



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 02:35 AM EDT

PDB ID : 8SDB / pdb\_00008sdb  
Title : Crystal Structure of E.Coli Branching Enzyme in complex with malto-octose  
Authors : Bingham, C.R.; Nayebi, H.; Fawaz, R.; Geiger, J.H.  
Deposited on : 2023-04-06  
Resolution : 3.00 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](mailto: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>.

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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)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
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

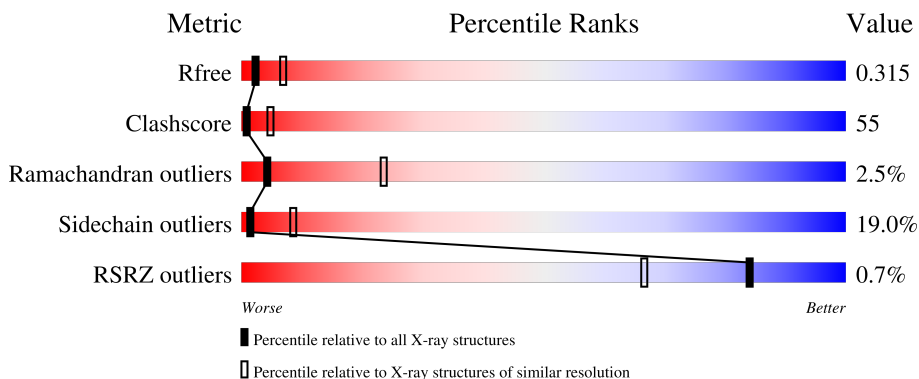
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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.







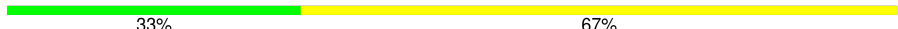
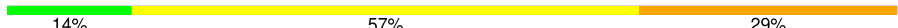

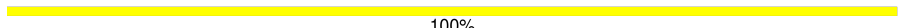

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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  $\geq 3$ , 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	613	
1	B	613	
1	C	613	
1	D	613	
2	E	5	

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Mol	Chain	Length	Quality of chain
2	F	5	 60% 40%
2	H	5	 40% 60%
3	G	4	 50% 50%
4	I	3	 67% 33%
4	M	3	 33% 67%
5	J	7	 14% 57% 29%
6	K	2	 100%
6	L	2	 100%
6	N	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GLC	J	5	-	-	X	-
5	GLC	J	6	-	-	X	-
6	GLC	L	1	-	-	X	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 19380 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
			Total	C	N	O	S			
1	A	600	Total 4938	C 3158	N 876	O 888	S 16	64	0	0
1	B	591	Total 4860	C 3108	N 862	O 874	S 16	43	0	0
1	C	604	Total 4972	C 3179	N 882	O 895	S 16	47	0	0
1	D	496	Total 4110	C 2636	N 722	O 741	S 11	128	0	0

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



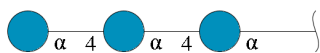
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
			Total	O			
2	E	5	56	30	12	0	0
2	F	5	56	30	12	0	0
2	H	5	56	30	9	0	0

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	G	4	Total	C	O	10	0	0
			45	24	21			

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	I	3	Total	C	O	2	0	0
			34	18	16			
4	M	3	Total	C	O	5	0	0
			34	18	16			

- Molecule 5 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



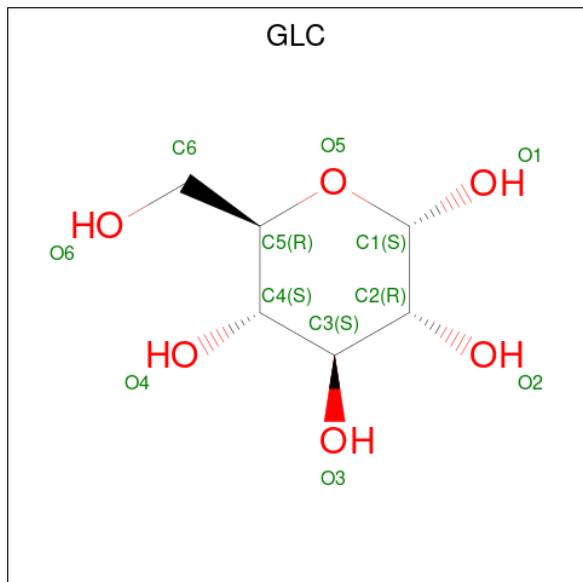
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
5	J	7	Total	C	O	16	0	0
			78	42	36			

- Molecule 6 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
6	K	2	Total	C	O	7	0	0
			23	12	11			
6	L	2	Total	C	O	4	0	0
			23	12	11			
6	N	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 7 is alpha-D-glucopyranose (CCD ID: GLC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).

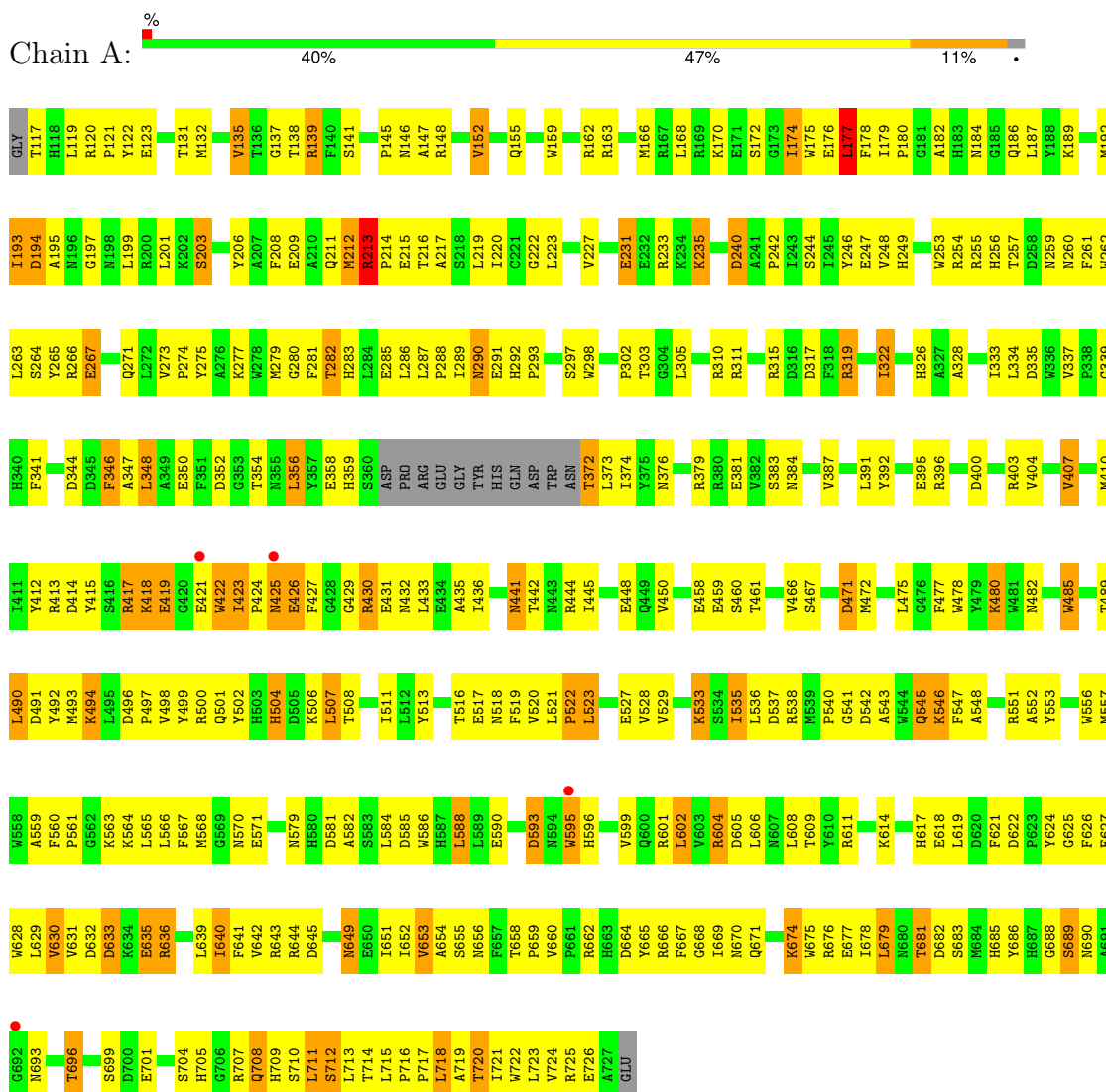


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 12 6 6	0	0
7	A	1	Total C O 12 6 6	1	0
7	A	1	Total C O 12 6 6	0	0
7	B	1	Total C O 12 6 6	1	0
7	B	1	Total C O 12 6 6	3	0
7	D	1	Total C O 12 6 6	0	0

### 3 Residue-property plots

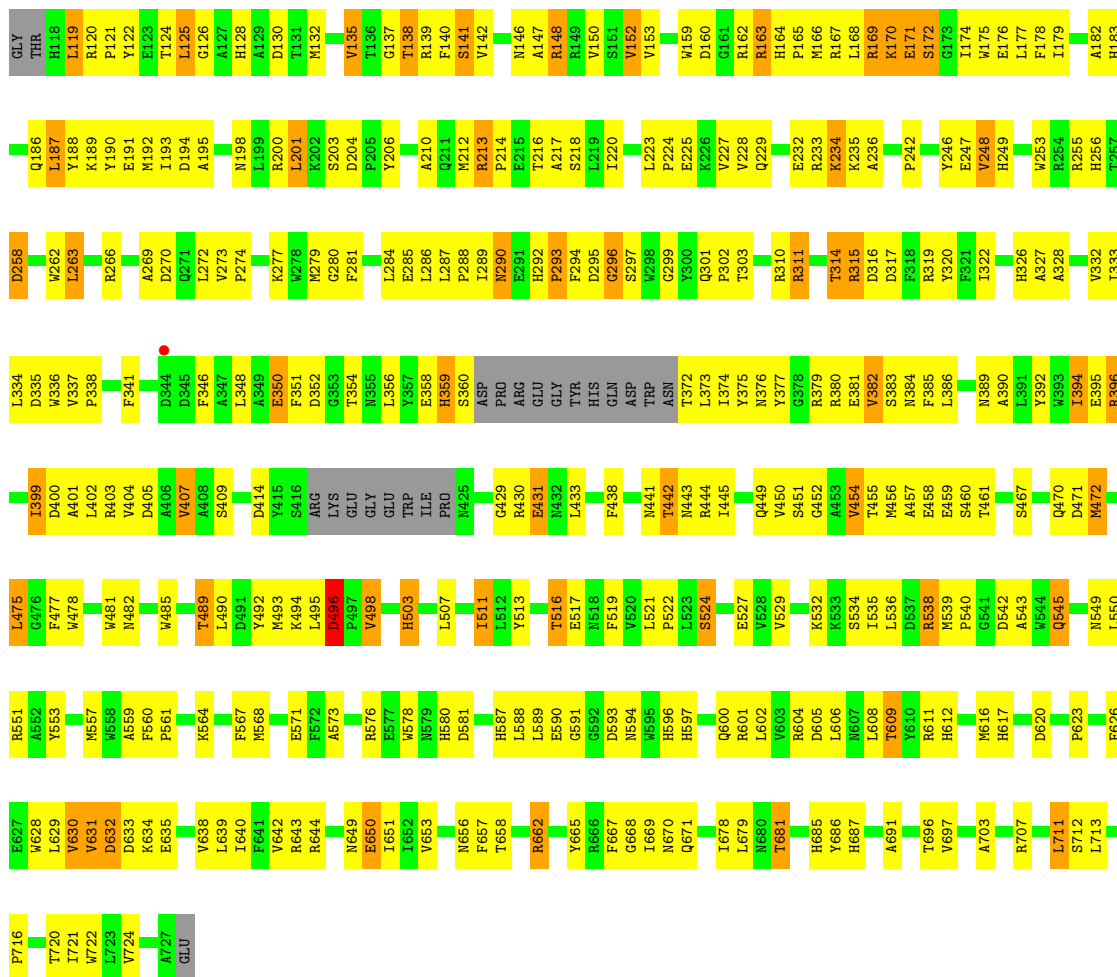
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

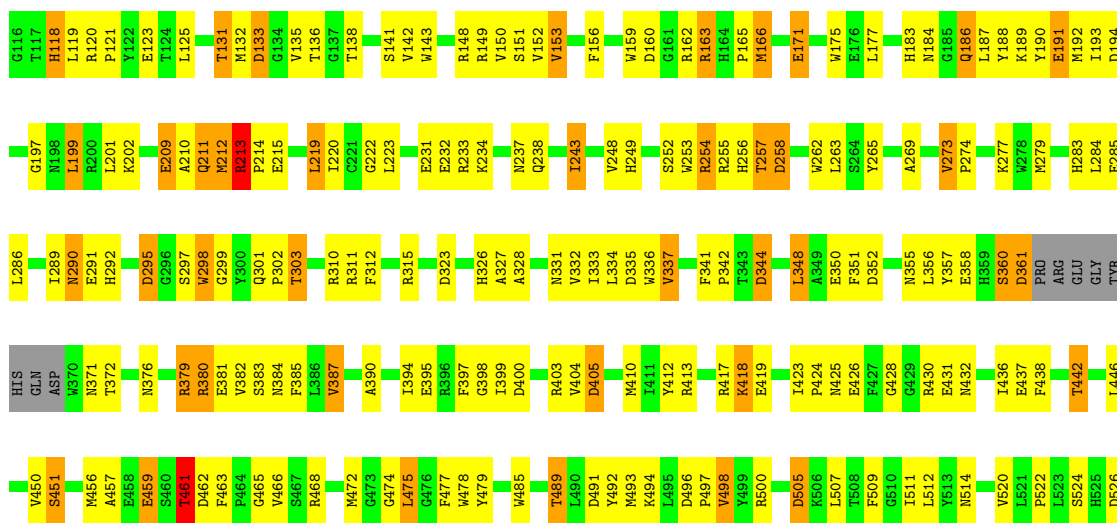


- Molecule 1: 1,4-alpha-glucan branching enzyme GlgB

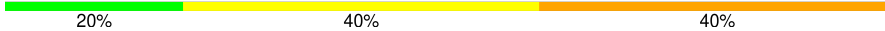




● Molecule 1: 1,4-alpha-glucan branching enzyme GlgB





Chain E:  20% 40% 40%



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

Chain F:  60% 40%



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

Chain H:  40% 60%



- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain G:  50% 50%

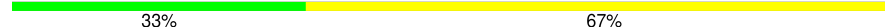


- Molecule 4: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain I:  67% 33%

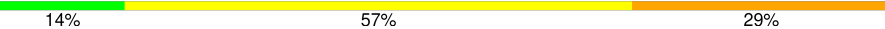


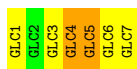
- Molecule 4: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain M:  33% 67%



- Molecule 5: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain J:  14% 57% 29%



- Molecule 6: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain K:  100%



- Molecule 6: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain L:  100%



- Molecule 6: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain N:  100%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.49Å 146.49Å 294.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.85 – 3.00 38.85 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.2 (38.85-3.00) 96.3 (38.85-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.214 , 0.315 0.217 , 0.315	Depositor DCC
$R_{free}$ test set	3623 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	82.5	Xtrriage
Anisotropy	0.006	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 66.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtrriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	19380	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GLC

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	0.64	0/5097	0.81	8/6923 (0.1%)
1	B	0.56	0/5015	0.75	2/6810 (0.0%)
1	C	0.54	0/5133	0.75	0/6973
1	D	0.58	2/4247 (0.0%)	0.91	18/5772 (0.3%)
All	All	0.58	2/19492 (0.0%)	0.80	28/26478 (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	B	0	1
1	D	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	261	PHE	CD2-CE2	-9.24	1.10	1.38
1	D	261	PHE	CB-CG	-8.50	1.31	1.50

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	341	PHE	CA-C-N	11.41	131.37	119.85
1	D	341	PHE	C-N-CA	11.41	131.37	119.85
1	D	253	TRP	CA-C-N	7.61	136.08	121.54
1	D	253	TRP	C-N-CA	7.61	136.08	121.54
1	A	422	TRP	N-CA-C	-7.29	95.26	110.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	359	HIS	Peptide
1	D	261	PHE	Sidechain
1	D	598	GLY	Peptide

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4938	0	4661	473	0
1	B	4860	0	4585	340	0
1	C	4972	0	4685	363	0
1	D	4110	0	3854	870	0
2	E	56	0	48	6	0
2	F	56	0	48	2	0
2	H	56	0	48	7	0
3	G	45	0	39	5	0
4	I	34	0	30	3	0
4	M	34	0	30	3	0
5	J	78	0	66	19	0
6	K	23	0	21	0	0
6	L	23	0	21	8	0
6	N	23	0	21	0	0
7	A	36	0	36	1	0
7	B	24	0	24	0	0
7	D	12	0	12	0	0
All	All	19380	0	18229	2045	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 55.

