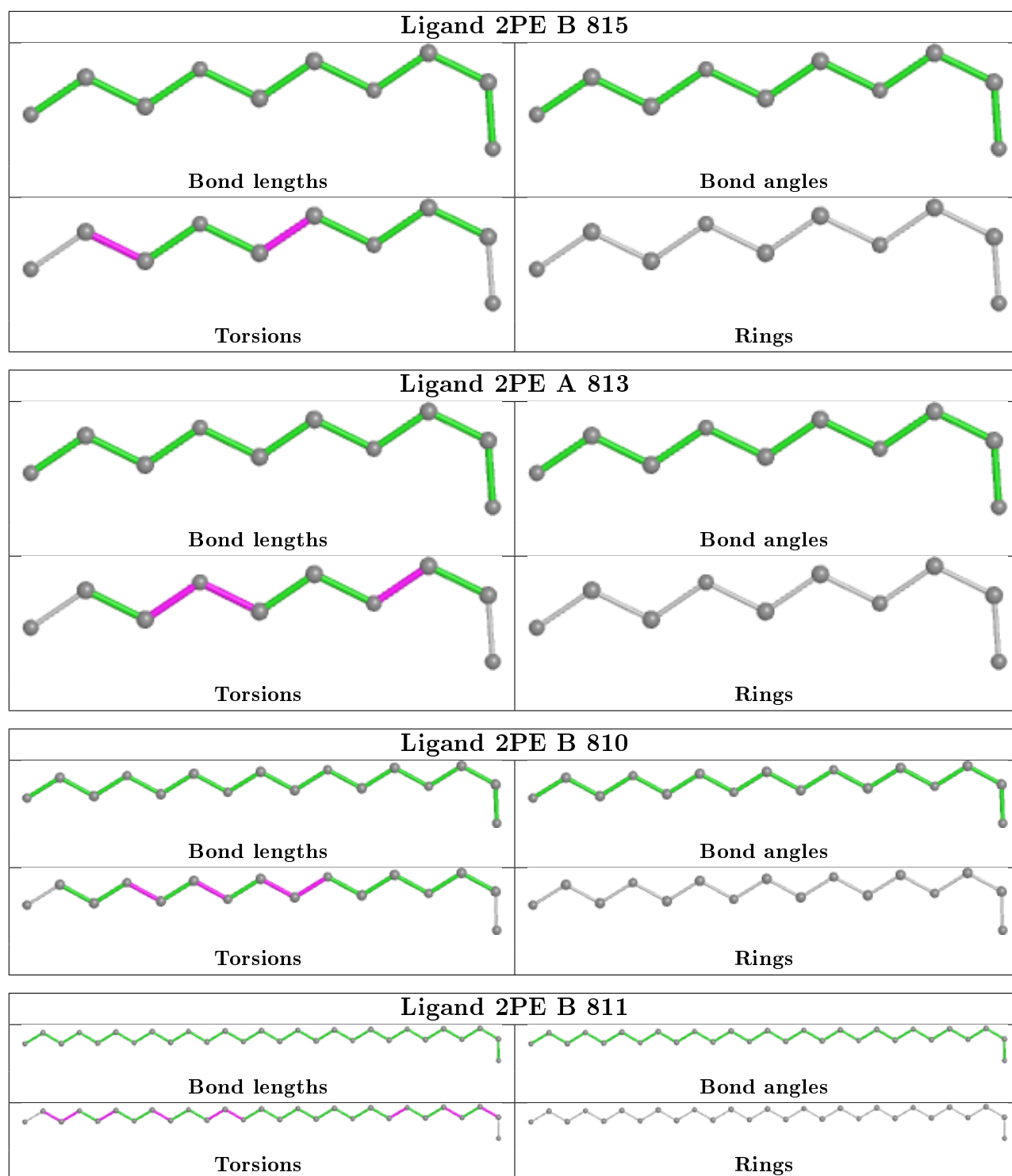
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	812	2PE	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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 ⓘ

