



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 27, 2022 – 06:50 PM JST

PDB ID : 7F95  
Title : Bifunctional xylosidase/glucosidase LXYL with intermediate substrate xylose for 2 min  
Authors : Gong, W.M.; Yang, L.Y.  
Deposited on : 2021-07-03  
Resolution : 2.43 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>.

---

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

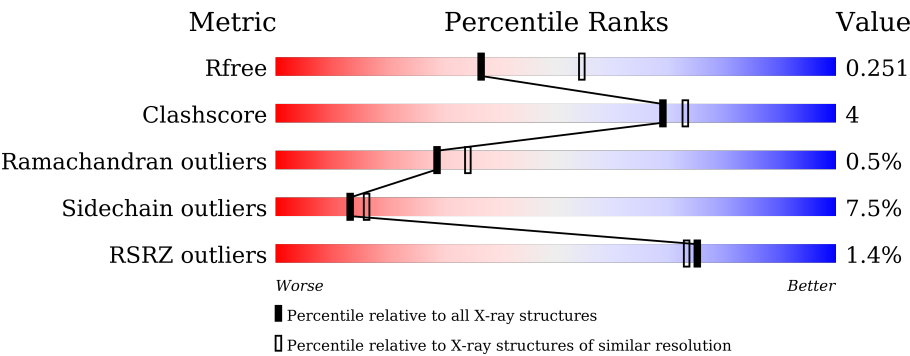
MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.29

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.43 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.




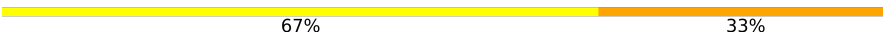
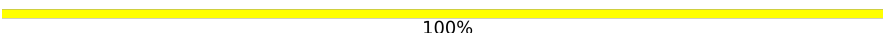
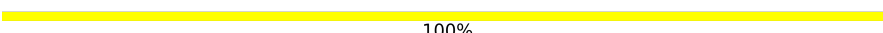
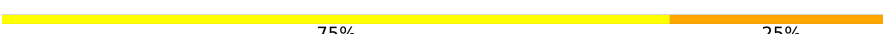
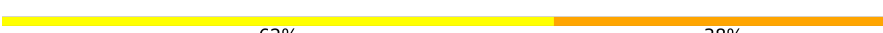




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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	803	<div><div></div><div>83%8%• 6%</div></div>
1	B	803	<div><div></div><div>83%10%• 6%</div></div>
1	C	803	<div><div>2%</div><div></div><div>82%10%• 6%</div></div>
1	D	803	<div><div>2%</div><div></div><div>80%12%• 6%</div></div>
2	E	8	<div><div></div><div>12%75%12%</div></div>
3	F	4	<div><div></div><div>25%75%</div></div>

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
4	G	9	
5	H	3	
5	J	3	
5	L	3	
6	I	8	
7	K	8	
8	M	2	
8	N	2	
8	O	2	
8	P	2	

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
13	MAN	B	909	-	-	-	X
14	BMA	B	908	-	-	X	-
7	NAG	K	1	-	-	X	-

## 2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 24674 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 Beta-D-xylosidase/beta-D-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	756	Total	C	N	O	S	0	2	0
			5719	3621	957	1124	17			
1	B	756	Total	C	N	O	S	0	4	0
			5736	3633	958	1128	17			
1	C	756	Total	C	N	O	S	0	2	0
			5716	3621	955	1123	17			
1	D	756	Total	C	N	O	S	0	2	0
			5720	3624	956	1123	17			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	8	Total	C	N	O	0	0	0
			92	50	1	41			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(4-3)-alpha-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
3	F	4	Total	C	N	O	0	0	0
			53	30	3	20			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-2)-beta-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
4	G	9	Total	C	N	O	0	0	0
			105	58	2	45			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	L	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[beta-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
6	I	8	Total	C	N	O	0	0	0
			94	52	2	40			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(6-4)]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
7	K	8	Total	C	N	O	0	0	0
			95	52	2	41			

- Molecule 8 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
8	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
8	N	2	Total	C	N	O	0	0	0
			28	16	2	10			
8	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



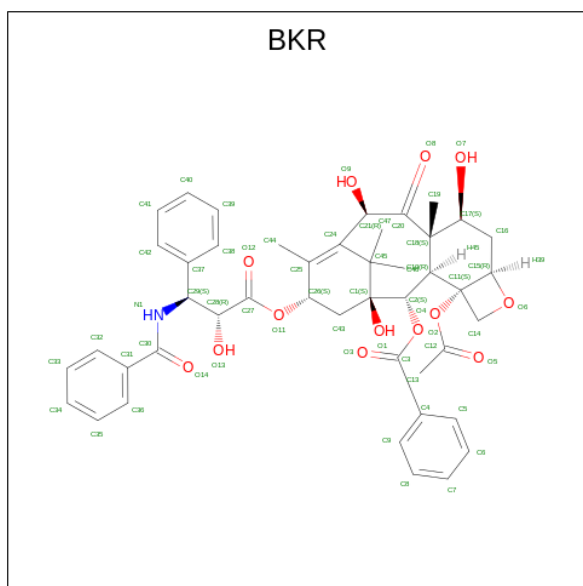
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			13	8	1	4		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	C	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

Continued from previous page...

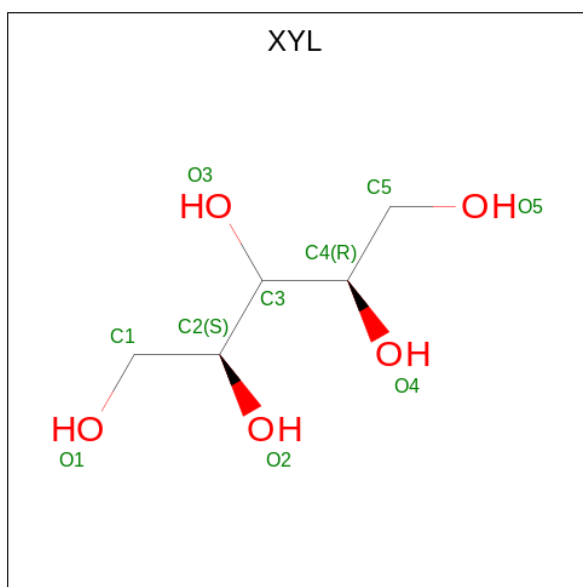
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	N	O	0	0
			14	8	1	5		
9	C	1	Total	C	N	O	0	0
			14	8	1	5		
9	D	1	Total	C	N	O	0	0
			14	8	1	5		
9	D	1	Total	C	N	O	0	0
			14	8	1	5		
9	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is Deacetyltaxol (three-letter code: BKR) (formula:  $C_{45}H_{49}NO_{13}$ ) (labeled as "Ligand of Interest" by depositor).



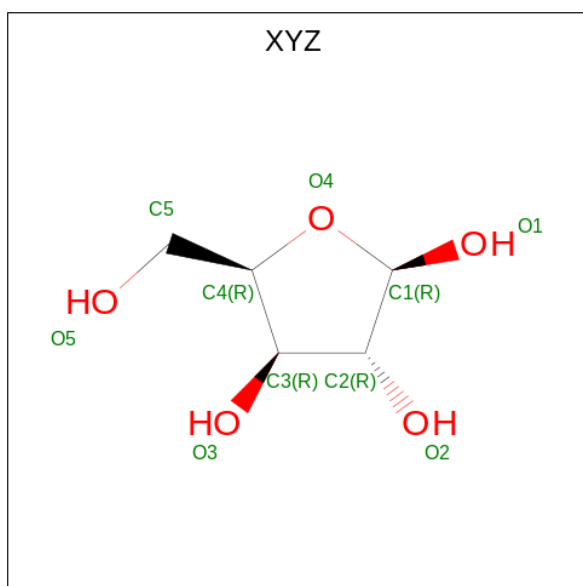
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	N	O	0	0
			59	45	1	13		
10	B	1	Total	C	N	O	0	0
			59	45	1	13		

- Molecule 11 is Xylitol (three-letter code: XYL) (formula:  $C_5H_{12}O_5$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			9	5	4		

