



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:20 AM UTC

PDB ID : 5E6Y / pdb_00005e6y
Title : Crystal structure of E.Coli branching enzyme in complex with alpha cyclodextrin
Authors : Feng, L.; Nosrati, M.; Geiger, J.H.
Deposited on : 2015-10-11
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

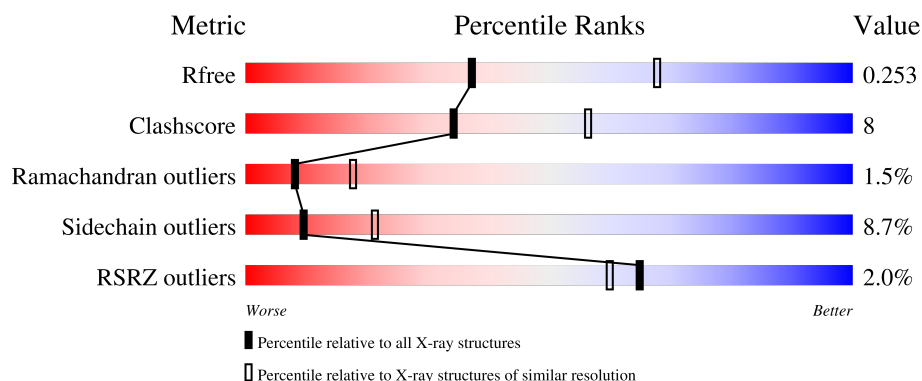
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



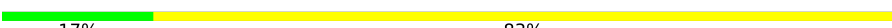
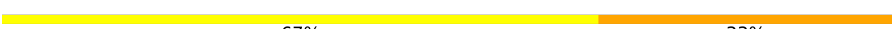
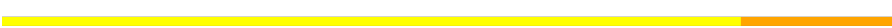
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	612	6% 72% 21% • •
1	B	612	% 72% 22% • •
1	C	612	75% 17% • 5%
1	D	612	% 74% 19% • •
2	E	6	83% 17%

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Mol	Chain	Length	Quality of chain
2	F	6	 33% 67%
2	G	6	 17% 83%
2	H	6	 33% 67%
2	I	6	 17% 83%
2	J	6	 67% 33%
2	K	6	 83% 17%
2	L	6	 17% 50% 33%
2	M	6	 83% 17%

2 Entry composition [i](#)

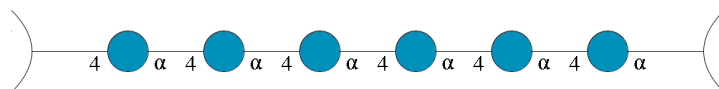
There are 4 unique types of molecules in this entry. The entry contains 20457 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1,4-alpha-glucan branching enzyme GlgB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	587	Total	C	N	O	S	0	0	0
			4729	3025	831	860	13			
1	B	594	Total	C	N	O	S	0	0	0
			4873	3116	861	880	16			
1	C	584	Total	C	N	O	S	0	1	0
			4814	3079	855	864	16			
1	D	589	Total	C	N	O	S	0	0	0
			4836	3090	860	870	16			

- Molecule 2 is an oligosaccharide called Cyclohexakis-(1-4)-(alpha-D-glucopyranose).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	6	Total	C	O	0	0	0
			66	36	30			
2	F	6	Total	C	O	0	0	0
			66	36	30			
2	G	6	Total	C	O	0	0	0
			66	36	30			
2	H	6	Total	C	O	0	0	0
			66	36	30			
2	I	6	Total	C	O	0	0	0
			66	36	30			
2	J	6	Total	C	O	0	0	0
			66	36	30			
2	K	6	Total	C	O	0	0	0
			66	36	30			
2	L	6	Total	C	O	0	0	0
			66	36	30			

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	M	6	Total	C	O	0	0	0
			66	36	30			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	128	Total	O	0	0
			128	128		
4	B	188	Total	O	0	0
			188	188		
4	C	72	Total	O	0	0
			72	72		

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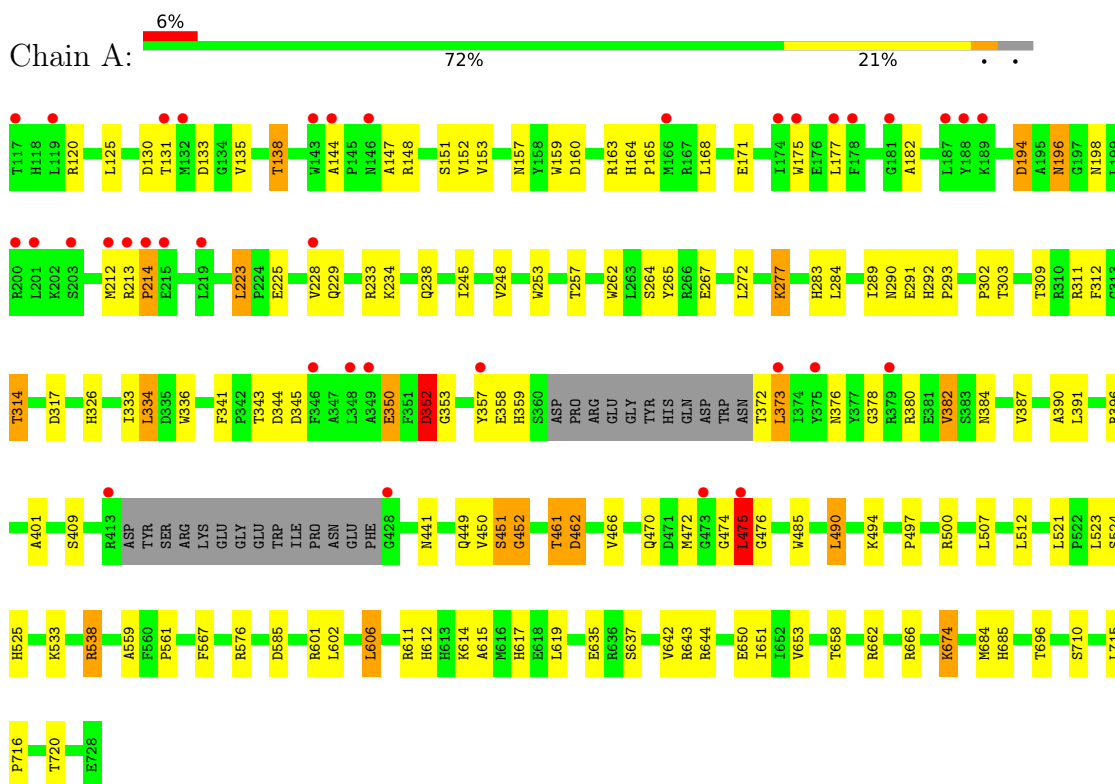
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	193	Total 193	O 193	0	0

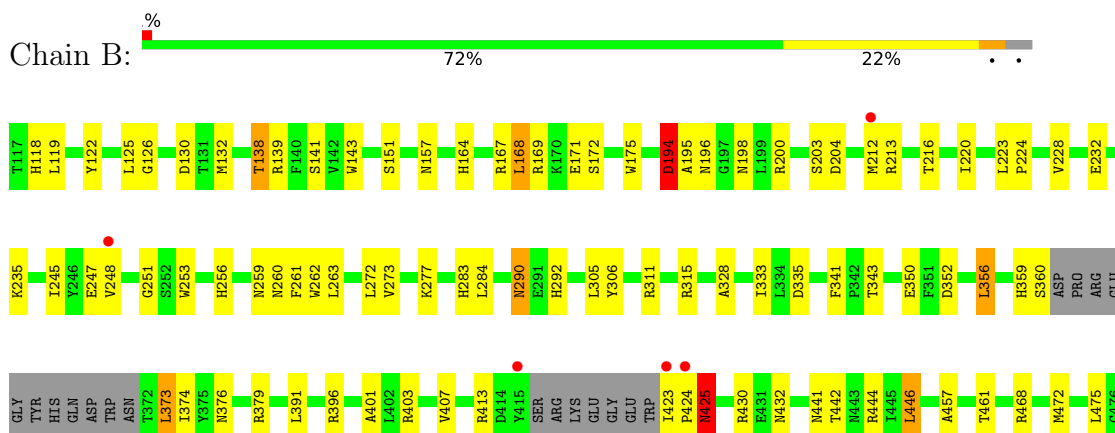
3 Residue-property plots

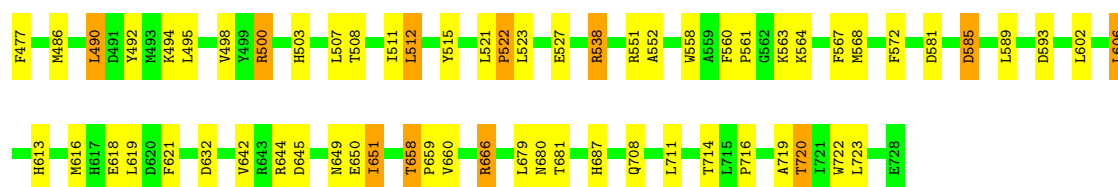
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: 1,4-alpha-glucan branching enzyme GlgB



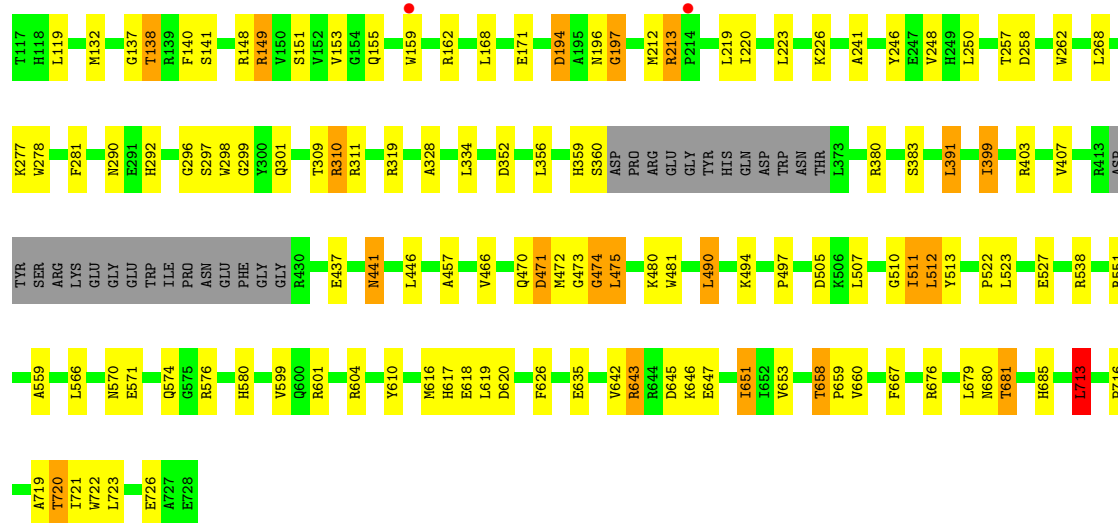
- Molecule 1: 1,4-alpha-glucan branching enzyme GlgB





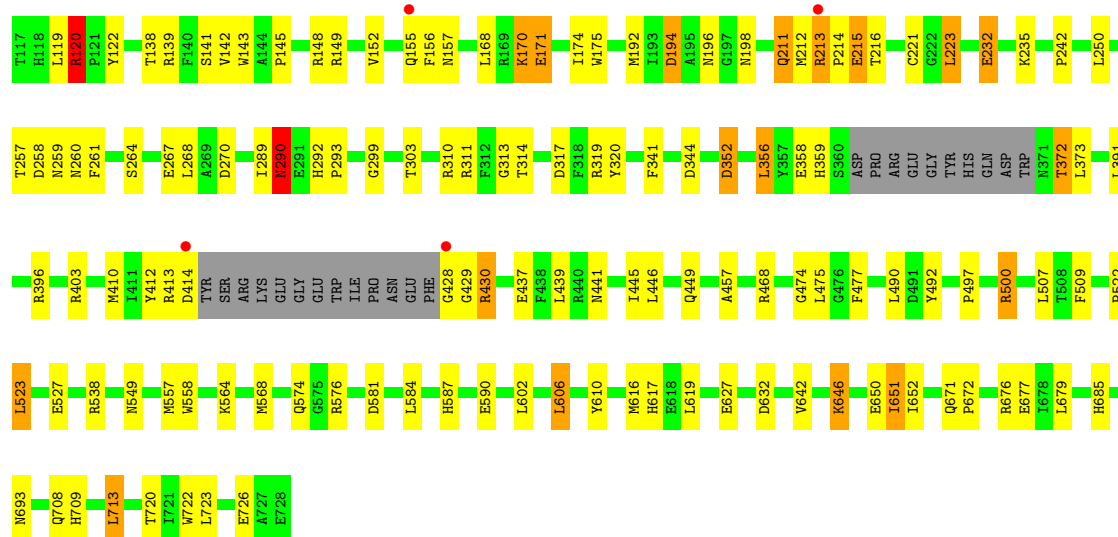
- Molecule 1: 1,4-alpha-glucan branching enzyme GlgB