The worst 5 of 2045 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:D:343:THR:HG21	1:D:370:TRP:CZ2	1.41	1.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:309:THR:HG21	1:D:318:PHE:CE2	1.42	1.52
1:B:256:HIS:CD2	5:J:6:GLC:O3	1.82	1.33
1:A:666:ARG:HG3	1:A:710:SER:OG	1.16	1.31
1:D:308:PRO:O	1:D:309:THR:CG2	1.78	1.31

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	596/613 (97%)	554 (93%)	32 (5%)	10 (2%)	7	32
1	B	585/613 (95%)	543 (93%)	35 (6%)	7 (1%)	10	40
1	C	600/613 (98%)	553 (92%)	41 (7%)	6 (1%)	12	45
1	D	492/613 (80%)	388 (79%)	70 (14%)	34 (7%)	1	5
All	All	2273/2452 (93%)	2038 (90%)	178 (8%)	57 (2%)	4	23

5 of 57 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	ARG
1	A	543	ALA
1	A	630	VAL
1	C	213	ARG
1	C	522	PRO

### 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	510/521 (98%)	422 (83%)	88 (17%)	2	10
1	B	502/521 (96%)	424 (84%)	78 (16%)	2	13
1	C	513/521 (98%)	431 (84%)	82 (16%)	2	12
1	D	426/521 (82%)	303 (71%)	123 (29%)	0	2
All	All	1951/2084 (94%)	1580 (81%)	371 (19%)	1	8

5 of 371 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	647	GLU
1	D	359	HIS
1	C	676	ARG
1	D	265	TYR
1	D	416	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	545	GLN
1	D	384	ASN
1	C	570	ASN
1	C	690	ASN
1	D	597	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](#)

38 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	12,12,12	0.47	0	17,17,17	0.52	0
2	GLC	E	2	2	11,11,12	0.26	0	15,15,17	0.54	0
2	GLC	E	3	2	11,11,12	0.50	0	15,15,17	1.78	2 (13%)
2	GLC	E	4	2	11,11,12	0.85	1 (9%)	15,15,17	1.82	2 (13%)
2	GLC	E	5	2	11,11,12	0.27	0	15,15,17	0.53	0
2	GLC	F	1	2	12,12,12	0.46	0	17,17,17	0.52	0
2	GLC	F	2	2	11,11,12	0.27	0	15,15,17	0.51	0
2	GLC	F	3	2	11,11,12	0.27	0	15,15,17	0.55	0
2	GLC	F	4	2	11,11,12	0.27	0	15,15,17	0.56	0
2	GLC	F	5	2	11,11,12	0.24	0	15,15,17	0.52	0
3	GLC	G	1	3	12,12,12	0.46	0	17,17,17	0.52	0
3	GLC	G	2	3	11,11,12	0.24	0	15,15,17	0.53	0
3	GLC	G	3	3	11,11,12	0.27	0	15,15,17	0.52	0
3	GLC	G	4	3	11,11,12	0.26	0	15,15,17	0.51	0
2	GLC	H	1	2	12,12,12	0.46	0	17,17,17	0.53	0
2	GLC	H	2	2	11,11,12	0.26	0	15,15,17	0.56	0
2	GLC	H	3	2	11,11,12	0.25	0	15,15,17	0.54	0
2	GLC	H	4	2	11,11,12	0.26	0	15,15,17	0.57	0
2	GLC	H	5	2	11,11,12	0.27	0	15,15,17	0.52	0
4	GLC	I	1	4	12,12,12	0.52	0	17,17,17	0.69	0
4	GLC	I	2	4	11,11,12	0.28	0	15,15,17	0.61	0
4	GLC	I	3	4	11,11,12	0.26	0	15,15,17	0.53	0
5	GLC	J	1	5	12,12,12	0.46	0	17,17,17	0.53	0
5	GLC	J	2	5	11,11,12	0.27	0	15,15,17	0.56	0
5	GLC	J	3	5	11,11,12	0.29	0	15,15,17	0.82	1 (6%)
5	GLC	J	4	5	11,11,12	0.51	0	15,15,17	1.74	3 (20%)
5	GLC	J	5	5	11,11,12	0.71	0	15,15,17	2.02	3 (20%)
5	GLC	J	6	5	11,11,12	0.26	0	15,15,17	0.55	0
5	GLC	J	7	5	11,11,12	0.25	0	15,15,17	0.51	0
6	GLC	K	1	6	12,12,12	0.46	0	17,17,17	0.51	0
6	GLC	K	2	6	11,11,12	0.26	0	15,15,17	0.52	0
6	GLC	L	1	6	12,12,12	0.46	0	17,17,17	0.52	0
6	GLC	L	2	6	11,11,12	0.26	0	15,15,17	0.51	0
4	GLC	M	1	4	12,12,12	0.46	0	17,17,17	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GLC	M	2	4	11,11,12	0.25	0	15,15,17	0.51	0
4	GLC	M	3	4	11,11,12	0.26	0	15,15,17	0.51	0
6	GLC	N	1	6	12,12,12	0.46	0	17,17,17	0.52	0
6	GLC	N	2	6	11,11,12	0.28	0	15,15,17	0.53	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	E	1	2	-	0/2/22/22	0/1/1/1
2	GLC	E	2	2	-	2/2/19/22	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	-	0/2/19/22	0/1/1/1
2	GLC	F	1	2	-	1/2/22/22	0/1/1/1
2	GLC	F	2	2	-	0/2/19/22	0/1/1/1
2	GLC	F	3	2	-	0/2/19/22	0/1/1/1
2	GLC	F	4	2	-	0/2/19/22	0/1/1/1
2	GLC	F	5	2	-	2/2/19/22	0/1/1/1
3	GLC	G	1	3	-	0/2/22/22	0/1/1/1
3	GLC	G	2	3	-	2/2/19/22	0/1/1/1
3	GLC	G	3	3	-	0/2/19/22	0/1/1/1
3	GLC	G	4	3	-	2/2/19/22	0/1/1/1
2	GLC	H	1	2	-	2/2/22/22	0/1/1/1
2	GLC	H	2	2	-	2/2/19/22	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	-	2/2/19/22	0/1/1/1
4	GLC	I	1	4	-	0/2/22/22	0/1/1/1
4	GLC	I	2	4	-	1/2/19/22	0/1/1/1
4	GLC	I	3	4	-	2/2/19/22	0/1/1/1
5	GLC	J	1	5	-	1/2/22/22	0/1/1/1
5	GLC	J	2	5	-	0/2/19/22	0/1/1/1
5	GLC	J	3	5	-	0/2/19/22	0/1/1/1
5	GLC	J	4	5	-	2/2/19/22	0/1/1/1
5	GLC	J	5	5	-	0/2/19/22	0/1/1/1
5	GLC	J	6	5	-	0/2/19/22	0/1/1/1
5	GLC	J	7	5	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GLC	K	1	6	-	0/2/22/22	0/1/1/1
6	GLC	K	2	6	-	2/2/19/22	0/1/1/1
6	GLC	L	1	6	-	2/2/22/22	0/1/1/1
6	GLC	L	2	6	-	2/2/19/22	0/1/1/1
4	GLC	M	1	4	-	2/2/22/22	0/1/1/1
4	GLC	M	2	4	-	2/2/19/22	0/1/1/1
4	GLC	M	3	4	-	2/2/19/22	0/1/1/1
6	GLC	N	1	6	-	1/2/22/22	0/1/1/1
6	GLC	N	2	6	-	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)
2	E	4	GLC	O5-C1	2.26	1.47	1.43

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	5	GLC	C1-C2-C3	5.10	117.08	109.64
2	E	3	GLC	C1-C2-C3	4.85	116.70	109.64
2	E	4	GLC	C1-C2-C3	4.80	116.63	109.64
2	E	3	GLC	C1-O5-C5	4.44	118.14	112.19
5	J	5	GLC	C1-O5-C5	4.42	118.11	112.19

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	GLC	O5-C5-C6-O6
2	E	4	GLC	C4-C5-C6-O6
6	L	2	GLC	O5-C5-C6-O6
2	H	1	GLC	O5-C5-C6-O6
6	K	2	GLC	O5-C5-C6-O6

There are no ring outliers.

21 monomers are involved in 53 short contacts:

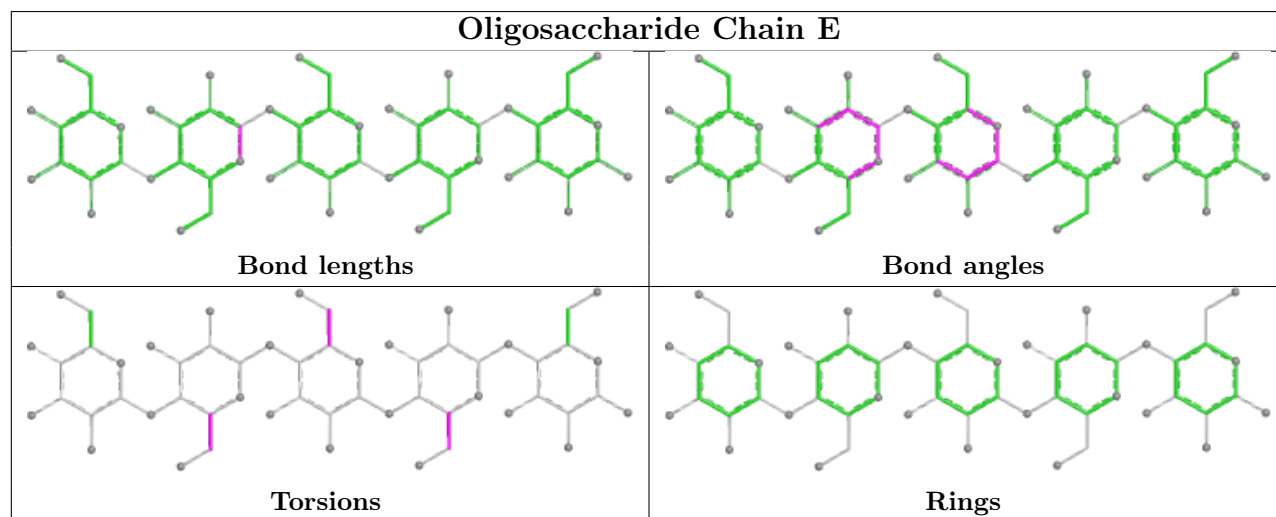
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	L	1	GLC	7	0