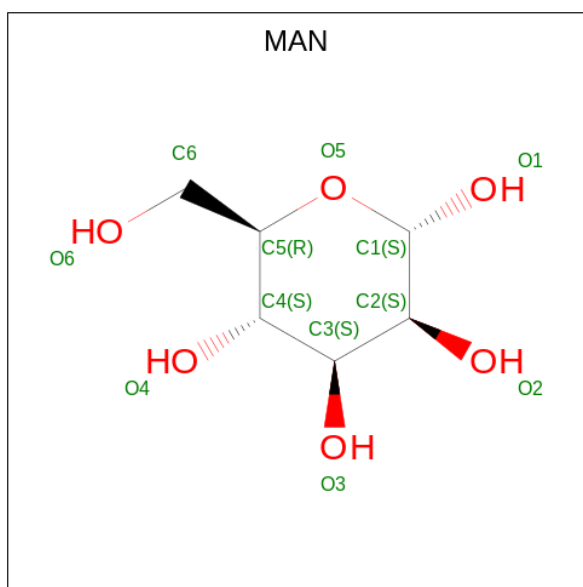
- Molecule 12 is beta-D-xylofuranose (three-letter code: XYZ) (formula:  $C_5H_{10}O_5$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	C	O	0	0
			10	5	5		

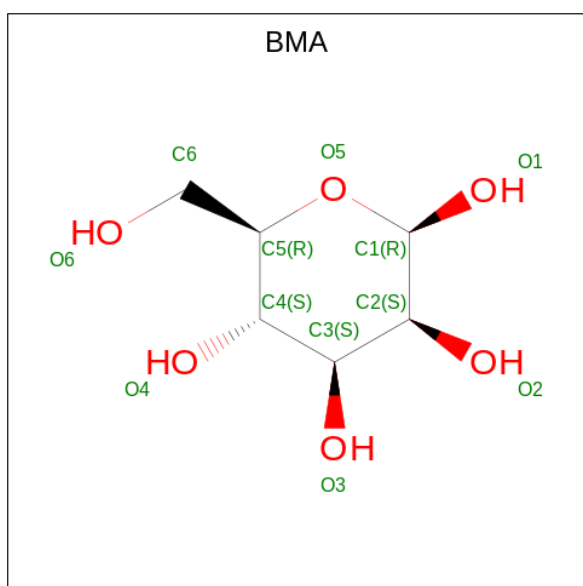
- Molecule 13 is alpha-D-mannopyranose (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	C	O	0	0
			11	6	5		
13	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 14 is beta-D-mannopyranose (three-letter code: BMA) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	B	1	Total	C	O	0	0
			11	6	5		

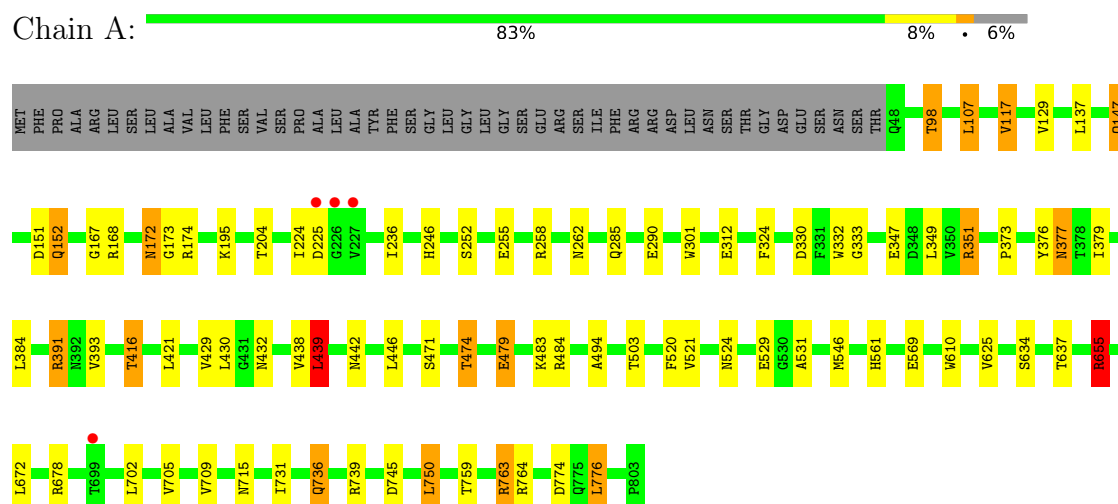
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	277	Total 277	O 277	0	0
15	B	240	Total 240	O 240	0	0
15	C	122	Total 122	O 122	0	0
15	D	96	Total 96	O 96	0	0

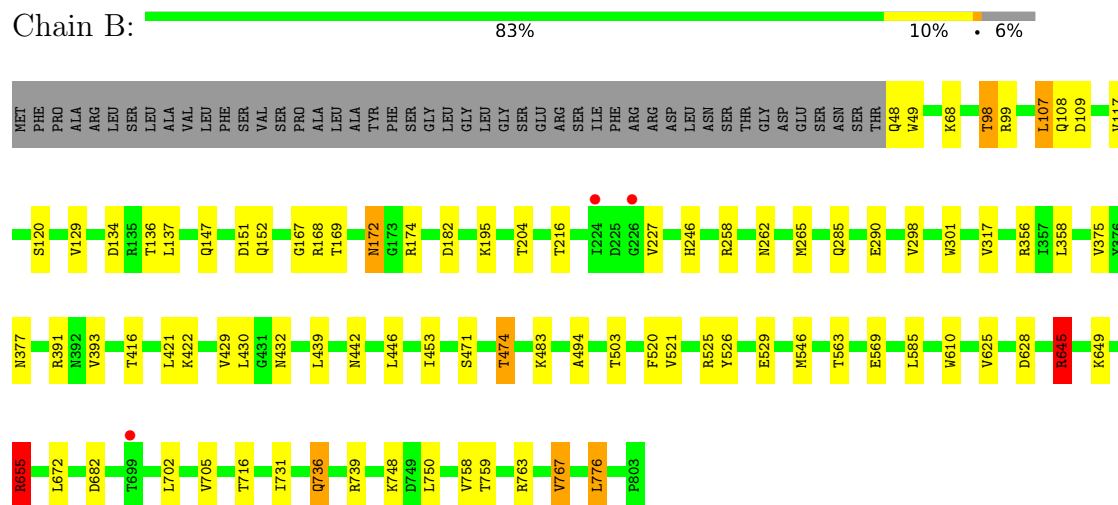
### 3 Residue-property plots [i](#)

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

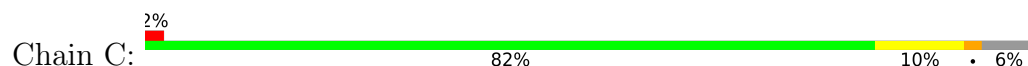
- Molecule 1: Beta-D-xylosidase/beta-D-glucosidase

