



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 20, 2023 – 07:57 AM EDT

PDB ID : 5JSA  
Title : Uncleaved prefusion optimized gp140 trimer with an engineered 10-residue HR1 turn bound to broadly neutralizing antibodies 8ANC195 and PGT128  
Authors : Kong, L.; Wilson, I.A.  
Deposited on : 2016-05-07  
Resolution : 6.31 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

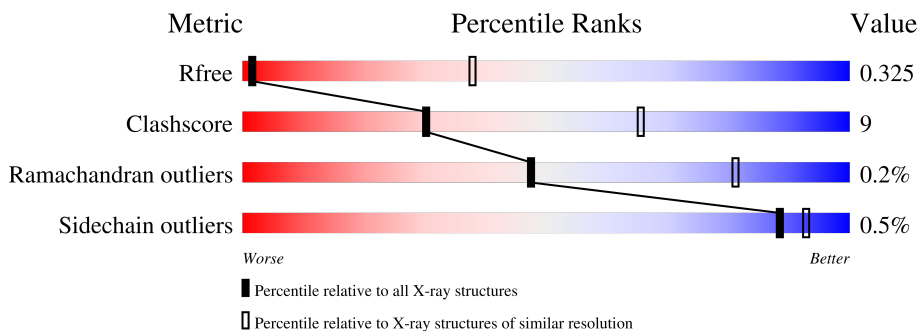
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 6.31 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	1009 (8.70-3.88)
Clashscore	141614	1058 (8.70-3.90)
Ramachandran outliers	138981	1006 (8.70-3.88)
Sidechain outliers	138945	1005 (8.70-3.84)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	239	74% 23% .
2	B	211	74% 22% .
3	C	480	71% 22% 7%
4	D	142	65% 25% . 7%
5	E	238	75% 19% 6%
6	F	215	82% 17% .
7	G	2	50% 50%

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Mol	Chain	Length	Quality of chain
7	H	2	 100%
7	I	2	 50% 50%
8	J	8	 25% 75%
9	K	10	 30% 40% 30%
10	L	9	 33% 67%
11	M	7	 71% 29%
12	N	5	 60% 40%
13	O	3	 100%
13	P	3	 100%
13	Q	3	 33% 67%
13	R	3	 100%
13	S	3	 100%
14	T	4	 25% 50% 25%
15	U	11	 27% 73%

## 2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 12075 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 broadly neutralizing antibody PGT128 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	230	1735	1105	292	332	6	0	0	0

- Molecule 2 is a protein called broadly neutralizing antibody PGT128 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	204	1514	950	254	306	4	0	0	0

- Molecule 3 is a protein called gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	447	3519	2210	622	659	28	0	0	0

- Molecule 4 is a protein called gp41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	132	1052	663	178	205	6	0	0	0

- Molecule 5 is a protein called broadly neutralizing antibody 8ANC195 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	224	1686	1072	284	325	5	0	0	0

- Molecule 6 is a protein called broadly neutralizing antibody 8ANC195 light chain.

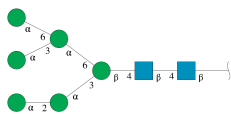
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	212	1626	1018	279	324	5	0	0	0

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



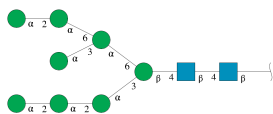
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
7	G	2	28	16	2	10	0	0	0
7	H	2	28	16	2	10	0	0	0
7	I	2	28	16	2	10	0	0	0

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
8	J	8	94	52	2	40	0	0	0

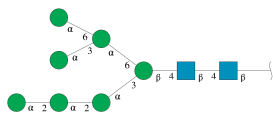
- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	K	10	116	64	2	50	0	0	0

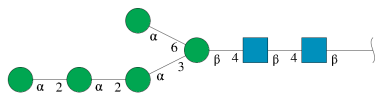
- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

ranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



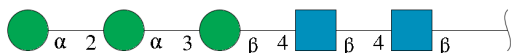
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
10	L	9	105	58	2	45	0	0	0

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(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)-2-acetamido-2-deoxy-beta-D-glucopyranose.



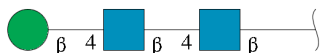
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
11	M	7	83	46	2	35	0	0	0

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 13 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



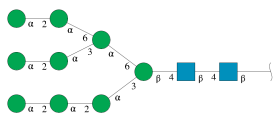
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	O	3	Total	C	N	O	0	0	0
			39	22	2	15			
13	P	3	Total	C	N	O	0	0	0
			39	22	2	15			
13	Q	3	Total	C	N	O	0	0	0
			39	22	2	15			
13	R	3	Total	C	N	O	0	0	0
			39	22	2	15			
13	S	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 14 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



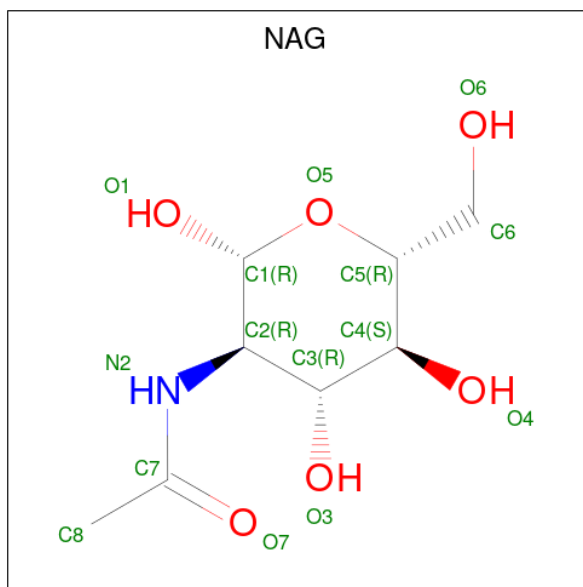
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	T	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 15 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	U	11	Total	C	N	O	0	0	0
			127	70	2	55			

- Molecule 16 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



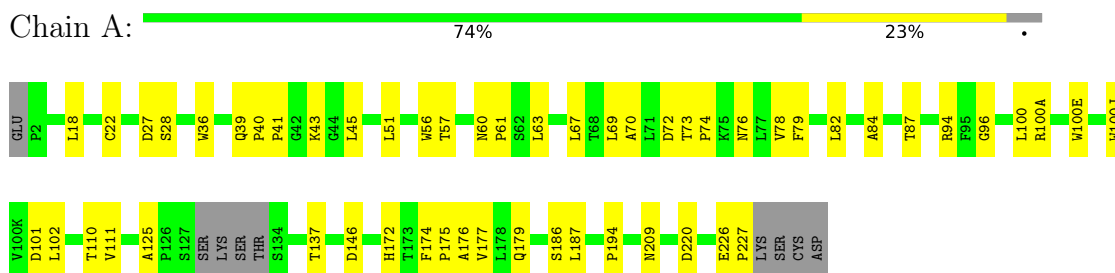
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
16	C	1	Total	C	N	O	0	0
			14	8	1	5		
16	D	1	Total	C	N	O	0	0
			14	8	1	5		



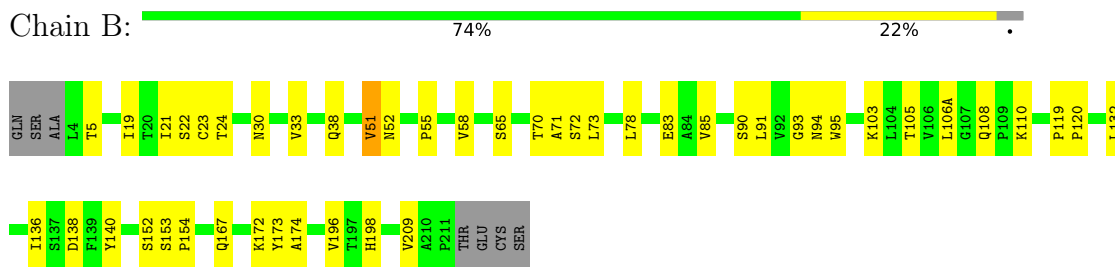
### 3 Residue-property plots [i](#)

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. 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. 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.

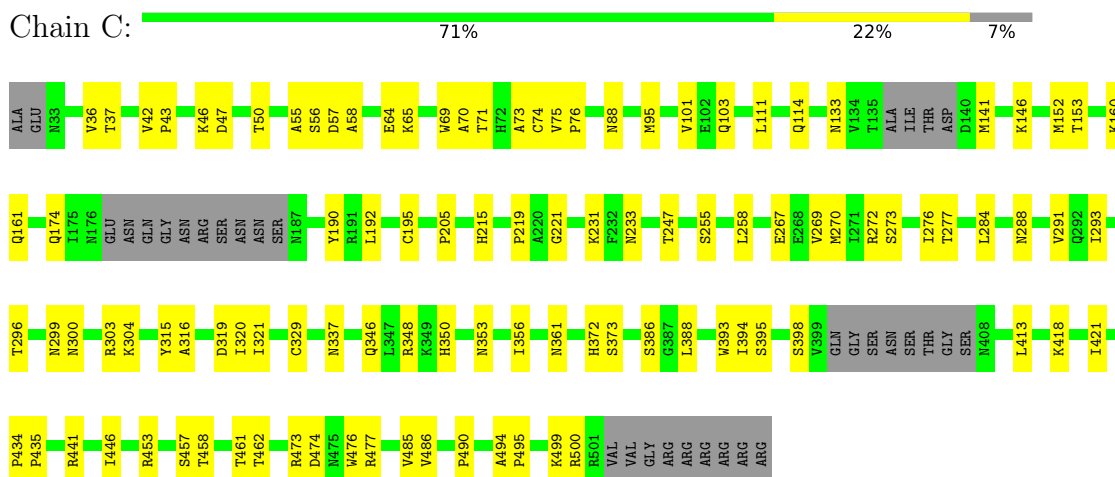
- Molecule 1: broadly neutralizing antibody PGT128 heavy chain



- Molecule 2: broadly neutralizing antibody PGT128 light chain

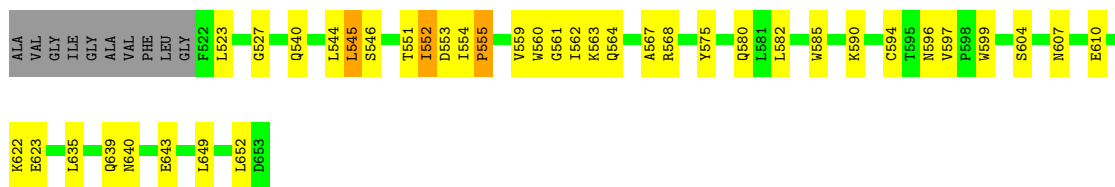


- Molecule 3: gp120



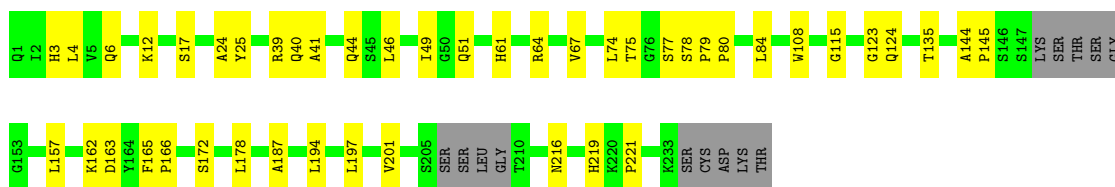
- Molecule 4: gp41

Chain D:  65% 25% 7%




- Molecule 5: broadly neutralizing antibody 8ANC195 heavy chain

Chain E:  75% 19% 6%



- Molecule 6: broadly neutralizing antibody 8ANC195 light chain

Chain F:  82% 17% 1%



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucofuranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucofuranose

Chain G:  50% 50%



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucofuranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucofuranose

Chain H:  100%



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucofuranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucofuranose

Chain I:  50% 50%

MAG1  
MAG2

- Molecule 8: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  25% 75%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
MAN6  
MAN7  
MAN8

- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  30% 40% 30%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
MAN6  
MAN7  
MAN8  
MAN9  
MAN10

- Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  33% 67%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
MAN6  
MAN7  
MAN8  
MAN9

- Molecule 11: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(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)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  71% 29%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
MAN6  
MAN7

- Molecule 12: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  60% 40%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5

- Molecule 13: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  100%

MAG1  
MAG2  
BMA3

- Molecule 13: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  100%

MAG1  
MAG2  
BMA3

- Molecule 13: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  33% 67%

MAG1  
MAG2  
BMA3

- Molecule 13: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:  100%

MAG1  
MAG2  
BMA3

- Molecule 13: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:  100%

MAG1  
MAG2  
BMA3

- Molecule 14: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:  25% 50% 25%

MAG1  
MAG2  
BMA3  
MAN4

- Molecule 15: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1

-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:  27% 73%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10
MAN11

## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	266.28Å 266.28Å 266.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.14 – 6.31 47.07 – 6.31	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.14-6.31) 99.9 (47.07-6.31)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 6.15Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.281 , 0.322 0.285 , 0.325	Depositor DCC
$R_{free}$ test set	685 reflections (9.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	357.6	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 304.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.049 for -l,-k,-h	Xtrriage
$F_o, F_c$ correlation	0.80	EDS
Total number of atoms	12075	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	350.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.31% 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: NAG, BMA, 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	0.20	0/1786	0.40	0/2449
2	B	0.21	0/1552	0.44	1/2121 (0.0%)
3	C	0.22	0/3592	0.42	0/4875
4	D	0.27	0/1072	0.58	1/1458 (0.1%)
5	E	0.21	0/1730	0.39	0/2361
6	F	0.22	0/1661	0.40	0/2256
All	All	0.22	0/11393	0.43	2/15520 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	545	LEU	CA-CB-CG	8.87	135.71	115.30
2	B	108	GLN	C-N-CD	-6.56	106.17	120.60

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1735	0	1690	37	0
2	B	1514	0	1473	35	0
3	C	3519	0	3461	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1052	0	1017	37	1
5	E	1686	0	1658	30	0
6	F	1626	0	1581	27	0
7	G	28	0	25	4	0
7	H	28	0	25	0	0
7	I	28	0	25	0	0
8	J	94	0	79	1	0
9	K	116	0	97	5	0
10	L	105	0	88	0	0
11	M	83	0	70	4	0
12	N	61	0	52	0	0
13	O	39	0	34	0	0
13	P	39	0	34	0	0
13	Q	39	0	34	1	0
13	R	39	0	34	0	0
13	S	39	0	34	0	0
14	T	50	0	43	2	0
15	U	127	0	104	0	0
16	C	14	0	13	0	0
16	D	14	0	13	0	0
All	All	12075	0	11684	220	1

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 9.