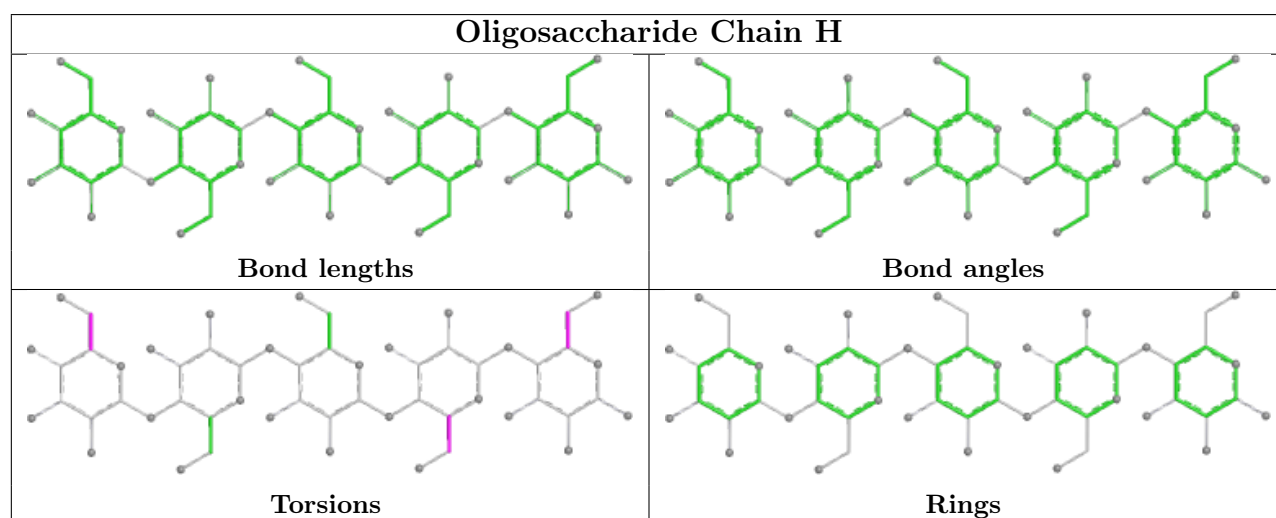
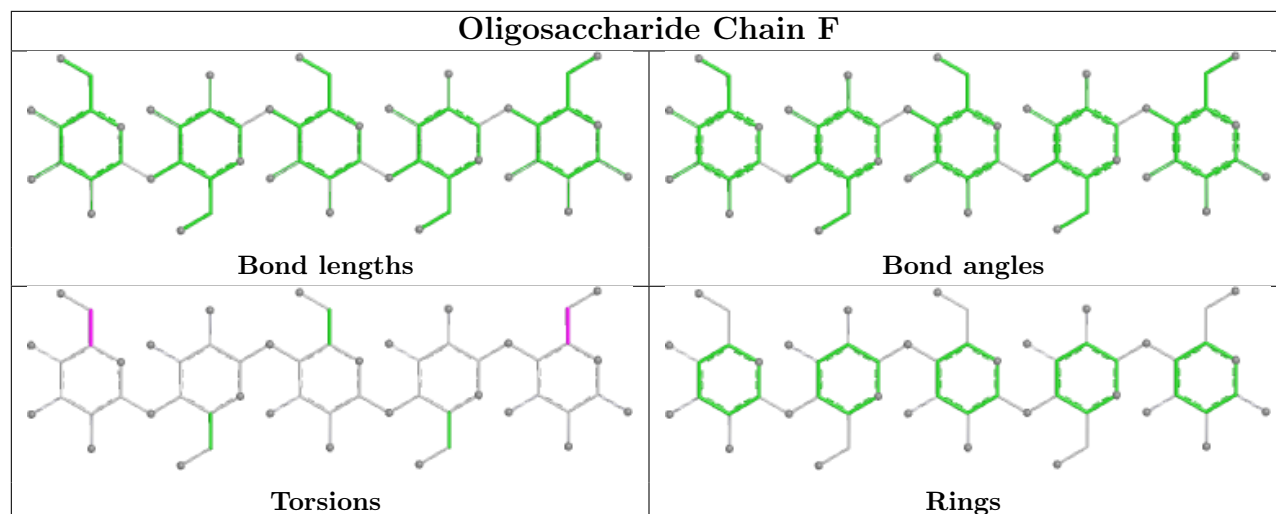
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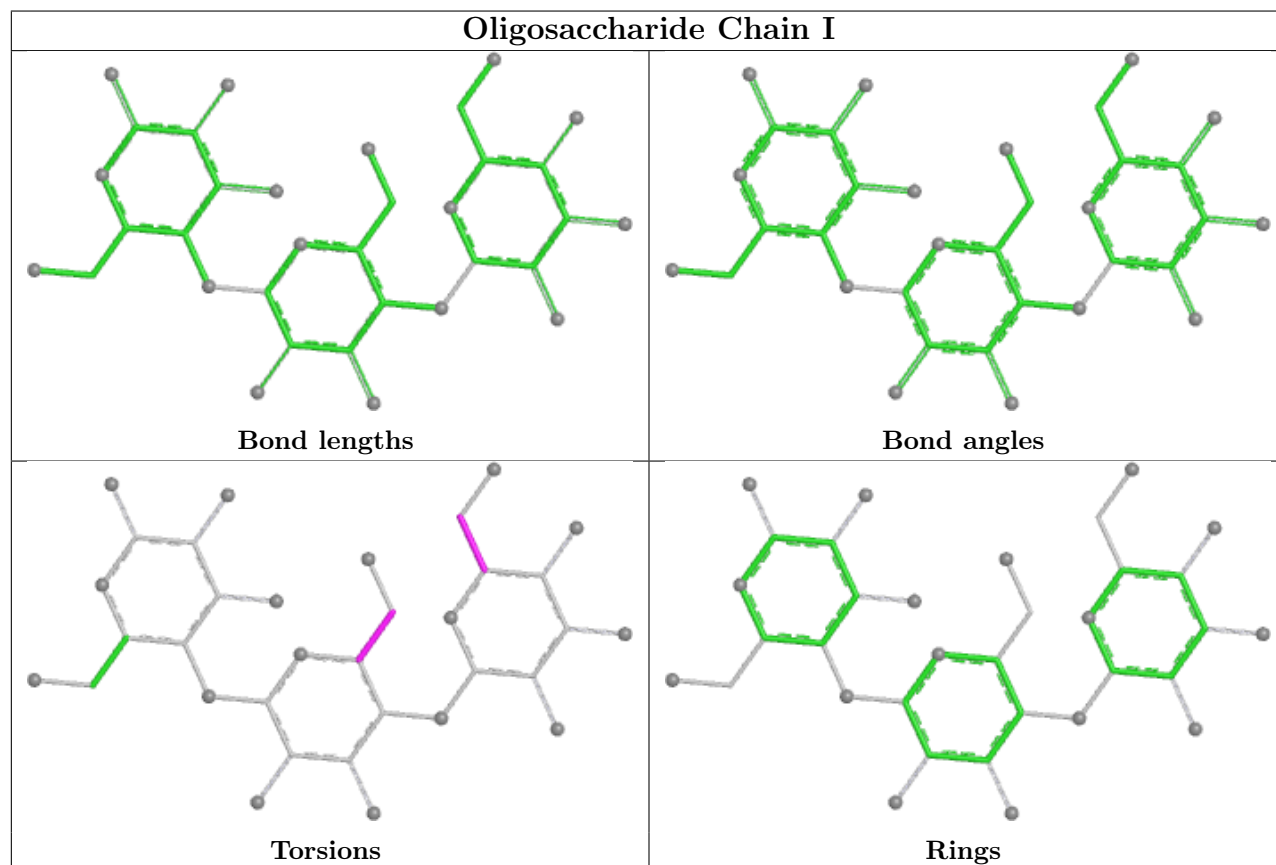
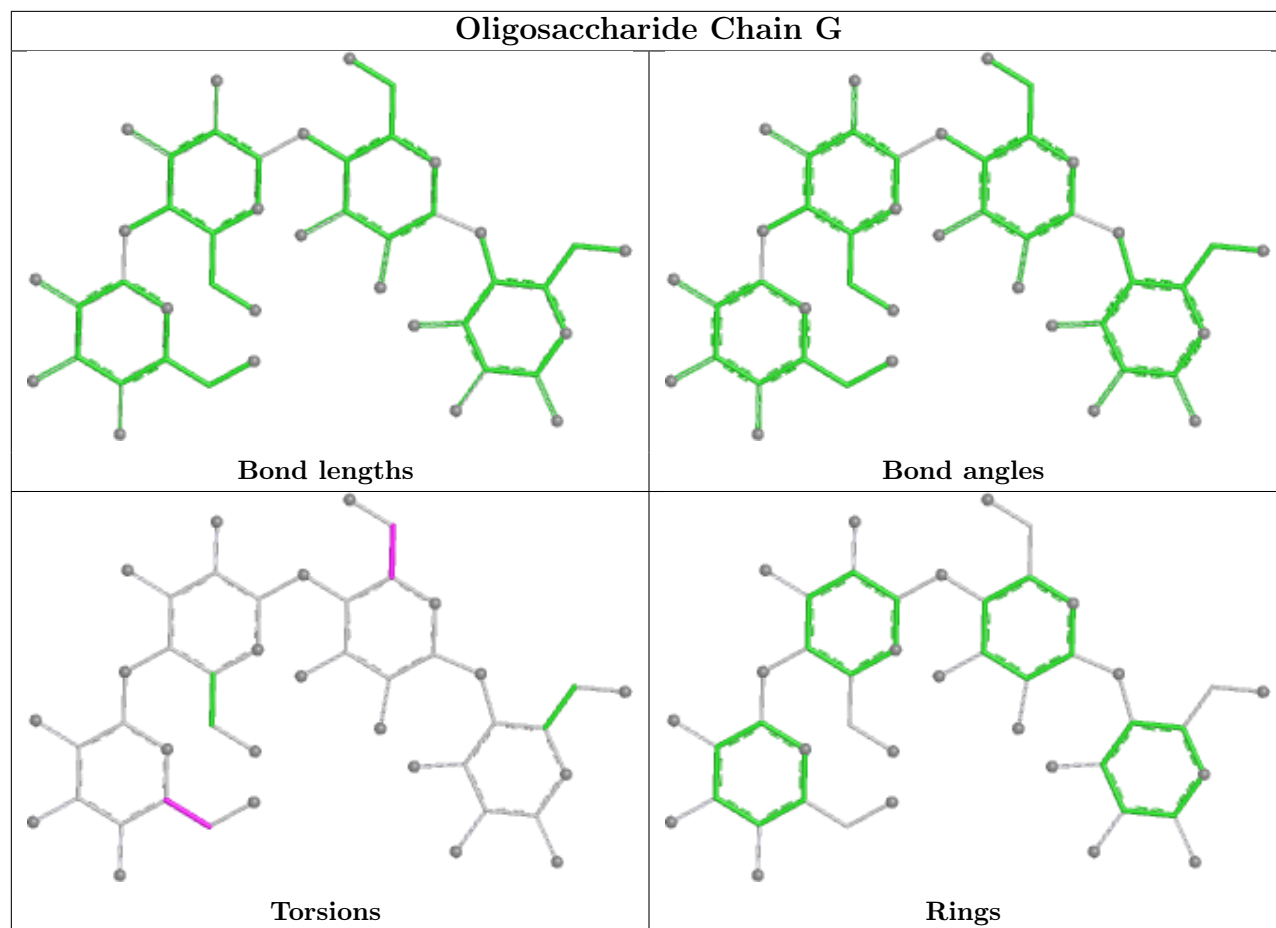
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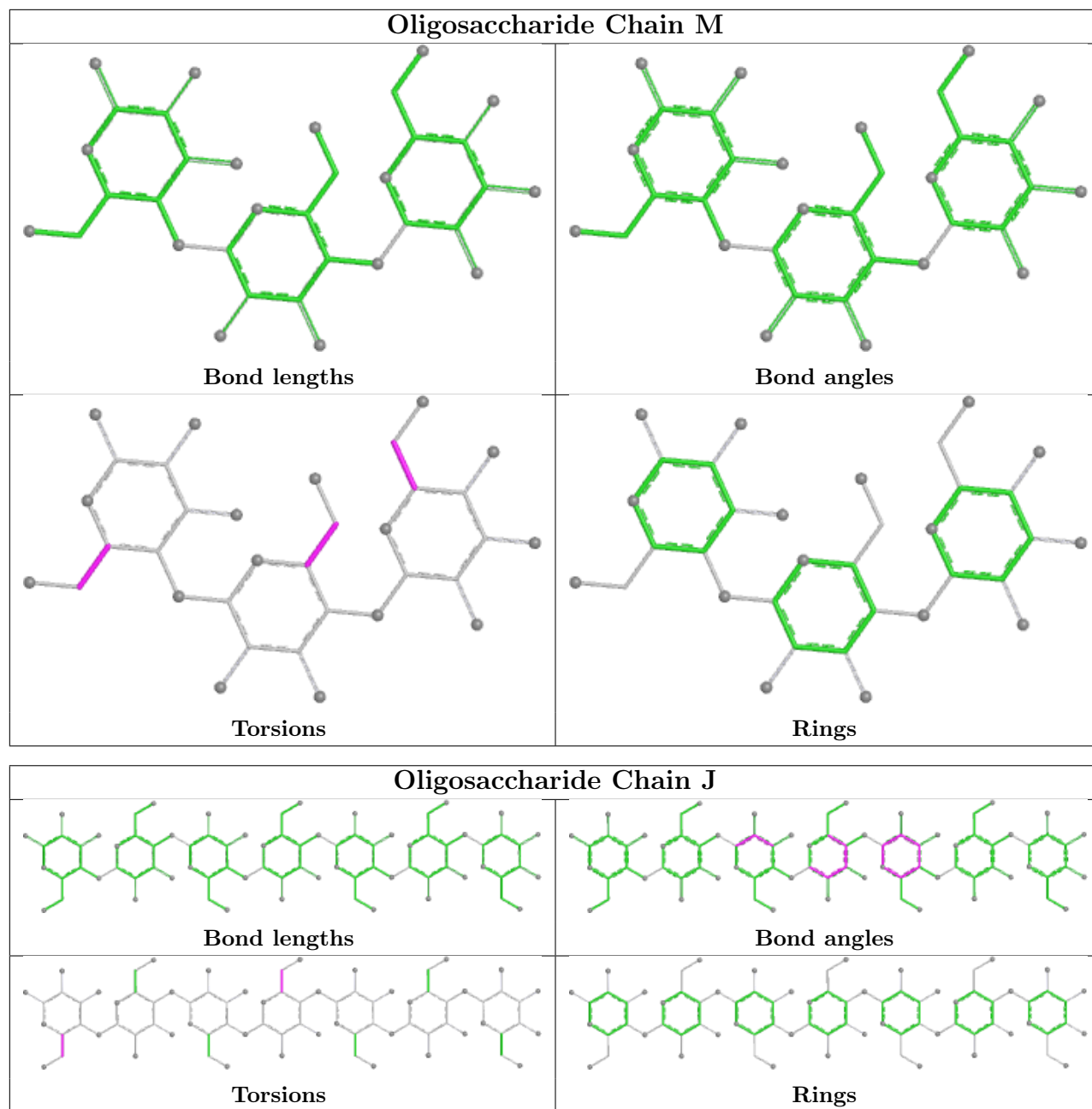
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	4	GLC	4	0
6	L	2	GLC	1	0
2	H	4	GLC	1	0
5	J	7	GLC	1	0
3	G	3	GLC	3	0
4	I	1	GLC	3	0
2	F	4	GLC	2	0
5	J	5	GLC	7	0
4	M	2	GLC	1	0
5	J	4	GLC	1	0
5	J	6	GLC	16	0
2	E	3	GLC	5	0
4	M	3	GLC	2	0
3	G	4	GLC	2	0
2	H	3	GLC	4	0
5	J	1	GLC	1	0
2	E	5	GLC	1	0
2	E	2	GLC	2	0
2	F	3	GLC	1	0
2	H	2	GLC	2	0

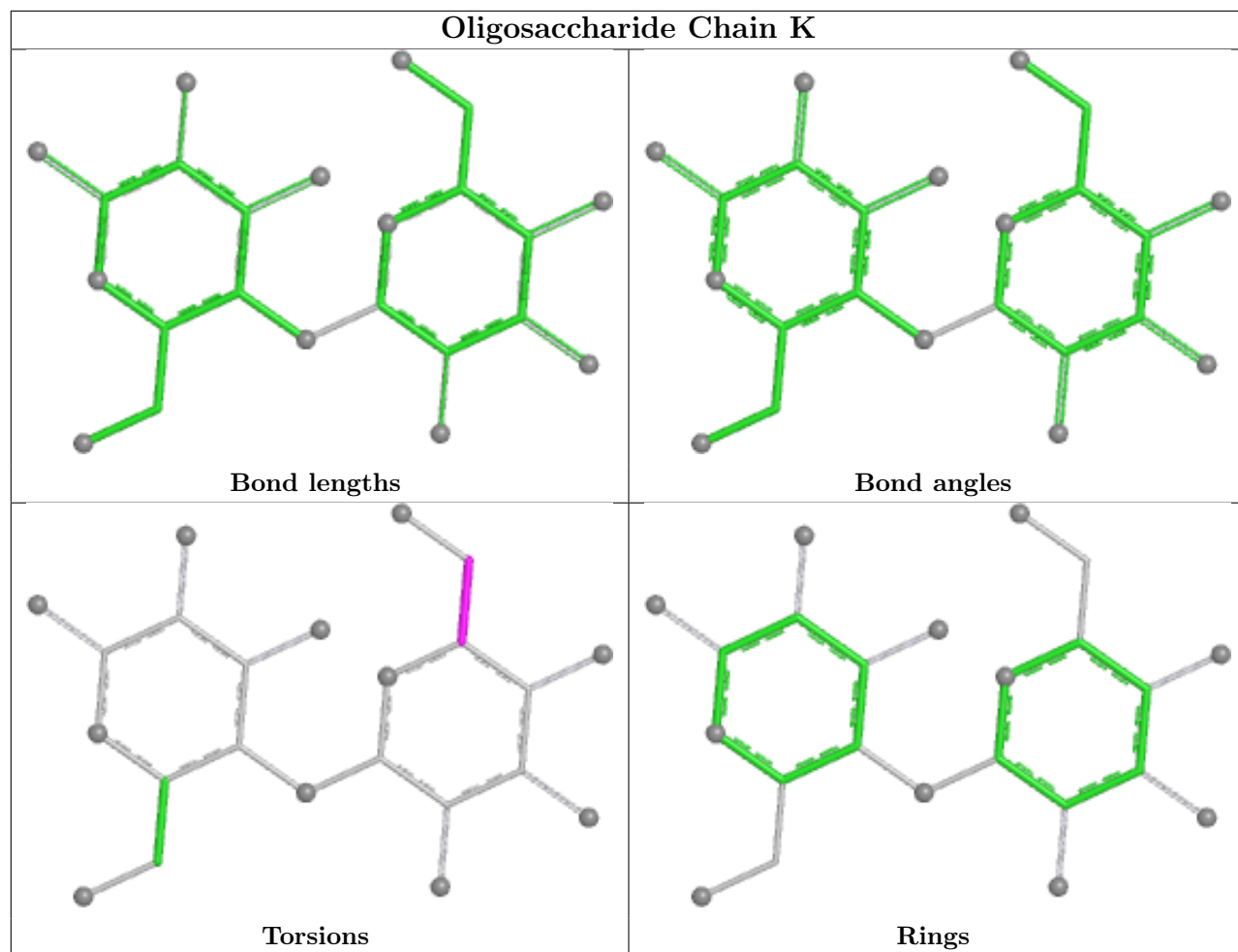
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