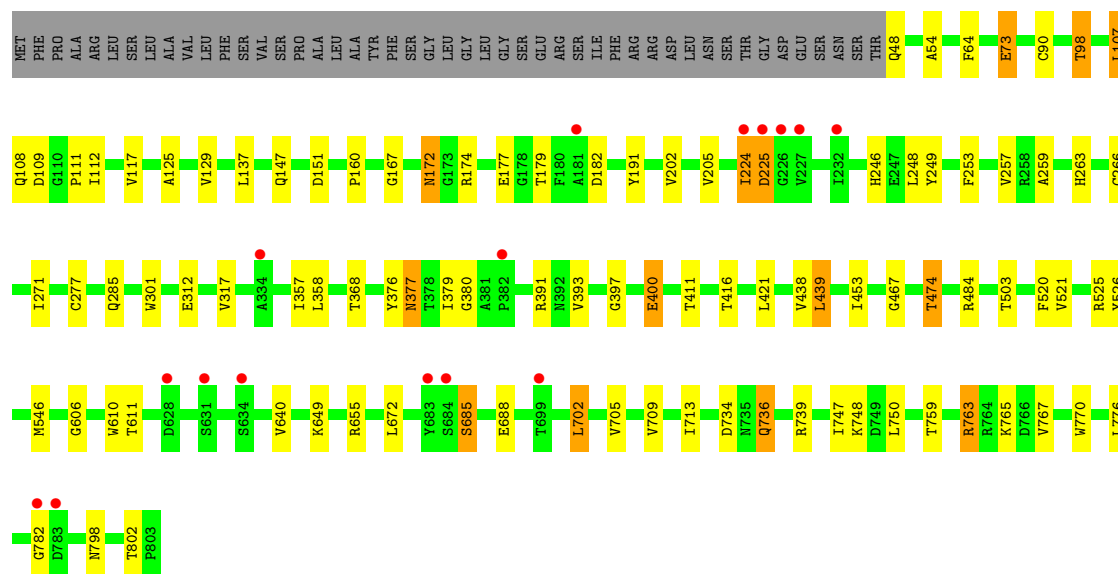


- Molecule 1: Beta-D-xylosidase/beta-D-glucosidase

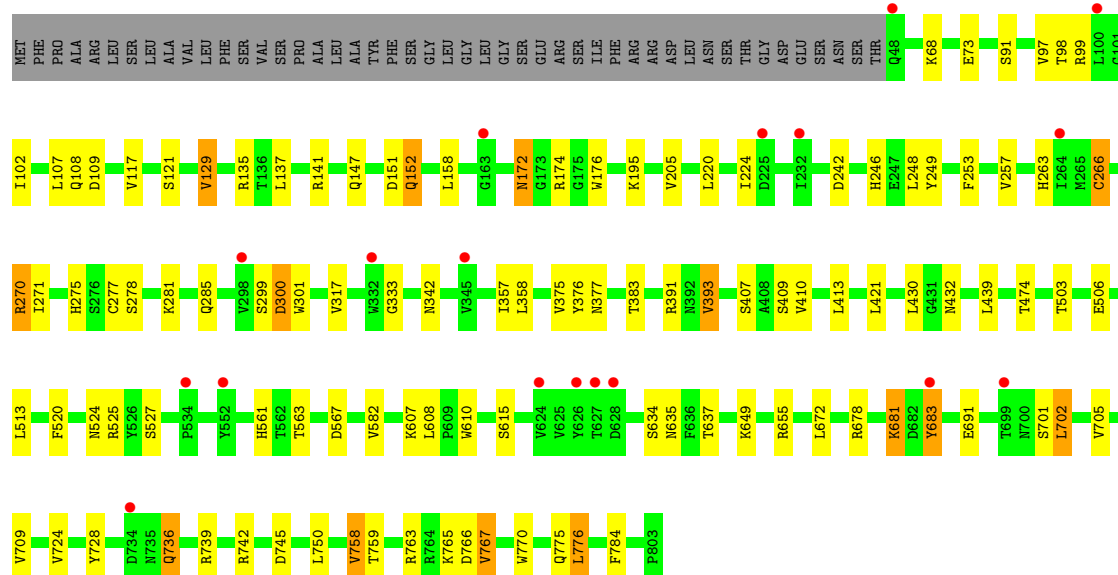
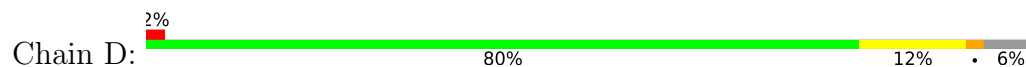


- Molecule 1: Beta-D-xylosidase/beta-D-glucosidase





• Molecule 1: Beta-D-xylosidase/beta-D-glucosidase



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



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

Chain F:  25% 75%

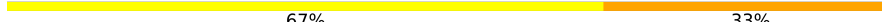


- Molecule 4: alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-2)-beta-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  11% 44% 44%

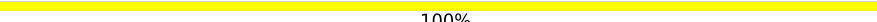


- Molecule 5: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  67% 33%

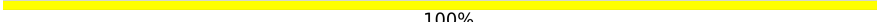


- Molecule 5: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  100%




- Molecule 5: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  100%



- Molecule 6: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[beta-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 I:  75% 25%



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(6-4)]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:  62% 38%

MAG1  
MAG2  
BMA3  
MAN4  
MAN5  
MAN6  
MAN7  
MAN8

- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  100%

MAG1  
MAG2

- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%

MAG1  
MAG2

- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  50% 50%

MAG1  
MAG2

- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  100%

MAG1  
MAG2

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	228.70Å 89.31Å 218.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	218.41 – 2.43 36.11 – 2.43	Depositor EDS
% Data completeness (in resolution range)	99.7 (218.41-2.43) 99.7 (36.11-2.43)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.198 , 0.246 0.209 , 0.251	Depositor DCC
$R_{free}$ test set	8500 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.8	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 26.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.010 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	24674	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, XYZ, XYL, MAN, BKR, NAG

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	0.75	1/5862 (0.0%)	0.91	17/8020 (0.2%)
1	B	0.75	0/5883	0.90	16/8049 (0.2%)
1	C	0.68	0/5863	0.82	5/8023 (0.1%)
1	D	0.70	0/5867	0.86	7/8027 (0.1%)
All	All	0.72	1/23475 (0.0%)	0.87	45/32119 (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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	479	GLU	CD-OE1	5.68	1.31	1.25

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	351	ARG	NE-CZ-NH1	9.32	124.96	120.30
1	A	351	ARG	NE-CZ-NH2	-8.63	115.98	120.30
1	B	391	ARG	NE-CZ-NH2	-8.40	116.10	120.30
1	A	484	ARG	NE-CZ-NH1	-7.68	116.46	120.30
1	A	391	ARG	NE-CZ-NH1	7.40	124.00	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	333	GLY	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5719	0	5511	31	0
1	B	5736	0	5528	30	0
1	C	5716	0	5508	39	0
1	D	5720	0	5517	51	0
2	E	92	0	78	2	0
3	F	53	0	46	0	0
4	G	105	0	88	5	0
5	H	39	0	34	3	0
5	J	39	0	34	0	0
5	L	39	0	34	0	0
6	I	94	0	79	1	0
7	K	95	0	76	12	0
8	M	28	0	25	4	0
8	N	28	0	25	5	0
8	O	28	0	25	5	0
8	P	28	0	24	0	0
9	A	69	0	63	2	0
9	B	56	0	52	0	0
9	C	42	0	39	0	0
9	D	42	0	39	0	0
10	A	59	0	0	1	0
10	B	59	0	0	2	0
11	A	9	0	9	0	0
12	B	10	0	7	2	0
13	B	23	0	22	2	0
14	B	11	0	10	6	0
15	A	277	0	0	4	0
15	B	240	0	0	4	0
15	C	122	0	0	1	0
15	D	96	0	0	4	0
All	All	24674	0	22873	174	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 4.

The worst 5 of 174 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)
8:M:1:NAG:O4	8:M:1:NAG:C4	1.82	1.27
4:G:1:NAG:C4	4:G:1:NAG:O4	1.81	1.27
8:N:1:NAG:O4	8:N:1:NAG:C4	1.84	1.25
9:A:901:NAG:C4	2:E:1:NAG:O1	1.92	1.17
1:B:216:THR:OG1	14:B:908:BMA:C1	1.93	1.15

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	756/803 (94%)	717 (95%)	38 (5%)	1 (0%)	51	64
1	B	758/803 (94%)	722 (95%)	34 (4%)	2 (0%)	41	49
1	C	756/803 (94%)	700 (93%)	49 (6%)	7 (1%)	17	20
1	D	756/803 (94%)	691 (91%)	61 (8%)	4 (0%)	29	34
All	All	3026/3212 (94%)	2830 (94%)	182 (6%)	14 (0%)	29	34

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	225	ASP
1	D	91	SER
1	D	224	ILE
1	C	73	GLU
1	C	179	THR

### 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	610/648 (94%)	570 (93%)	40 (7%)	16	20
1	B	613/648 (95%)	569 (93%)	44 (7%)	14	17
1	C	610/648 (94%)	565 (93%)	45 (7%)	13	16
1	D	611/648 (94%)	557 (91%)	54 (9%)	10	10
All	All	2444/2592 (94%)	2261 (92%)	183 (8%)	13	16

5 of 183 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	672	LEU
1	D	270	ARG
1	C	709	VAL
1	D	73	GLU
1	D	358	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	442	ASN
1	D	229	GLN
1	C	676	HIS
1	D	147	GLN
1	D	262	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