The worst 5 of 220 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)
2:B:95:TRP:HE1	9:K:6:MAN:HO4	1.12	0.93
4:D:553:ASP:OD1	4:D:564:GLN:NE2	2.07	0.85
3:C:499:LYS:HG2	3:C:500:ARG:H	1.50	0.77
2:B:95:TRP:NE1	9:K:6:MAN:O4	2.16	0.75
3:C:394:ILE:HG22	3:C:395:SER:H	1.53	0.72

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:546:SER:OG	4:D:580:GLN:OE1[5_555]	2.09	0.11



## 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	226/239 (95%)	212 (94%)	14 (6%)	0	100	100
2	B	202/211 (96%)	194 (96%)	7 (4%)	1 (0%)	29	69
3	C	439/480 (92%)	417 (95%)	22 (5%)	0	100	100
4	D	130/142 (92%)	119 (92%)	9 (7%)	2 (2%)	10	45
5	E	218/238 (92%)	209 (96%)	9 (4%)	0	100	100
6	F	210/215 (98%)	205 (98%)	5 (2%)	0	100	100
All	All	1425/1525 (93%)	1356 (95%)	66 (5%)	3 (0%)	47	81

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	552	ILE
2	B	51	VAL
4	D	555	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	194/203 (96%)	194 (100%)	0	100	100
2	B	171/177 (97%)	170 (99%)	1 (1%)	86	92
3	C	399/426 (94%)	396 (99%)	3 (1%)	81	89
4	D	115/120 (96%)	113 (98%)	2 (2%)	60	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	192/204 (94%)	192 (100%)	0	100	100
6	F	180/182 (99%)	180 (100%)	0	100	100
All	All	1251/1312 (95%)	1245 (100%)	6 (0%)	88	93

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	337	ASN
4	D	562	ILE
4	D	563	LYS
3	C	233	ASN
2	B	152	SER

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

Mol	Chain	Res	Type
3	C	114	GLN
3	C	194	ASN

### 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](#)

75 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
7	NAG	G	1	3,7	14,14,15	0.30	0	17,19,21	0.63	0
7	NAG	G	2	7	14,14,15	0.20	0	17,19,21	0.38	0
7	NAG	H	1	3,7	14,14,15	0.22	0	17,19,21	0.42	0
7	NAG	H	2	7	14,14,15	0.28	0	17,19,21	0.41	0
7	NAG	I	1	3,7	14,14,15	0.23	0	17,19,21	1.02	1 (5%)
7	NAG	I	2	7	14,14,15	0.24	0	17,19,21	0.37	0
8	NAG	J	1	3,8	14,14,15	0.60	0	17,19,21	0.53	0
8	NAG	J	2	8	14,14,15	0.58	0	17,19,21	0.48	0
8	BMA	J	3	8	11,11,12	0.55	0	15,15,17	0.69	0
8	MAN	J	4	8	11,11,12	0.69	0	15,15,17	1.07	1 (6%)
8	MAN	J	5	8	11,11,12	0.59	0	15,15,17	1.04	1 (6%)
8	MAN	J	6	8	11,11,12	0.90	0	15,15,17	0.92	2 (13%)
8	MAN	J	7	8	11,11,12	0.64	0	15,15,17	1.03	2 (13%)
8	MAN	J	8	8	11,11,12	0.82	1 (9%)	15,15,17	1.47	2 (13%)
9	NAG	K	1	3,9	14,14,15	0.25	0	17,19,21	0.44	0
9	MAN	K	10	9	11,11,12	0.69	0	15,15,17	1.00	2 (13%)
9	NAG	K	2	9	14,14,15	0.23	0	17,19,21	0.39	0
9	BMA	K	3	9	11,11,12	0.81	0	15,15,17	0.87	0
9	MAN	K	4	9	11,11,12	0.76	1 (9%)	15,15,17	1.14	2 (13%)
9	MAN	K	5	9	11,11,12	0.68	0	15,15,17	1.14	2 (13%)
9	MAN	K	6	9	11,11,12	0.80	0	15,15,17	0.96	1 (6%)
9	MAN	K	7	9	11,11,12	0.69	0	15,15,17	1.05	2 (13%)
9	MAN	K	8	9	11,11,12	0.68	0	15,15,17	1.24	2 (13%)
9	MAN	K	9	9	11,11,12	0.70	0	15,15,17	0.92	1 (6%)
10	NAG	L	1	3,10	14,14,15	0.51	0	17,19,21	0.63	0
10	NAG	L	2	10	14,14,15	0.20	0	17,19,21	0.71	0
10	BMA	L	3	10	11,11,12	0.82	0	15,15,17	1.03	0
10	MAN	L	4	10	11,11,12	0.79	0	15,15,17	1.35	2 (13%)
10	MAN	L	5	10	11,11,12	0.61	0	15,15,17	1.15	2 (13%)
10	MAN	L	6	10	11,11,12	0.61	0	15,15,17	1.16	2 (13%)
10	MAN	L	7	10	11,11,12	0.72	0	15,15,17	0.98	2 (13%)
10	MAN	L	8	10	11,11,12	0.68	0	15,15,17	0.97	2 (13%)
10	MAN	L	9	10	11,11,12	0.64	0	15,15,17	1.01	2 (13%)
11	NAG	M	1	11,3	14,14,15	0.30	0	17,19,21	0.45	0
11	NAG	M	2	11	14,14,15	0.41	0	17,19,21	0.52	0
11	BMA	M	3	11	11,11,12	0.66	0	15,15,17	1.03	1 (6%)
11	MAN	M	4	11	11,11,12	0.71	0	15,15,17	1.35	1 (6%)
11	MAN	M	5	11	11,11,12	0.55	0	15,15,17	1.15	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
11	MAN	M	6	11	11,11,12	0.68	0	15,15,17	1.28	2 (13%)
11	MAN	M	7	11	11,11,12	0.77	1 (9%)	15,15,17	1.17	2 (13%)
12	NAG	N	1	3,12	14,14,15	0.47	0	17,19,21	0.45	0
12	NAG	N	2	12	14,14,15	0.23	0	17,19,21	0.60	0
12	BMA	N	3	12	11,11,12	0.66	0	15,15,17	1.23	1 (6%)
12	MAN	N	4	12	11,11,12	0.63	0	15,15,17	1.33	2 (13%)
12	MAN	N	5	12	11,11,12	0.22	0	15,15,17	0.59	0
13	NAG	O	1	3,13	14,14,15	0.41	0	17,19,21	0.40	0
13	NAG	O	2	13	14,14,15	0.28	0	17,19,21	0.62	0
13	BMA	O	3	13	11,11,12	0.65	0	15,15,17	0.78	0
13	NAG	P	1	3,13	14,14,15	0.31	0	17,19,21	0.49	0
13	NAG	P	2	13	14,14,15	0.39	0	17,19,21	0.62	0
13	BMA	P	3	13	11,11,12	0.69	0	15,15,17	0.81	0
13	NAG	Q	1	3,13	14,14,15	0.31	0	17,19,21	0.74	0
13	NAG	Q	2	13	14,14,15	0.24	0	17,19,21	0.67	1 (5%)
13	BMA	Q	3	13	11,11,12	0.64	0	15,15,17	0.76	0
13	NAG	R	1	3,13	14,14,15	0.32	0	17,19,21	0.50	0
13	NAG	R	2	13	14,14,15	0.39	0	17,19,21	0.62	0
13	BMA	R	3	13	11,11,12	0.69	0	15,15,17	0.80	0
13	NAG	S	1	3,13	14,14,15	0.32	0	17,19,21	0.50	0
13	NAG	S	2	13	14,14,15	0.39	0	17,19,21	0.61	0
13	BMA	S	3	13	11,11,12	0.69	0	15,15,17	0.80	0
14	NAG	T	1	4,14	14,14,15	0.26	0	17,19,21	0.41	0
14	NAG	T	2	14	14,14,15	0.42	0	17,19,21	1.52	3 (17%)
14	BMA	T	3	14	11,11,12	0.74	0	15,15,17	0.98	0
14	MAN	T	4	14	11,11,12	1.55	3 (27%)	15,15,17	1.38	2 (13%)
15	NAG	U	1	3,15	14,14,15	0.18	0	17,19,21	0.38	0
15	MAN	U	10	15	11,11,12	0.64	0	15,15,17	1.19	2 (13%)
15	MAN	U	11	15	11,11,12	0.67	0	15,15,17	0.96	2 (13%)
15	NAG	U	2	15	14,14,15	0.38	0	17,19,21	0.45	0
15	BMA	U	3	15	11,11,12	0.53	0	15,15,17	0.70	0
15	MAN	U	4	15	11,11,12	0.54	0	15,15,17	1.12	2 (13%)
15	MAN	U	5	15	11,11,12	0.73	0	15,15,17	1.07	1 (6%)
15	MAN	U	6	15	11,11,12	0.55	0	15,15,17	1.00	2 (13%)
15	MAN	U	7	15	11,11,12	0.59	0	15,15,17	1.17	2 (13%)
15	MAN	U	8	15	11,11,12	0.85	0	15,15,17	1.43	3 (20%)
15	MAN	U	9	15	11,11,12	0.59	0	15,15,17	1.04	2 (13%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	G	1	3,7	-	4/6/23/26	0/1/1/1
7	NAG	G	2	7	-	2/6/23/26	0/1/1/1
7	NAG	H	1	3,7	-	2/6/23/26	0/1/1/1
7	NAG	H	2	7	-	2/6/23/26	0/1/1/1
7	NAG	I	1	3,7	-	1/6/23/26	0/1/1/1
7	NAG	I	2	7	-	0/6/23/26	0/1/1/1
8	NAG	J	1	3,8	-	2/6/23/26	0/1/1/1
8	NAG	J	2	8	-	2/6/23/26	0/1/1/1
8	BMA	J	3	8	-	0/2/19/22	0/1/1/1
8	MAN	J	4	8	-	0/2/19/22	0/1/1/1
8	MAN	J	5	8	-	0/2/19/22	0/1/1/1
8	MAN	J	6	8	-	2/2/19/22	0/1/1/1
8	MAN	J	7	8	-	0/2/19/22	0/1/1/1
8	MAN	J	8	8	-	0/2/19/22	0/1/1/1
9	NAG	K	1	3,9	-	0/6/23/26	0/1/1/1
9	MAN	K	10	9	-	1/2/19/22	0/1/1/1
9	NAG	K	2	9	-	2/6/23/26	0/1/1/1
9	BMA	K	3	9	-	0/2/19/22	0/1/1/1
9	MAN	K	4	9	-	1/2/19/22	0/1/1/1
9	MAN	K	5	9	-	0/2/19/22	0/1/1/1
9	MAN	K	6	9	-	0/2/19/22	0/1/1/1
9	MAN	K	7	9	-	0/2/19/22	0/1/1/1
9	MAN	K	8	9	-	0/2/19/22	0/1/1/1
9	MAN	K	9	9	-	0/2/19/22	0/1/1/1
10	NAG	L	1	3,10	-	1/6/23/26	0/1/1/1
10	NAG	L	2	10	-	1/6/23/26	0/1/1/1
10	BMA	L	3	10	-	0/2/19/22	0/1/1/1
10	MAN	L	4	10	-	0/2/19/22	0/1/1/1
10	MAN	L	5	10	-	0/2/19/22	0/1/1/1
10	MAN	L	6	10	-	0/2/19/22	0/1/1/1
10	MAN	L	7	10	-	0/2/19/22	0/1/1/1
10	MAN	L	8	10	-	0/2/19/22	0/1/1/1
10	MAN	L	9	10	-	0/2/19/22	0/1/1/1
11	NAG	M	1	11,3	-	0/6/23/26	0/1/1/1
11	NAG	M	2	11	-	0/6/23/26	0/1/1/1
11	BMA	M	3	11	-	0/2/19/22	0/1/1/1
11	MAN	M	4	11	-	1/2/19/22	0/1/1/1
11	MAN	M	5	11	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	MAN	M	6	11	-	1/2/19/22	0/1/1/1
11	MAN	M	7	11	-	0/2/19/22	0/1/1/1
12	NAG	N	1	3,12	-	0/6/23/26	0/1/1/1
12	NAG	N	2	12	-	2/6/23/26	0/1/1/1
12	BMA	N	3	12	-	0/2/19/22	0/1/1/1
12	MAN	N	4	12	-	2/2/19/22	0/1/1/1
12	MAN	N	5	12	-	0/2/19/22	0/1/1/1
13	NAG	O	1	3,13	-	0/6/23/26	0/1/1/1
13	NAG	O	2	13	-	1/6/23/26	0/1/1/1
13	BMA	O	3	13	-	0/2/19/22	0/1/1/1
13	NAG	P	1	3,13	-	0/6/23/26	0/1/1/1
13	NAG	P	2	13	-	2/6/23/26	0/1/1/1
13	BMA	P	3	13	-	0/2/19/22	0/1/1/1
13	NAG	Q	1	3,13	-	4/6/23/26	0/1/1/1
13	NAG	Q	2	13	-	0/6/23/26	0/1/1/1
13	BMA	Q	3	13	-	0/2/19/22	0/1/1/1
13	NAG	R	1	3,13	-	0/6/23/26	0/1/1/1
13	NAG	R	2	13	-	2/6/23/26	0/1/1/1
13	BMA	R	3	13	-	0/2/19/22	0/1/1/1
13	NAG	S	1	3,13	-	0/6/23/26	0/1/1/1
13	NAG	S	2	13	-	2/6/23/26	0/1/1/1
13	BMA	S	3	13	-	0/2/19/22	0/1/1/1
14	NAG	T	1	4,14	-	1/6/23/26	0/1/1/1
14	NAG	T	2	14	-	5/6/23/26	0/1/1/1
14	BMA	T	3	14	-	2/2/19/22	0/1/1/1
14	MAN	T	4	14	-	2/2/19/22	0/1/1/1
15	NAG	U	1	3,15	-	2/6/23/26	0/1/1/1
15	MAN	U	10	15	-	2/2/19/22	0/1/1/1
15	MAN	U	11	15	-	2/2/19/22	0/1/1/1
15	NAG	U	2	15	-	2/6/23/26	0/1/1/1
15	BMA	U	3	15	-	0/2/19/22	0/1/1/1
15	MAN	U	4	15	-	0/2/19/22	0/1/1/1
15	MAN	U	5	15	-	2/2/19/22	0/1/1/1
15	MAN	U	6	15	-	0/2/19/22	0/1/1/1
15	MAN	U	7	15	-	0/2/19/22	0/1/1/1
15	MAN	U	8	15	-	0/2/19/22	0/1/1/1
15	MAN	U	9	15	-	1/2/19/22	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	T	4	MAN	C2-C3	2.98	1.56	1.52
14	T	4	MAN	O2-C2	2.74	1.49	1.43
14	T	4	MAN	C1-C2	2.66	1.58	1.52
11	M	7	MAN	C1-C2	2.30	1.57	1.52
8	J	8	MAN	C1-C2	2.23	1.57	1.52