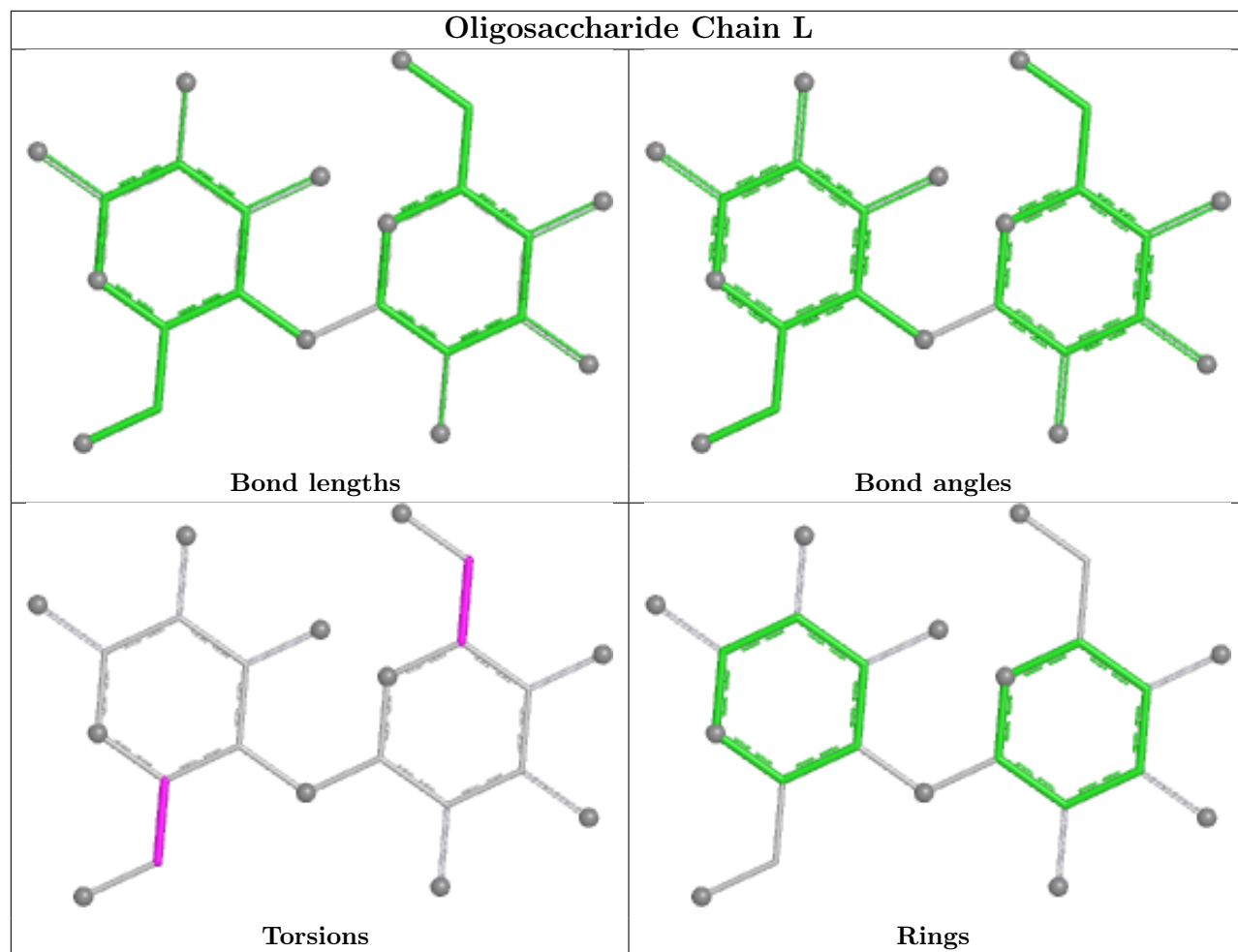


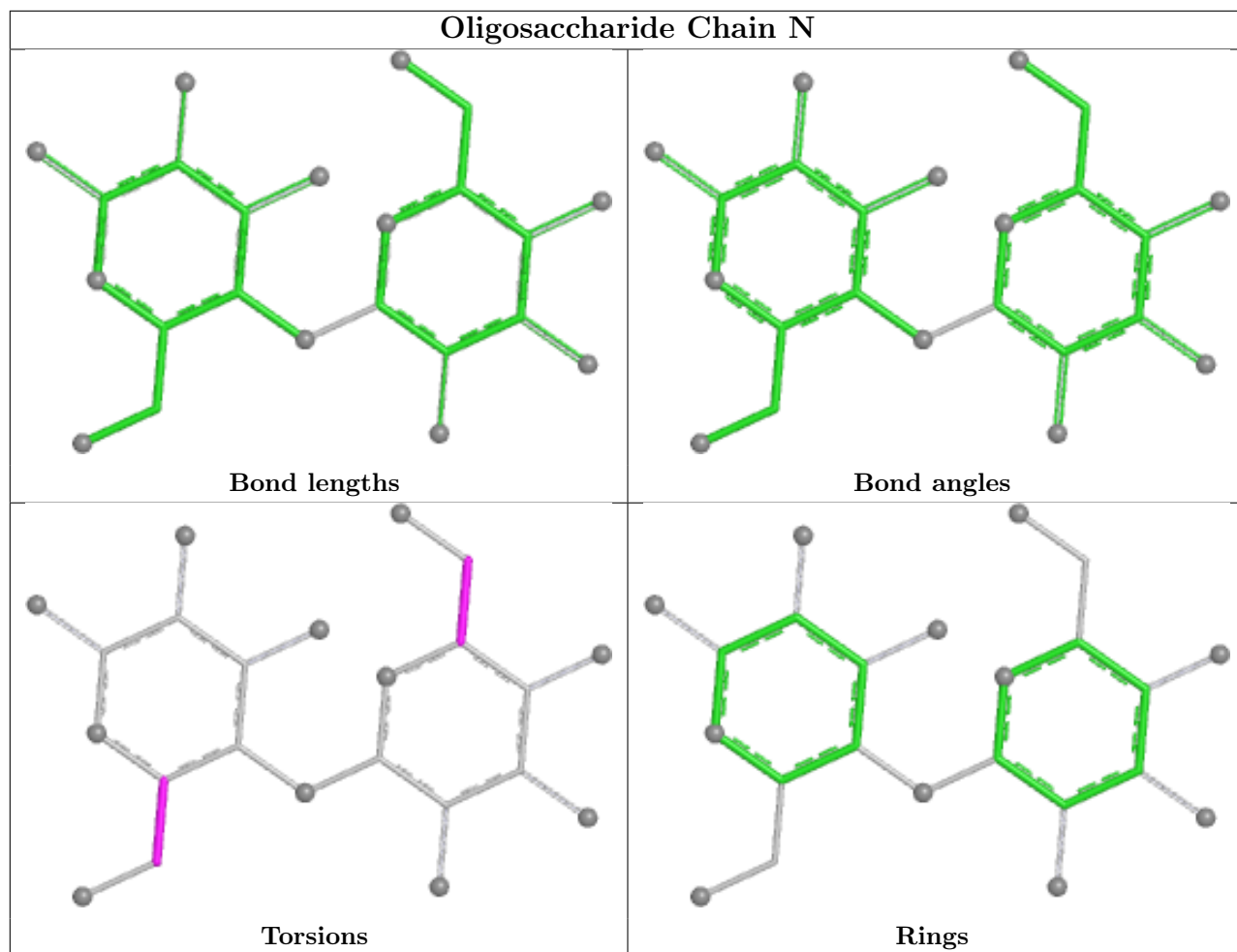












## 5.6 Ligand geometry [i](#)

6 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	$\# Z  > 2$
7	GLC	A	802	-	12,12,12	0.46	0	17,17,17	0.52	0
7	GLC	B	802	-	12,12,12	0.46	0	17,17,17	0.53	0
7	GLC	D	801	-	12,12,12	0.49	0	17,17,17	0.62	0
7	GLC	B	801	-	12,12,12	0.45	0	17,17,17	0.52	0
7	GLC	A	801	-	12,12,12	0.46	0	17,17,17	0.52	0
7	GLC	A	803	-	12,12,12	0.46	0	17,17,17	0.52	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
7	GLC	A	802	-	-	1/2/22/22	0/1/1/1
7	GLC	B	802	-	-	0/2/22/22	0/1/1/1
7	GLC	D	801	-	-	0/2/22/22	0/1/1/1
7	GLC	B	801	-	-	1/2/22/22	0/1/1/1
7	GLC	A	801	-	-	2/2/22/22	0/1/1/1
7	GLC	A	803	-	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

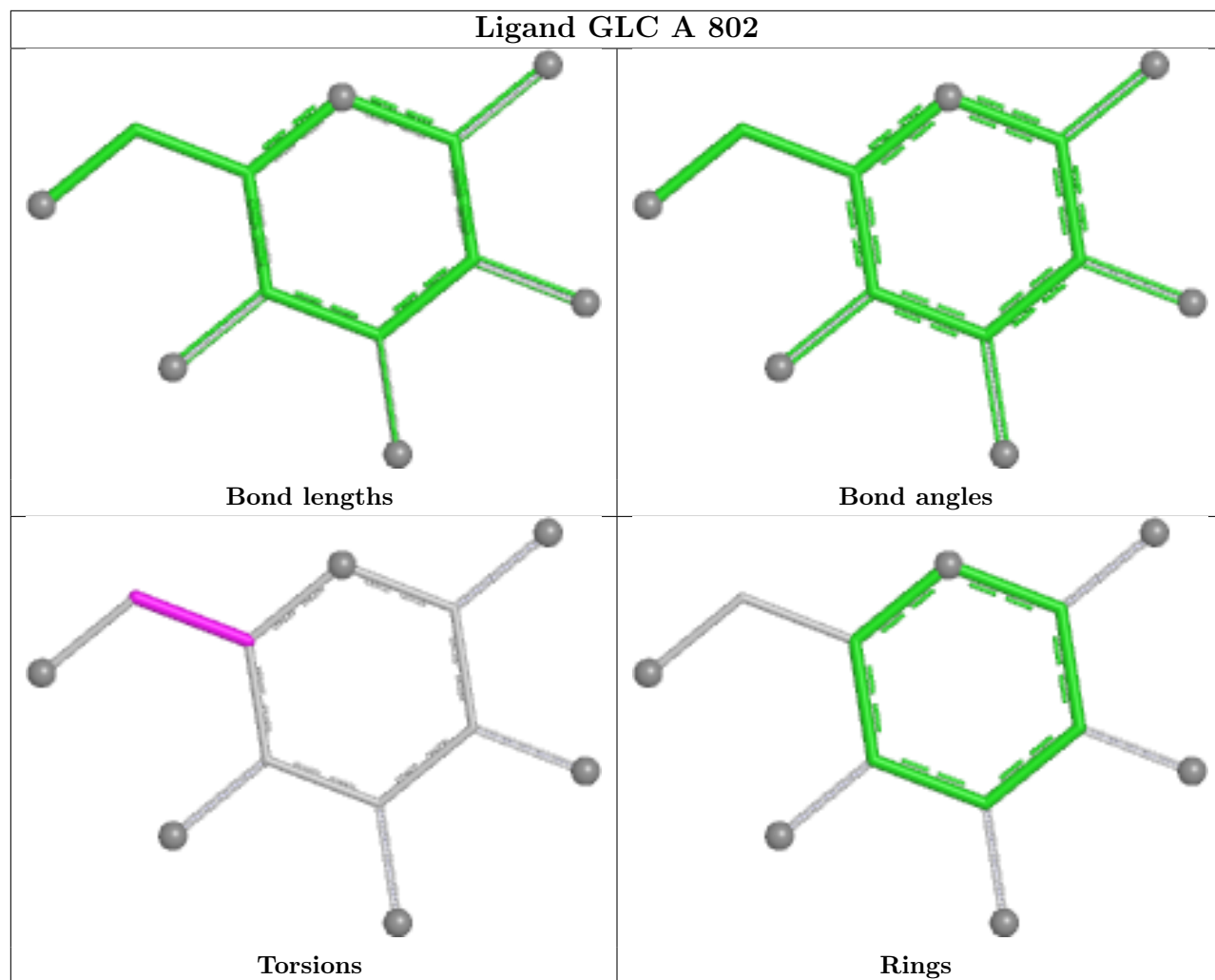
Mol	Chain	Res	Type	Atoms
7	A	801	GLC	C4-C5-C6-O6
7	A	801	GLC	O5-C5-C6-O6
7	B	801	GLC	O5-C5-C6-O6
7	A	802	GLC	C4-C5-C6-O6

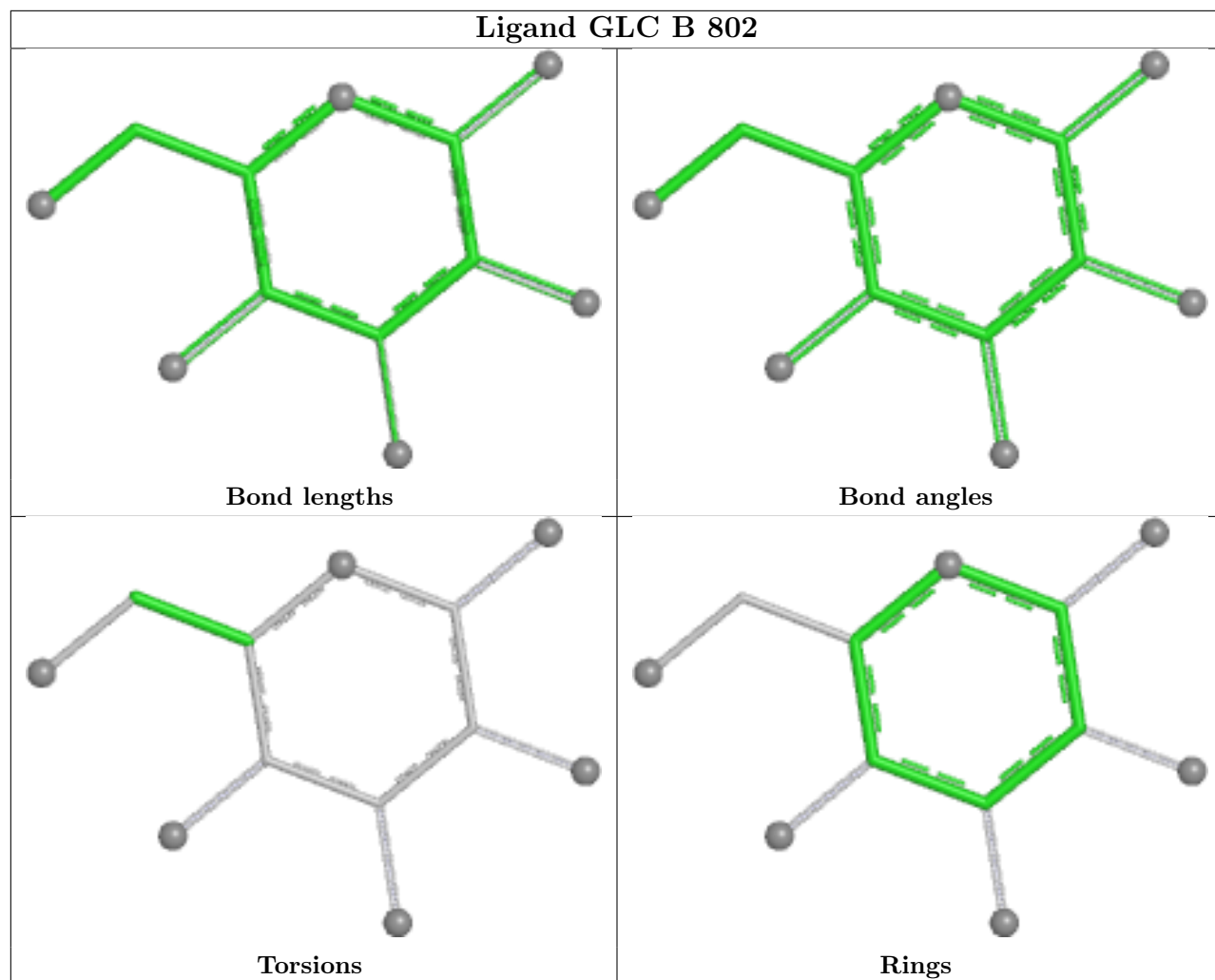
There are no ring outliers.