54 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	NAG	E	1	2	15,15,15	0.52	0	21,21,21	1.61	3 (14%)
2	BMA	E	2	2	11,11,12	0.99	0	15,15,17	1.49	1 (6%)
2	MAN	E	3	2	11,11,12	0.79	0	15,15,17	2.73	4 (26%)
2	BMA	E	4	2	11,11,12	0.99	1 (9%)	15,15,17	2.86	2 (13%)
2	MAN	E	5	2	11,11,12	0.76	0	15,15,17	2.16	6 (40%)
2	MAN	E	6	2	11,11,12	0.64	0	15,15,17	0.98	0
2	MAN	E	7	2	11,11,12	0.70	0	15,15,17	2.10	3 (20%)
2	MAN	E	8	2	11,11,12	0.63	0	15,15,17	1.42	2 (13%)
3	NAG	F	1	3,1	14,14,15	0.55	0	17,19,21	0.89	0
3	NAG	F	2	3	14,14,15	0.50	0	17,19,21	1.23	2 (11%)
3	MAN	F	3	3	11,11,12	0.80	0	15,15,17	1.97	5 (33%)
3	NAG	F	4	3	14,14,15	2.89	3 (21%)	19,19,21	3.83	10 (52%)
4	NAG	G	1	4,1	14,14,15	4.39	1 (7%)	17,19,21	1.86	5 (29%)
4	NAG	G	2	4	14,14,15	0.67	0	17,19,21	1.72	5 (29%)
4	BMA	G	3	4	11,11,12	1.06	0	15,15,17	1.69	2 (13%)
4	MAN	G	4	4	11,11,12	0.77	0	15,15,17	2.37	7 (46%)
4	BMA	G	5	4	11,11,12	0.34	0	15,15,17	1.19	1 (6%)
4	MAN	G	6	4	11,11,12	0.73	0	15,15,17	1.76	2 (13%)
4	MAN	G	7	4	11,11,12	0.60	0	15,15,17	1.20	1 (6%)
4	BMA	G	8	4	11,11,12	0.26	0	15,15,17	0.64	0
4	MAN	G	9	4	11,11,12	0.93	1 (9%)	15,15,17	1.96	3 (20%)
5	NAG	H	1	1,5	14,14,15	0.71	0	17,19,21	1.06	1 (5%)
5	NAG	H	2	5	14,14,15	0.47	0	17,19,21	1.70	3 (17%)
5	MAN	H	3	5	11,11,12	1.13	1 (9%)	15,15,17	2.41	7 (46%)
6	NAG	I	1	6,1	14,14,15	1.10	1 (7%)	17,19,21	1.16	2 (11%)
6	NAG	I	2	6	14,14,15	0.47	0	17,19,21	1.35	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	BMA	I	3	6	11,11,12	0.79	0	15,15,17	2.42	5 (33%)
6	MAN	I	4	6	11,11,12	0.89	0	15,15,17	2.64	4 (26%)
6	MAN	I	5	6	11,11,12	0.98	0	15,15,17	2.08	6 (40%)
6	MAN	I	6	6	11,11,12	0.75	0	15,15,17	2.38	6 (40%)
6	MAN	I	7	6	11,11,12	0.24	0	15,15,17	1.03	1 (6%)
6	BMA	I	8	6	11,11,12	0.56	0	15,15,17	1.71	4 (26%)
5	NAG	J	1	1,5	14,14,15	0.35	0	17,19,21	0.80	1 (5%)
5	NAG	J	2	5	14,14,15	0.74	0	17,19,21	1.19	2 (11%)
5	MAN	J	3	5	11,11,12	1.53	3 (27%)	15,15,17	2.61	5 (33%)
7	NAG	K	1	7,1	14,14,15	1.03	1 (7%)	17,19,21	2.22	3 (17%)
7	NAG	K	2	7	14,14,15	0.58	0	17,19,21	1.91	3 (17%)
7	BMA	K	3	7	11,11,12	0.97	1 (9%)	15,15,17	2.15	5 (33%)
7	MAN	K	4	7	11,11,12	0.29	0	15,15,17	0.68	0
7	MAN	K	5	7	11,11,12	1.16	1 (9%)	15,15,17	1.66	2 (13%)
7	MAN	K	6	7	11,11,12	1.29	3 (27%)	15,15,17	2.87	7 (46%)
7	MAN	K	7	7	11,11,12	0.50	0	15,15,17	1.93	3 (20%)
7	MAN	K	8	7	12,12,12	1.29	1 (8%)	17,17,17	1.53	2 (11%)
5	NAG	L	1	1,5	14,14,15	0.62	0	17,19,21	1.54	3 (17%)
5	NAG	L	2	5	14,14,15	0.65	0	17,19,21	1.64	4 (23%)
5	MAN	L	3	5	11,11,12	1.27	0	15,15,17	2.12	4 (26%)
8	NAG	M	1	8,1	14,14,15	4.57	1 (7%)	17,19,21	1.41	3 (17%)
8	NAG	M	2	8	14,14,15	0.86	0	17,19,21	1.76	5 (29%)
8	NAG	N	1	8,1	14,14,15	4.80	1 (7%)	17,19,21	1.43	2 (11%)
8	NAG	N	2	8	14,14,15	0.91	0	17,19,21	1.83	5 (29%)
8	NAG	O	1	8,1	14,14,15	1.10	1 (7%)	17,19,21	1.61	3 (17%)
8	NAG	O	2	8	14,14,15	1.02	1 (7%)	17,19,21	1.51	3 (17%)
8	NAG	P	1	8,1	14,14,15	0.78	0	17,19,21	1.94	4 (23%)
8	NAG	P	2	8	14,14,15	0.69	0	17,19,21	1.60	3 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	2	-	2/6/26/26	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

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

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	K	6	7	-	2/2/19/22	0/1/1/1
7	MAN	K	7	7	-	2/2/19/22	0/1/1/1
7	MAN	K	8	7	-	2/2/22/22	0/1/1/1
5	NAG	L	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	L	2	5	-	2/6/23/26	0/1/1/1
5	MAN	L	3	5	-	2/2/19/22	0/1/1/1
8	NAG	M	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	M	2	8	-	0/6/23/26	0/1/1/1
8	NAG	N	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	N	2	8	-	1/6/23/26	0/1/1/1
8	NAG	O	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	O	2	8	-	0/6/23/26	0/1/1/1
8	NAG	P	1	8,1	-	0/6/23/26	0/1/1/1
8	NAG	P	2	8	-	0/6/23/26	0/1/1/1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	N	1	NAG	O4-C4	17.63	1.84	1.43
8	M	1	NAG	O4-C4	16.93	1.82	1.43
4	G	1	NAG	O4-C4	16.24	1.81	1.43
3	F	4	NAG	C3-C2	9.44	1.61	1.53
3	F	4	NAG	C2-N2	3.40	1.51	1.45

The worst 5 of 178 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	4	BMA	C1-C2-C3	-9.97	97.41	109.67
3	F	4	NAG	C1-C2-N2	-8.60	100.76	110.73
6	I	4	MAN	C1-O5-C5	7.73	122.66	112.19
3	F	4	NAG	C3-C2-N2	7.21	124.64	110.38
3	F	4	NAG	C4-C3-C2	7.18	120.14	111.46

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	K	2	NAG	C3-C2-N2-C7
4	G	6	MAN	O5-C5-C6-O6
5	L	3	MAN	O5-C5-C6-O6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
7	K	6	MAN	C4-C5-C6-O6
7	K	5	MAN	O5-C5-C6-O6

All (2) ring outliers are listed below:

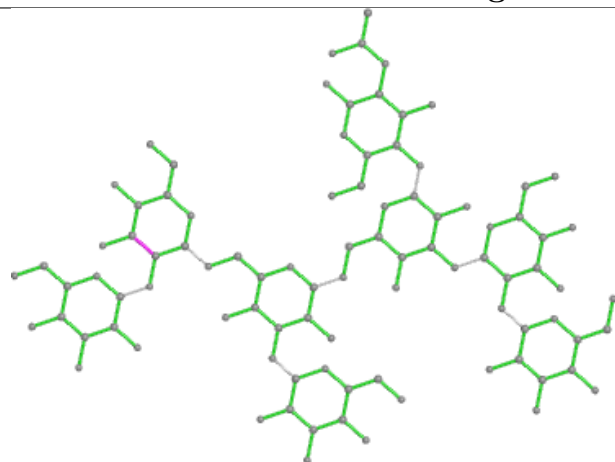
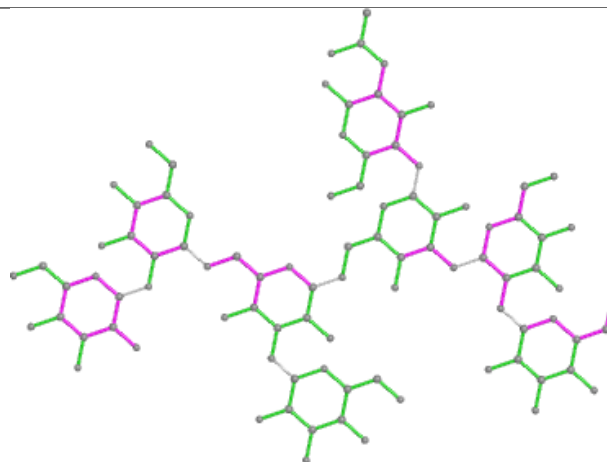
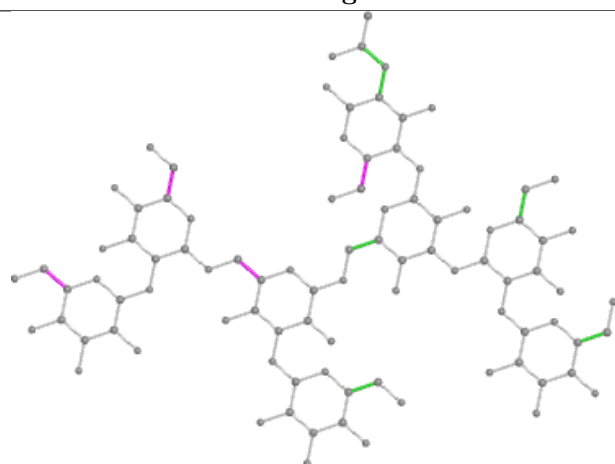
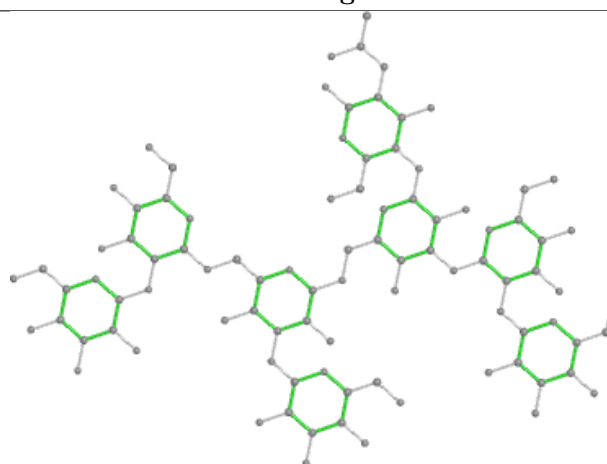
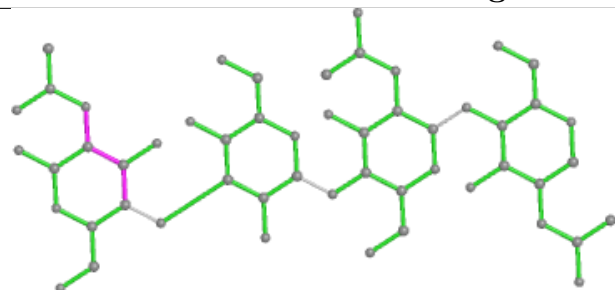
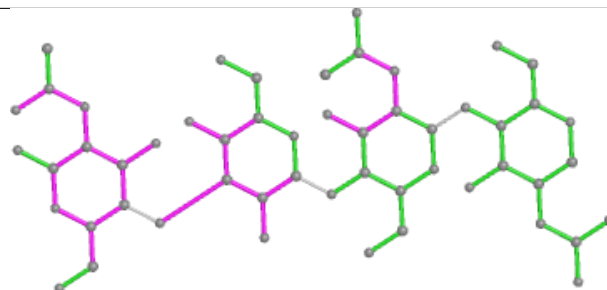
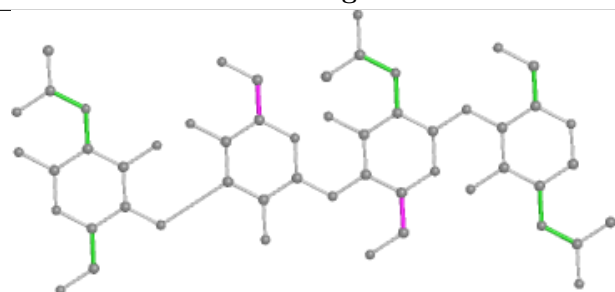
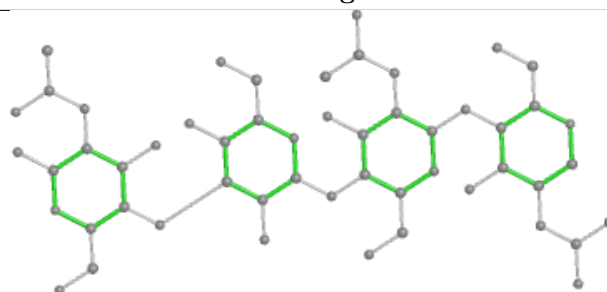
Mol	Chain	Res	Type	Atoms
4	G	6	MAN	C1-C2-C3-C4-C5-O5
6	I	6	MAN	C1-C2-C3-C4-C5-O5

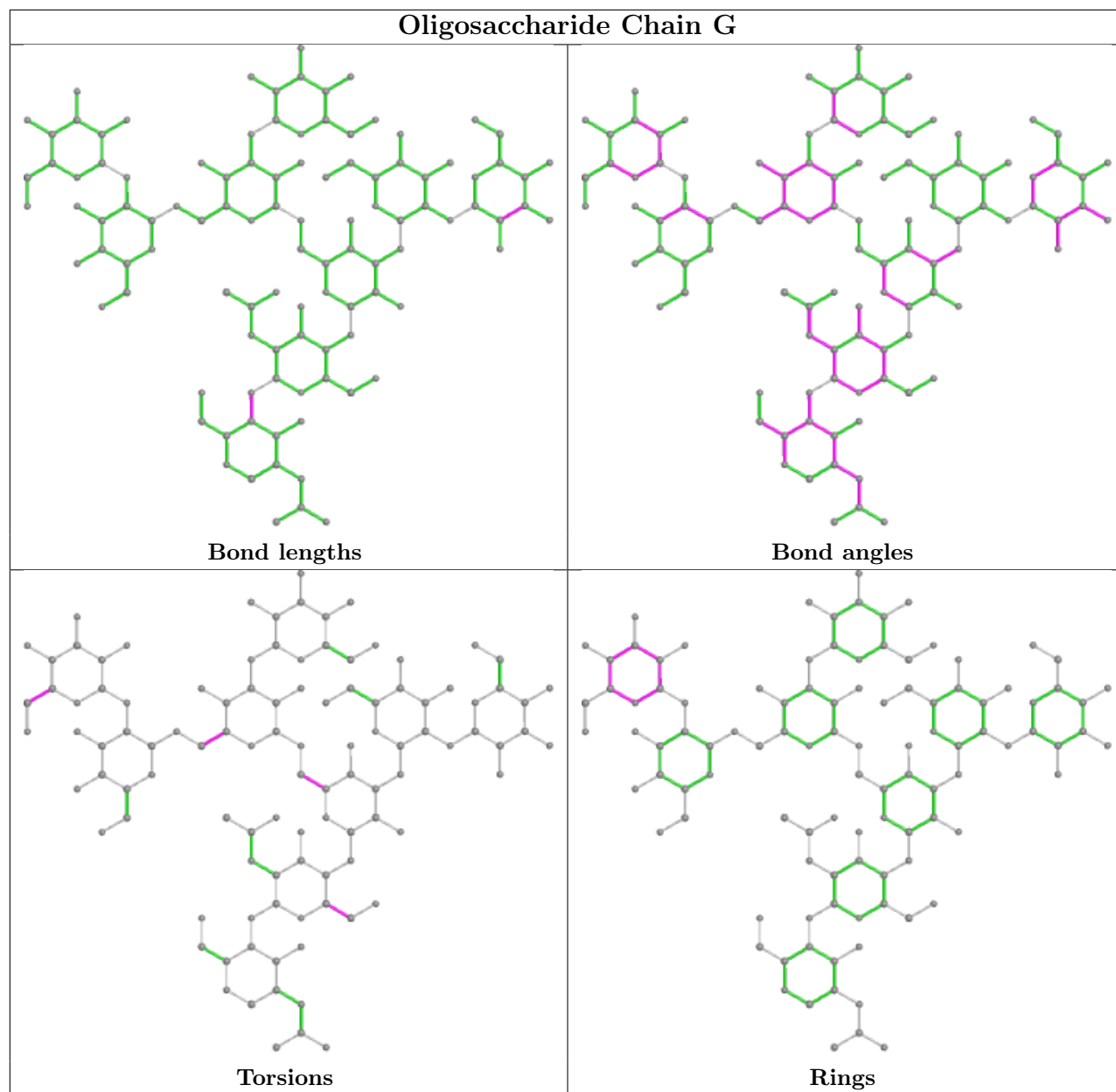
17 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	O	1	NAG	5	0
4	G	2	NAG	1	0
7	K	3	BMA	1	0
4	G	1	NAG	3	0
4	G	6	MAN	2	0
8	N	2	NAG	2	0
5	H	3	MAN	3	0
4	G	5	BMA	2	0
6	I	4	MAN	1	0
8	M	2	NAG	1	0
2	E	1	NAG	2	0
8	N	1	NAG	4	0
7	K	2	NAG	1	0
6	I	5	MAN	1	0
8	M	1	NAG	4	0
7	K	1	NAG	8	0
7	K	4	MAN	4	0