Chain C: 75% 17% 5%



- Molecule 1: 1,4-alpha-glucan branching enzyme GlgB

Chain D: 74% 19% 7%

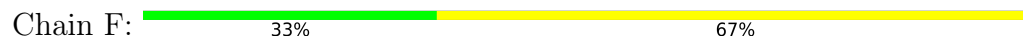


- Molecule 2: Cyclohexakis-(1-4)-(alpha-D-glucopyranose)

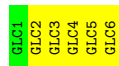
Chain E: 83% 17%



- Molecule 2: Cyclohexakis-(1-4)-(alpha-D-glucopyranose)



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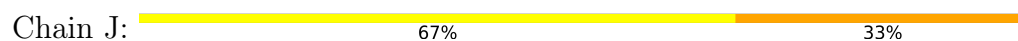
- Molecule 2: Cyclohexakis-(1-4)-(alpha-D-glucopyranose)



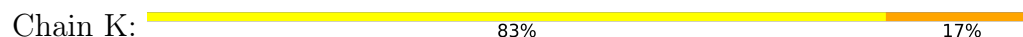
- Molecule 2: Cyclohexakis-(1-4)-(alpha-D-glucopyranose)



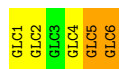
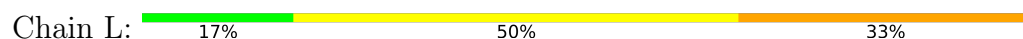
- Molecule 2: Cyclohexakis-(1-4)-(alpha-D-glucopyranose)



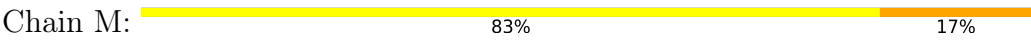
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GLD1
GLD2
GLD3
GLD4
GLD5
GLD6

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.02Å 103.81Å 186.08Å 90.00° 91.97° 90.00°	Depositor
Resolution (Å)	42.43 – 2.60 42.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.2 (42.43-2.60) 95.4 (42.43-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.7.2_869	Depositor
R, R_{free}	0.190 , 0.256 0.190 , 0.253	Depositor DCC
R_{free} test set	10357 reflections (9.56%)	wwPDB-VP
Wilson B-factor (Å ²)	53.1	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20457	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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: GLC, GOL

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	0.49	1/4882 (0.0%)	0.86	3/6644 (0.0%)
1	B	0.58	0/5029	0.89	7/6832 (0.1%)
1	C	0.51	0/4970	0.86	5/6748 (0.1%)
1	D	0.63	0/4989	0.94	12/6774 (0.2%)
All	All	0.56	1/19870 (0.0%)	0.89	27/26998 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	716	PRO	CA-C	5.85	1.55	1.51

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	215	GLU	N-CA-C	9.10	123.10	112.72
1	D	223	LEU	CA-C-N	-8.45	112.10	120.21
1	D	223	LEU	C-N-CA	-8.45	112.10	120.21
1	A	611	ARG	N-CA-C	-7.51	101.17	110.41
1	A	382	VAL	N-CA-C	-7.40	105.45	111.81

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	473	GLY	Peptide
1	D	289	ILE	Peptide

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	4729	0	4365	78	0
1	B	4873	0	4580	87	0
1	C	4814	0	4554	63	0
1	D	4836	0	4567	68	0
2	E	66	0	54	1	0
2	F	66	0	54	0	0
2	G	66	0	54	1	0
2	H	66	0	54	0	0
2	I	66	0	54	0	0
2	J	66	0	54	2	0
2	K	66	0	54	1	0
2	L	66	0	54	2	0
2	M	66	0	54	1	0
3	A	12	0	16	0	0
3	B	12	0	16	1	0
3	D	6	0	8	0	0
4	A	128	0	0	3	0
4	B	188	0	0	8	0
4	C	72	0	0	2	0
4	D	193	0	0	5	0
All	All	20457	0	18592	293	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 8.

The worst 5 of 293 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:157:ASN:HD21	1:A:164:HIS:HB2	1.37	0.90
1:C:149:ARG:HH12	1:C:151:SER:HB2	1.38	0.88
1:C:470:GLN:HA	1:C:474:GLY:HA2	1.57	0.86
1:B:292:HIS:O	1:B:311:ARG:NH1	2.15	0.80
1:A:644:ARG:NH2	1:A:650:GLU:OE1	2.15	0.79

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	581/612 (95%)	506 (87%)	62 (11%)	13 (2%)	5	10
1	B	588/612 (96%)	546 (93%)	38 (6%)	4 (1%)	18	38
1	C	579/612 (95%)	532 (92%)	41 (7%)	6 (1%)	12	28
1	D	583/612 (95%)	543 (93%)	29 (5%)	11 (2%)	6	13
All	All	2331/2448 (95%)	2127 (91%)	170 (7%)	34 (2%)	8	18

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	ARG
1	A	225	GLU
1	A	451	SER
1	B	194	ASP
1	B	212	MET

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	475/521 (91%)	435 (92%)	40 (8%)	10	23
1	B	502/521 (96%)	458 (91%)	44 (9%)	9	21
1	C	498/521 (96%)	449 (90%)	49 (10%)	7	17
1	D	499/521 (96%)	461 (92%)	38 (8%)	12	27
All	All	1974/2084 (95%)	1803 (91%)	171 (9%)	9	21

5 of 171 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	507	LEU
1	D	223	LEU
1	C	601	ARG
1	C	713	LEU
1	D	352	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	487	HIS
1	D	617	HIS
1	C	580	HIS
1	D	685	HIS
1	D	290	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 ⓘ

54 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	GLC	E	1	2	11,11,12	0.99	1 (9%)	15,15,17	1.52	3 (20%)
2	GLC	E	2	2	11,11,12	2.46	1 (9%)	15,15,17	1.83	5 (33%)
2	GLC	E	3	2	11,11,12	0.87	0	15,15,17	2.10	3 (20%)
2	GLC	E	4	2	11,11,12	1.08	1 (9%)	15,15,17	1.83	3 (20%)
2	GLC	E	5	2	11,11,12	0.91	0	15,15,17	1.23	2 (13%)
2	GLC	E	6	2	11,11,12	0.91	0	15,15,17	1.17	1 (6%)
2	GLC	F	1	2	11,11,12	0.77	0	15,15,17	1.44	3 (20%)
2	GLC	F	2	2	11,11,12	2.63	1 (9%)	15,15,17	1.79	3 (20%)
2	GLC	F	3	2	11,11,12	1.11	0	15,15,17	1.70	3 (20%)
2	GLC	F	4	2	11,11,12	1.01	0	15,15,17	0.86	0
2	GLC	F	5	2	11,11,12	0.93	0	15,15,17	0.80	0
2	GLC	F	6	2	11,11,12	0.93	0	15,15,17	1.17	1 (6%)
2	GLC	G	1	2	11,11,12	0.78	0	15,15,17	0.90	0
2	GLC	G	2	2	11,11,12	2.29	1 (9%)	15,15,17	1.24	1 (6%)
2	GLC	G	3	2	11,11,12	1.03	0	15,15,17	1.91	3 (20%)
2	GLC	G	4	2	11,11,12	0.87	0	15,15,17	1.35	4 (26%)
2	GLC	G	5	2	11,11,12	0.94	0	15,15,17	0.82	0
2	GLC	G	6	2	11,11,12	1.02	0	15,15,17	1.42	4 (26%)
2	GLC	H	1	2	11,11,12	0.90	0	15,15,17	1.32	3 (20%)
2	GLC	H	2	2	11,11,12	2.26	1 (9%)	15,15,17	1.32	1 (6%)
2	GLC	H	3	2	11,11,12	0.94	0	15,15,17	1.01	1 (6%)
2	GLC	H	4	2	11,11,12	0.85	0	15,15,17	0.77	0
2	GLC	H	5	2	11,11,12	0.82	0	15,15,17	0.86	0
2	GLC	H	6	2	11,11,12	0.88	0	15,15,17	1.01	1 (6%)
2	GLC	I	1	2	11,11,12	1.00	1 (9%)	15,15,17	1.50	3 (20%)
2	GLC	I	2	2	11,11,12	2.47	1 (9%)	15,15,17	1.41	3 (20%)
2	GLC	I	3	2	11,11,12	1.01	0	15,15,17	1.52	3 (20%)
2	GLC	I	4	2	11,11,12	0.89	0	15,15,17	1.20	1 (6%)
2	GLC	I	5	2	11,11,12	0.91	0	15,15,17	0.79	0
2	GLC	I	6	2	11,11,12	0.96	0	15,15,17	1.18	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	J	1	2	11,11,12	0.78	0	15,15,17	1.16	1 (6%)
2	GLC	J	2	2	11,11,12	2.47	1 (9%)	15,15,17	1.22	1 (6%)
2	GLC	J	3	2	11,11,12	0.85	0	15,15,17	1.20	2 (13%)
2	GLC	J	4	2	11,11,12	0.87	0	15,15,17	1.29	2 (13%)
2	GLC	J	5	2	11,11,12	0.90	0	15,15,17	1.22	2 (13%)
2	GLC	J	6	2	11,11,12	0.81	0	15,15,17	1.18	1 (6%)
2	GLC	K	1	2	11,11,12	0.89	0	15,15,17	2.19	6 (40%)
2	GLC	K	2	2	11,11,12	2.55	1 (9%)	15,15,17	1.87	4 (26%)
2	GLC	K	3	2	11,11,12	1.10	1 (9%)	15,15,17	1.37	2 (13%)
2	GLC	K	4	2	11,11,12	0.96	1 (9%)	15,15,17	1.81	3 (20%)
2	GLC	K	5	2	11,11,12	1.02	0	15,15,17	0.96	1 (6%)
2	GLC	K	6	2	11,11,12	0.94	0	15,15,17	1.13	2 (13%)
2	GLC	L	1	2	11,11,12	1.02	1 (9%)	15,15,17	1.35	3 (20%)
2	GLC	L	2	2	11,11,12	2.52	1 (9%)	15,15,17	1.39	3 (20%)
2	GLC	L	3	2	11,11,12	0.96	0	15,15,17	1.01	0
2	GLC	L	4	2	11,11,12	1.01	0	15,15,17	1.13	1 (6%)
2	GLC	L	5	2	11,11,12	1.17	1 (9%)	15,15,17	1.37	2 (13%)
2	GLC	L	6	2	11,11,12	0.82	0	15,15,17	1.15	3 (20%)
2	GLC	M	1	2	11,11,12	0.94	1 (9%)	15,15,17	1.01	0
2	GLC	M	2	2	11,11,12	2.35	1 (9%)	15,15,17	1.13	0
2	GLC	M	3	2	11,11,12	0.85	0	15,15,17	1.11	2 (13%)
2	GLC	M	4	2	11,11,12	0.95	1 (9%)	15,15,17	0.76	0
2	GLC	M	5	2	11,11,12	0.88	0	15,15,17	1.21	1 (6%)
2	GLC	M	6	2	11,11,12	0.82	0	15,15,17	1.14	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	E	1	2	-	2/2/19/22	0/1/1/1
2	GLC	E	2	2	-	0/2/19/22	0/1/1/1
2	GLC	E	3	2	-	2/2/19/22	0/1/1/1
2	GLC	E	4	2	-	2/2/19/22	0/1/1/1
2	GLC	E	5	2	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	E	6	2	-	2/2/19/22	0/1/1/1
2	GLC	F	1	2	-	2/2/19/22	0/1/1/1
2	GLC	F	2	2	-	0/2/19/22	0/1/1/1
2	GLC	F	3	2	-	1/2/19/22	0/1/1/1
2	GLC	F	4	2	-	0/2/19/22	0/1/1/1
2	GLC	F	5	2	-	0/2/19/22	0/1/1/1
2	GLC	F	6	2	-	0/2/19/22	0/1/1/1
2	GLC	G	1	2	-	0/2/19/22	0/1/1/1
2	GLC	G	2	2	-	2/2/19/22	0/1/1/1
2	GLC	G	3	2	-	1/2/19/22	0/1/1/1
2	GLC	G	4	2	-	0/2/19/22	0/1/1/1
2	GLC	G	5	2	-	0/2/19/22	0/1/1/1
2	GLC	G	6	2	-	2/2/19/22	0/1/1/1
2	GLC	H	1	2	-	2/2/19/22	0/1/1/1
2	GLC	H	2	2	-	0/2/19/22	0/1/1/1
2	GLC	H	3	2	-	0/2/19/22	0/1/1/1
2	GLC	H	4	2	-	0/2/19/22	0/1/1/1
2	GLC	H	5	2	-	0/2/19/22	0/1/1/1
2	GLC	H	6	2	-	0/2/19/22	0/1/1/1
2	GLC	I	1	2	-	1/2/19/22	0/1/1/1
2	GLC	I	2	2	-	2/2/19/22	0/1/1/1
2	GLC	I	3	2	-	0/2/19/22	0/1/1/1
2	GLC	I	4	2	-	2/2/19/22	0/1/1/1
2	GLC	I	5	2	-	2/2/19/22	0/1/1/1
2	GLC	I	6	2	-	0/2/19/22	0/1/1/1
2	GLC	J	1	2	-	0/2/19/22	0/1/1/1
2	GLC	J	2	2	-	1/2/19/22	0/1/1/1
2	GLC	J	3	2	-	2/2/19/22	0/1/1/1
2	GLC	J	4	2	-	2/2/19/22	0/1/1/1
2	GLC	J	5	2	-	0/2/19/22	0/1/1/1
2	GLC	J	6	2	-	2/2/19/22	0/1/1/1
2	GLC	K	1	2	-	2/2/19/22	0/1/1/1
2	GLC	K	2	2	-	2/2/19/22	0/1/1/1
2	GLC	K	3	2	-	0/2/19/22	0/1/1/1
2	GLC	K	4	2	-	2/2/19/22	0/1/1/1
2	GLC	K	5	2	-	2/2/19/22	0/1/1/1
2	GLC	K	6	2	-	0/2/19/22	0/1/1/1
2	GLC	L	1	2	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	L	2	2	-	2/2/19/22	0/1/1/1
2	GLC	L	3	2	-	2/2/19/22	0/1/1/1
2	GLC	L	4	2	-	0/2/19/22	0/1/1/1
2	GLC	L	5	2	-	1/2/19/22	0/1/1/1
2	GLC	L	6	2	-	0/2/19/22	0/1/1/1
2	GLC	M	1	2	-	0/2/19/22	0/1/1/1
2	GLC	M	2	2	-	0/2/19/22	0/1/1/1
2	GLC	M	3	2	-	0/2/19/22	0/1/1/1
2	GLC	M	4	2	-	2/2/19/22	0/1/1/1
2	GLC	M	5	2	-	2/2/19/22	0/1/1/1
2	GLC	M	6	2	-	1/2/19/22	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	GLC	O5-C1	8.18	1.57	1.43
2	K	2	GLC	O5-C1	8.04	1.57	1.43
2	L	2	GLC	O5-C1	7.90	1.57	1.43
2	I	2	GLC	O5-C1	7.89	1.57	1.43
2	J	2	GLC	O5-C1	7.72	1.56	1.43