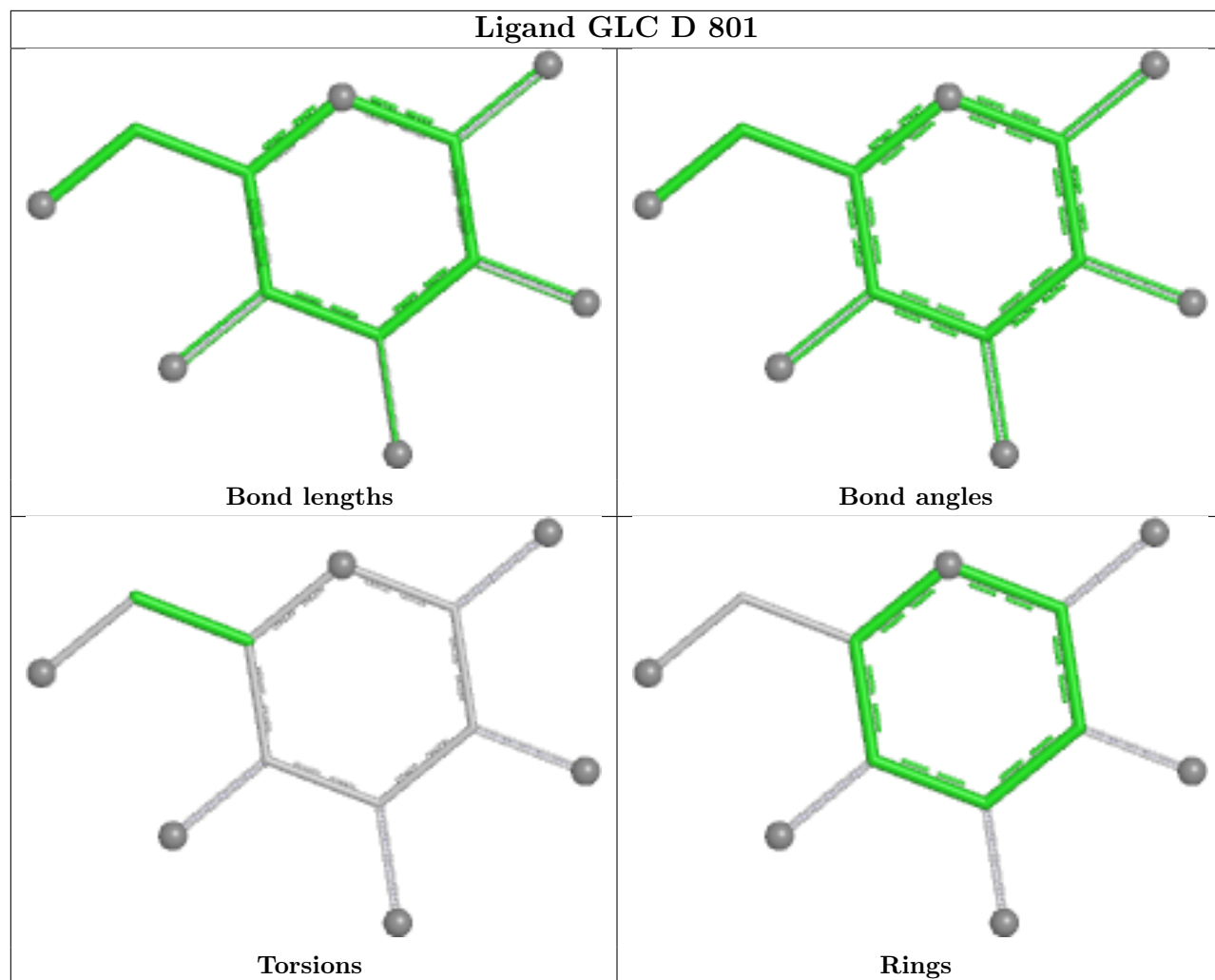
1 monomer is involved in 1 short contact:

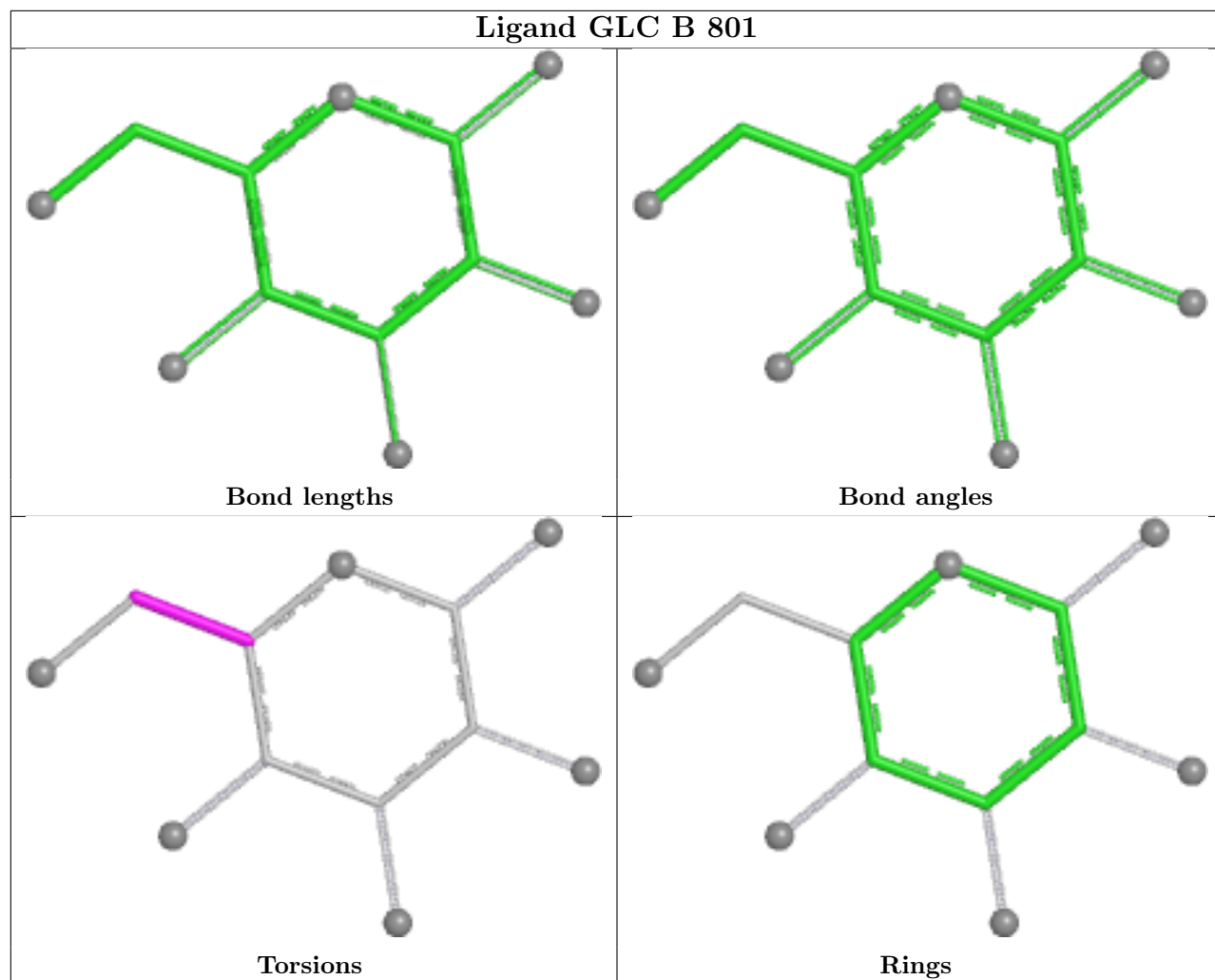
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	803	GLC	1	0

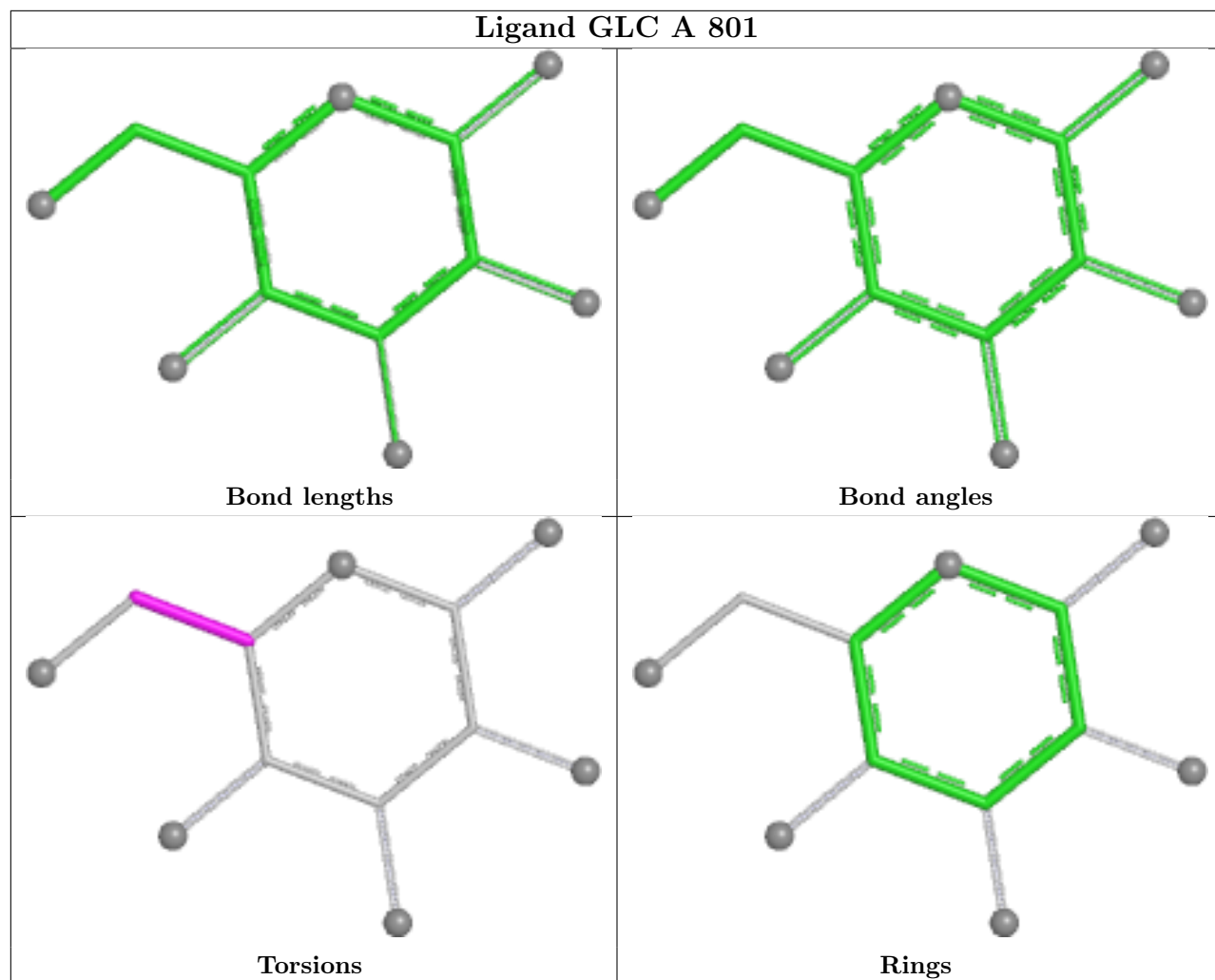
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

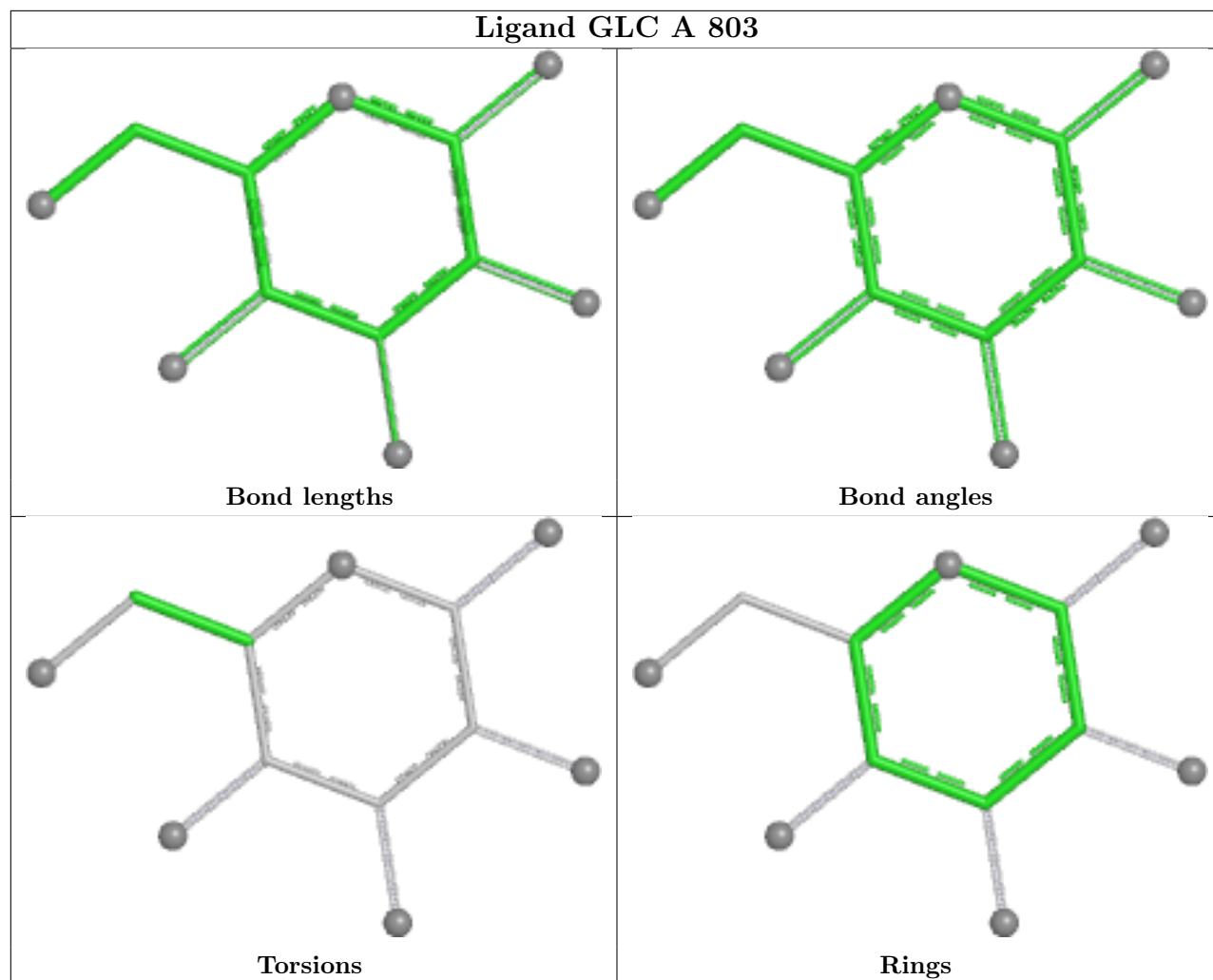












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	600/613 (97%)	-0.25	4 (0%) 84 66	35, 51, 72, 108	440 (73%)
1	B	591/613 (96%)	-0.37	1 (0%) 91 83	32, 49, 62, 73	436 (73%)
1	C	604/613 (98%)	-0.33	1 (0%) 91 83	33, 49, 62, 86	461 (76%)
1	D	496/613 (80%)	0.32	10 (2%) 65 41	46, 74, 100, 117	448 (90%)
All	All	2291/2452 (93%)	-0.18	16 (0%) 84 66	32, 52, 84, 117	1785 (77%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	694	GLY	4.2
1	D	362	PRO	3.1
1	D	305	LEU	2.9
1	D	347	ALA	2.7
1	A	425	ASN	2.5