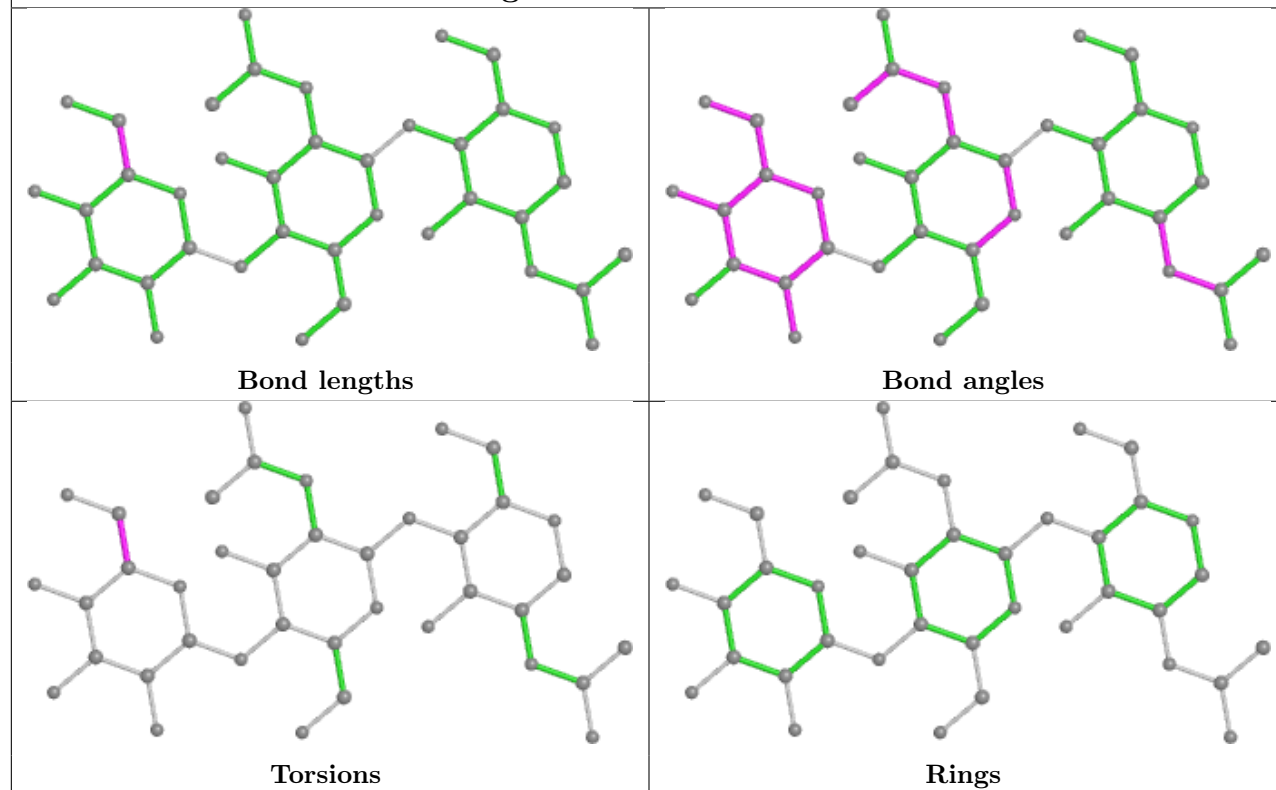
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



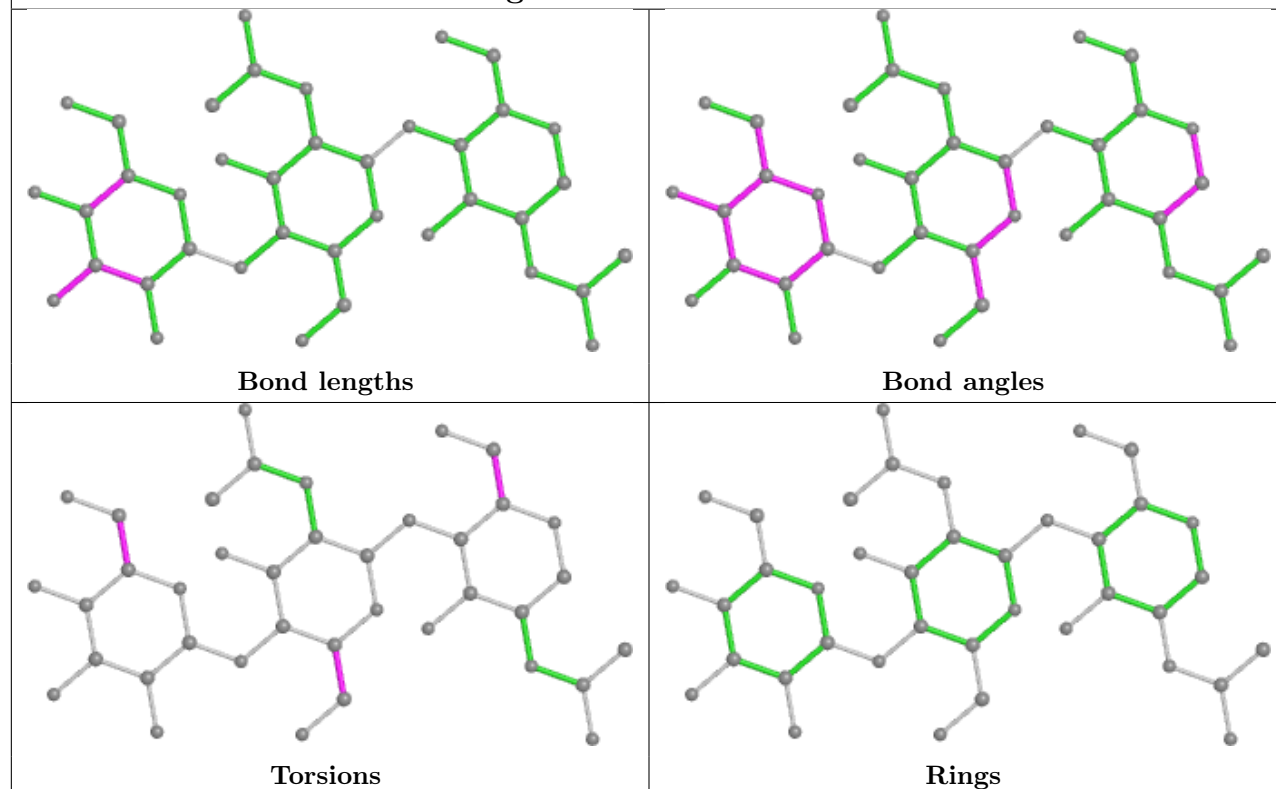
**Oligosaccharide Chain E****Bond lengths****Bond angles****Torsions****Rings****Oligosaccharide Chain F****Bond lengths****Bond angles****Torsions****Rings**