The worst 5 of 100 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	3	GLC	C1-O5-C5	5.41	119.44	112.19
2	E	3	GLC	C1-O5-C5	5.40	119.43	112.19
2	K	4	GLC	C1-O5-C5	4.86	118.70	112.19
2	E	4	GLC	C1-C2-C3	4.86	116.72	109.64
2	F	3	GLC	C1-C2-C3	4.46	116.13	109.64

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

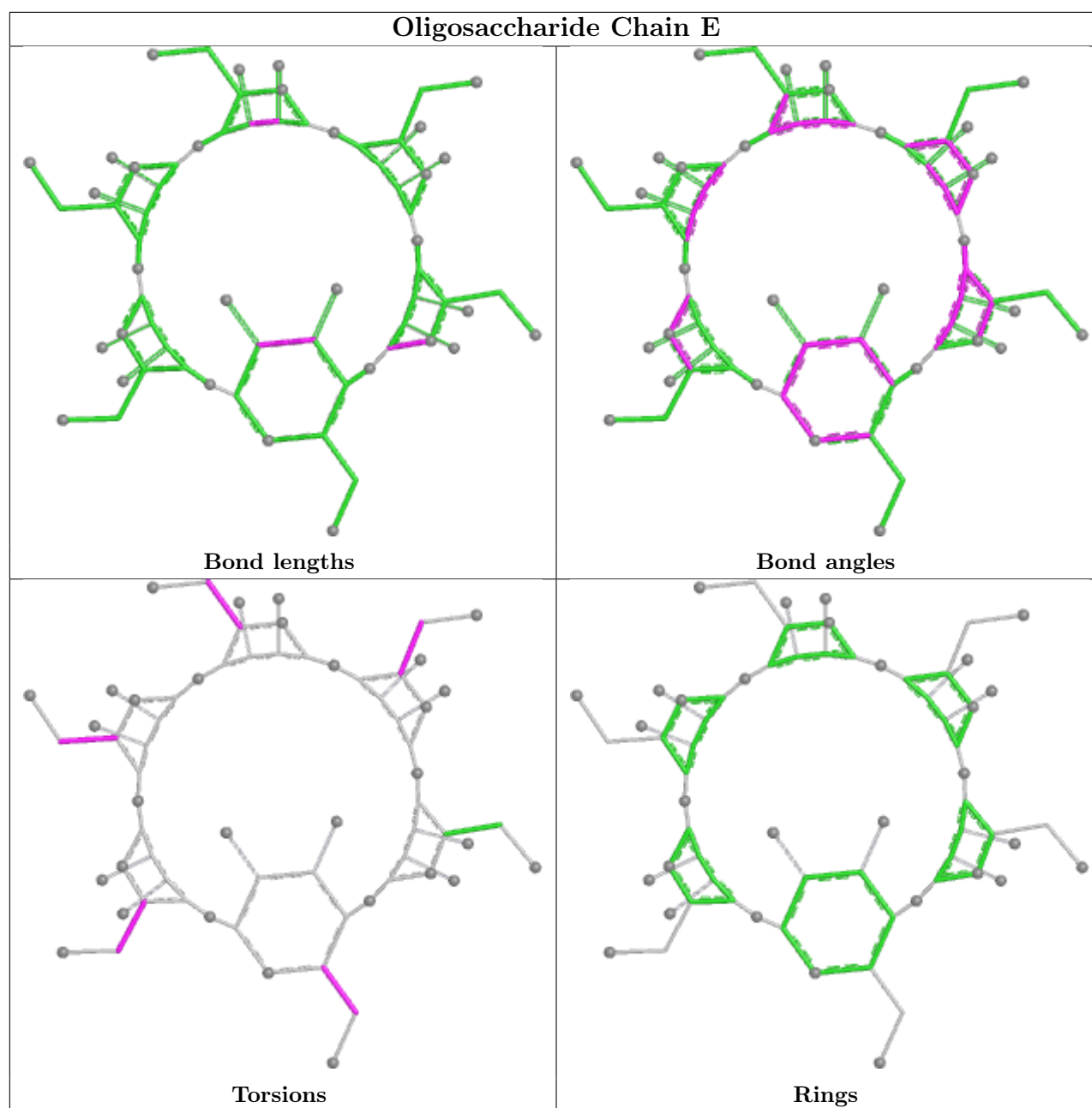
Mol	Chain	Res	Type	Atoms
2	K	4	GLC	O5-C5-C6-O6
2	L	2	GLC	O5-C5-C6-O6
2	E	1	GLC	O5-C5-C6-O6
2	E	3	GLC	O5-C5-C6-O6
2	H	1	GLC	O5-C5-C6-O6

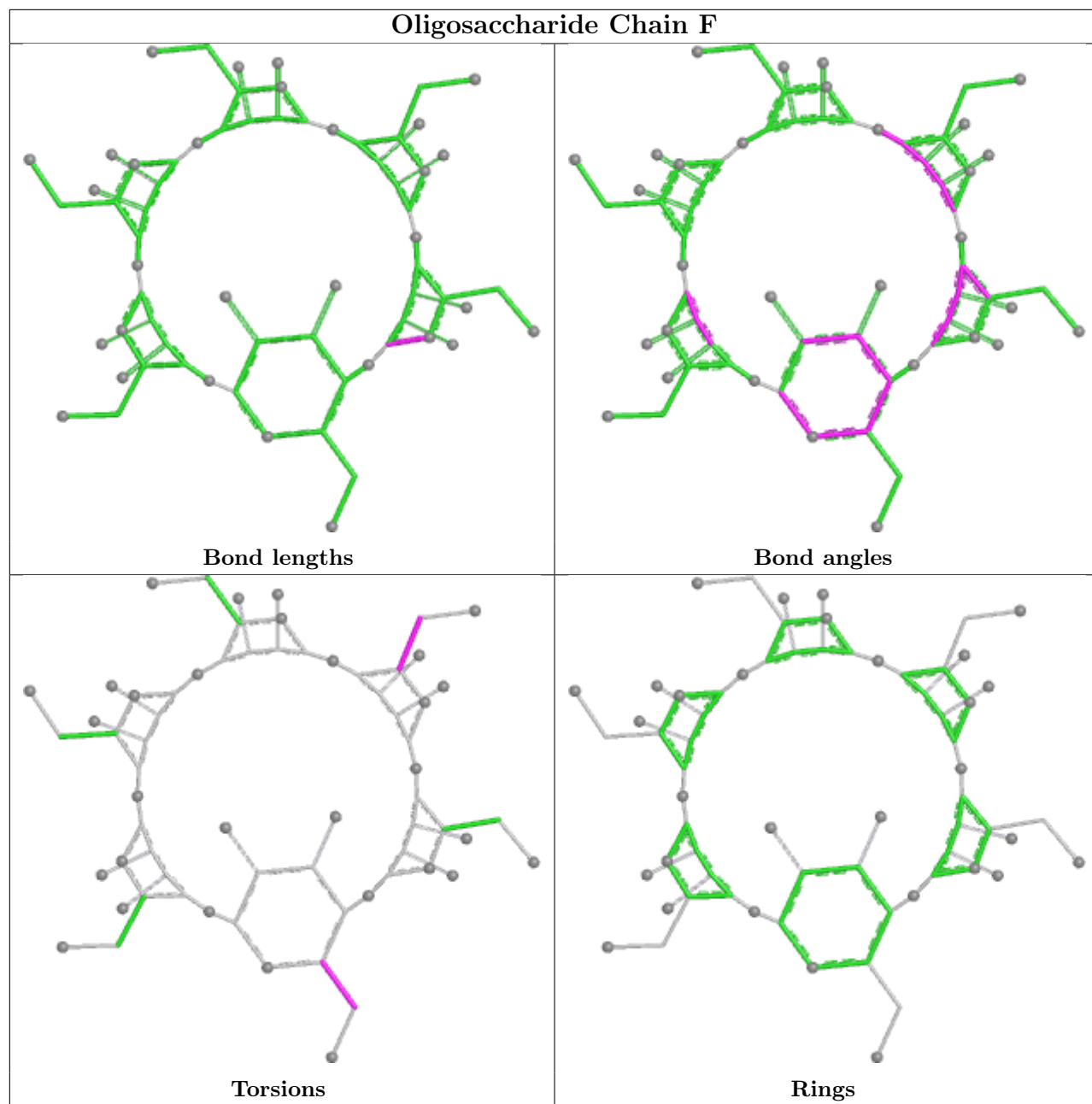
There are no ring outliers.