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	GLC	G	4	11/12	0.27	0.25	88,93,100,111	5
3	GLC	G	2	11/12	0.33	0.35	104,111,117,119	4

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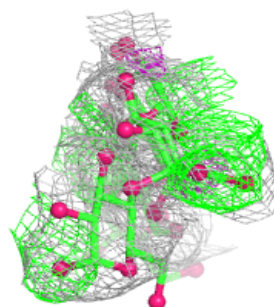
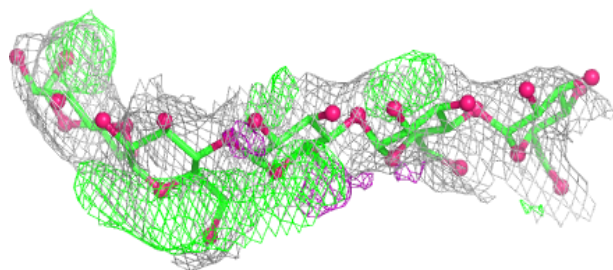
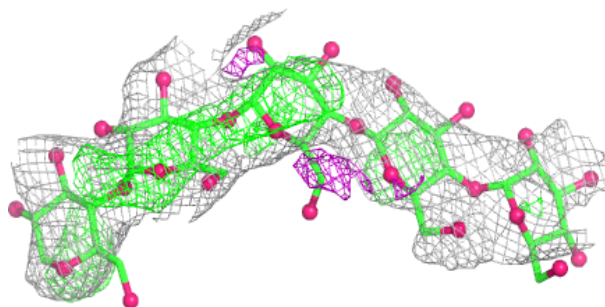
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	GLC	J	5	11/12	0.43	0.25	89,98,105,125	5
5	GLC	J	6	11/12	0.44	0.24	98,108,114,114	4
2	GLC	H	5	11/12	0.45	0.17	103,113,124,126	4
5	GLC	J	7	11/12	0.50	0.18	107,115,122,126	4
4	GLC	M	1	12/12	0.51	0.13	114,123,124,129	5
3	GLC	G	3	11/12	0.51	0.34	88,96,107,110	4
2	GLC	H	1	12/12	0.51	0.18	106,115,119,128	5
4	GLC	I	3	11/12	0.51	0.14	98,102,109,110	8
5	GLC	J	4	11/12	0.53	0.21	86,92,103,108	1
3	GLC	G	1	12/12	0.56	0.37	20,20,20,20	0
2	GLC	H	2	11/12	0.57	0.15	96,108,116,120	6
4	GLC	M	2	11/12	0.58	0.17	88,102,108,111	3
2	GLC	H	3	11/12	0.59	0.24	93,105,120,126	3
6	GLC	N	1	12/12	0.60	0.16	20,20,20,20	0
6	GLC	N	2	11/12	0.60	0.16	20,20,20,20	0
5	GLC	J	3	11/12	0.63	0.19	59,67,83,88	3
2	GLC	E	4	11/12	0.66	0.21	92,100,105,114	6
2	GLC	F	1	12/12	0.66	0.17	74,79,82,95	7
6	GLC	K	1	12/12	0.69	0.21	76,81,85,90	6
2	GLC	F	2	11/12	0.71	0.17	64,71,79,87	3
6	GLC	K	2	11/12	0.71	0.18	68,72,76,80	5
6	GLC	L	1	12/12	0.73	0.15	75,84,90,92	8
2	GLC	E	5	11/12	0.74	0.17	106,110,118,124	6
2	GLC	E	2	11/12	0.74	0.20	70,80,87,102	4
2	GLC	E	1	12/12	0.74	0.17	76,80,91,97	6
2	GLC	E	3	11/12	0.75	0.28	73,84,97,107	5
5	GLC	J	2	11/12	0.76	0.23	61,72,100,102	4
2	GLC	H	4	11/12	0.77	0.12	92,99,102,107	3
5	GLC	J	1	12/12	0.78	0.21	78,89,93,107	7
4	GLC	M	3	11/12	0.79	0.17	90,92,102,104	4
6	GLC	L	2	11/12	0.80	0.19	77,87,92,111	4
4	GLC	I	2	11/12	0.81	0.17	81,87,99,108	6
2	GLC	F	5	11/12	0.84	0.15	57,67,71,77	6
4	GLC	I	1	12/12	0.87	0.14	76,79,83,85	6
2	GLC	F	4	11/12	0.89	0.16	56,61,64,64	7
2	GLC	F	3	11/12	0.90	0.12	61,65,72,74	5

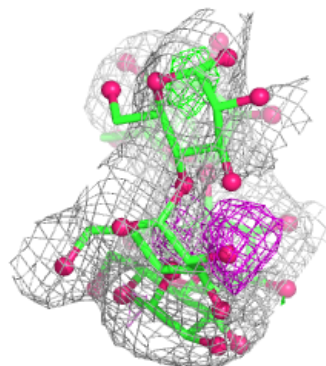
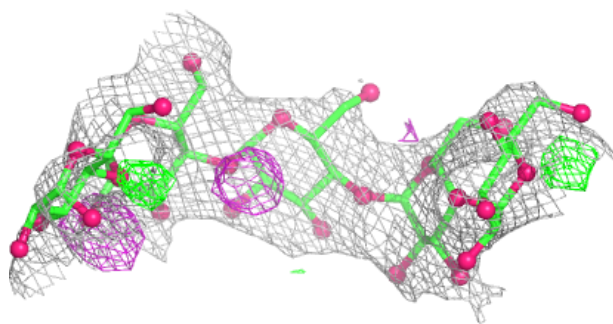
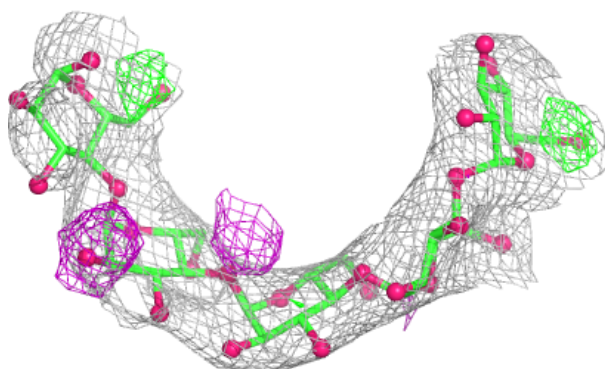
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**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)

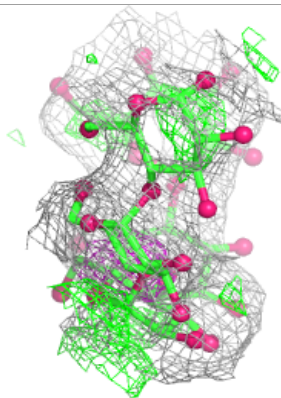
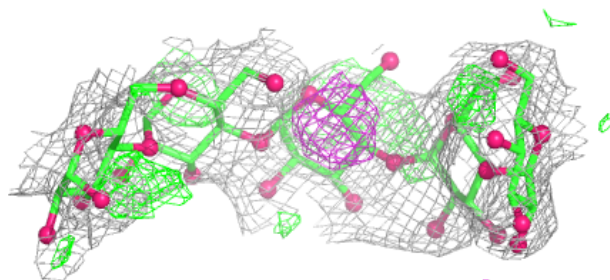
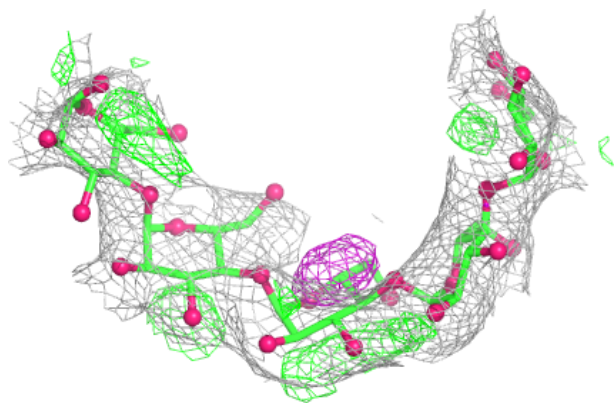
**Electron density around Chain F:**

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

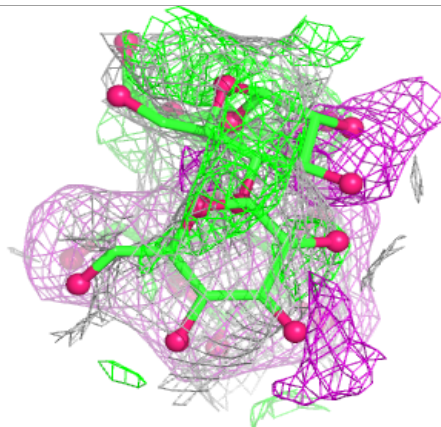
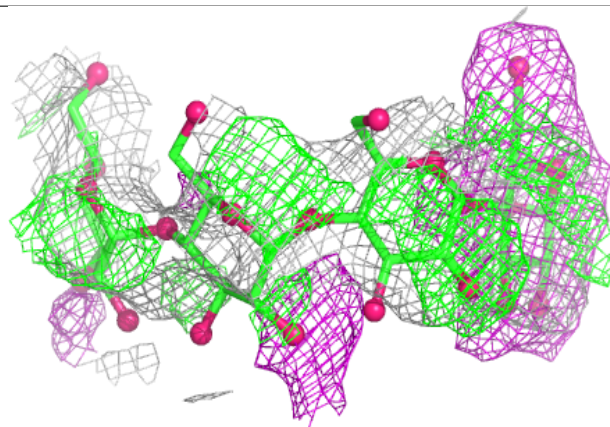
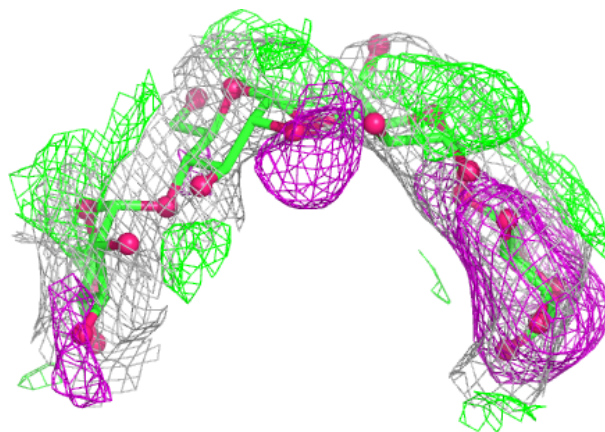


**Electron density around Chain H:**

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

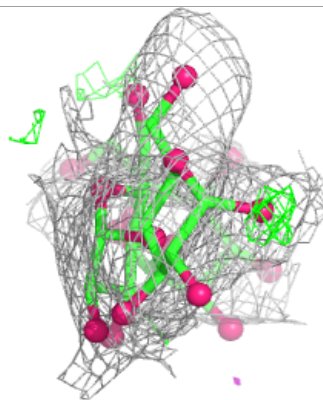
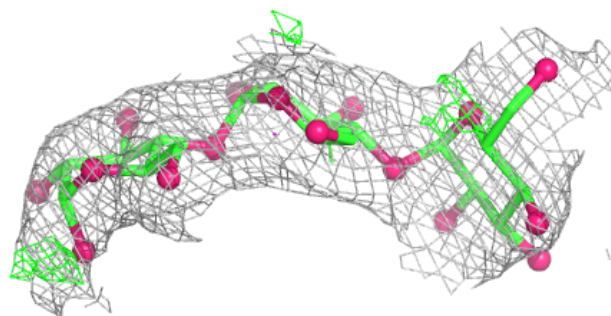
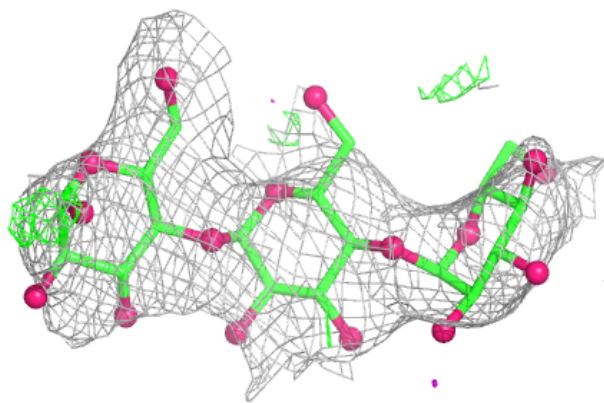
**Electron density around Chain G:**

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

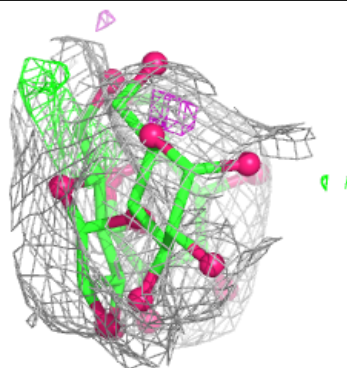
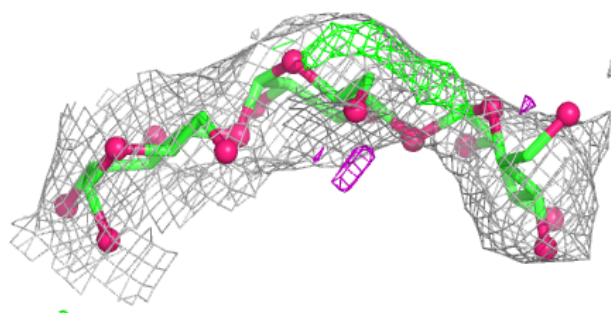
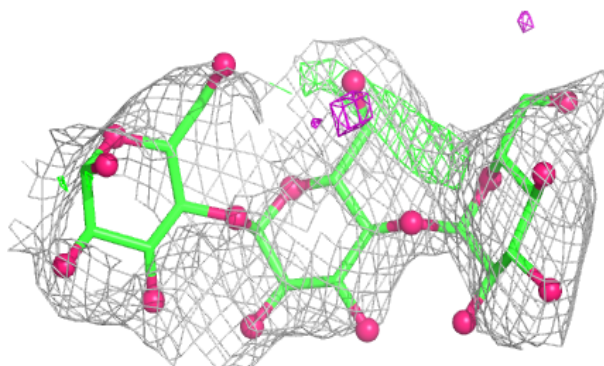