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	390/398 (97%)	0.12	18 (4%) 32 38	18, 33, 59, 101	0
1	B	391/398 (98%)	0.15	15 (3%) 40 46	18, 30, 59, 120	0
All	All	781/796 (98%)	0.13	33 (4%) 36 42	18, 31, 59, 120	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	421	MET	8.5
1	A	420	THR	7.0
1	B	422	GLN	6.8
1	A	421	MET	6.1
1	B	175	ASP	5.4
1	B	420	THR	4.4
1	A	56[A]	CYS	4.0
1	B	396	PHE	3.9
1	B	57	GLN	3.8
1	B	399	TRP	3.4
1	A	177	LEU	3.2
1	A	209	TRP	3.1
1	A	175	ASP	3.0
1	A	57	GLN	2.8
1	B	202[A]	CYS	2.7
1	A	251	GLU	2.6
1	A	211	PHE	2.6
1	A	178	GLU	2.6
1	B	45	LEU	2.6
1	A	293	PRO	2.5
1	B	209	TRP	2.4
1	B	211	PHE	2.4
1	A	212	GLN	2.4
1	A	347	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	398	GLU	2.3
1	B	133	ILE	2.2
1	B	295	PHE	2.2
1	B	201	SER	2.2
1	A	294	LEU	2.2
1	A	295	PHE	2.2
1	B	167	LEU	2.1
1	A	133	ILE	2.0
1	A	202[A]	CYS	2.0

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

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

6.3 Carbohydrates [i](#)

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

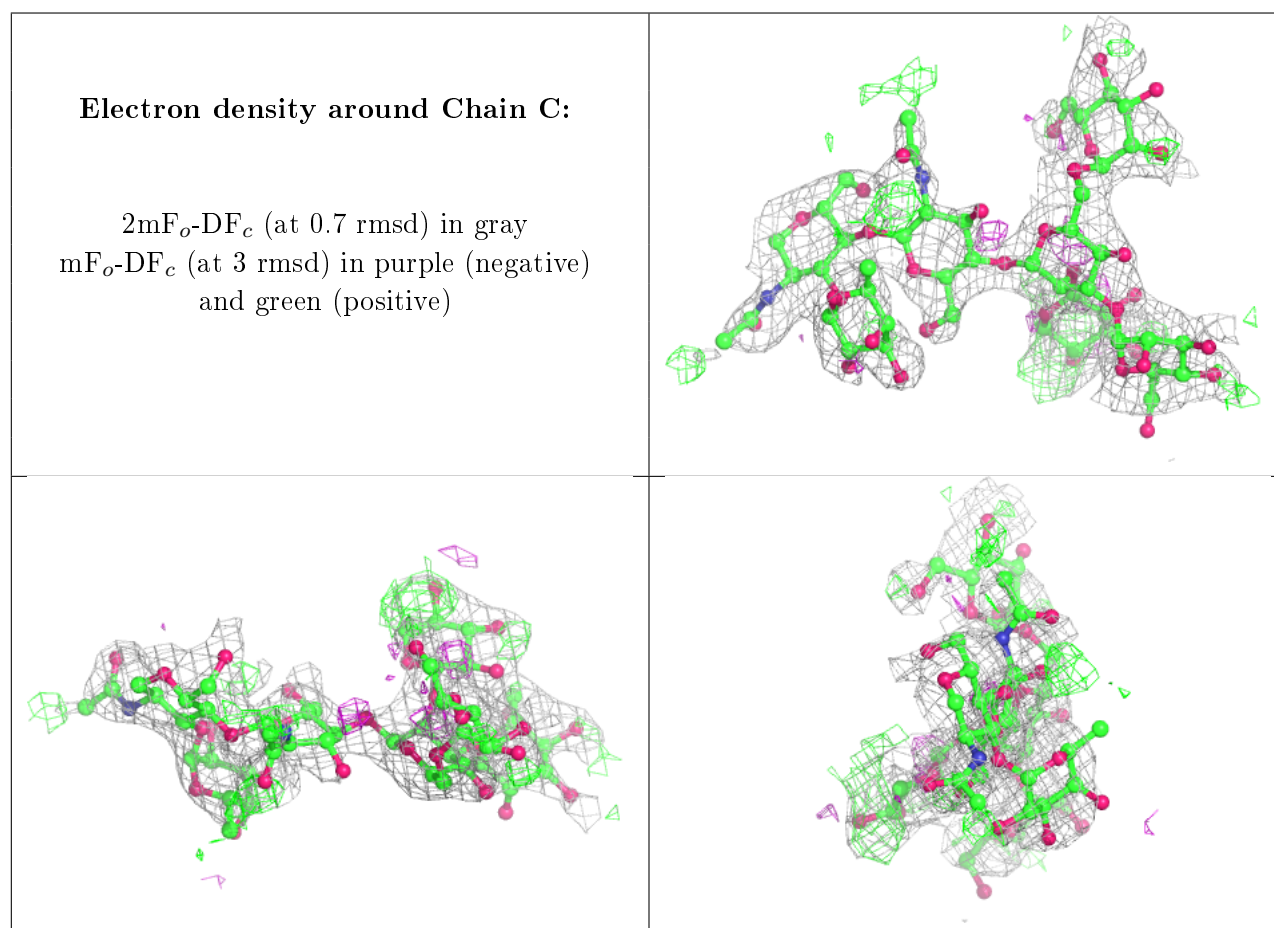
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	XYP	C	4	9/10	0.46	0.39	97,105,109,111	0
2	MAN	C	5	11/12	0.49	0.41	112,116,118,119	0
2	NAG	C	2	14/15	0.64	0.48	97,103,105,106	0
2	BMA	C	3	11/12	0.70	0.33	99,105,108,111	0
3	BMA	D	3	11/12	0.71	0.32	83,88,96,98	0
2	MAN	C	6	11/12	0.71	0.32	89,96,98,101	0
3	FUC	D	5	10/11	0.72	0.44	80,87,92,92	0
6	BMA	G	3	11/12	0.75	0.34	104,110,112,112	0
3	XYP	D	4	9/10	0.81	0.28	79,84,85,88	0
2	NAG	C	1	14/15	0.82	0.35	72,80,91,93	0
2	FUC	C	7	10/11	0.83	0.50	94,96,98,99	0
5	XYP	F	4	9/10	0.86	0.26	79,82,84,85	0
5	BMA	F	3	11/12	0.87	0.23	75,81,86,91	0
4	FUC	E	2	10/11	0.88	0.42	91,93,94,95	0
5	MAN	F	5	11/12	0.88	0.20	70,78,80,81	0
4	NAG	E	1	14/15	0.90	0.29	69,80,88,93	0
4	NAG	E	3	14/15	0.90	0.36	95,99,104,106	0
3	NAG	D	2	14/15	0.90	0.23	46,64,71,72	0
6	NAG	G	2	14/15	0.91	0.25	44,68,85,95	0