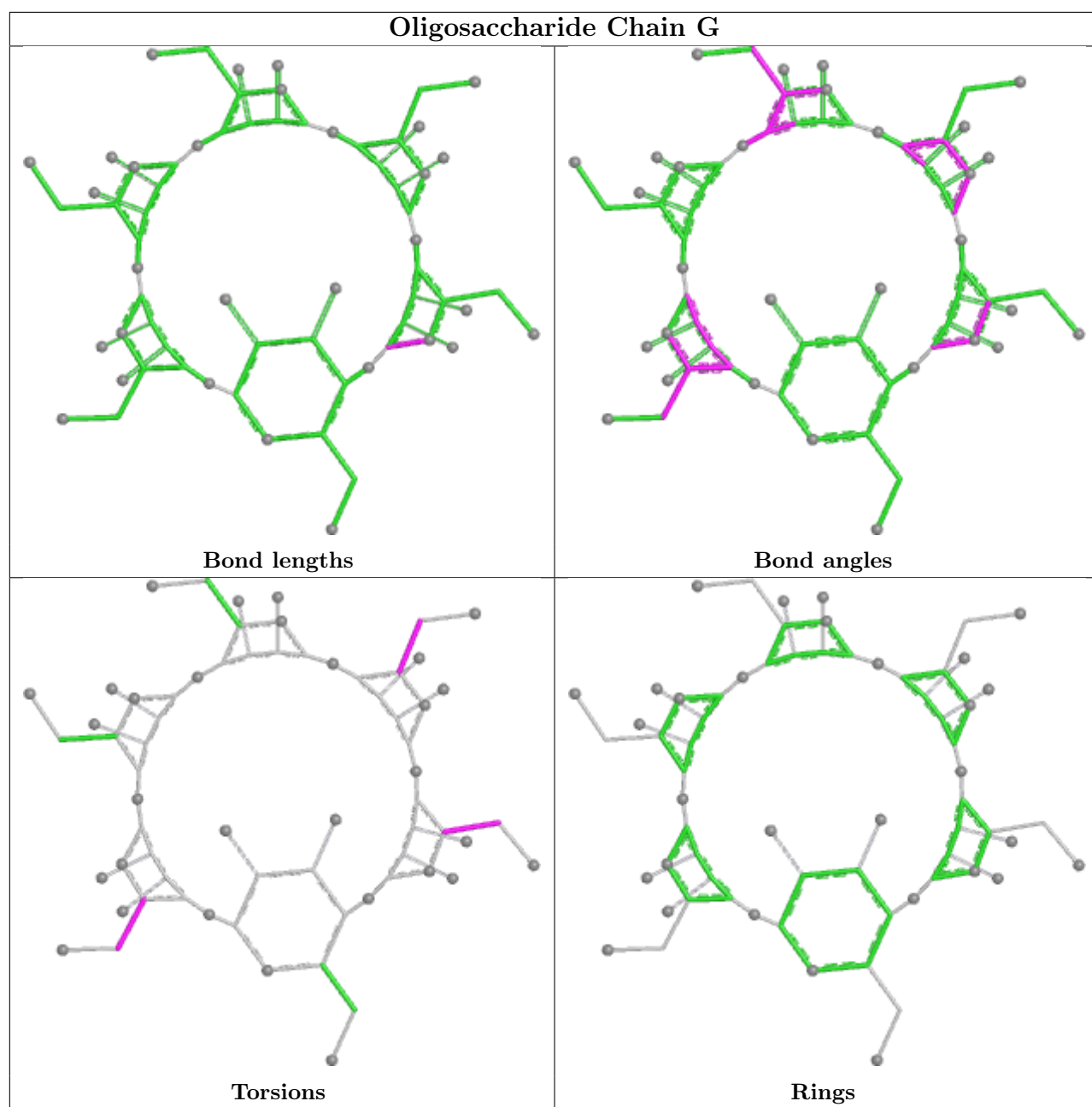
8 monomers are involved in 8 short contacts:

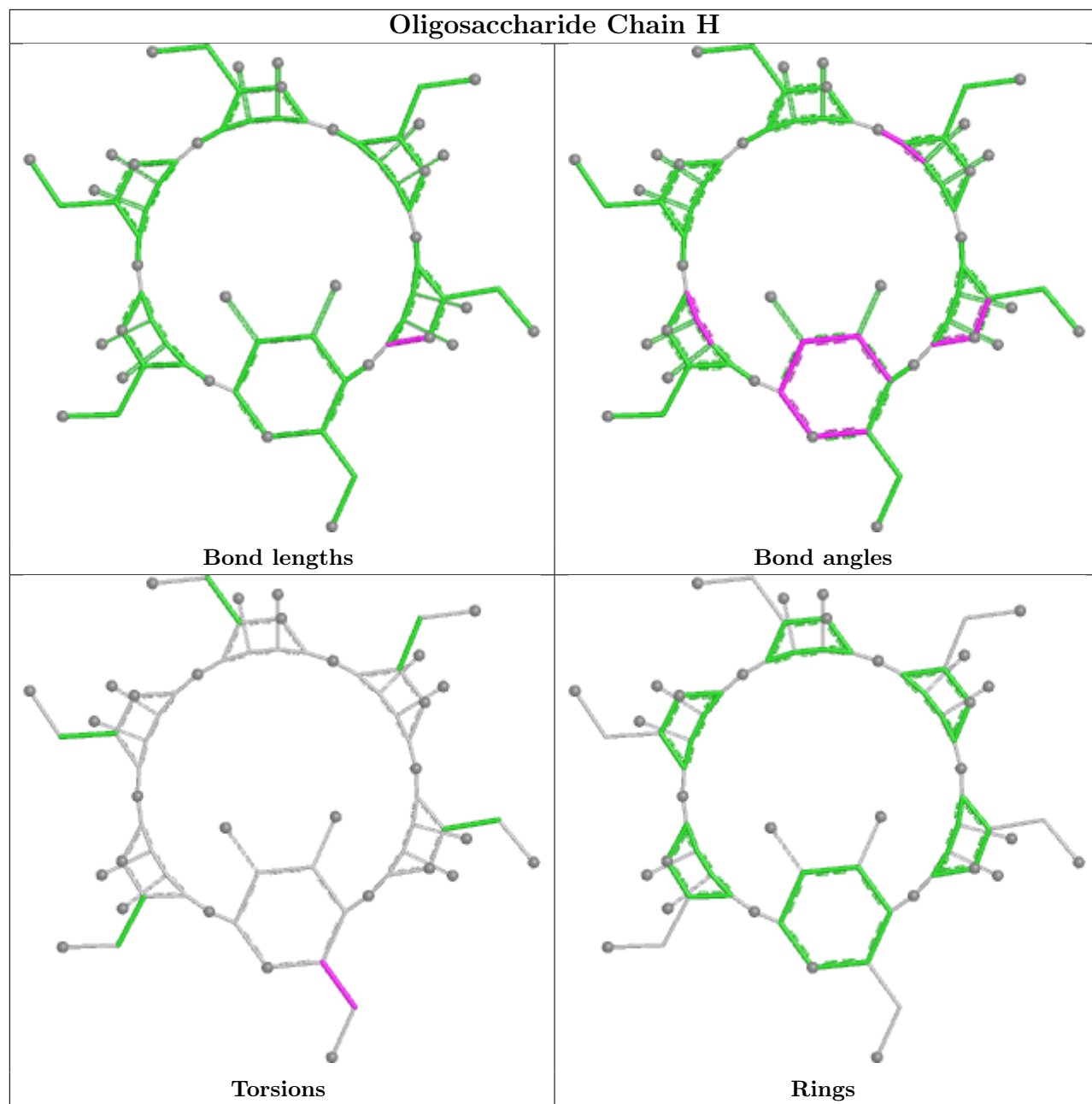
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	4	GLC	1	0
2	J	4	GLC	1	0
2	E	3	GLC	1	0
2	J	1	GLC	1	0
2	L	6	GLC	1	0
2	G	5	GLC	1	0
2	L	5	GLC	1	0
2	M	3	GLC	1	0

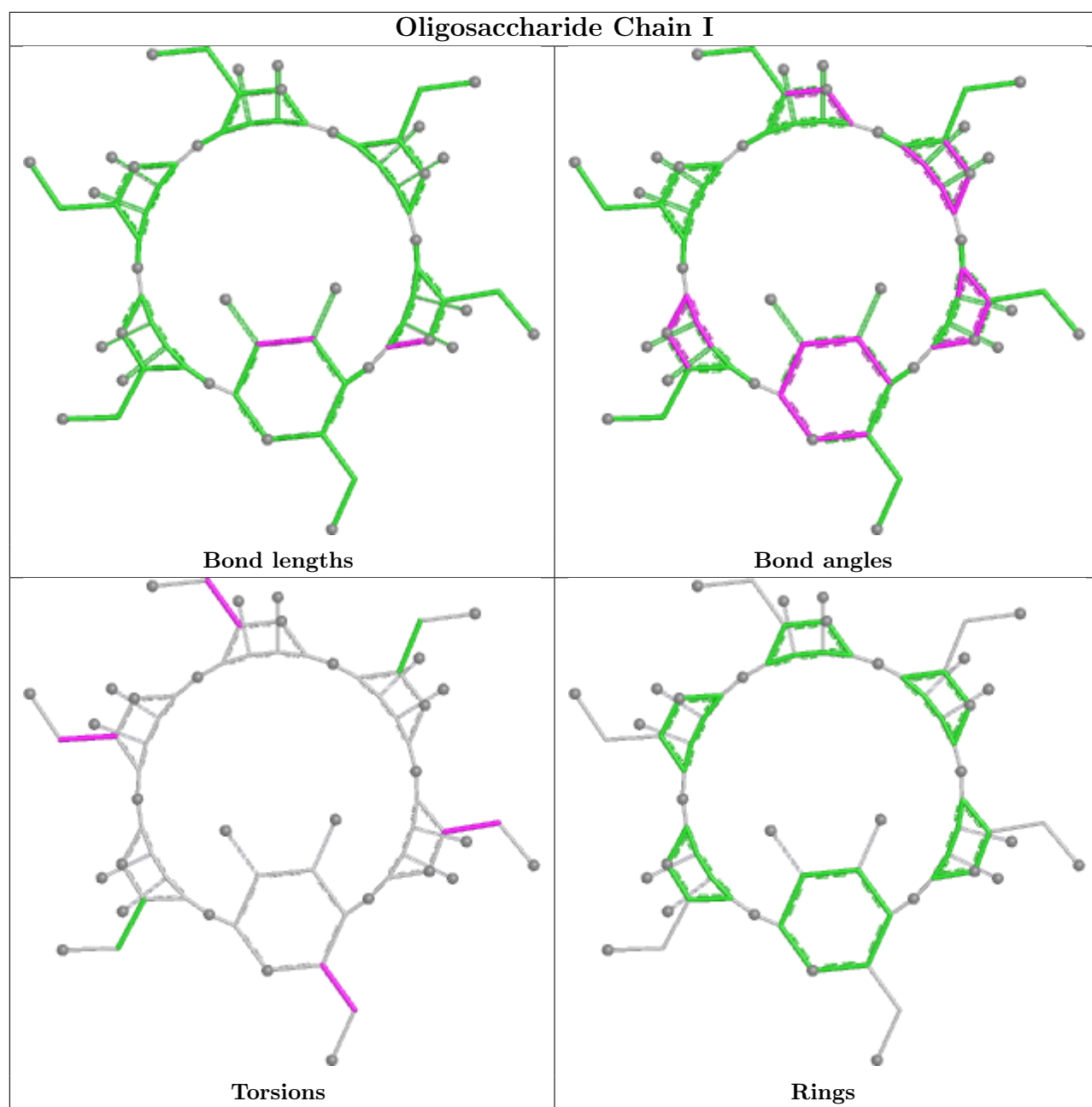
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