**Electron density around Chain I:**

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

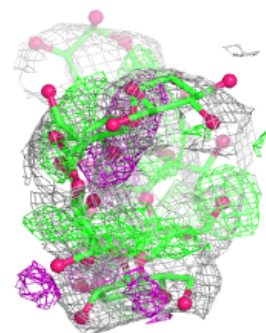
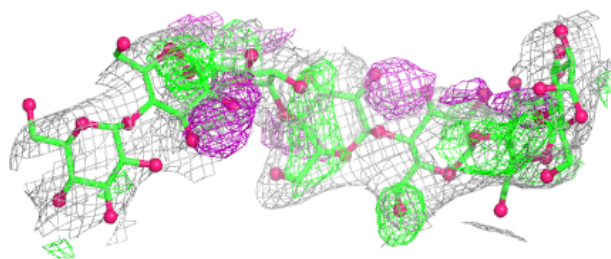
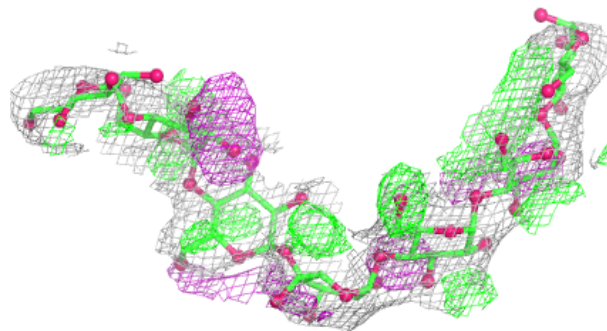
**Electron density around Chain M:**

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

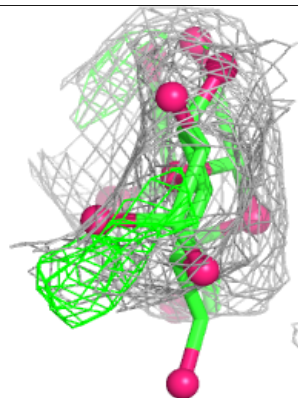
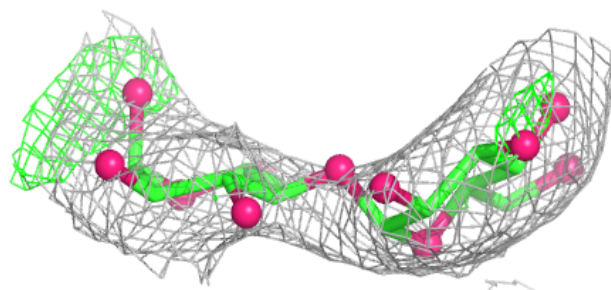
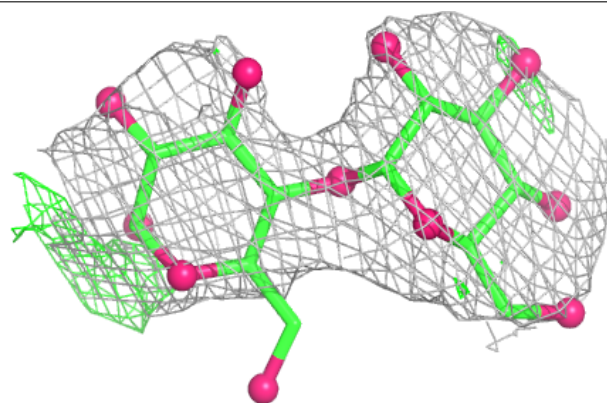


**Electron density around Chain J:**

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

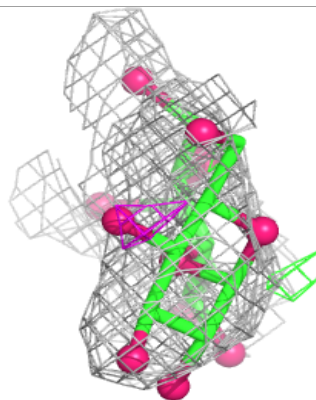
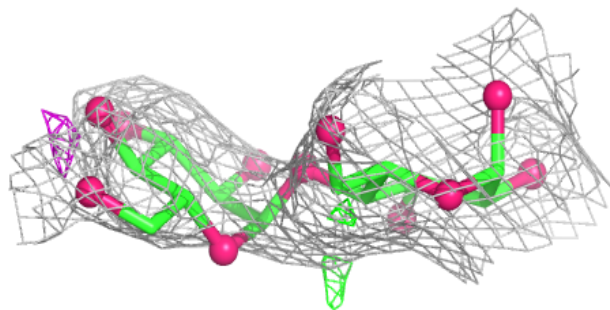
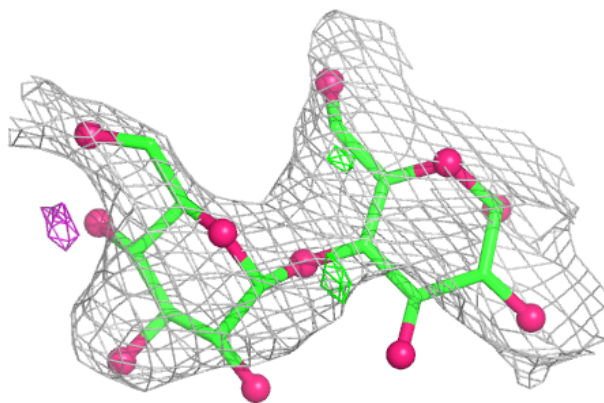
**Electron density around Chain K:**

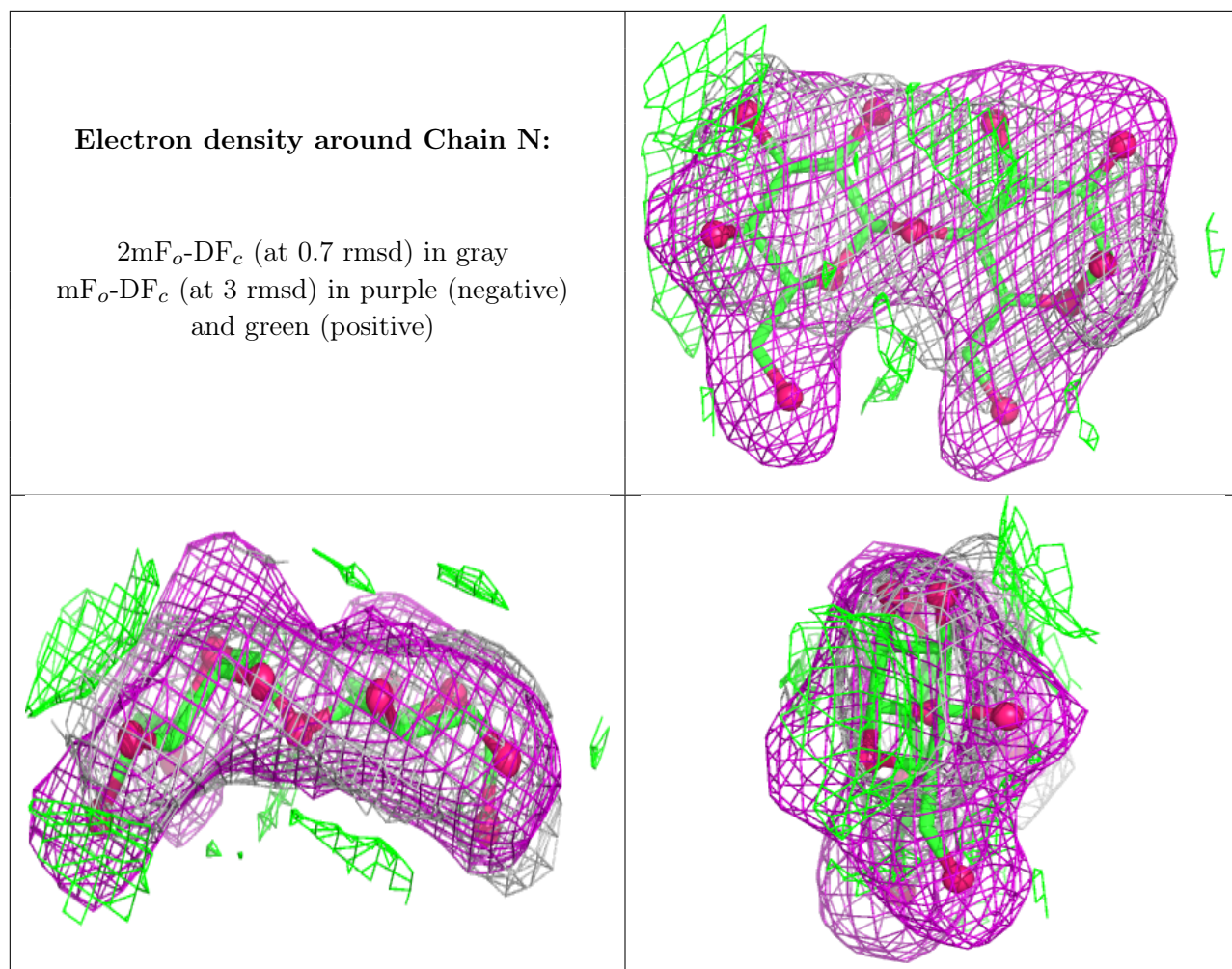
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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)





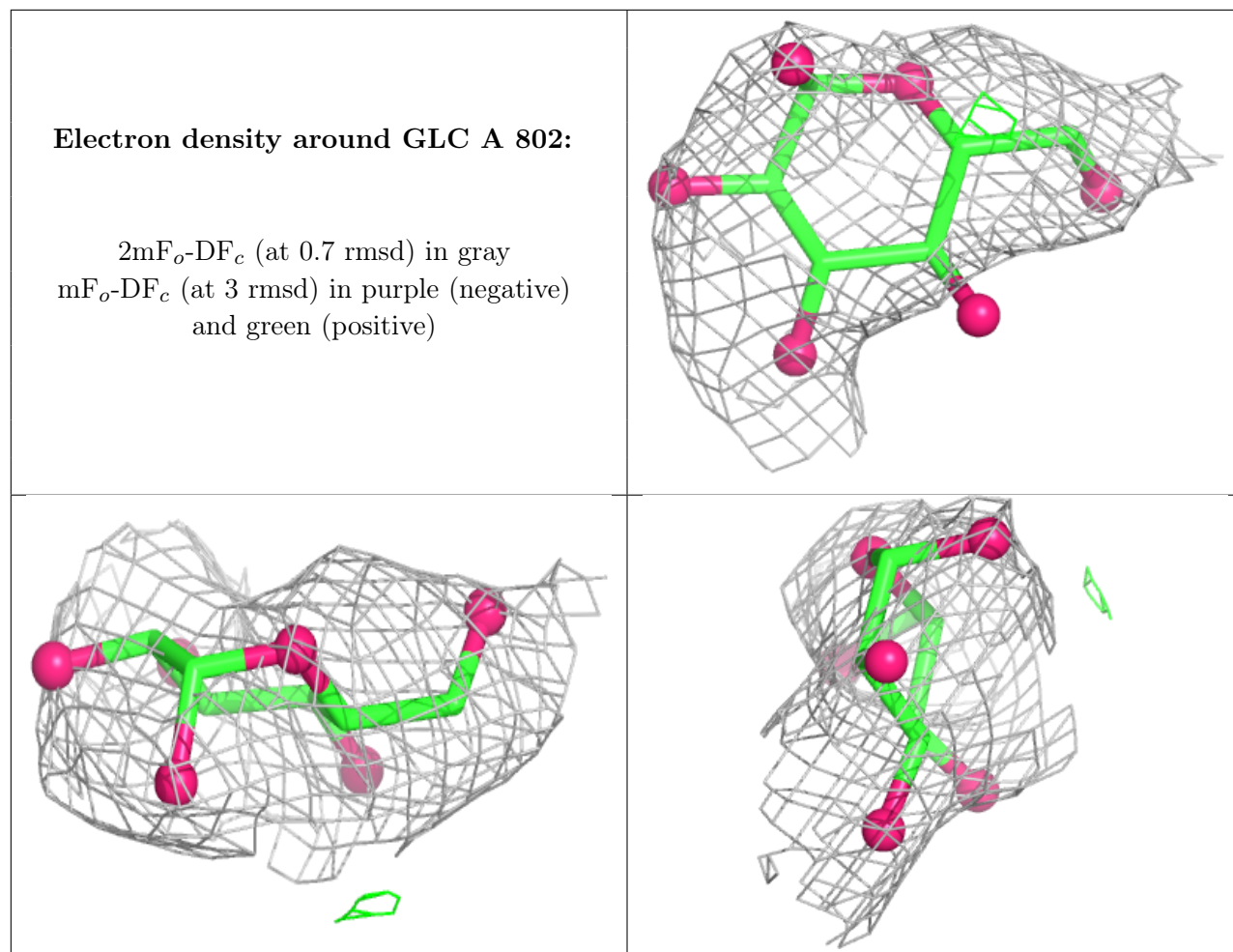
## 6.4 Ligands [i](#)

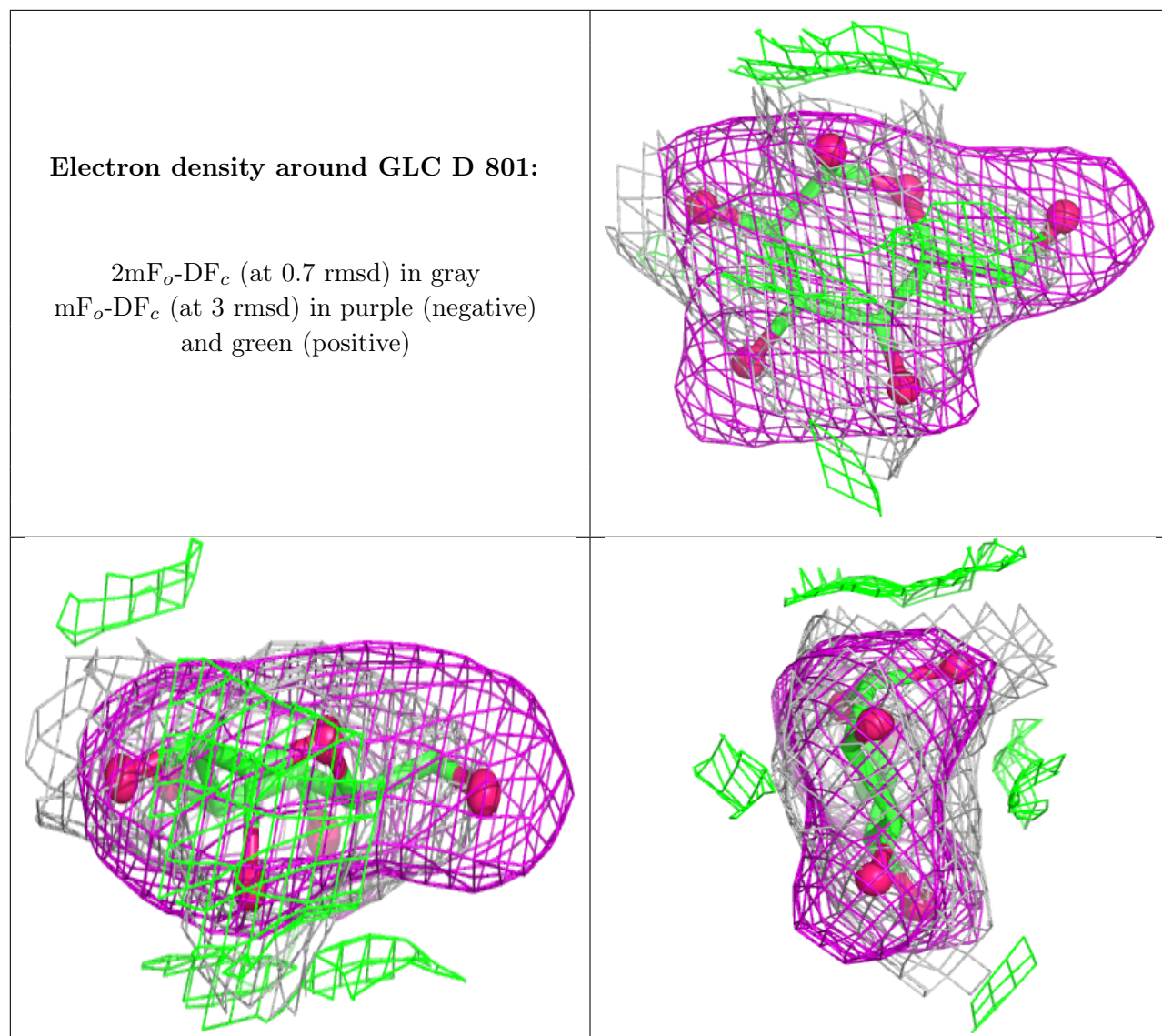
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