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	J	8	MAN	C1-O5-C5	4.62	118.46	112.19
11	M	4	MAN	C1-O5-C5	4.51	118.30	112.19
14	T	2	NAG	C2-N2-C7	4.50	129.31	122.90
10	L	4	MAN	C1-O5-C5	4.34	118.08	112.19
11	M	6	MAN	C1-O5-C5	4.02	117.64	112.19

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

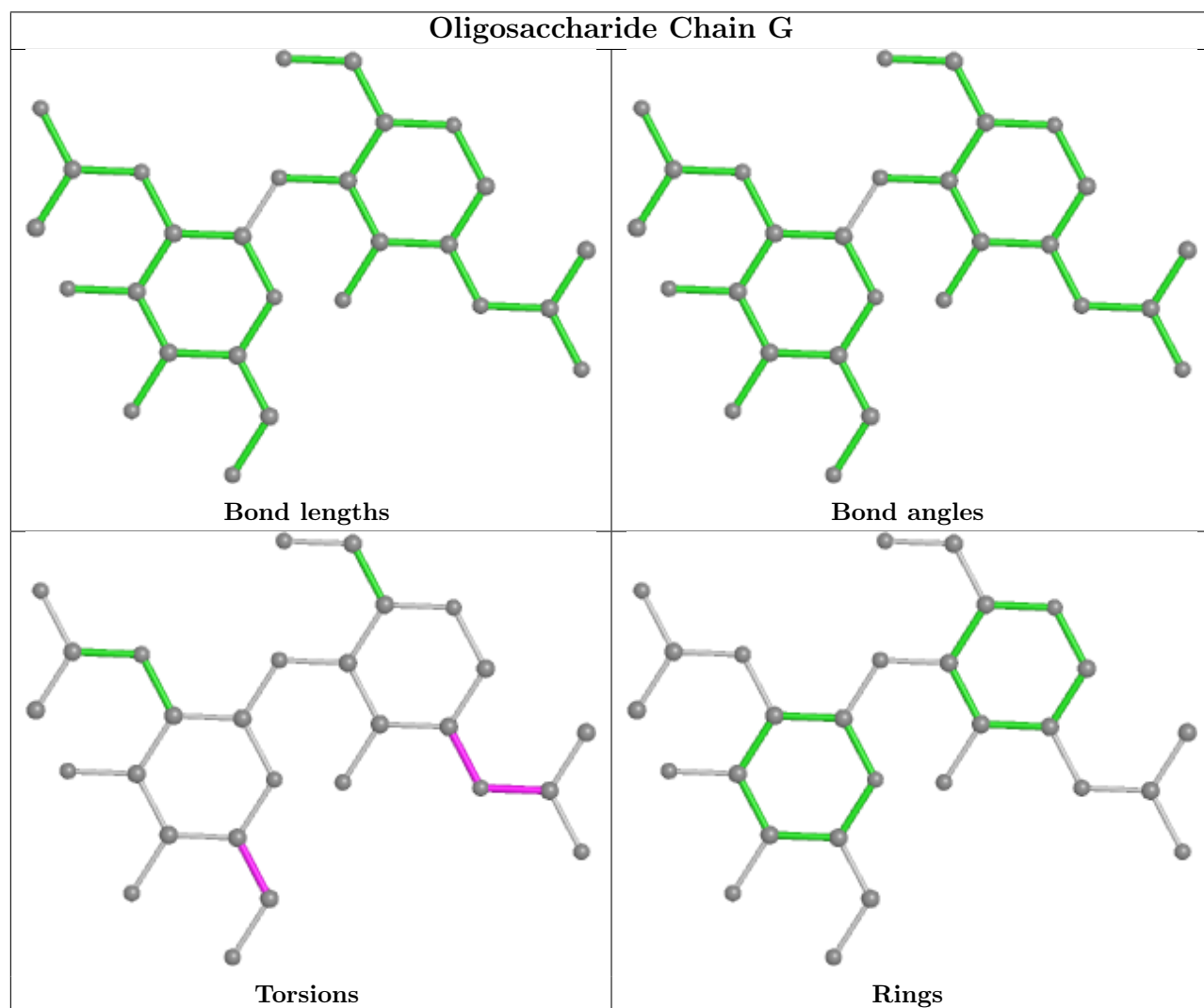
Mol	Chain	Res	Type	Atoms
7	G	1	NAG	C3-C2-N2-C7
7	G	1	NAG	C8-C7-N2-C2
7	G	1	NAG	O7-C7-N2-C2
7	I	1	NAG	C3-C2-N2-C7
13	Q	1	NAG	C8-C7-N2-C2

There are no ring outliers.

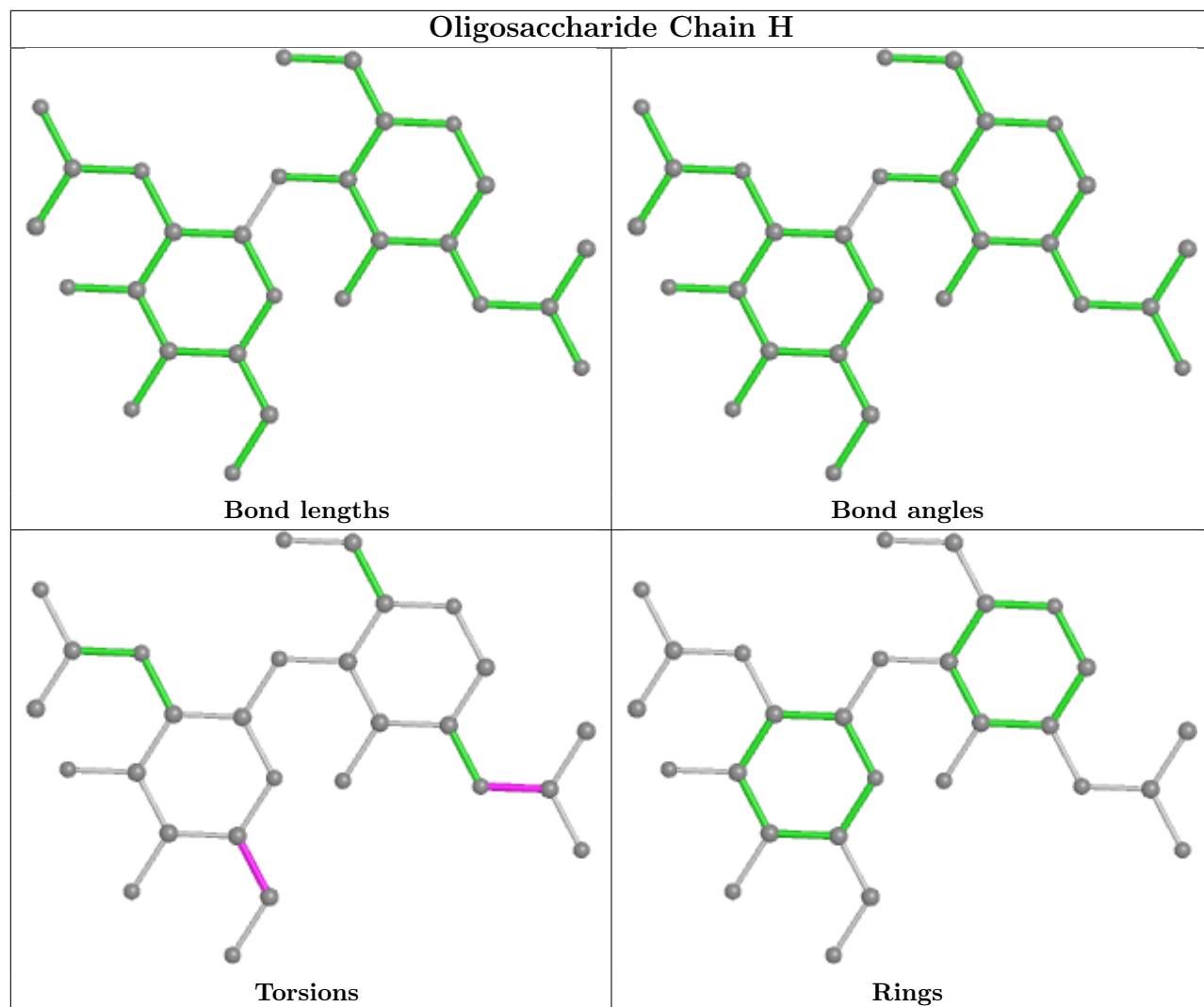
12 monomers are involved in 17 short contacts:

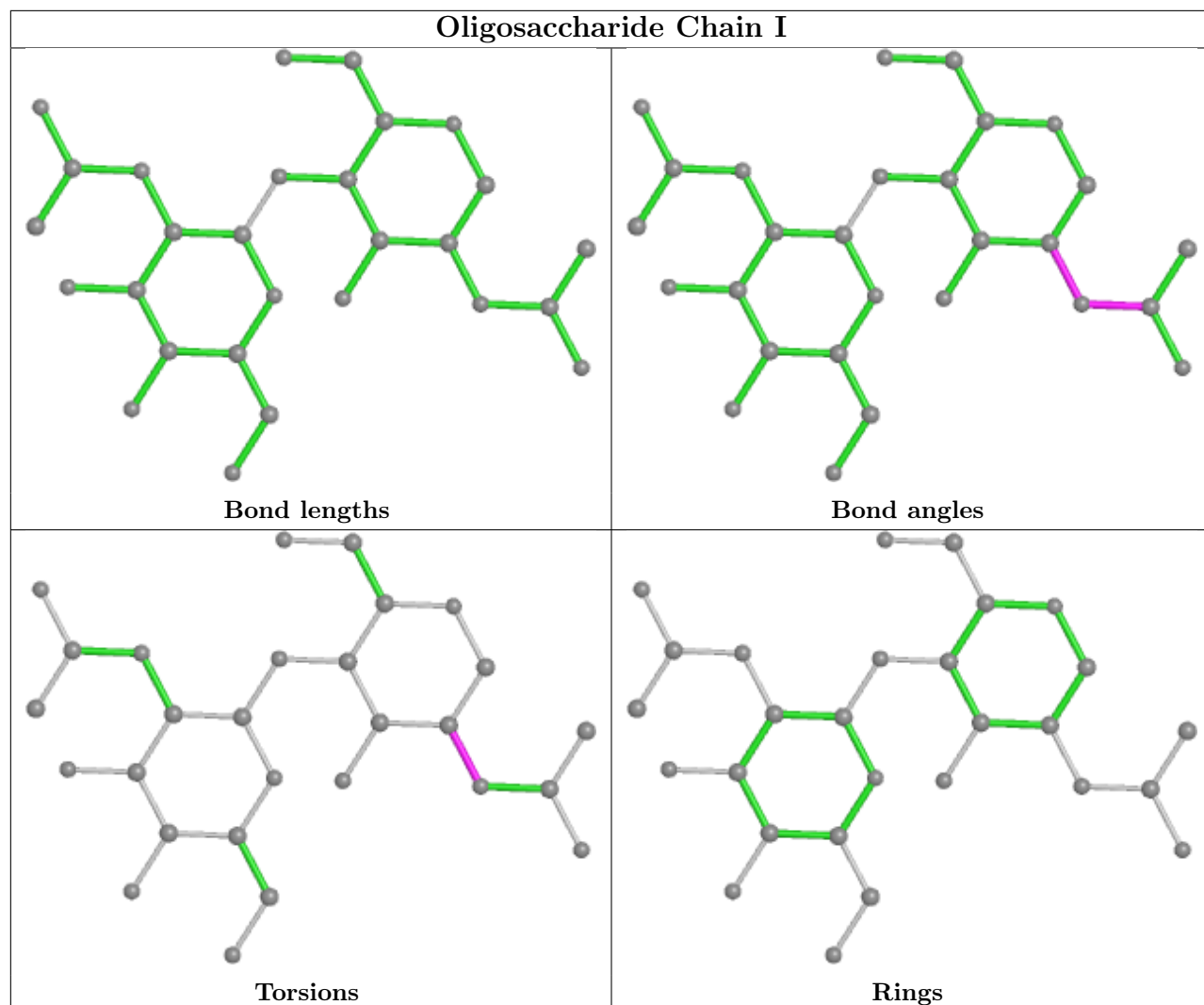
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	G	1	NAG	4	0
11	M	2	NAG	2	0
14	T	2	NAG	2	0
13	Q	1	NAG	1	0
11	M	6	MAN	2	0
14	T	3	BMA	1	0
9	K	5	MAN	2	0
8	J	2	NAG	1	0
9	K	9	MAN	1	0
11	M	1	NAG	2	0
9	K	6	MAN	2	0
11	M	4	MAN	2	0