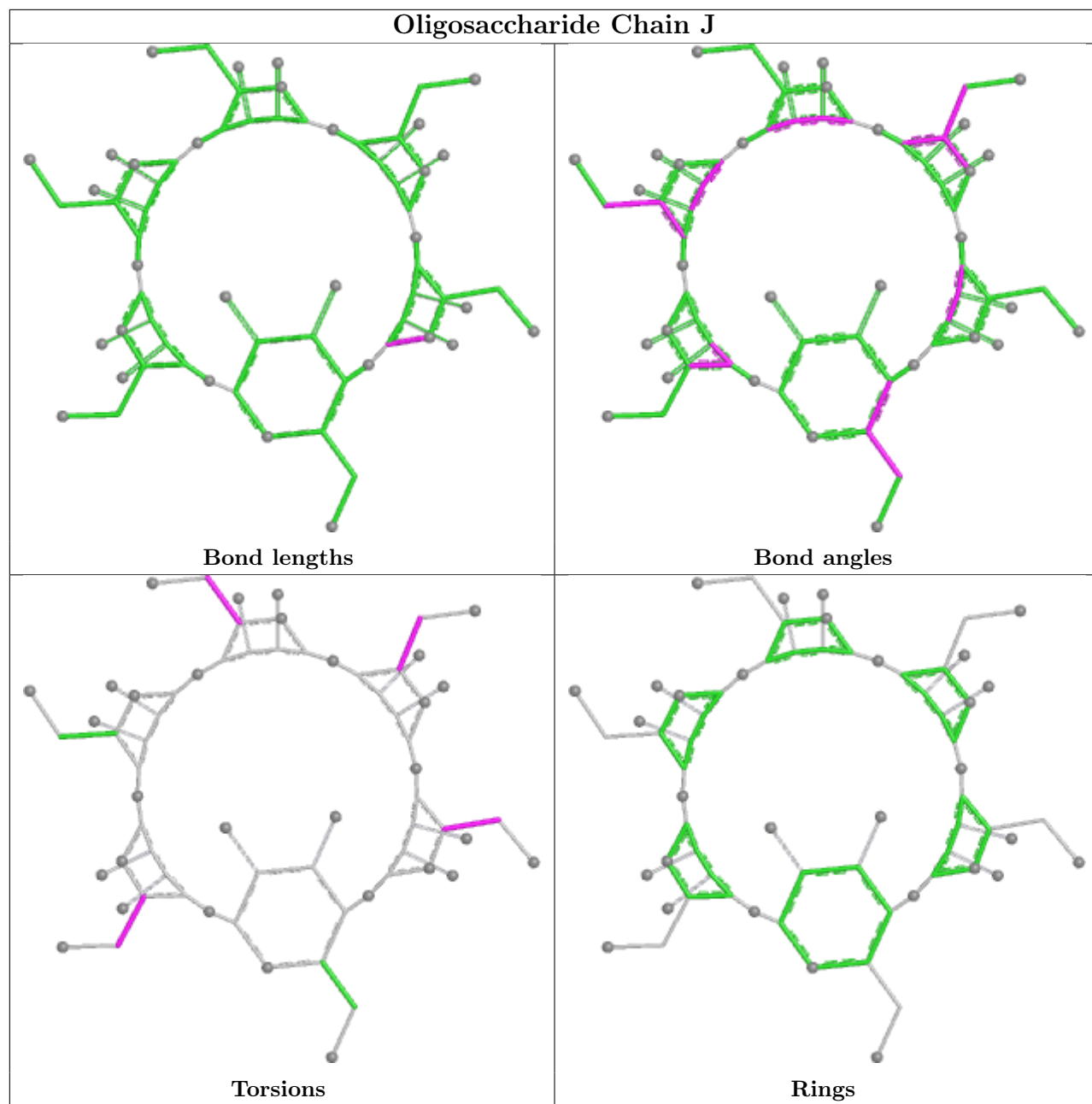


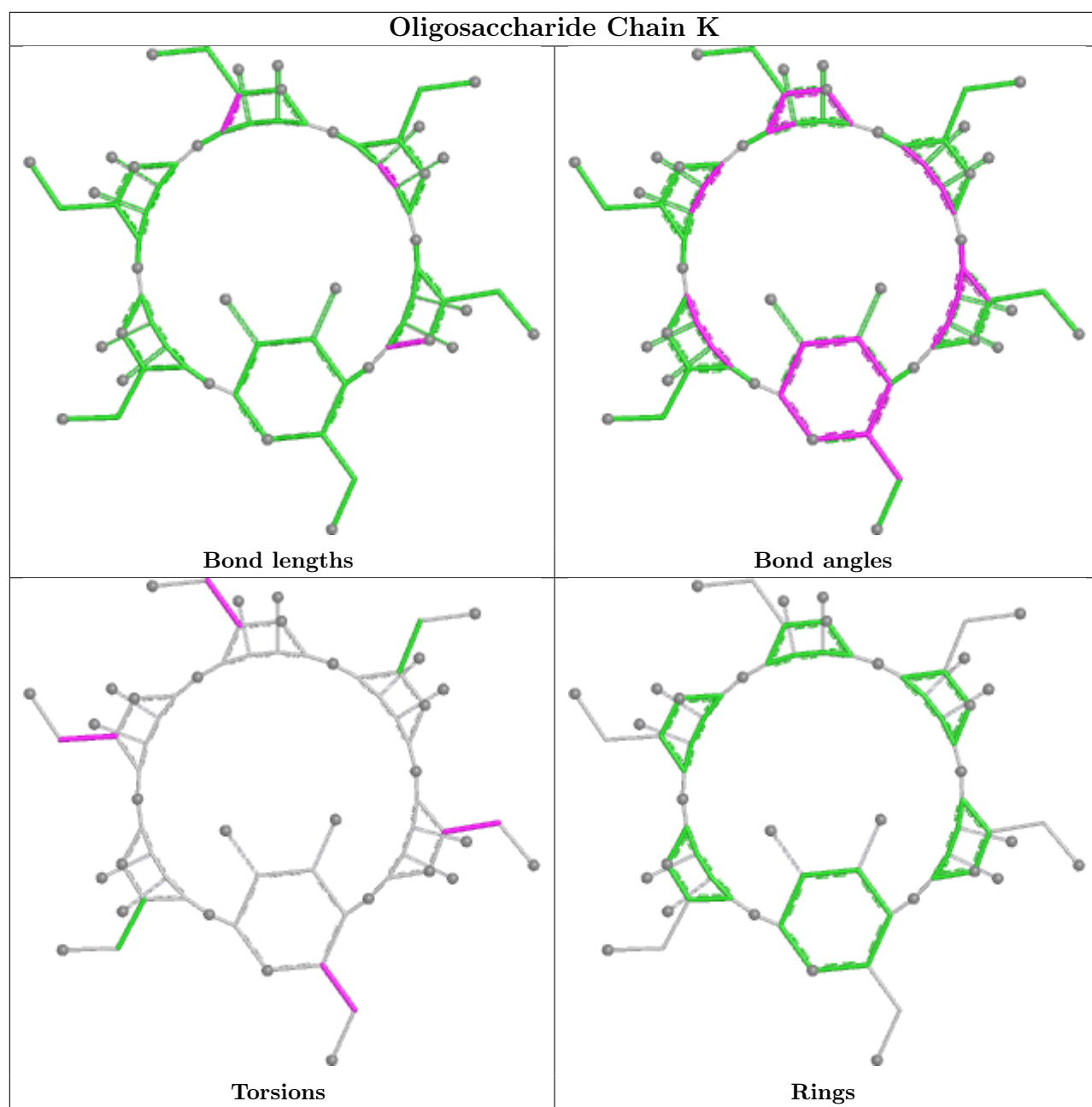


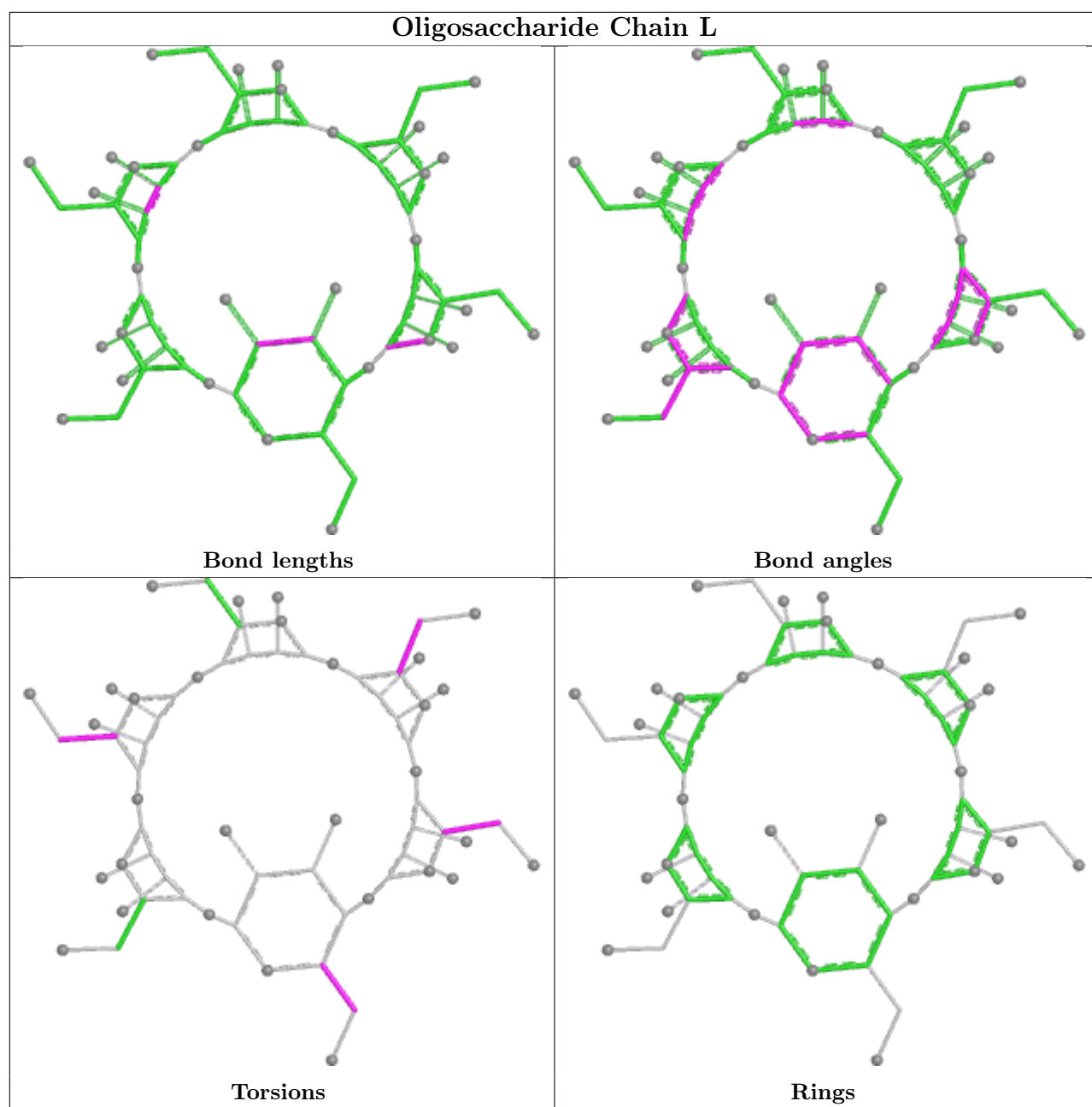


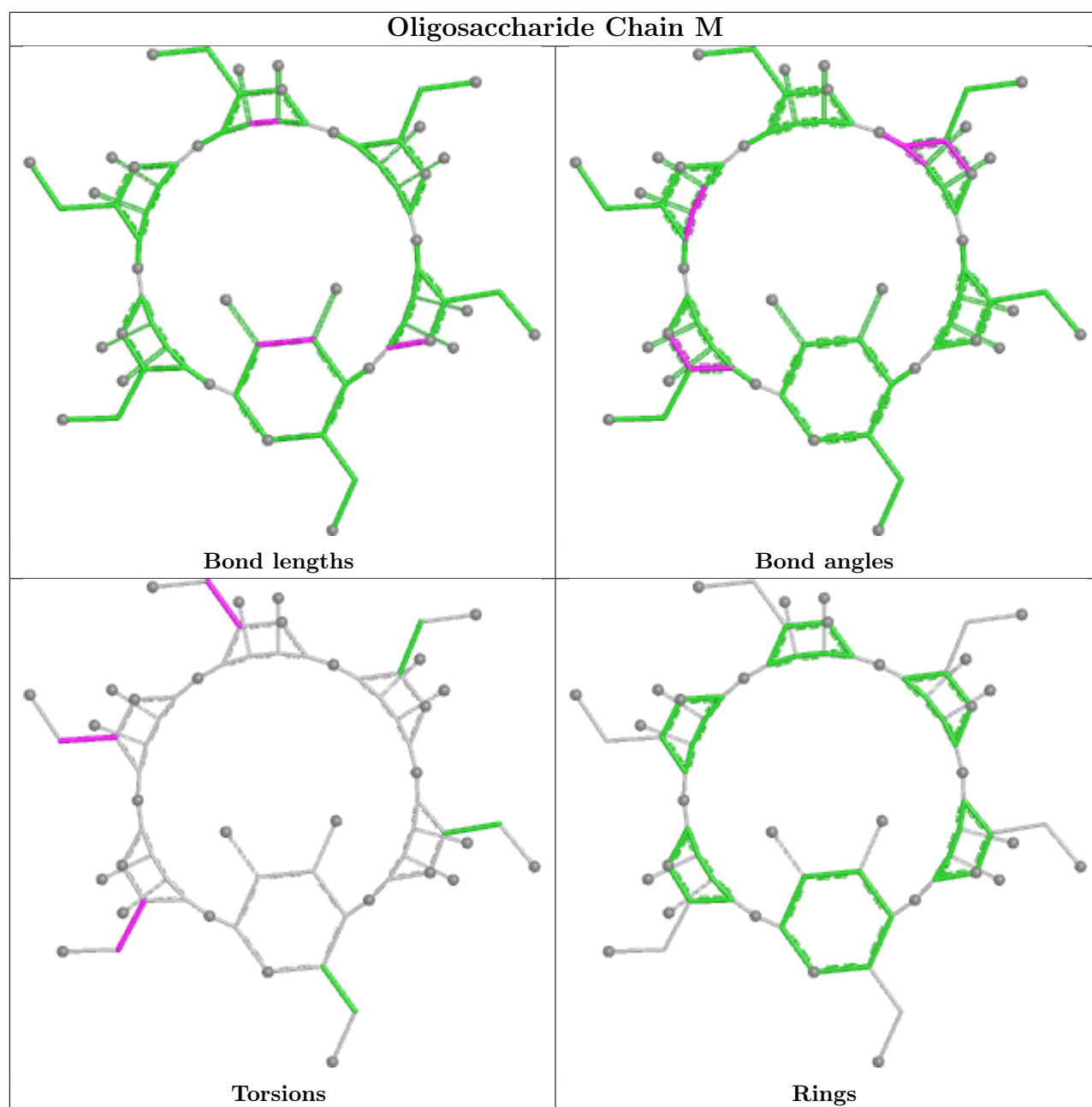












5.6 Ligand geometry [i](#)

5 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
3	GOL	A	803	-	5,5,5	0.42	0	5,5,5	0.32	0
3	GOL	A	804	-	5,5,5	0.39	0	5,5,5	0.23	0
3	GOL	B	803	-	5,5,5	0.39	0	5,5,5	0.34	0
3	GOL	D	804	-	5,5,5	0.27	0	5,5,5	0.46	0
3	GOL	B	802	-	5,5,5	0.43	0	5,5,5	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	803	-	-	0/4/4/4	-
3	GOL	A	804	-	-	0/4/4/4	-
3	GOL	B	803	-	-	4/4/4/4	-
3	GOL	D	804	-	-	4/4/4/4	-
3	GOL	B	802	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	802	GOL	O1-C1-C2-C3
3	B	803	GOL	O1-C1-C2-C3
3	D	804	GOL	C1-C2-C3-O3
3	B	803	GOL	C1-C2-C3-O3
3	D	804	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	802	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	587/612 (95%)	0.26	36 (6%) 27 22	33, 64, 136, 151	2 (0%)
1	B	594/612 (97%)	-0.15	5 (0%) 82 80	34, 53, 84, 104	2 (0%)
1	C	584/612 (95%)	-0.29	2 (0%) 90 88	23, 55, 79, 96	1 (0%)
1	D	589/612 (96%)	-0.41	4 (0%) 84 82	30, 43, 69, 97	1 (0%)
All	All	2354/2448 (96%)	-0.15	47 (1%) 65 60	23, 53, 106, 151	6 (0%)

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	373	LEU	4.5
1	A	428	GLY	3.7
1	A	187	LEU	3.6
1	A	146	ASN	3.4
1	A	201	LEU	3.2

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
2	GLC	K	1	11/12	0.47	0.14	116,128,135,136	0
2	GLC	K	2	11/12	0.63	0.11	125,132,137,139	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	K	4	11/12	0.66	0.12	103,115,120,123	0
2	GLC	F	2	11/12	0.68	0.10	99,104,106,107	0
2	GLC	K	3	11/12	0.69	0.13	124,128,134,134	0
2	GLC	I	5	11/12	0.74	0.11	87,95,102,104	0
2	GLC	G	2	11/12	0.78	0.11	90,97,100,101	0
2	GLC	J	4	11/12	0.78	0.10	87,95,99,100	0
2	GLC	I	3	11/12	0.78	0.11	84,94,98,103	0
2	GLC	F	3	11/12	0.79	0.12	86,90,98,100	0
2	GLC	I	4	11/12	0.79	0.11	95,100,104,106	0
2	GLC	E	2	11/12	0.79	0.12	76,91,95,98	0