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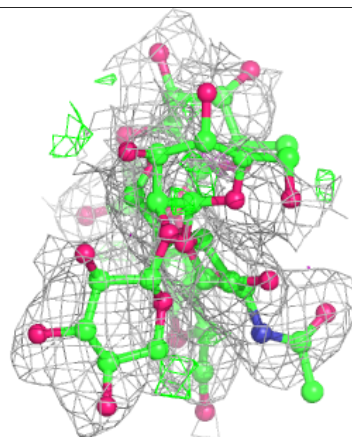
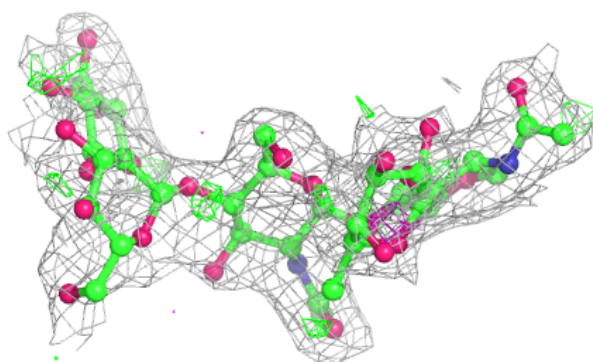
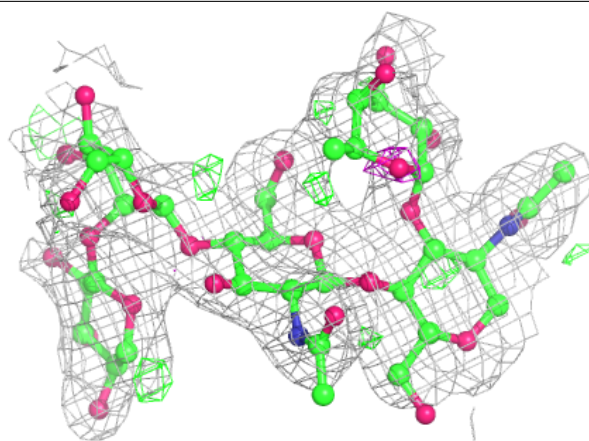
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	F	2	14/15	0.91	0.20	54,64,74,77	0
6	FUC	G	4	10/11	0.92	0.24	51,60,65,70	0
6	NAG	G	1	14/15	0.92	0.12	37,44,52,60	0
5	NAG	F	1	14/15	0.94	0.14	32,43,49,56	0
3	NAG	D	1	14/15	0.94	0.12	31,41,57,65	0

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.