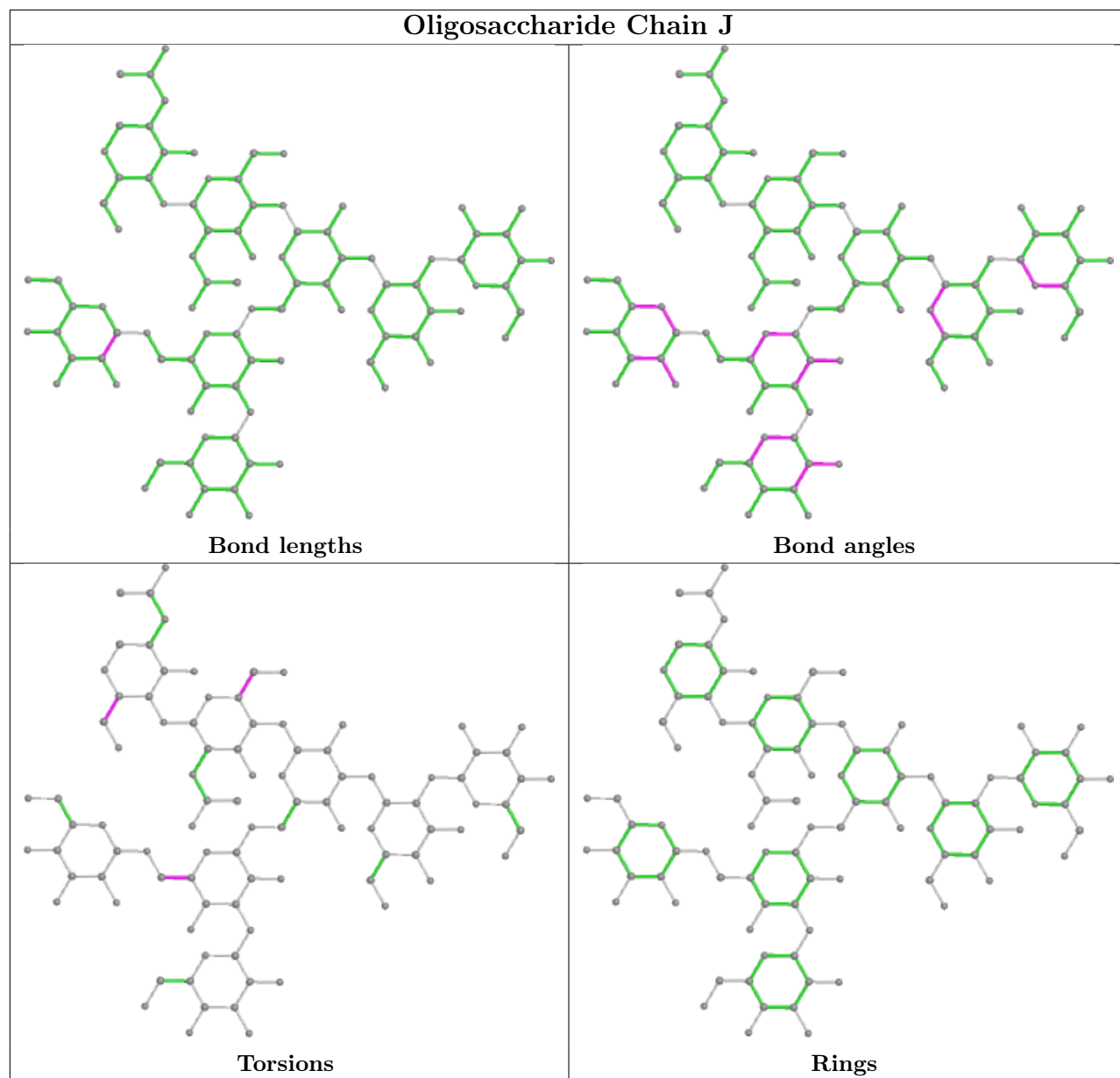
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