2	GLC	H	5	11/12	0.79	0.10	81,85,88,89	0
2	GLC	F	1	11/12	0.80	0.10	91,99,105,113	0
2	GLC	G	1	11/12	0.80	0.10	85,92,101,102	0
2	GLC	E	4	11/12	0.81	0.11	85,94,101,102	0
2	GLC	J	5	11/12	0.81	0.10	93,98,100,102	0
2	GLC	E	3	11/12	0.81	0.11	74,84,89,91	0
2	GLC	K	6	11/12	0.81	0.13	88,102,118,126	0
2	GLC	L	4	11/12	0.81	0.10	76,82,87,87	0
2	GLC	G	3	11/12	0.82	0.10	93,100,103,107	0
2	GLC	G	4	11/12	0.82	0.10	82,87,92,93	0
2	GLC	G	6	11/12	0.82	0.12	60,80,87,89	0
2	GLC	M	5	11/12	0.82	0.09	77,81,89,90	0
2	GLC	J	3	11/12	0.83	0.09	87,90,96,100	0
2	GLC	L	2	11/12	0.83	0.10	82,92,98,102	0
2	GLC	E	6	11/12	0.84	0.09	85,95,102,103	0
2	GLC	L	5	11/12	0.84	0.11	73,82,86,89	0
2	GLC	E	5	11/12	0.84	0.09	94,96,99,101	0
2	GLC	J	6	11/12	0.85	0.09	87,94,99,101	0
2	GLC	I	6	11/12	0.85	0.09	81,89,98,101	0
2	GLC	F	6	11/12	0.86	0.11	78,87,98,99	0
2	GLC	I	1	11/12	0.86	0.10	86,91,93,95	0
2	GLC	K	5	11/12	0.86	0.10	87,99,103,115	0
2	GLC	E	1	11/12	0.86	0.10	84,90,99,104	0
2	GLC	L	1	11/12	0.87	0.10	65,80,90,98	0
2	GLC	F	4	11/12	0.88	0.11	67,77,85,89	0
2	GLC	J	2	11/12	0.89	0.08	69,73,81,84	0
2	GLC	F	5	11/12	0.89	0.10	69,74,85,86	0
2	GLC	H	1	11/12	0.89	0.07	71,77,81,85	0
2	GLC	J	1	11/12	0.89	0.10	65,73,82,84	0
2	GLC	H	6	11/12	0.90	0.08	75,79,84,84	0
2	GLC	H	4	11/12	0.90	0.09	71,77,86,87	0
2	GLC	M	4	11/12	0.90	0.07	61,68,72,80	0

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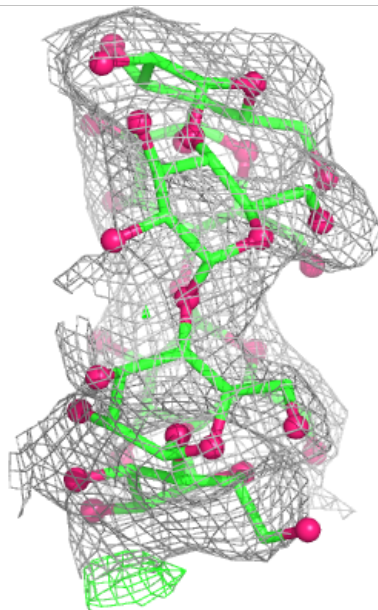
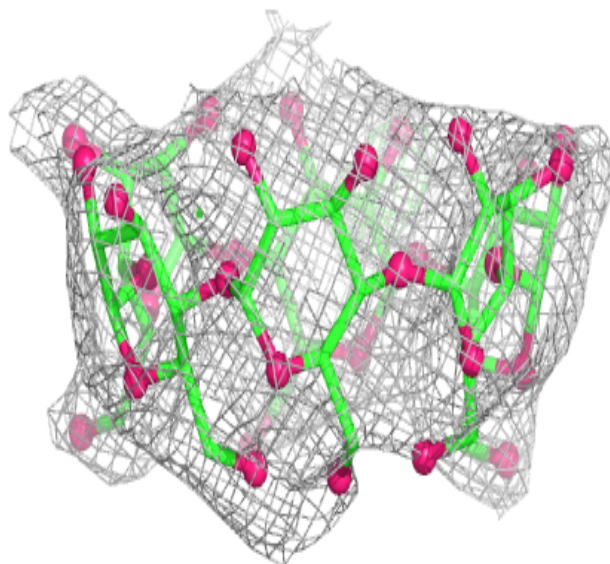
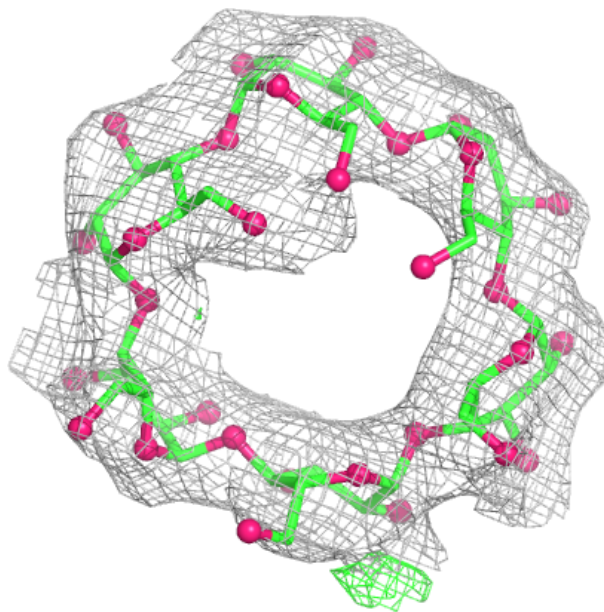
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	I	2	11/12	0.90	0.09	73,80,87,90	0
2	GLC	H	3	11/12	0.91	0.08	53,58,65,67	0
2	GLC	M	1	11/12	0.92	0.08	61,73,78,80	0
2	GLC	G	5	11/12	0.92	0.09	55,71,74,79	0
2	GLC	L	3	11/12	0.92	0.07	82,90,92,94	0
2	GLC	M	6	11/12	0.92	0.07	68,75,81,82	0
2	GLC	L	6	11/12	0.93	0.08	55,65,73,74	0
2	GLC	M	3	11/12	0.94	0.06	54,55,63,66	0
2	GLC	M	2	11/12	0.95	0.07	46,57,61,66	0
2	GLC	H	2	11/12	0.96	0.07	56,60,64,67	0