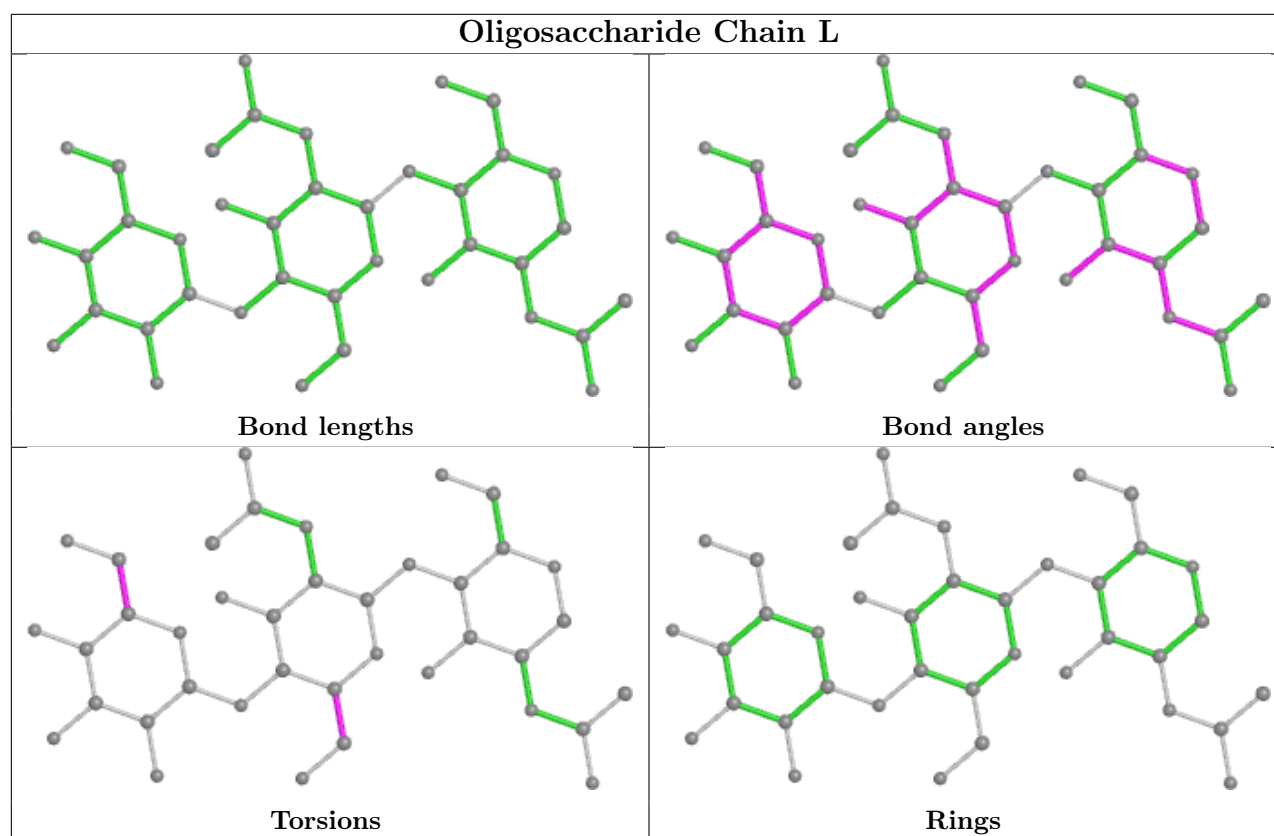


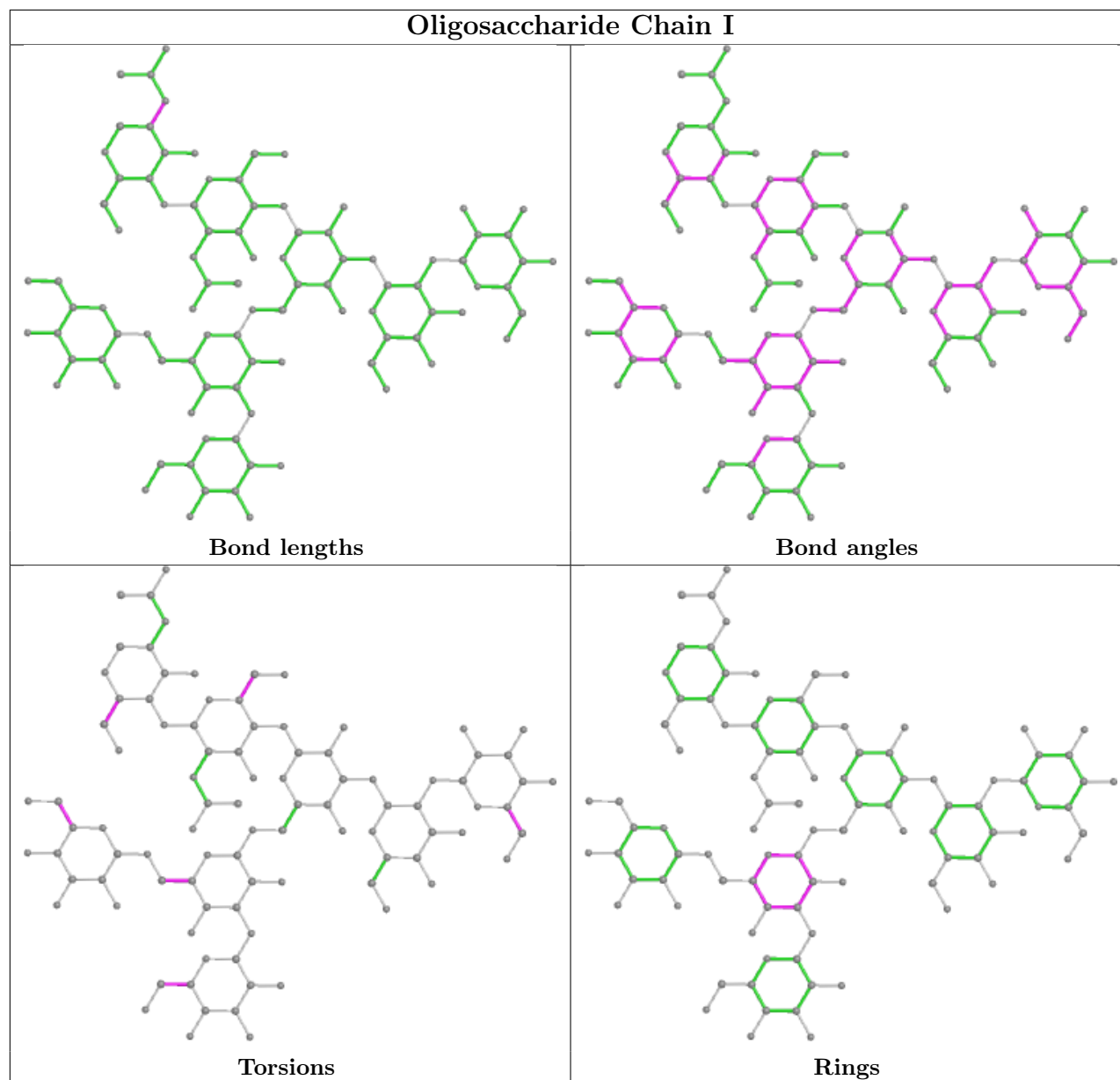
## Oligosaccharide Chain H



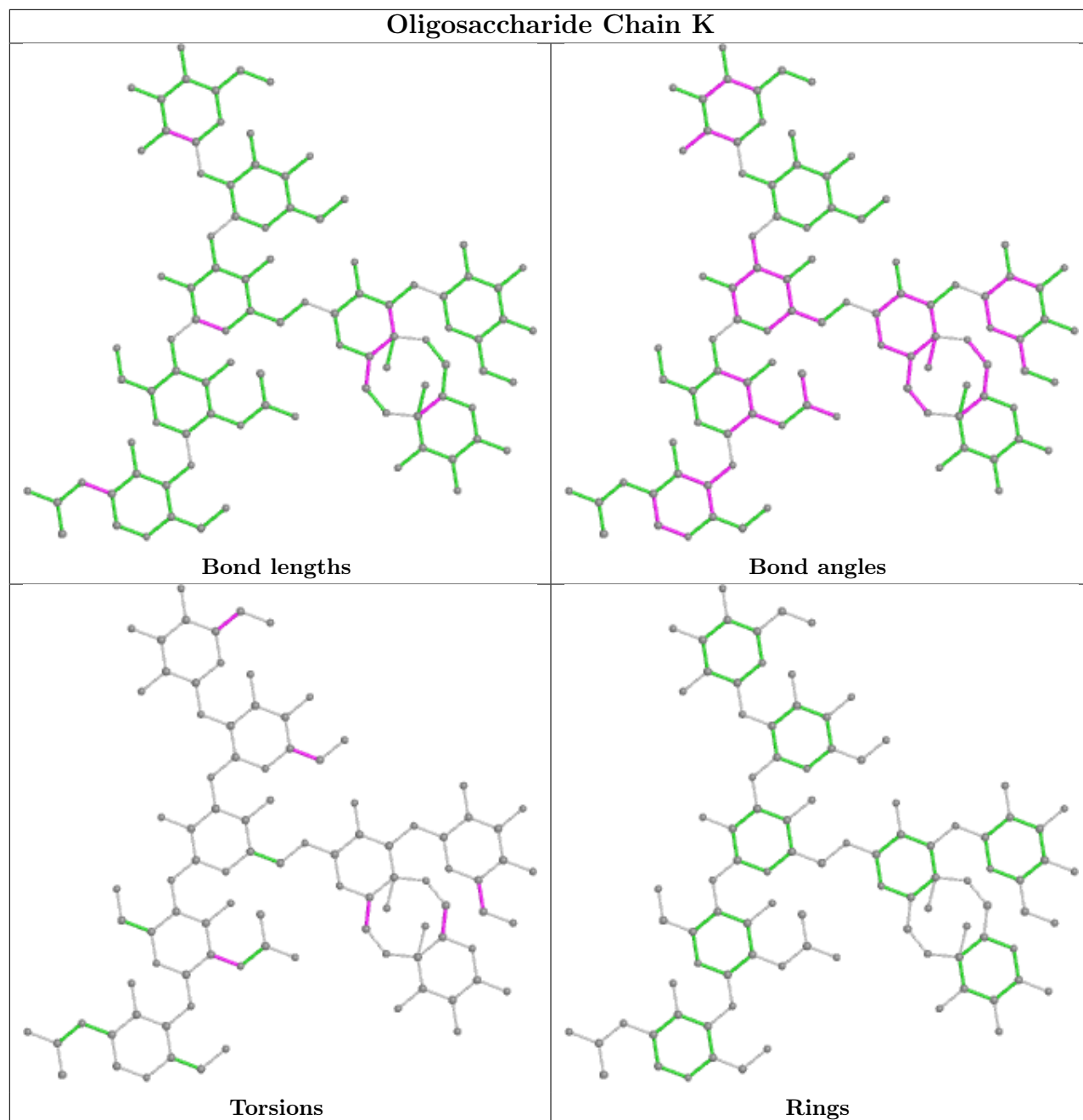