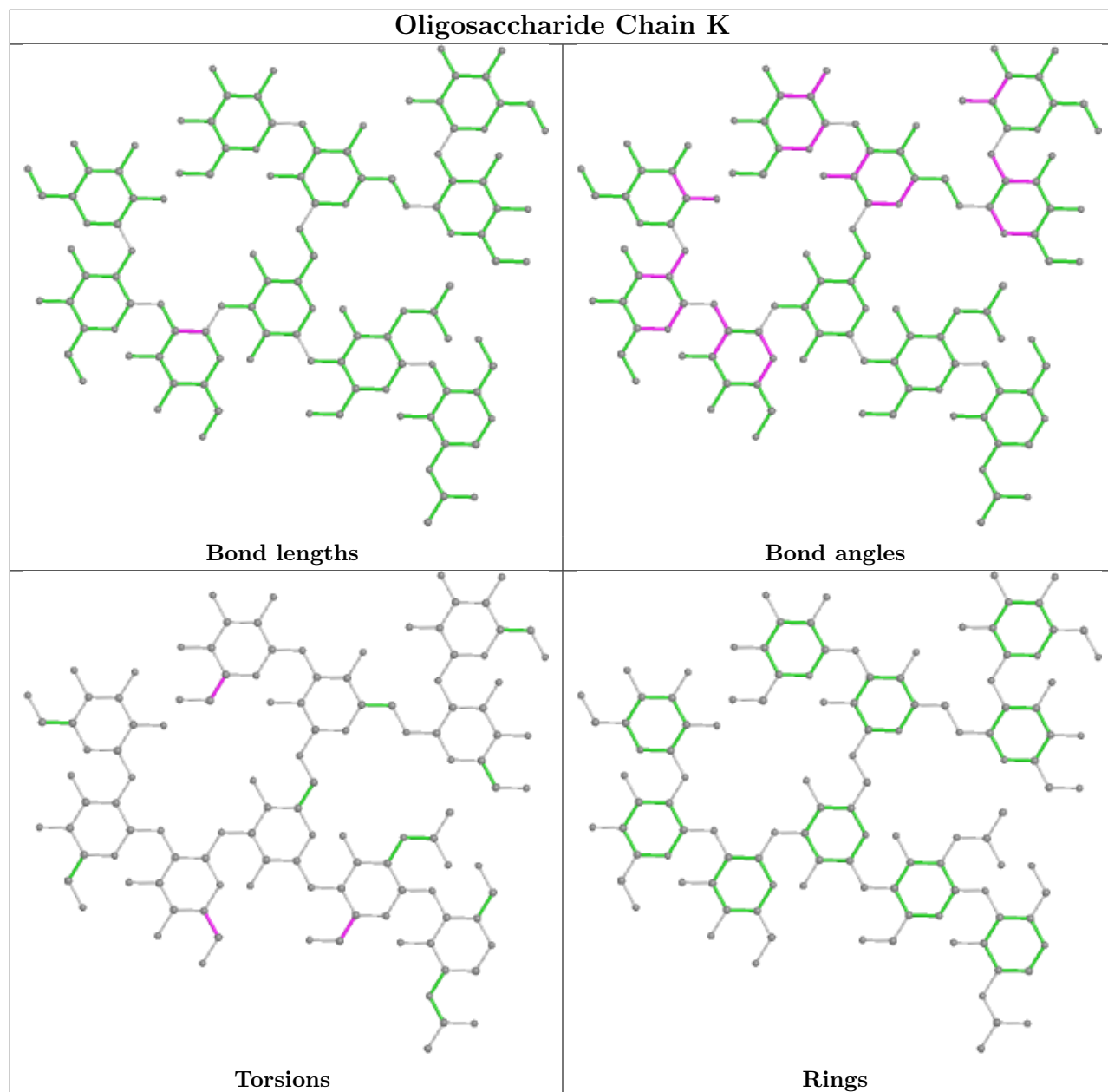


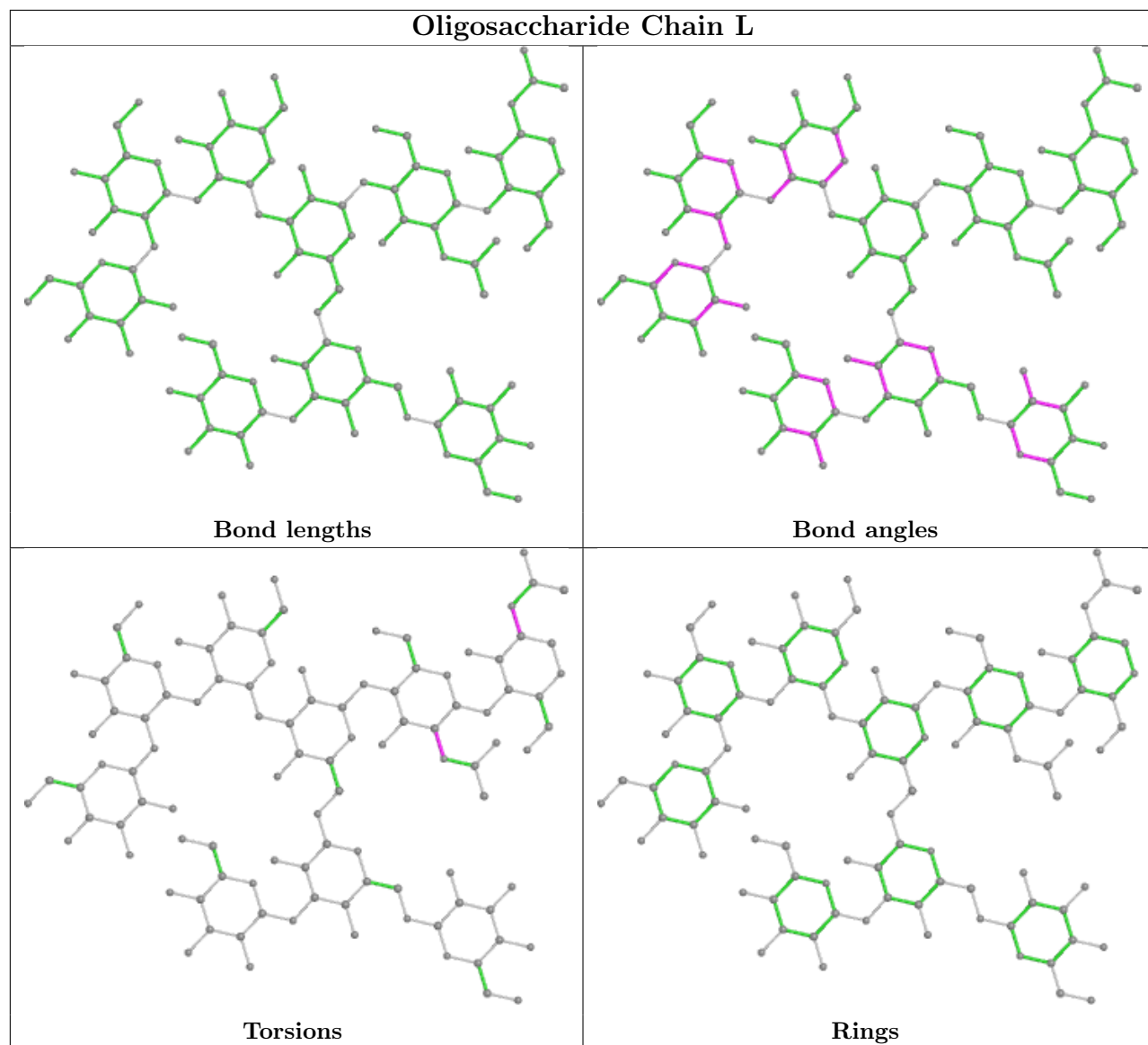


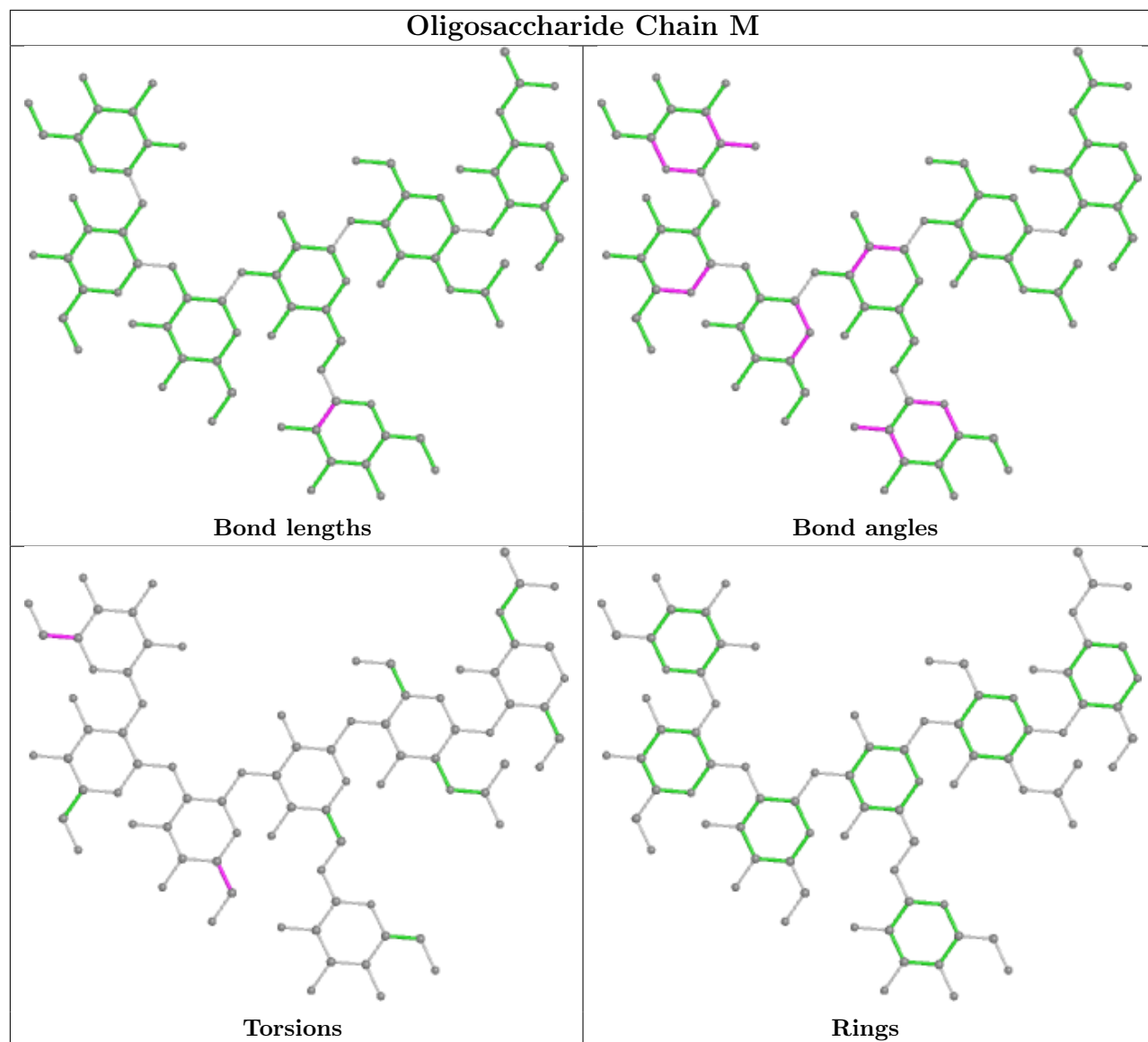


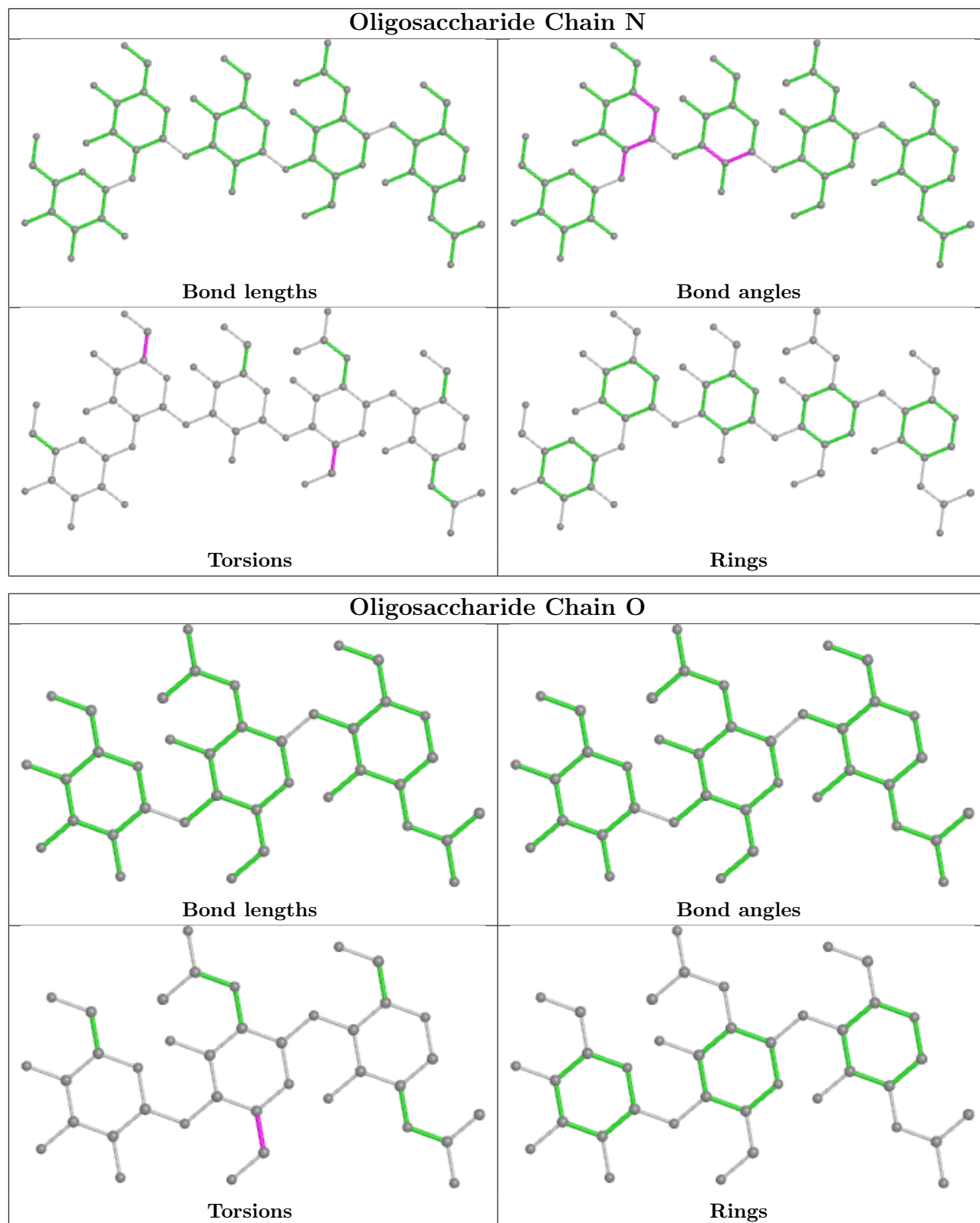


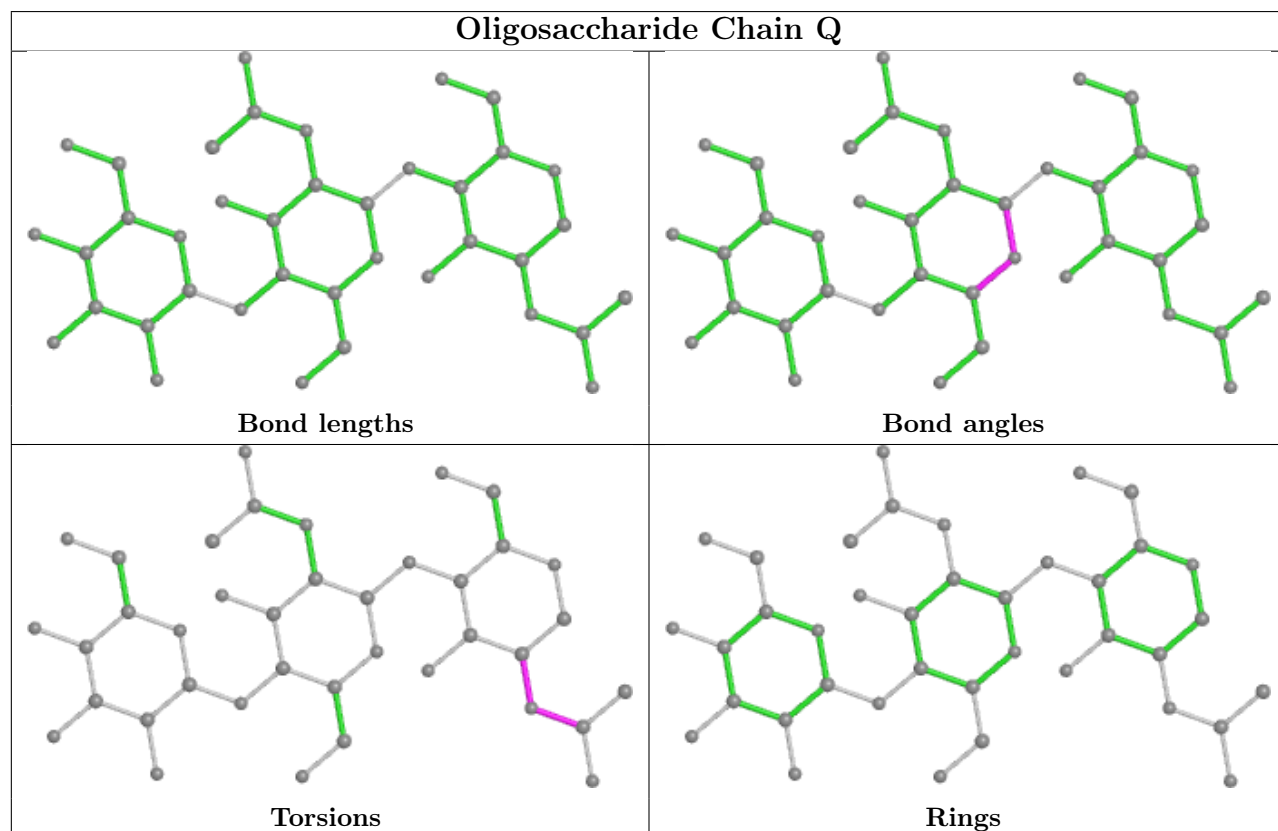
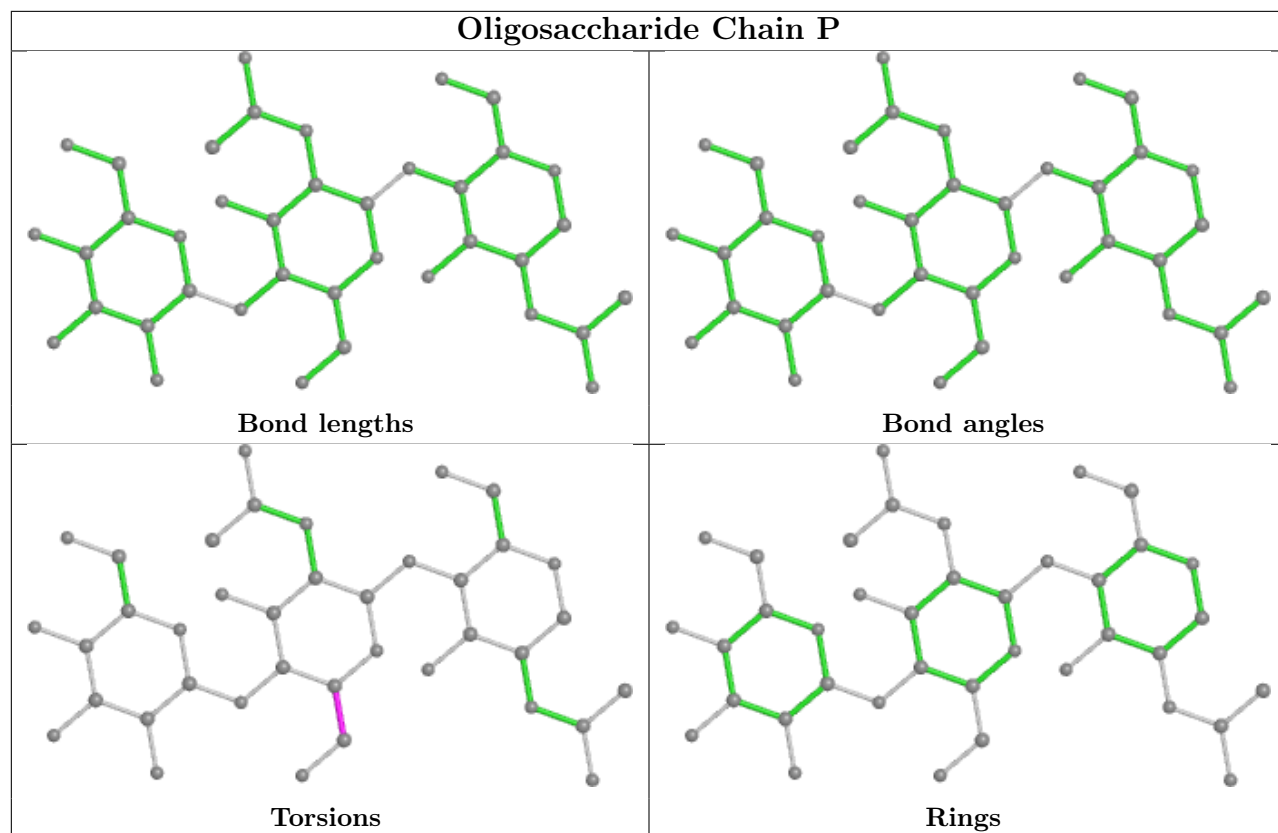




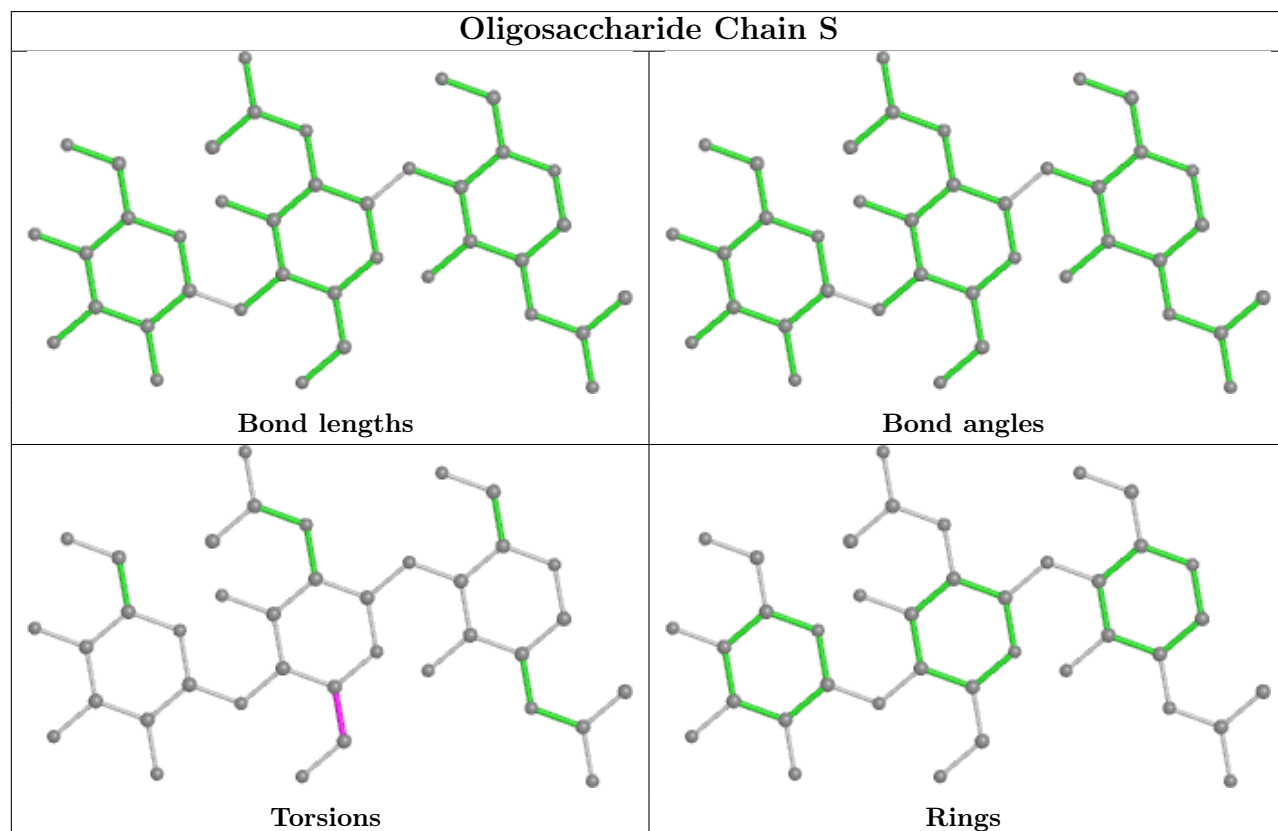
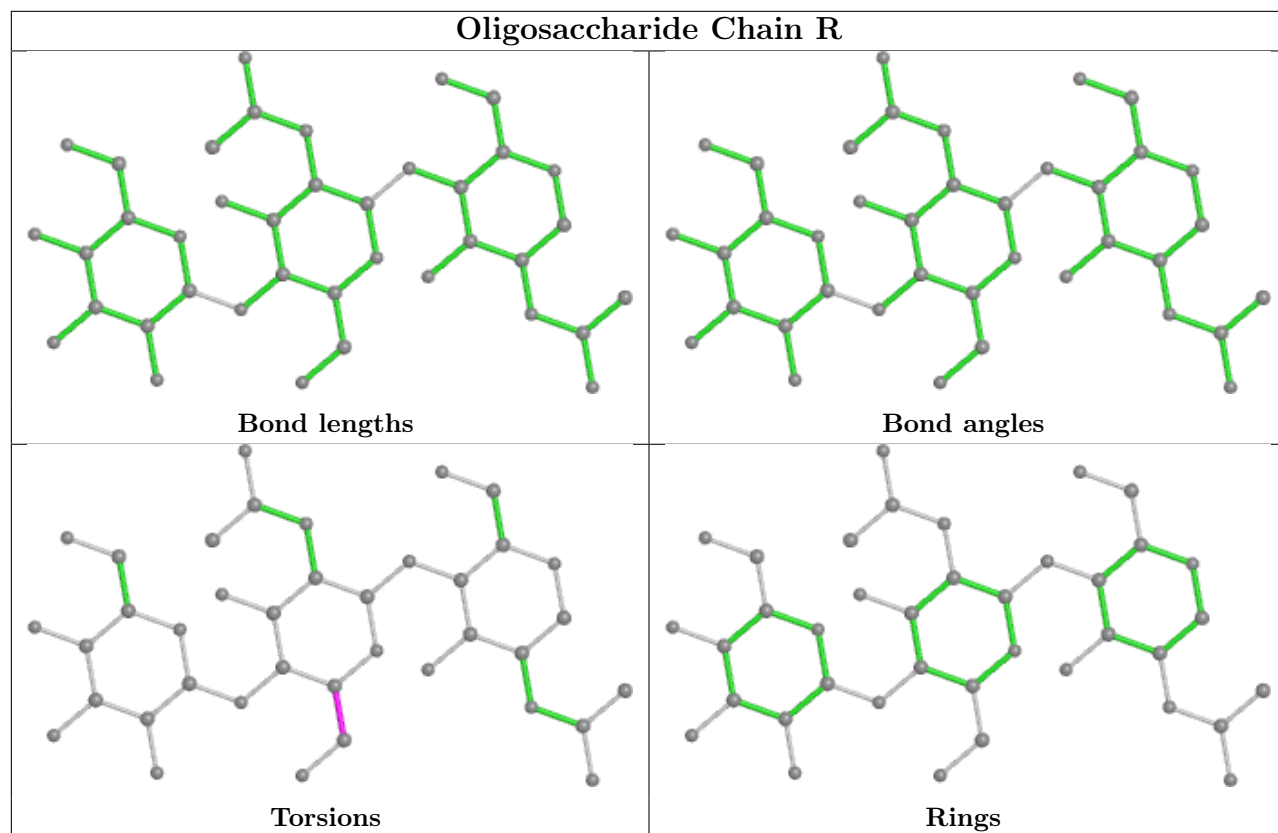