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

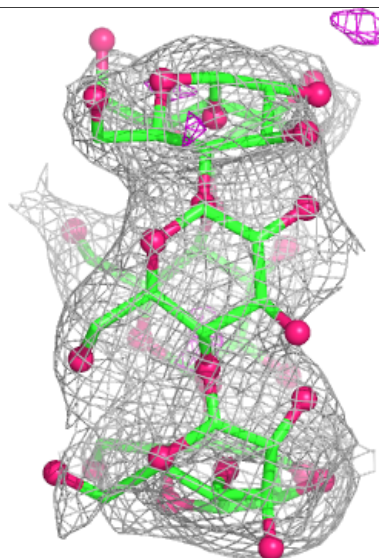
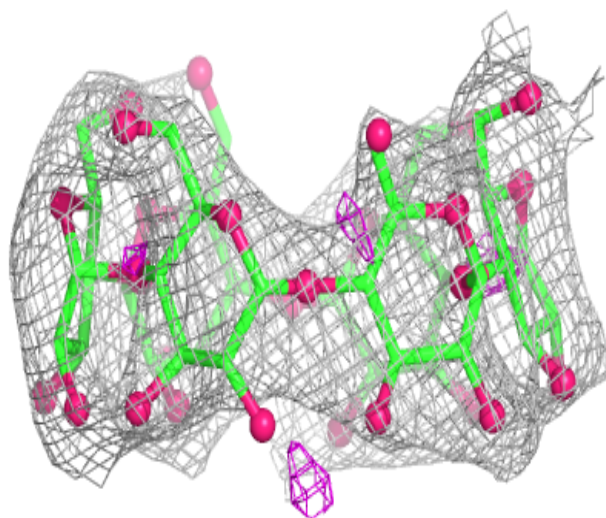
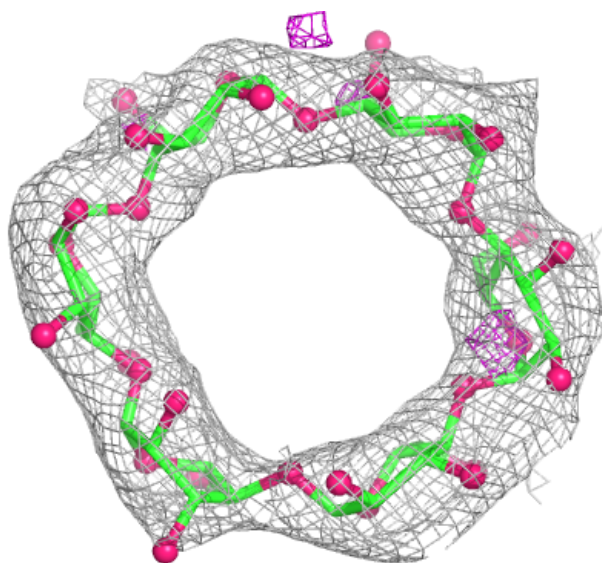
Electron density around Chain E:

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



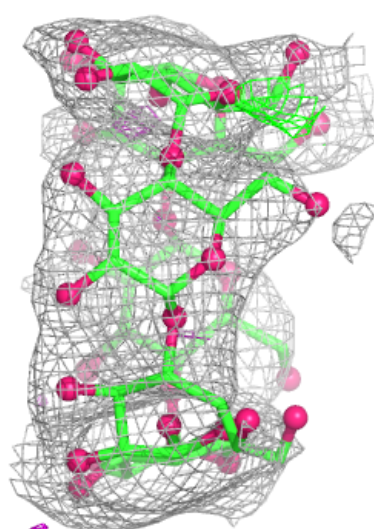
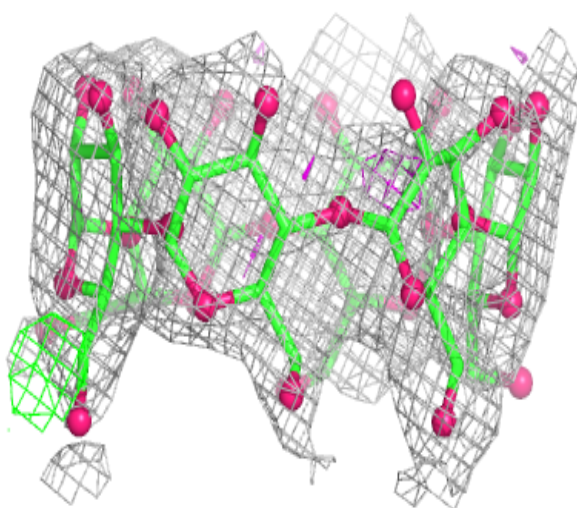
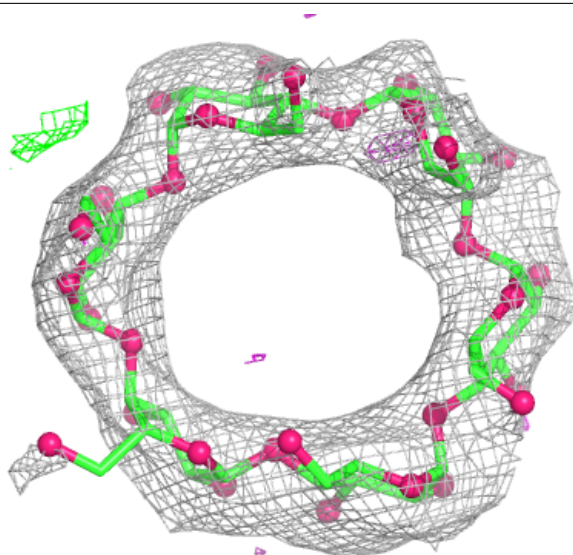
Electron density around Chain F:

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



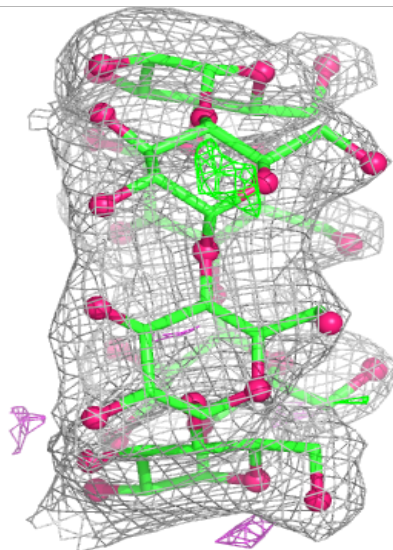
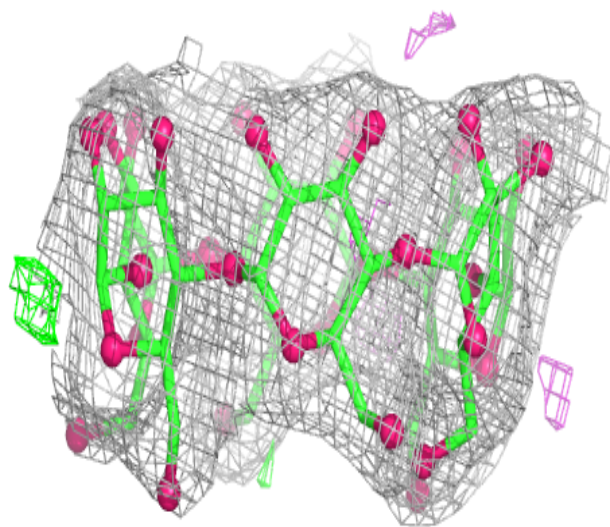
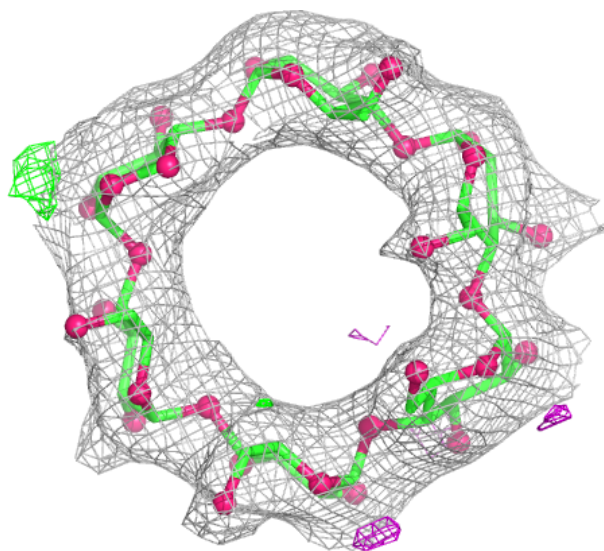
Electron density around Chain G:

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



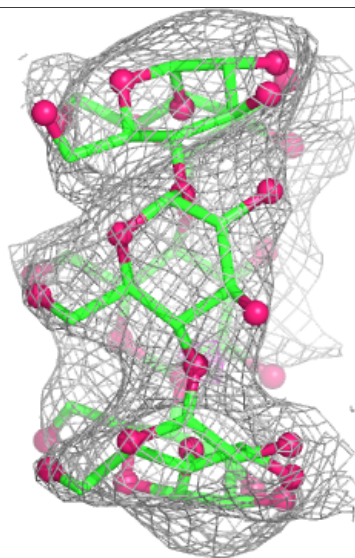
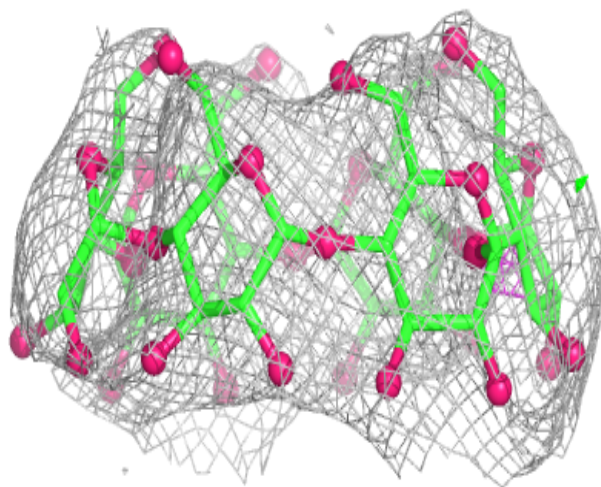
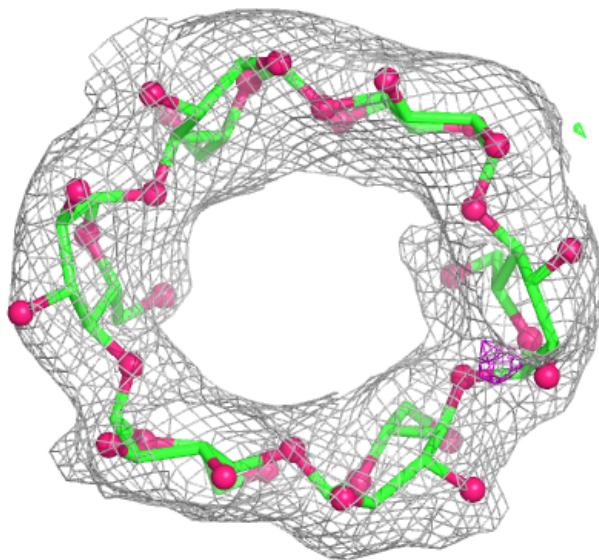
Electron density around Chain H:

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



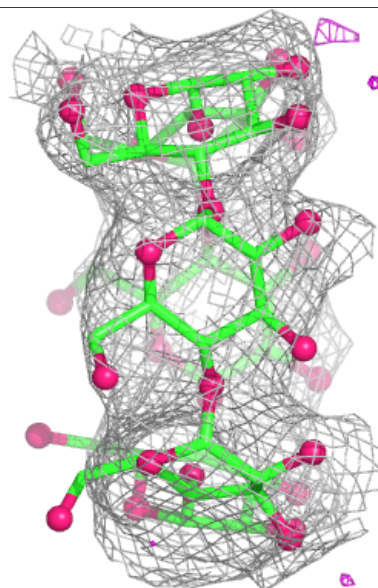
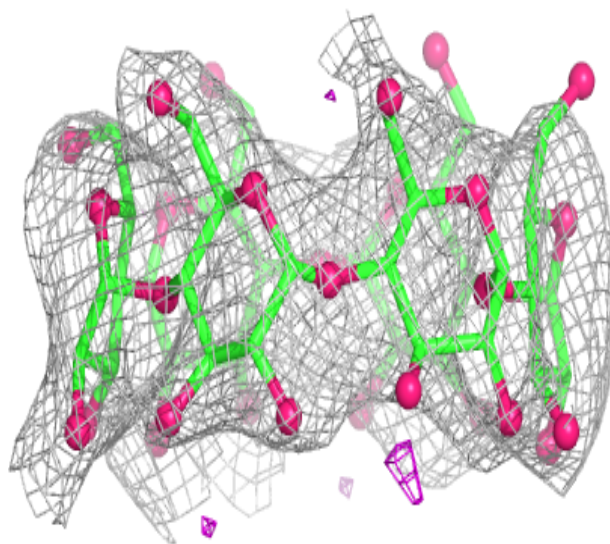
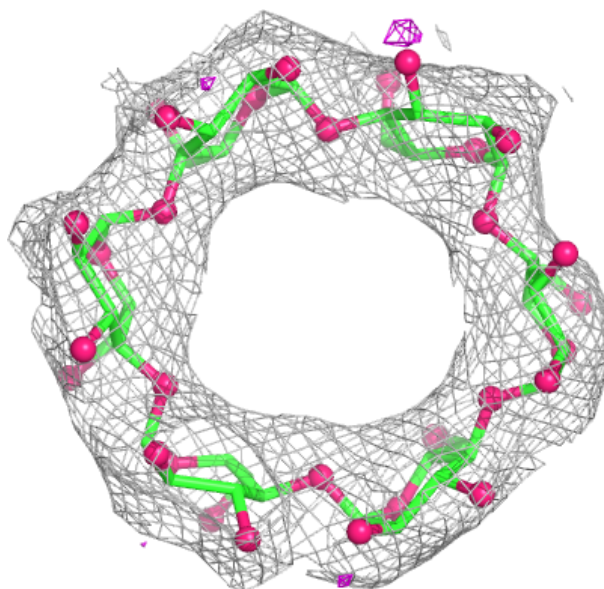
Electron density around Chain I:

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



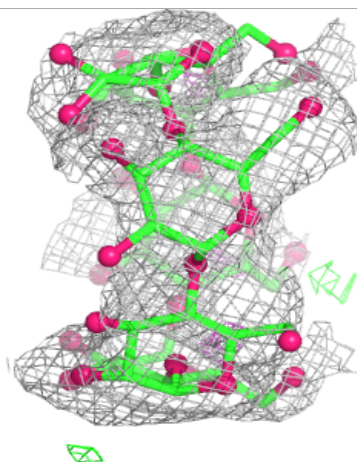
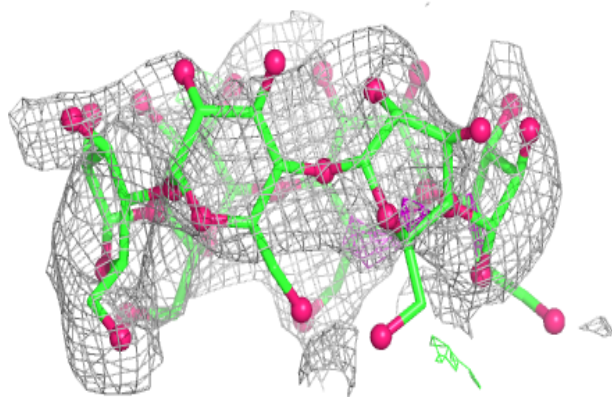
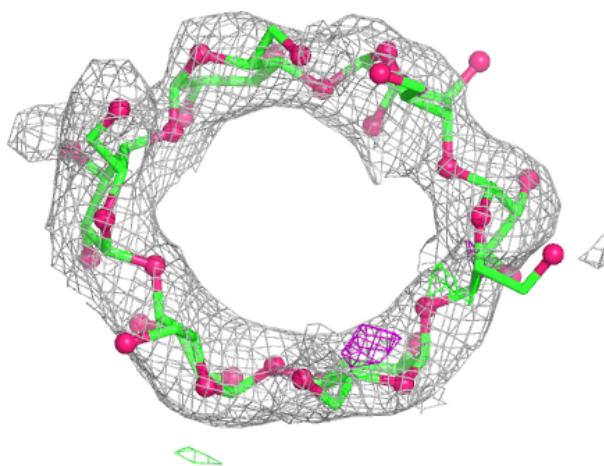
Electron density around Chain J:

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



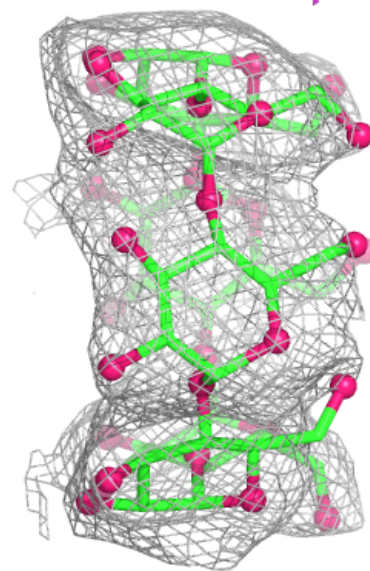
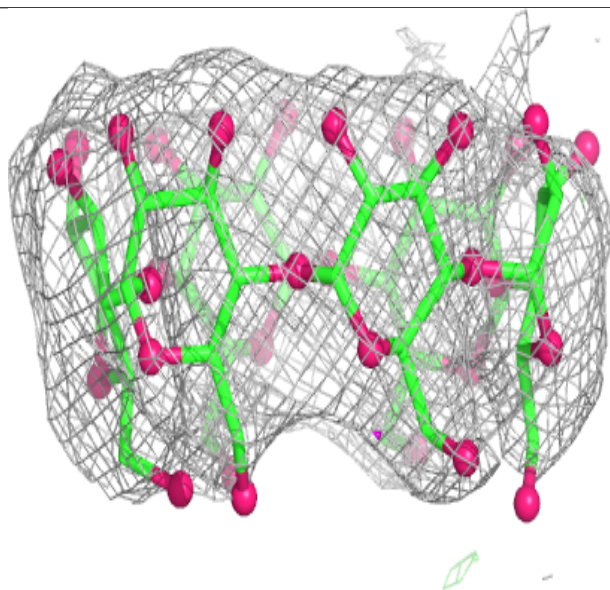
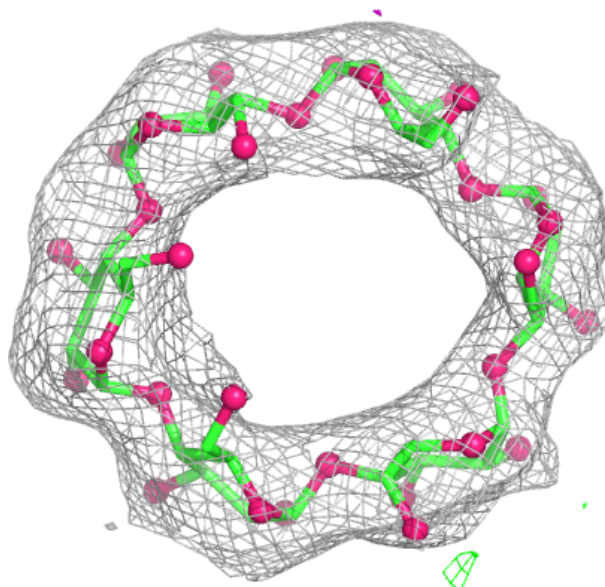
Electron density around Chain K:

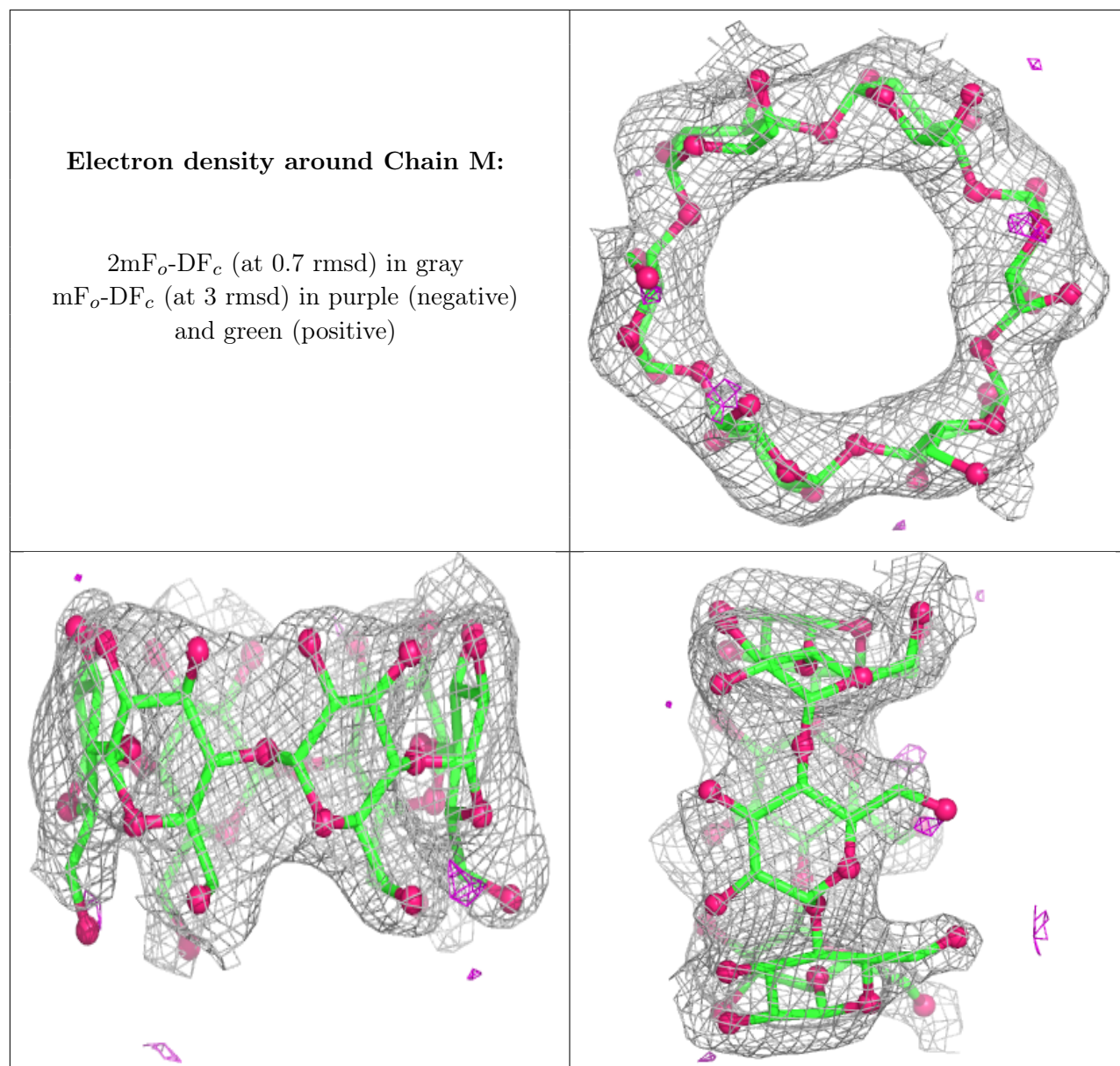
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain L:

$2mF_o-DF_c$ (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(Å ²)	Q<0.9
3	GOL	B	803	6/6	0.81	0.17	70,74,75,76	0
3	GOL	A	803	6/6	0.88	0.12	58,59,64,66	0
3	GOL	B	802	6/6	0.94	0.08	45,51,58,62	0
3	GOL	A	804	6/6	0.94	0.09	44,47,52,58	0
3	GOL	D	804	6/6	0.94	0.09	48,51,53,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.