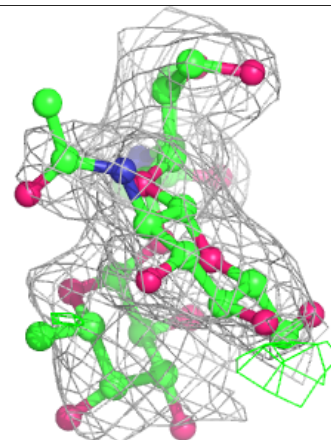
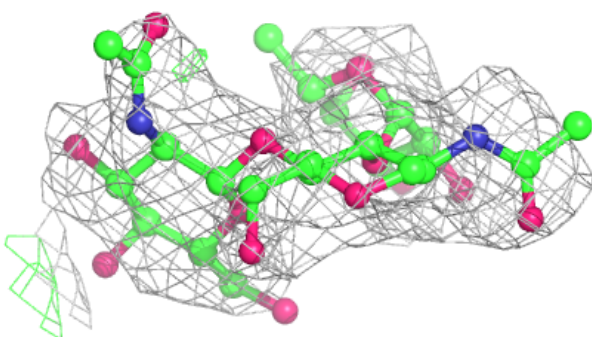
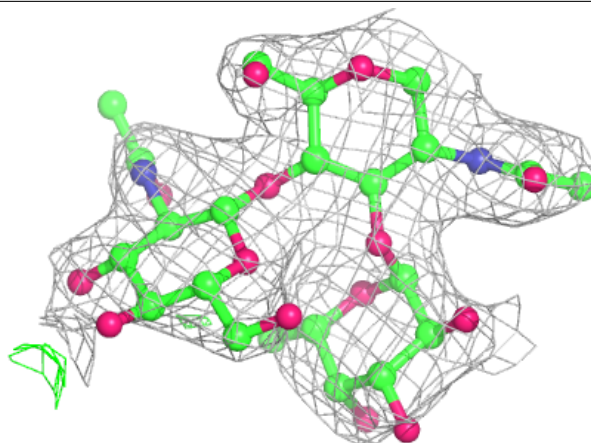
Electron density around Chain D:

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

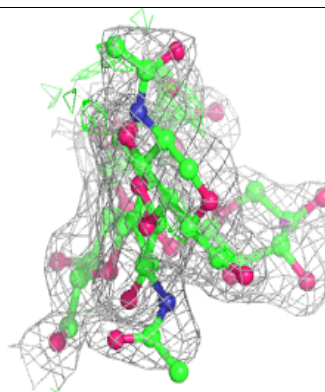
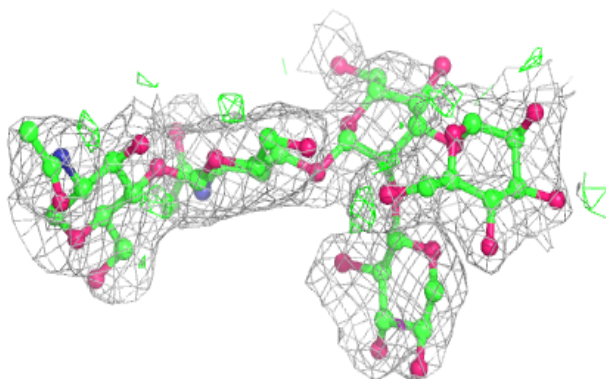
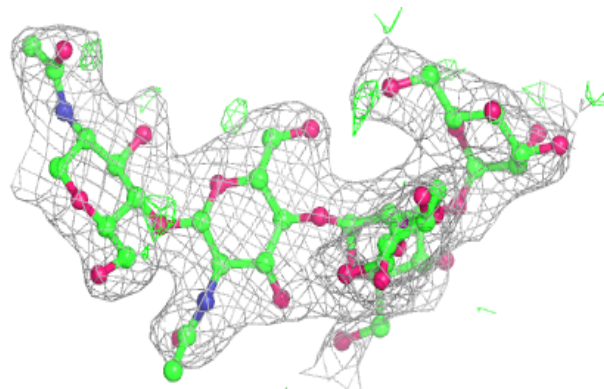