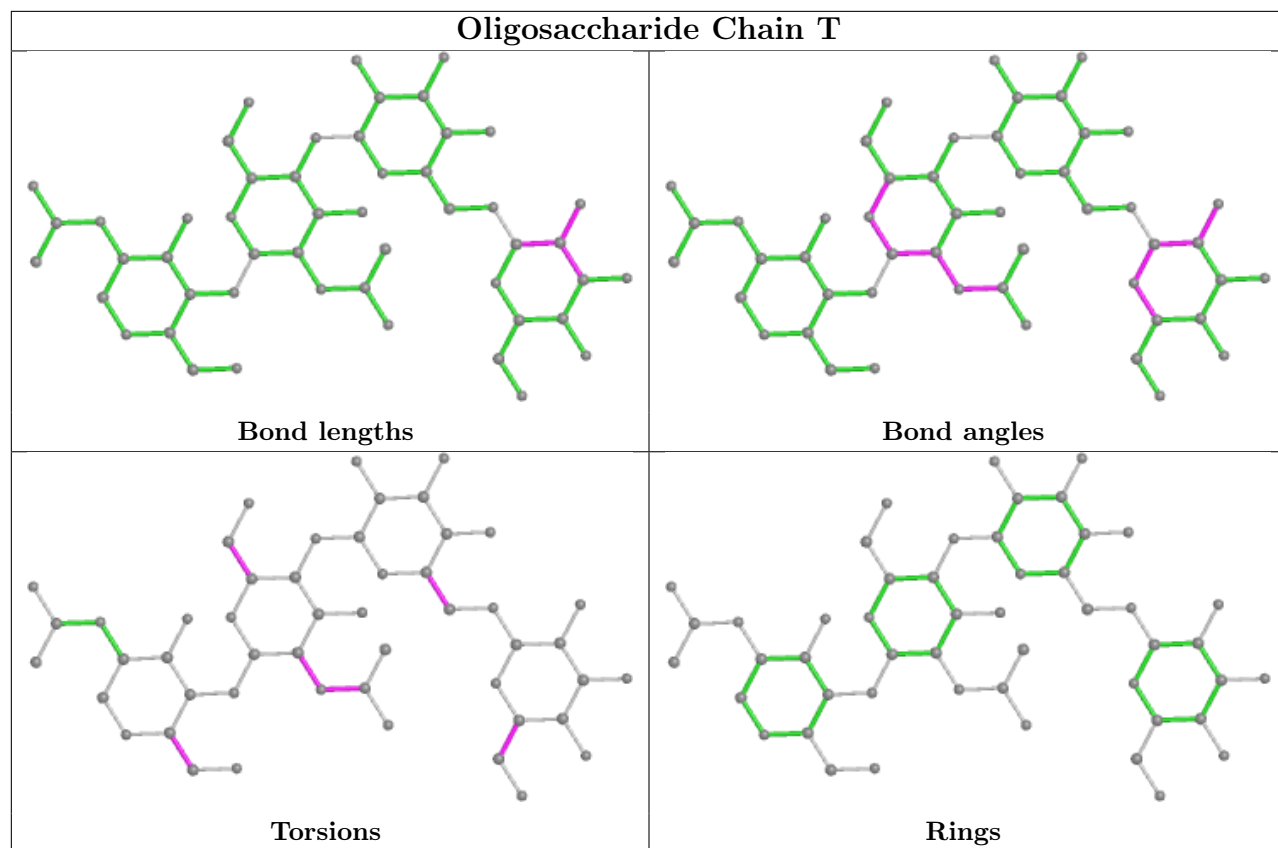


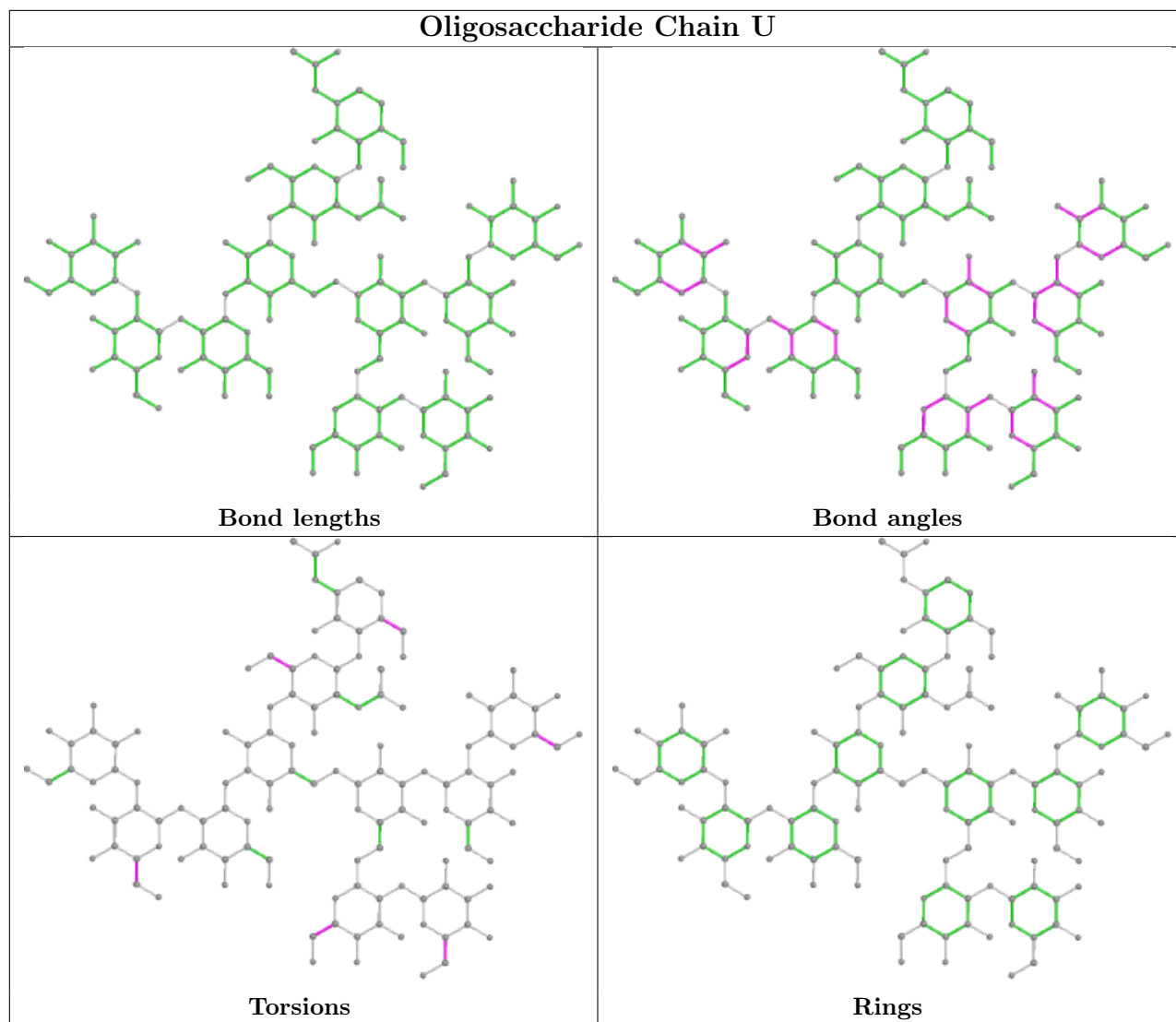












## 5.6 Ligand geometry [i](#)

2 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	$\# Z  > 2$
16	NAG	D	705	4	14,14,15	0.21	0	17,19,21	0.40	0
16	NAG	C	615	3	14,14,15	0.35	0	17,19,21	0.35	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
16	NAG	D	705	4	-	2/6/23/26	0/1/1/1
16	NAG	C	615	3	-	2/6/23/26	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
16	D	705	NAG	O5-C5-C6-O6
16	C	615	NAG	C4-C5-C6-O6
16	C	615	NAG	O5-C5-C6-O6
16	D	705	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

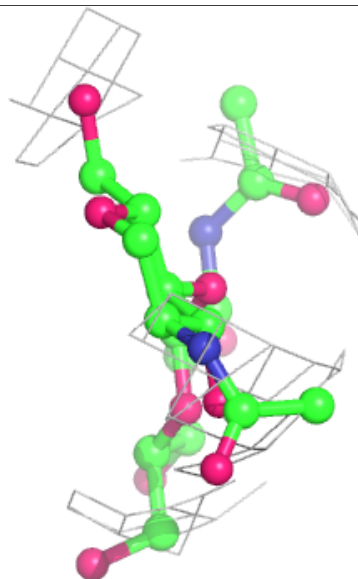
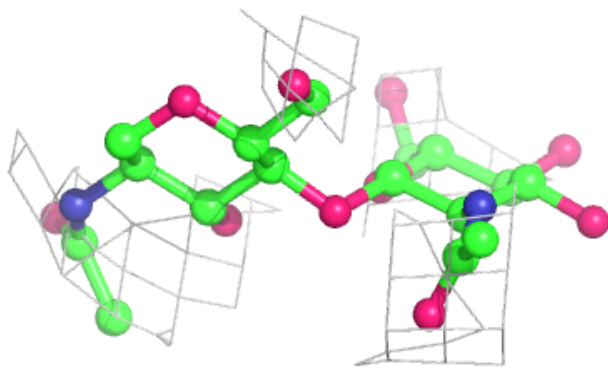
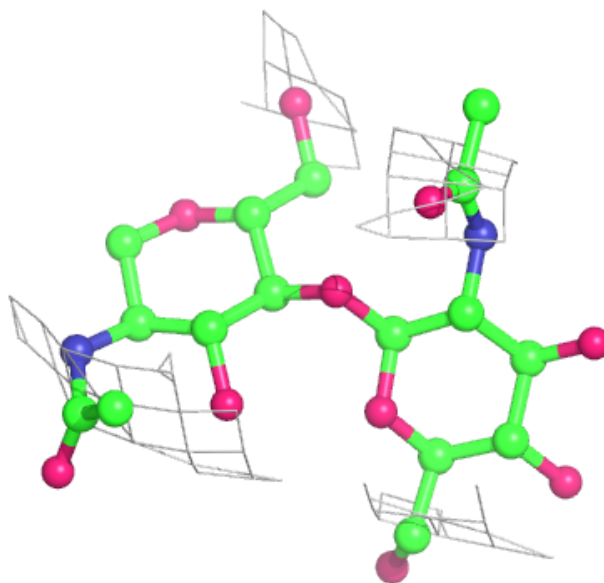
### 6.3 Carbohydrates

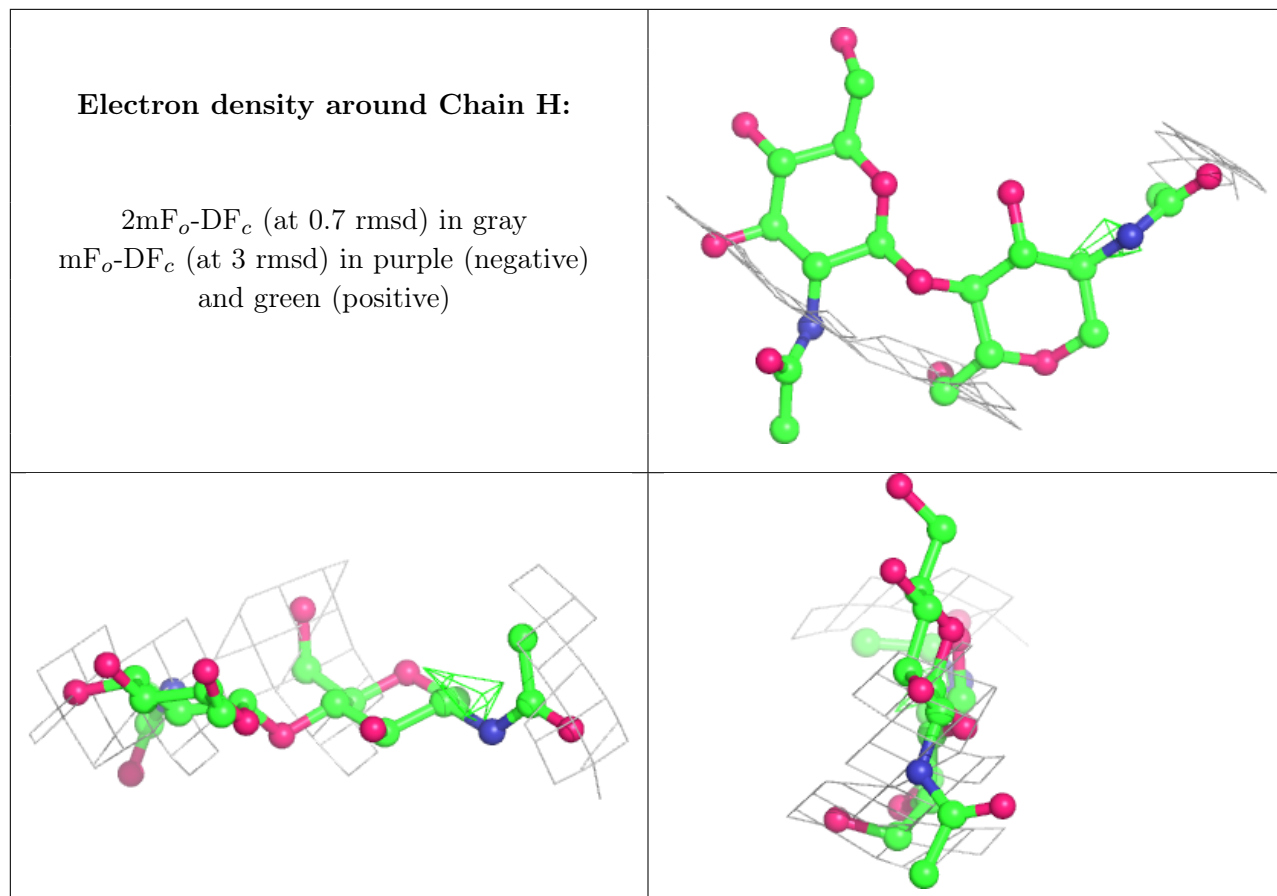
Unable to reproduce the depositors R factor - this section is therefore empty.