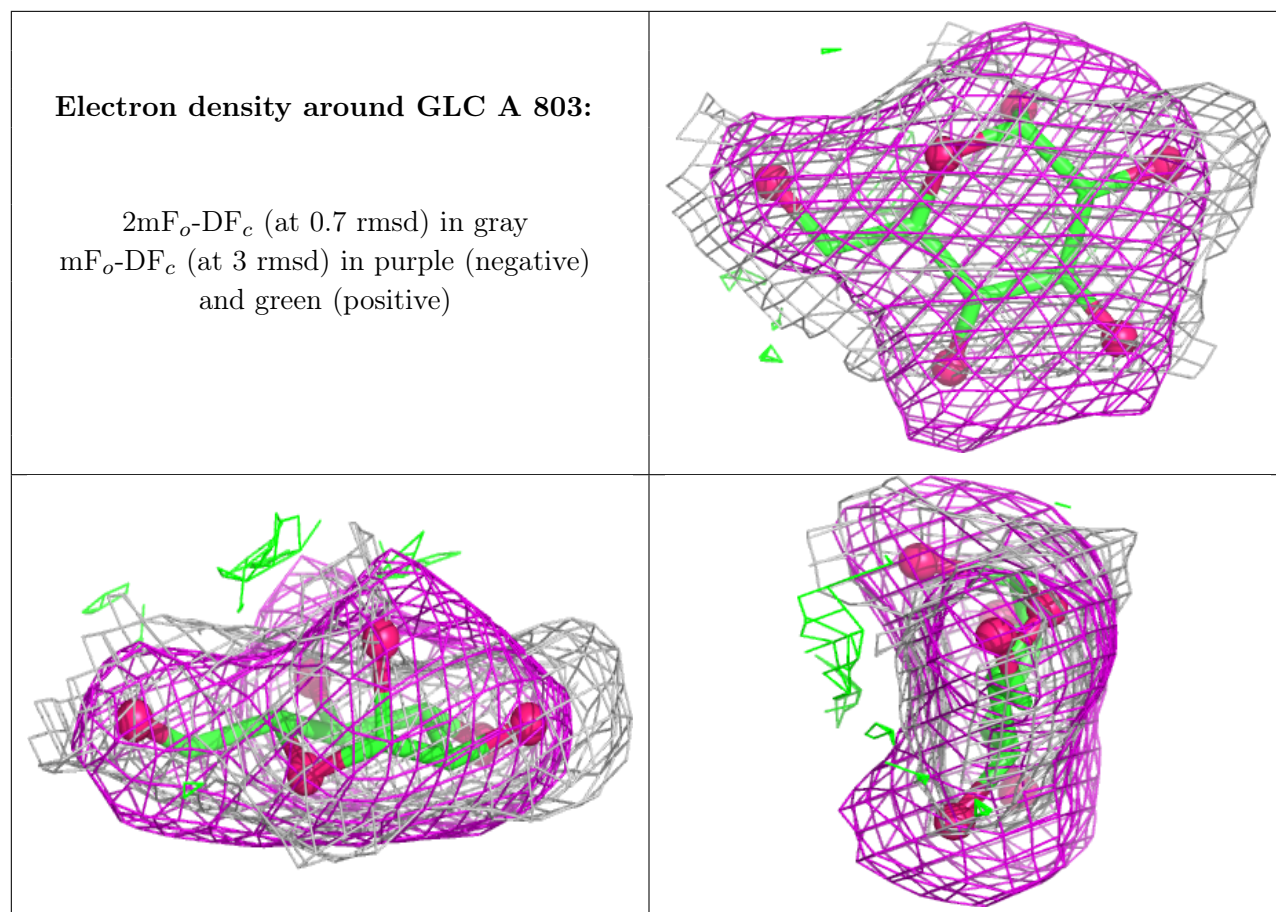
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
7	GLC	A	802	12/12	0.55	0.17	93,102,107,114	5
7	GLC	D	801	12/12	0.70	0.35	20,20,20,20	0
7	GLC	A	803	12/12	0.73	0.39	20,20,20,20	0
7	GLC	B	802	12/12	0.76	0.26	73,77,85,86	9
7	GLC	A	801	12/12	0.80	0.15	70,87,93,94	5
7	GLC	B	801	12/12	0.83	0.16	64,74,84,85	6

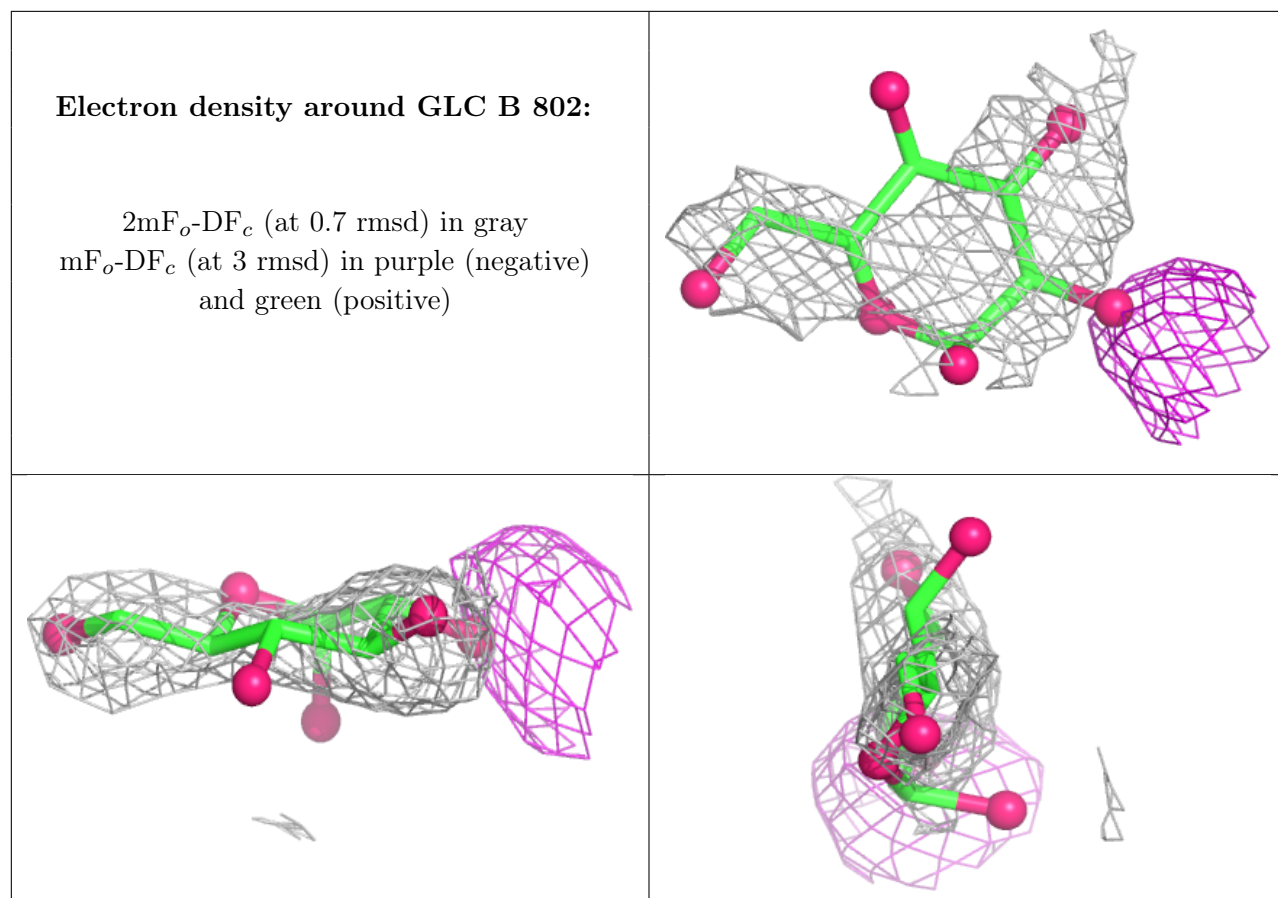
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different

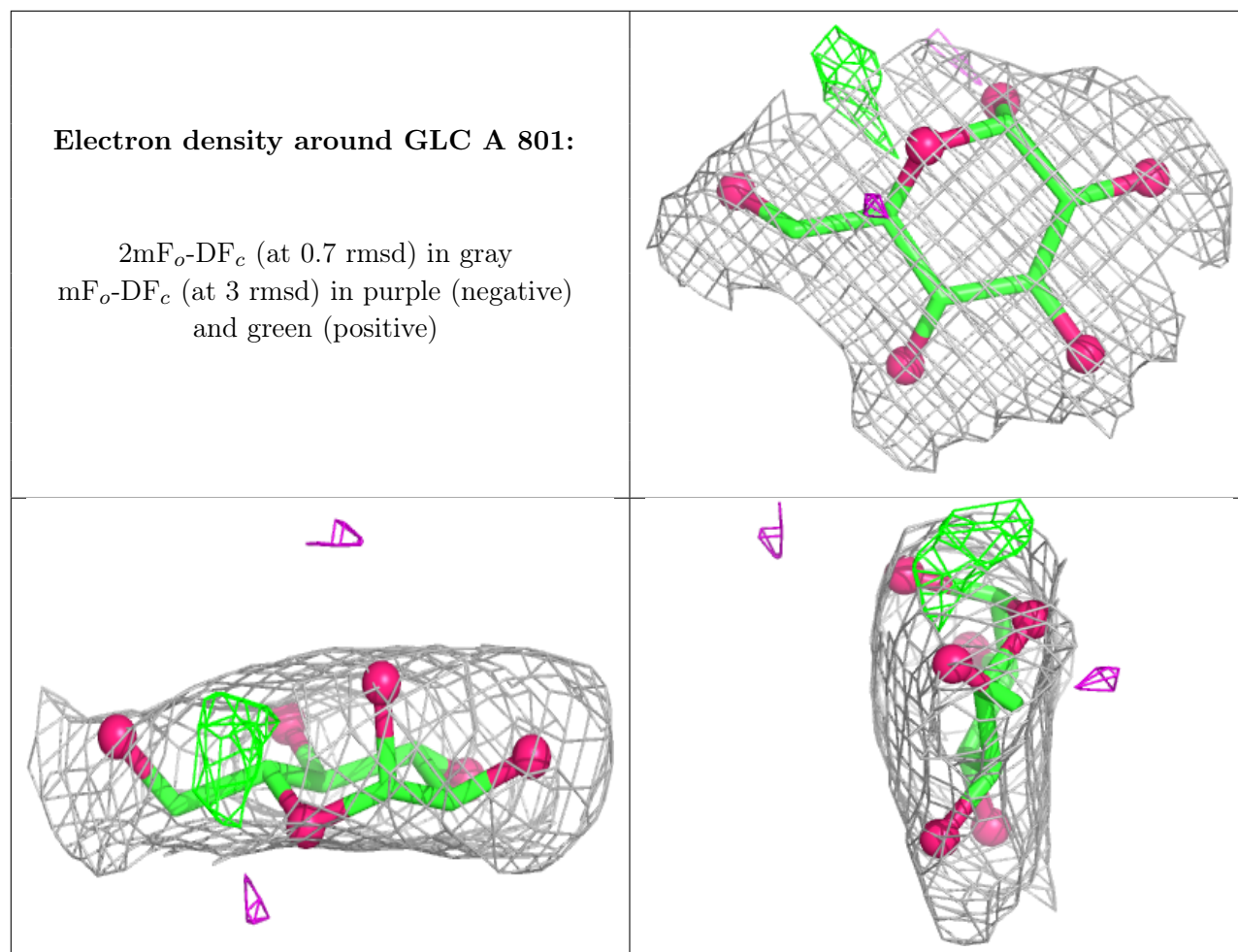
orientation to approximate a three-dimensional view.

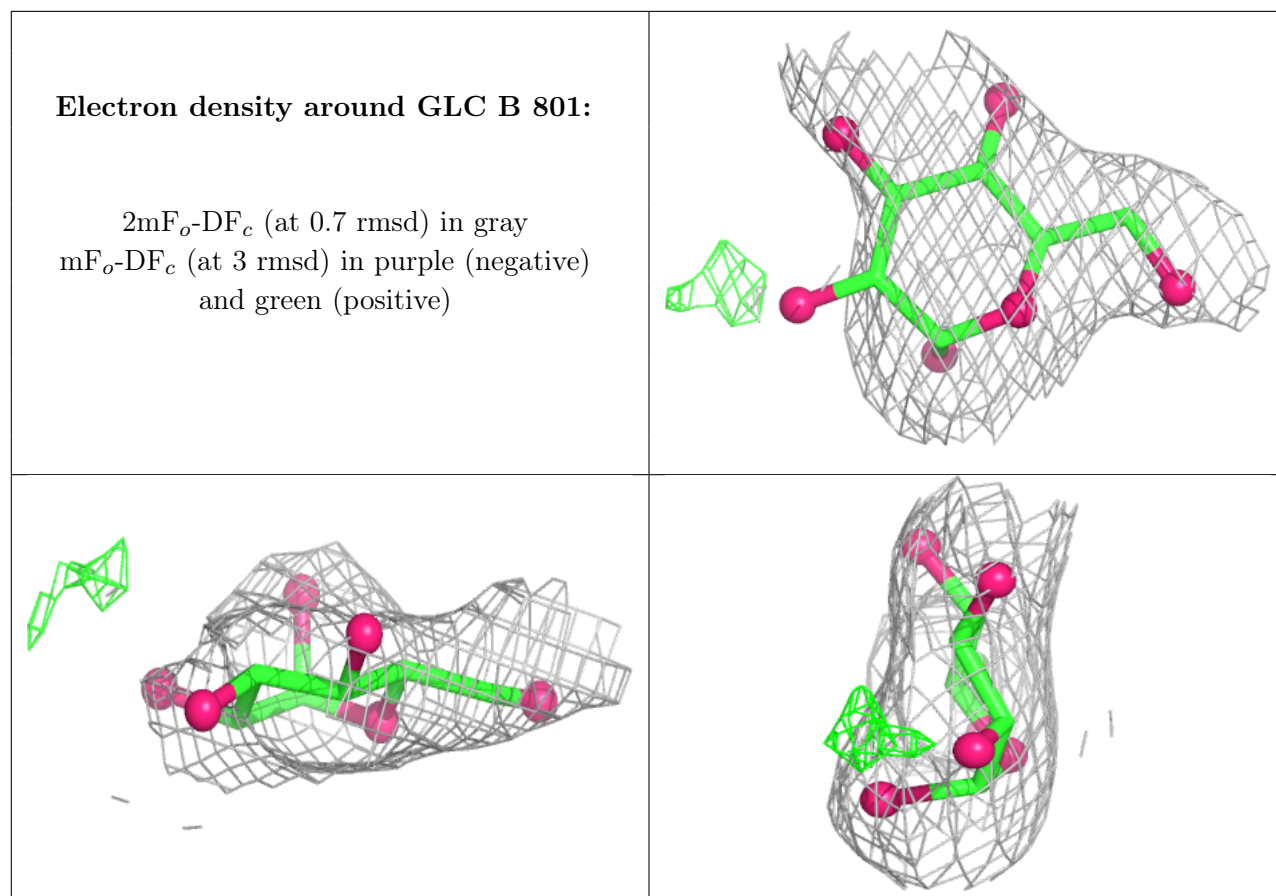












## 6.5 Other polymers [i](#)

There are no such residues in this entry.