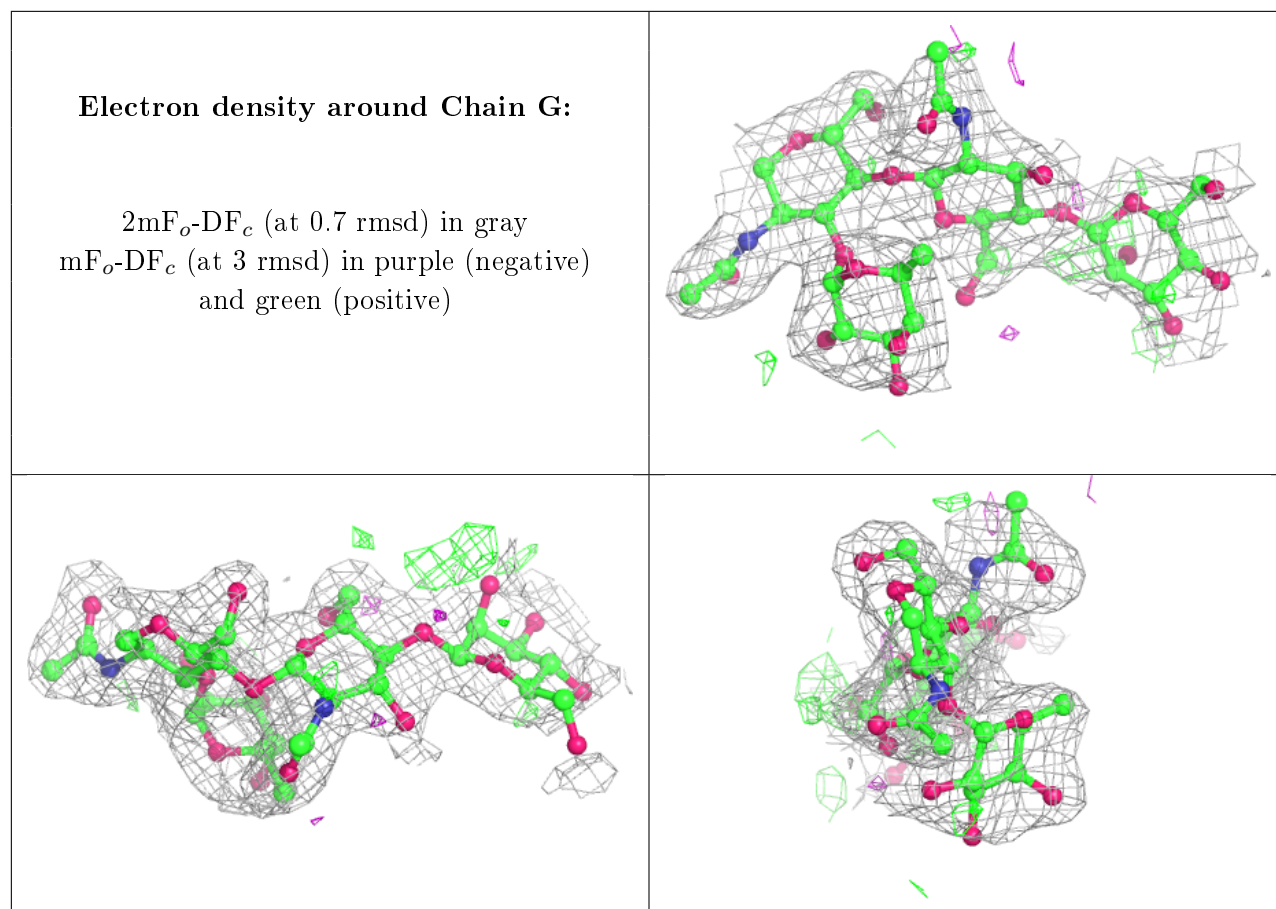
Electron density around Chain E:

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

**Electron density around Chain F:**

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





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.