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 G:**

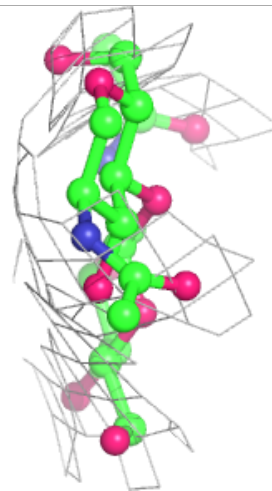
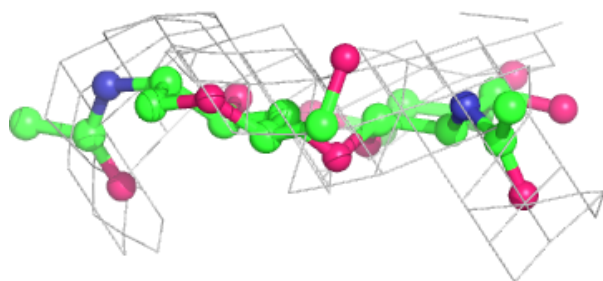
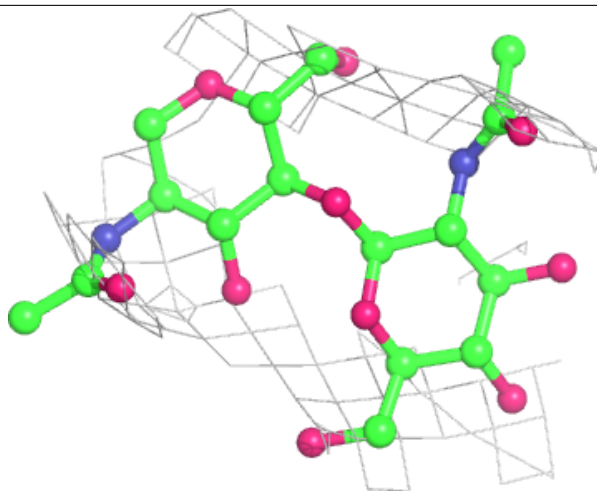
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



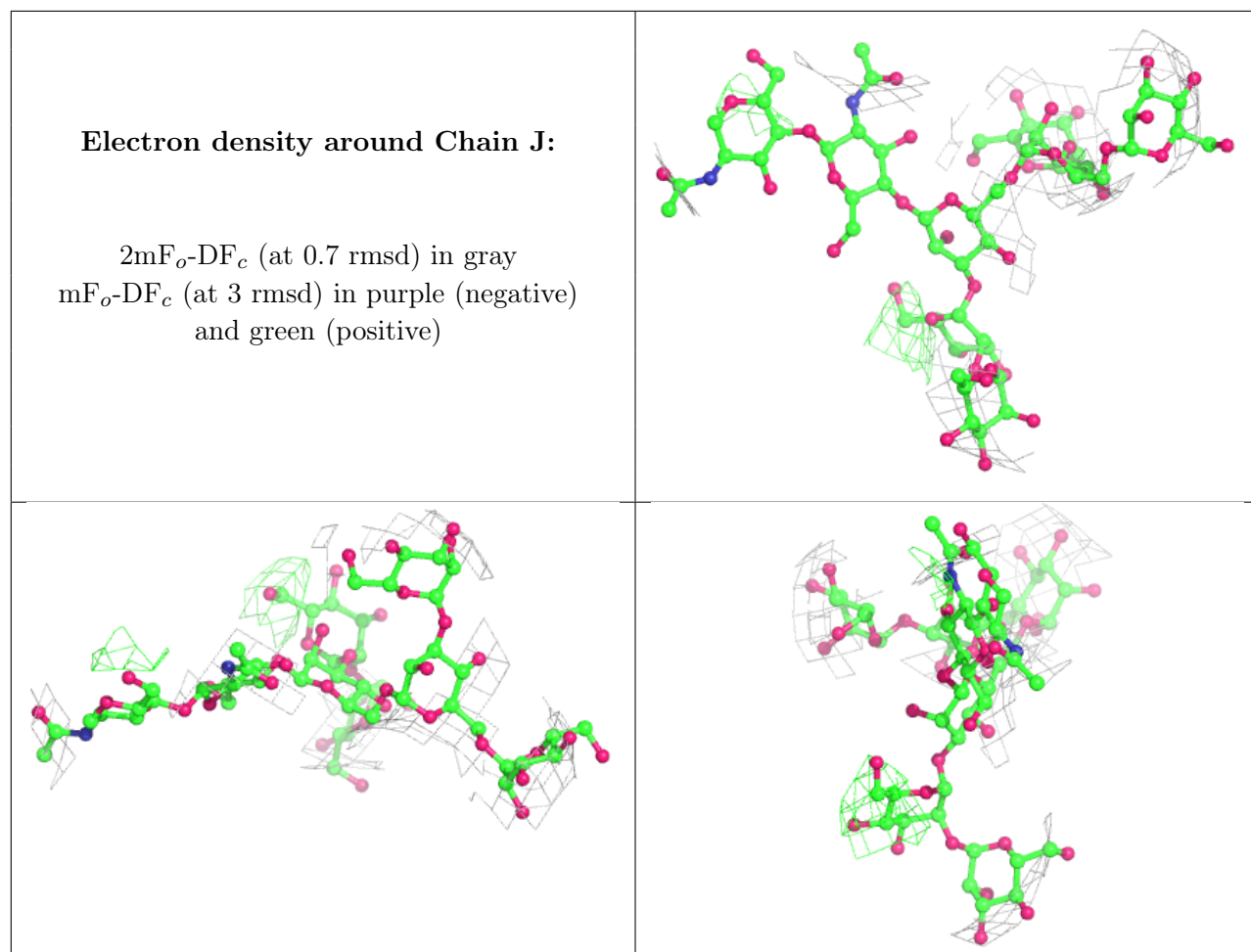


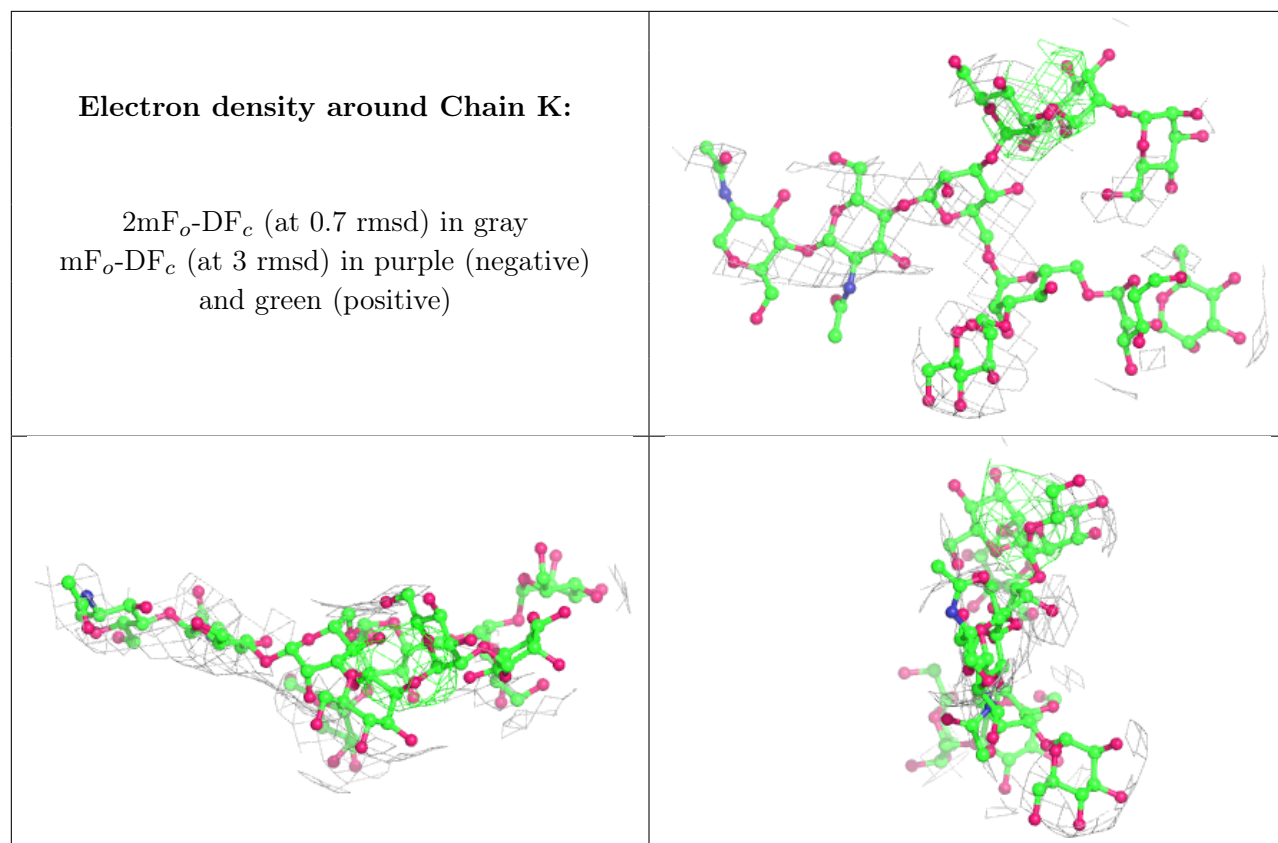
**Electron density around Chain I:**

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



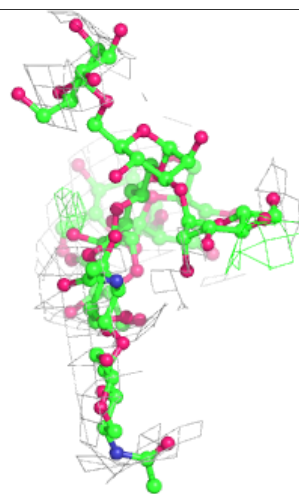
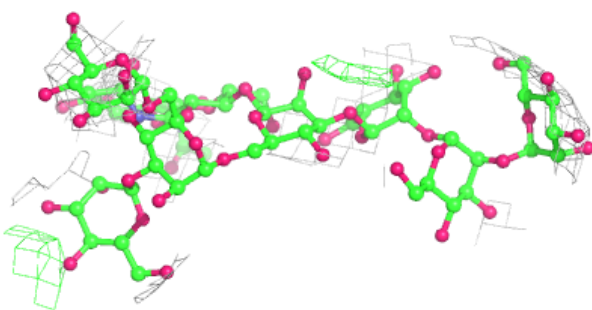
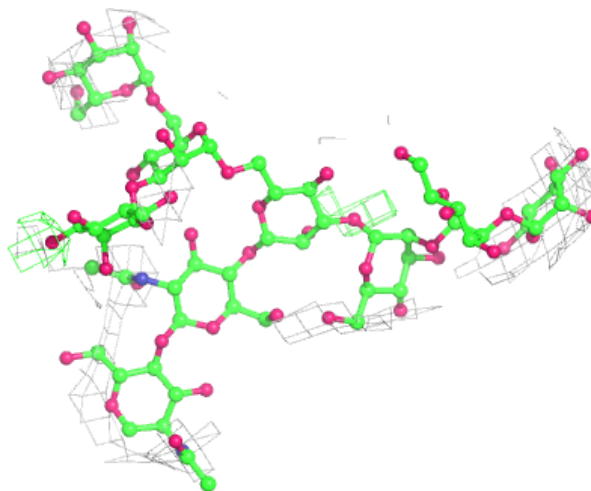






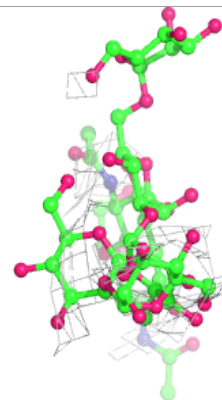
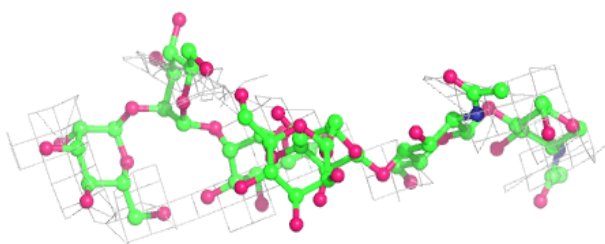
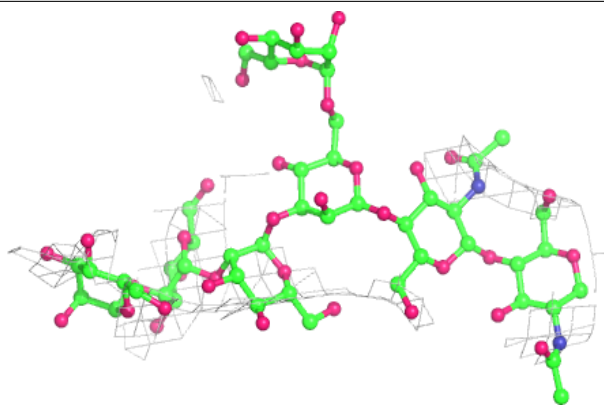
**Electron density around Chain L:**