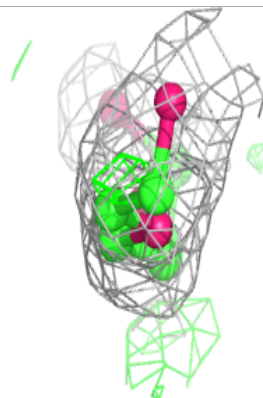
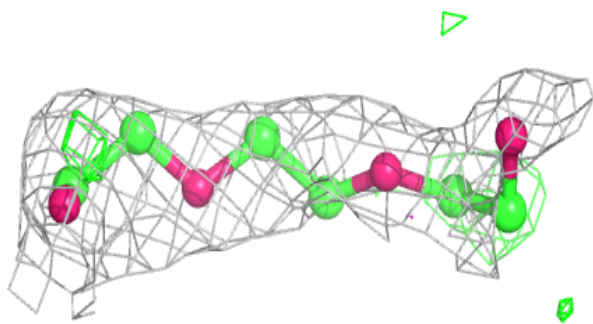
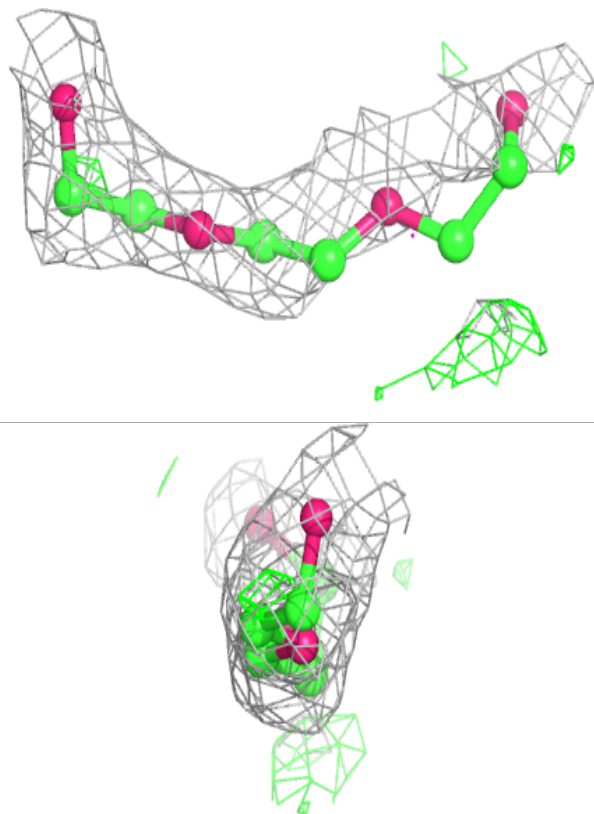
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
11	ACY	B	842	4/4	0.56	0.46	67,72,73,73	0
8	2PE	B	815	10/28	0.59	0.36	77,87,96,97	0
9	NAG	B	639	14/15	0.59	0.49	85,96,101,101	0
8	2PE	B	812	7/28	0.64	0.21	50,53,57,59	0
11	ACY	B	843	4/4	0.75	0.32	71,72,73,74	0
8	2PE	B	810	16/28	0.79	0.30	59,78,97,97	0
8	2PE	B	811	28/28	0.81	0.26	58,72,95,95	0
10	EDO	B	814	4/4	0.83	0.20	60,64,68,72	0
8	2PE	A	813	10/28	0.83	0.17	65,75,76,77	0
7	DGJ	B	802	11/11	0.96	0.14	18,21,23,24	0
7	DGJ	A	801	11/11	0.97	0.14	24,27,30,31	0