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

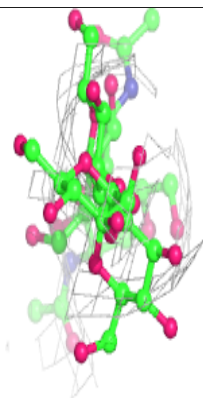
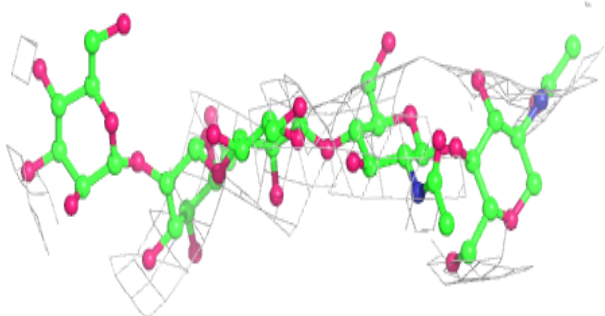
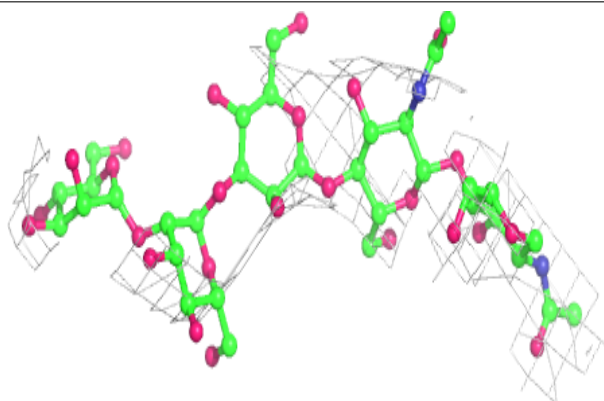


**Electron density around Chain M:**

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

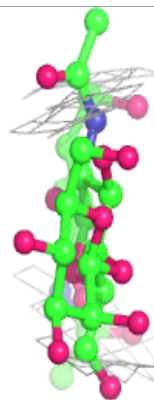
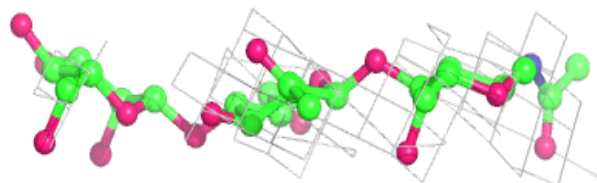
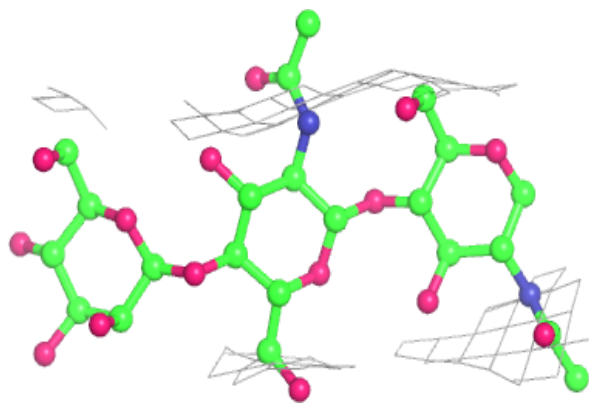
**Electron density around Chain N:**

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

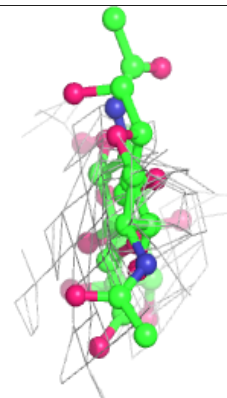
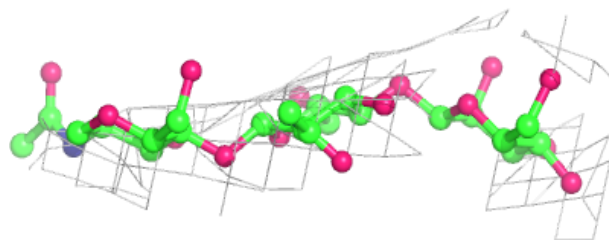
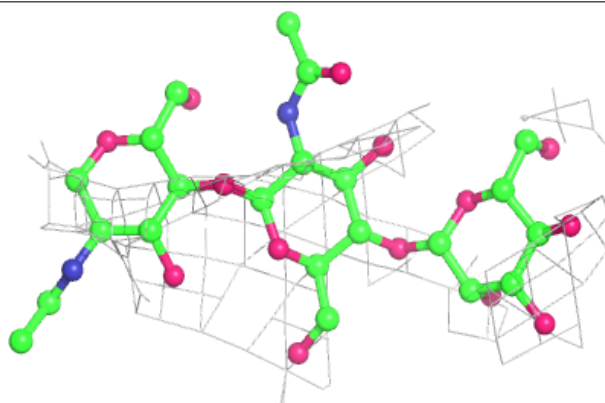


**Electron density around Chain O:**

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

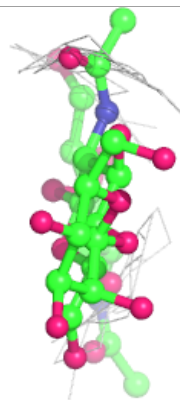
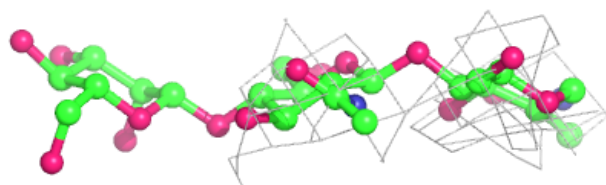
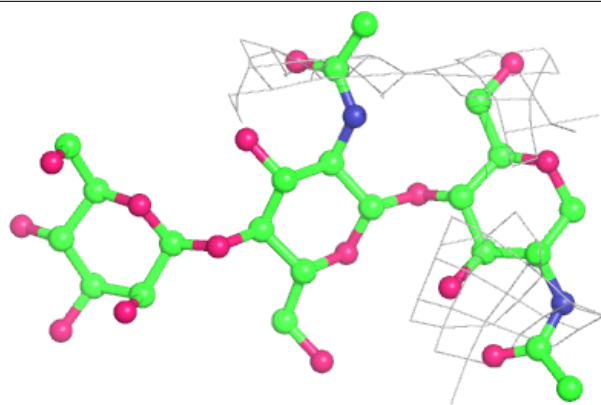
**Electron density around Chain P:**

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

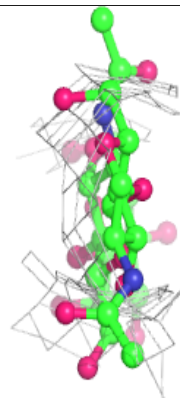
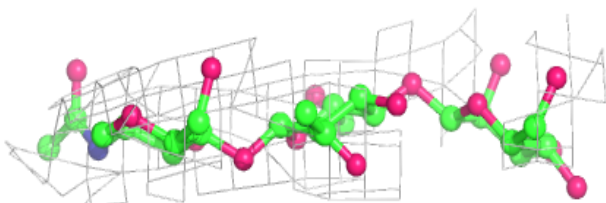
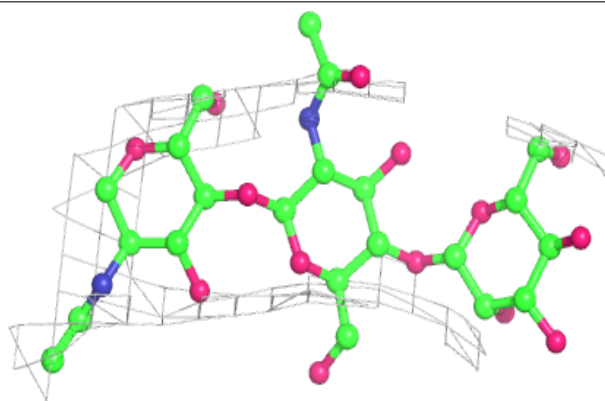


**Electron density around Chain Q:**

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

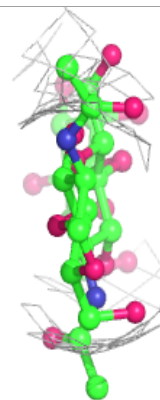
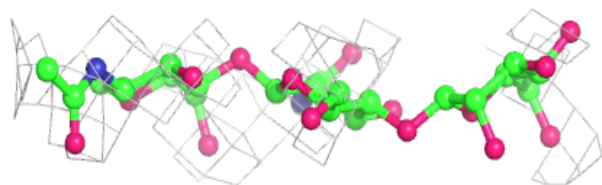
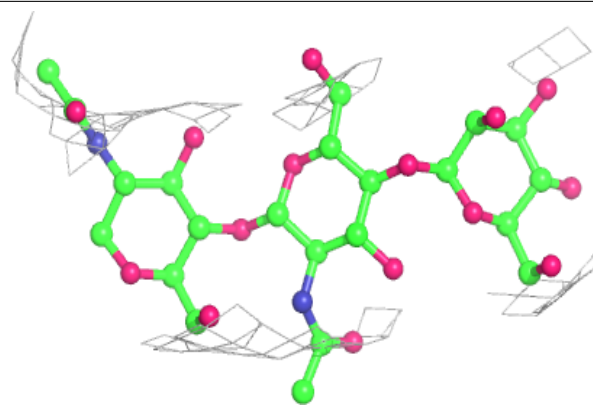
**Electron density around Chain R:**

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

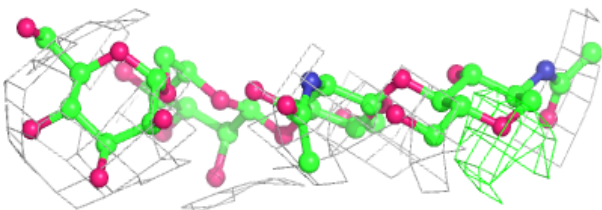
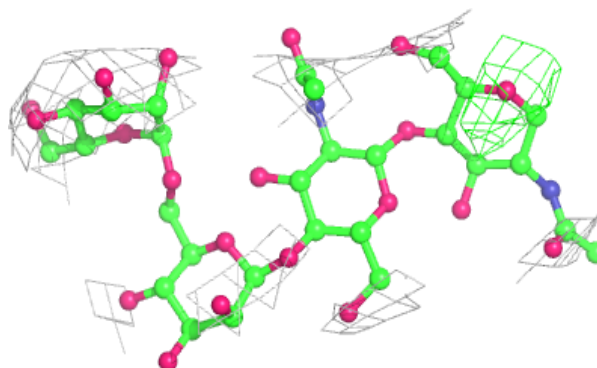


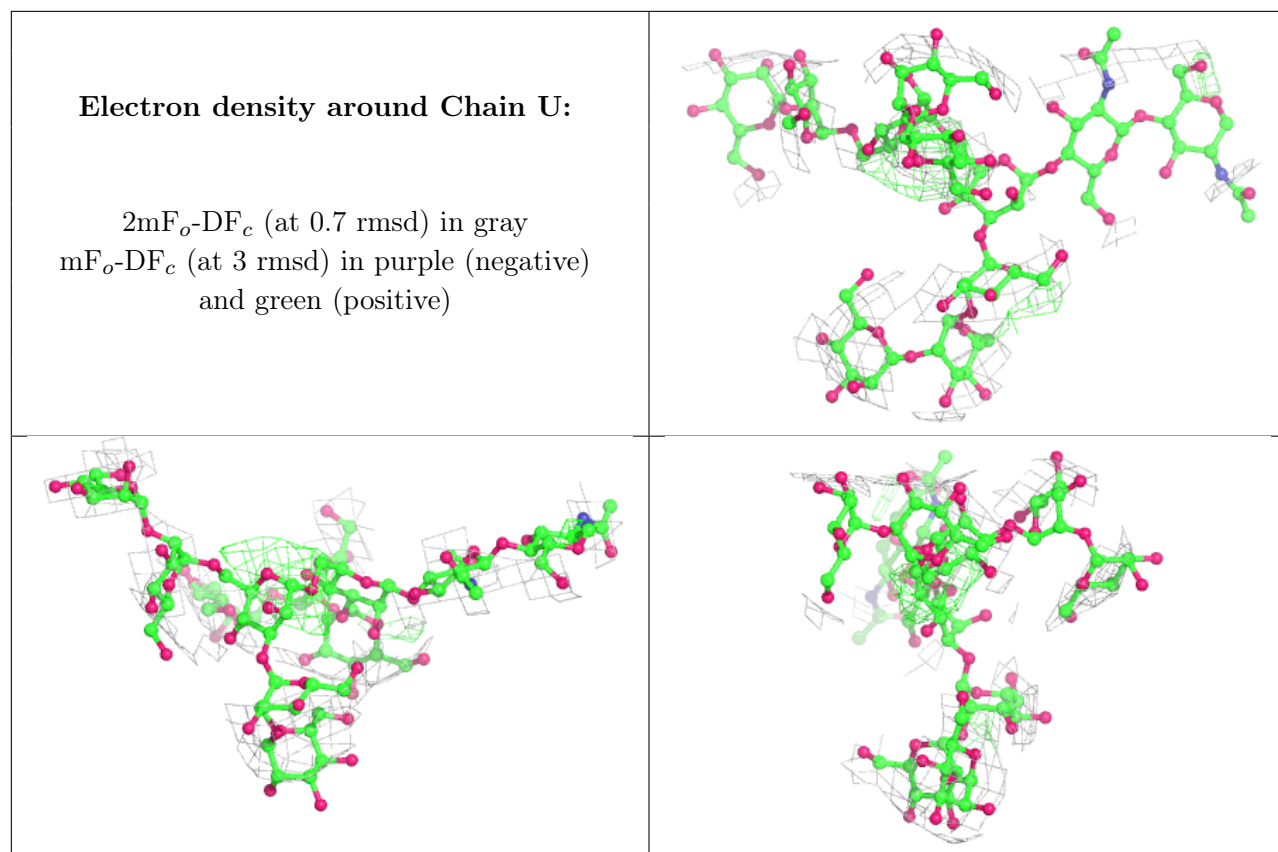
**Electron density around Chain S:**

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

**Electron density around Chain T:**

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





## 6.4 Ligands [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.

## 6.5 Other polymers [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.