The following is a graphical depiction of the model fit to experimental electron density of all

instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

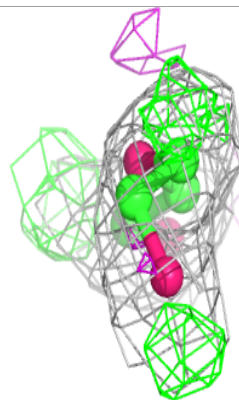
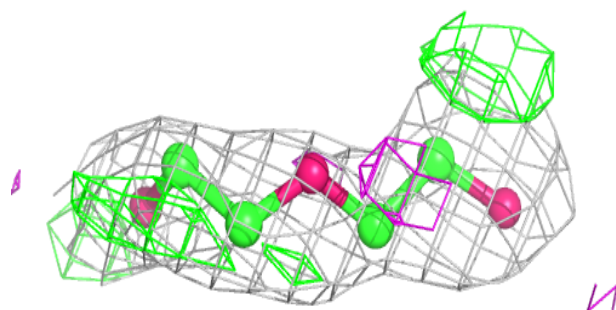
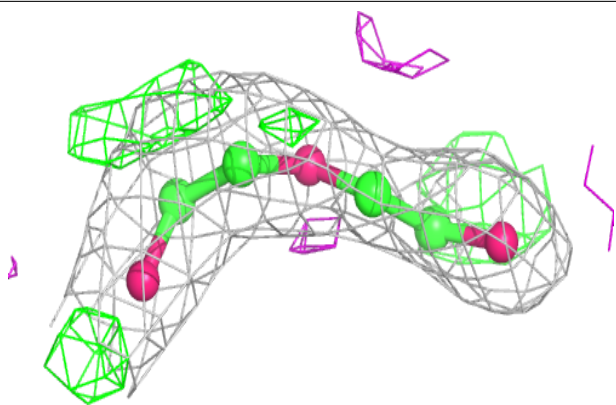
Electron density around 2PE B 815:

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



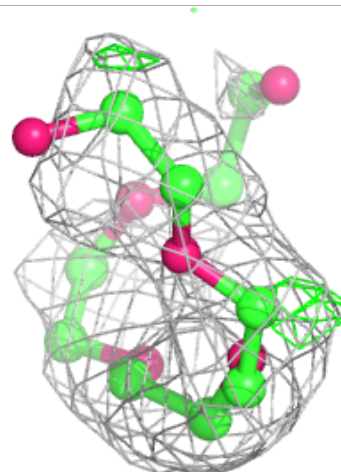
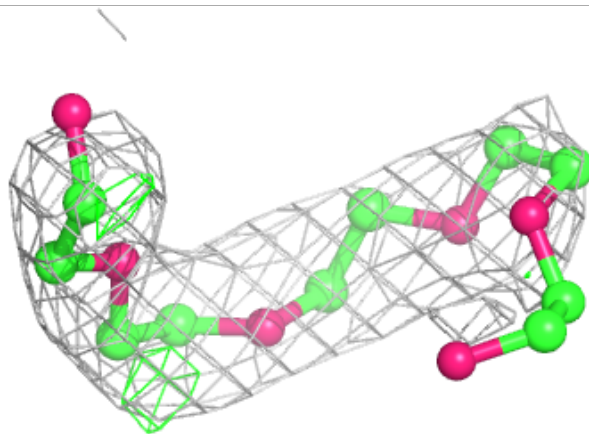
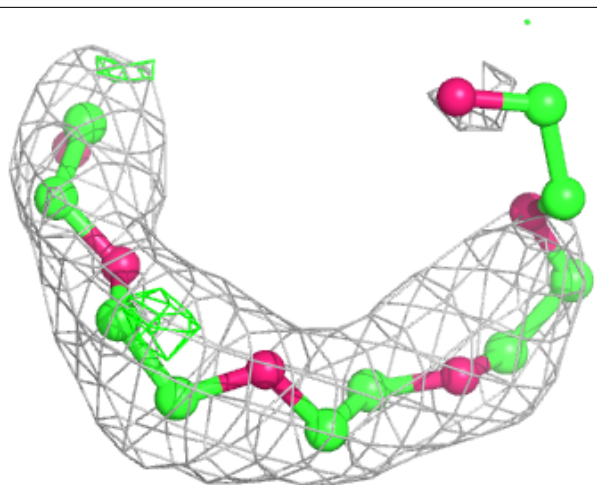
Electron density around 2PE B 812:

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



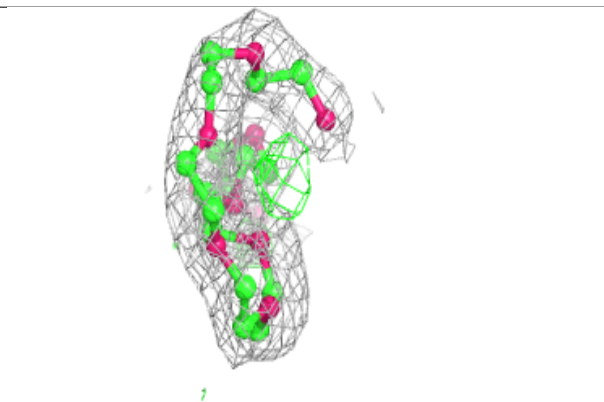
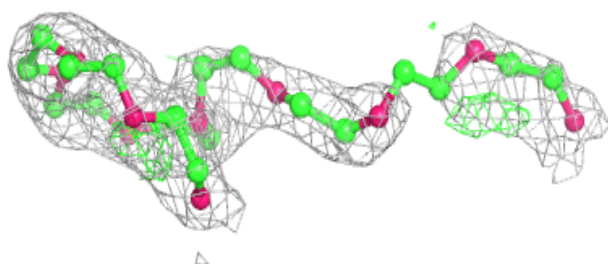
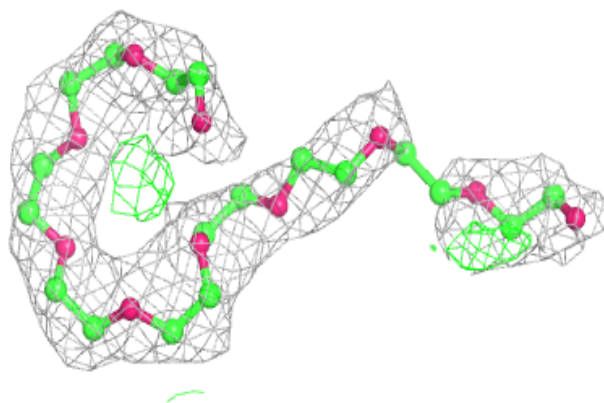
Electron density around 2PE B 810:

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

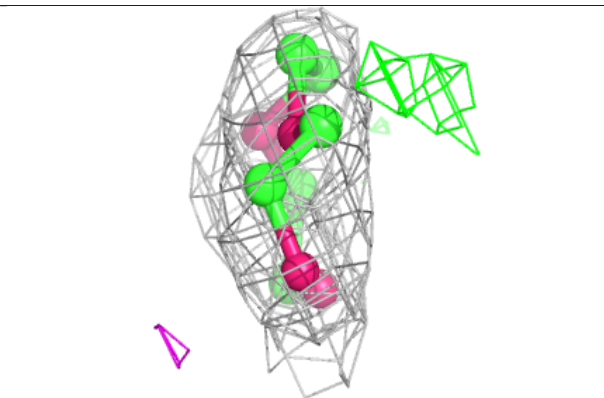
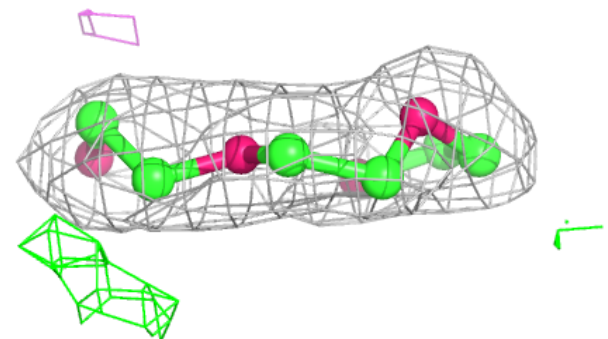
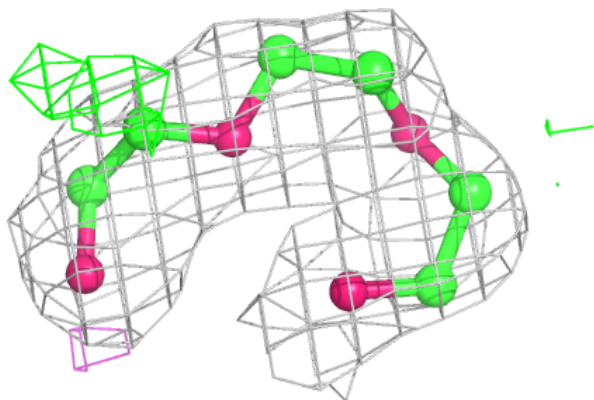


Electron density around 2PE B 811:

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

**Electron density around 2PE A 813:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.