## Oligosaccharide Chain J

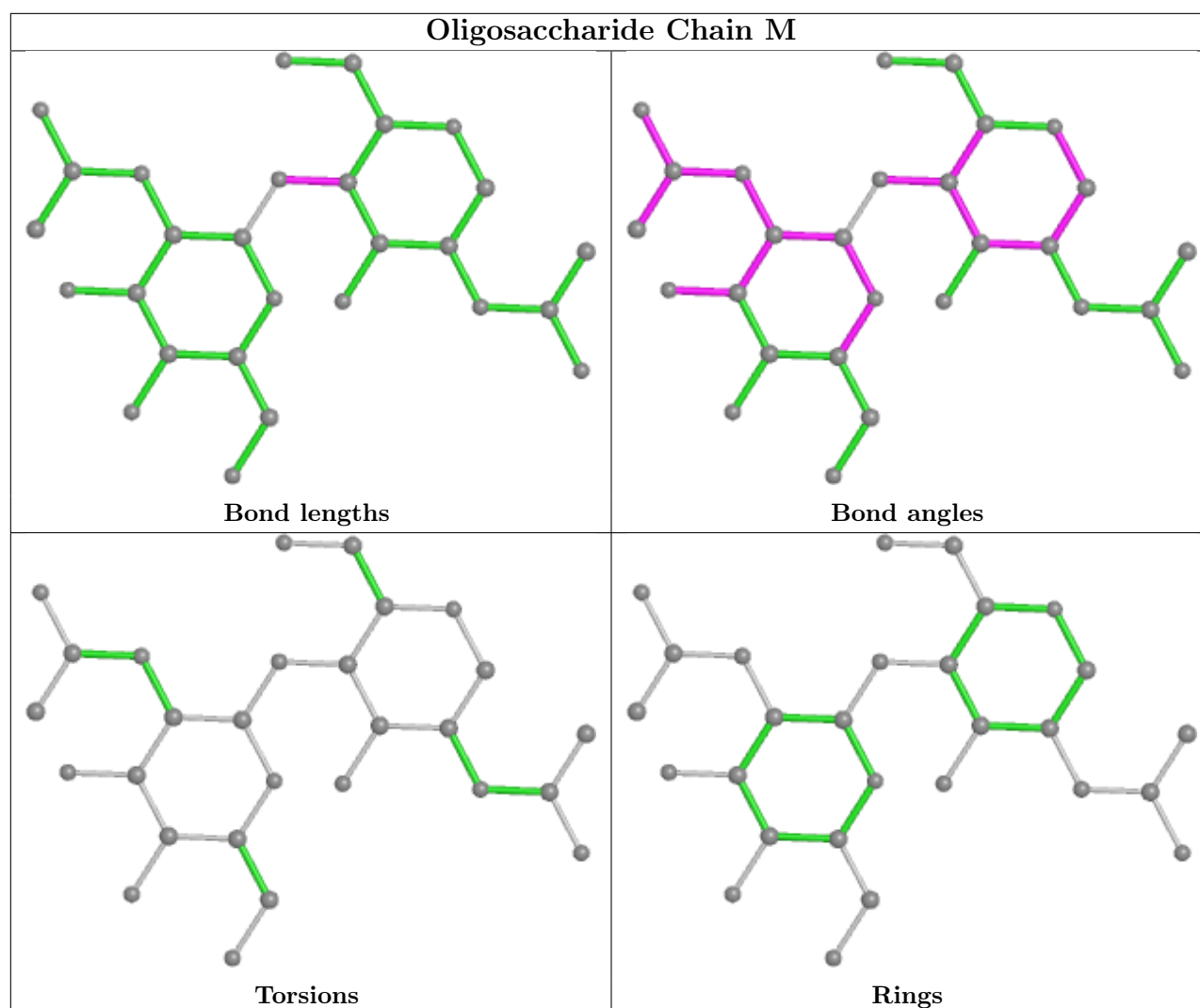


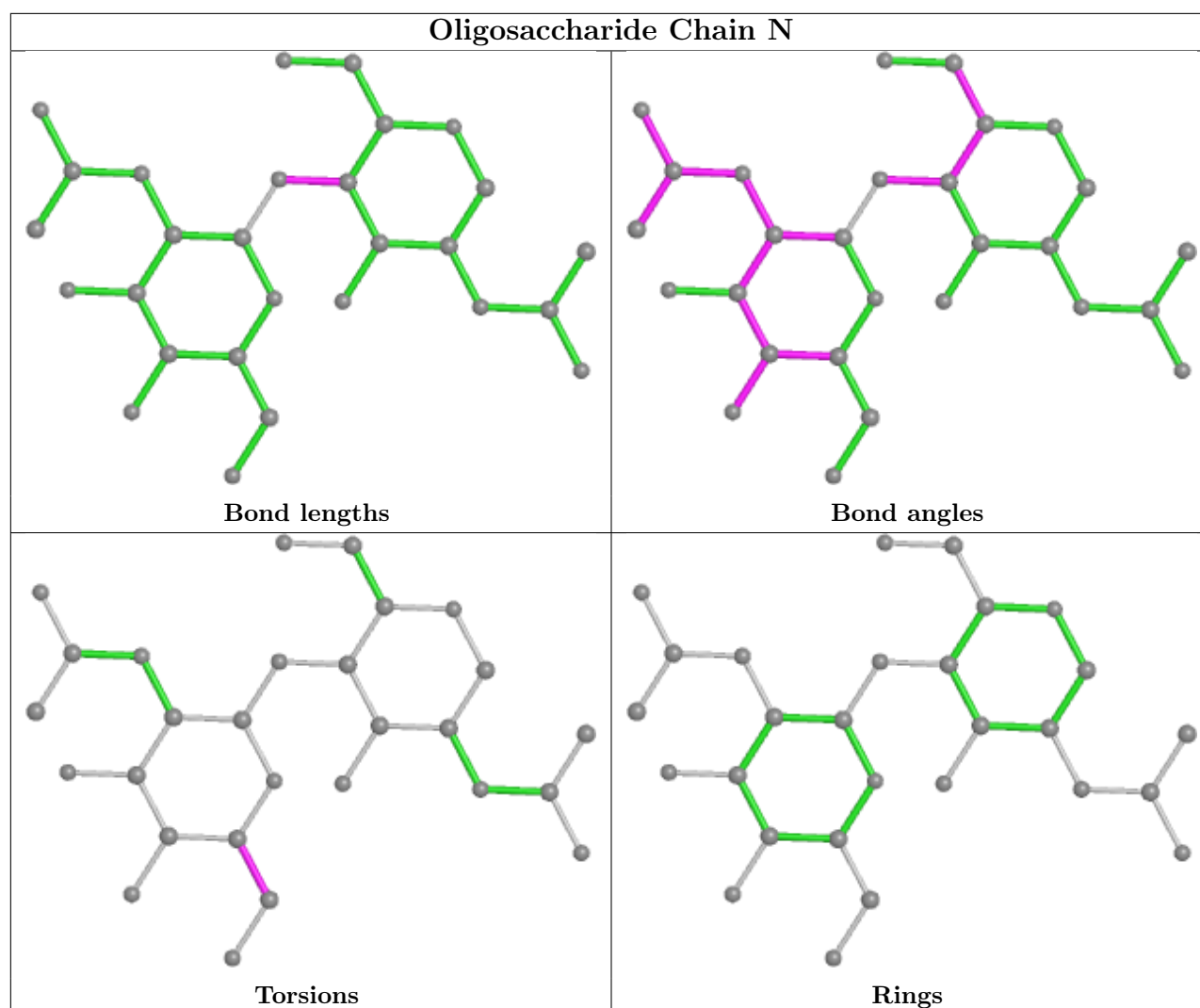




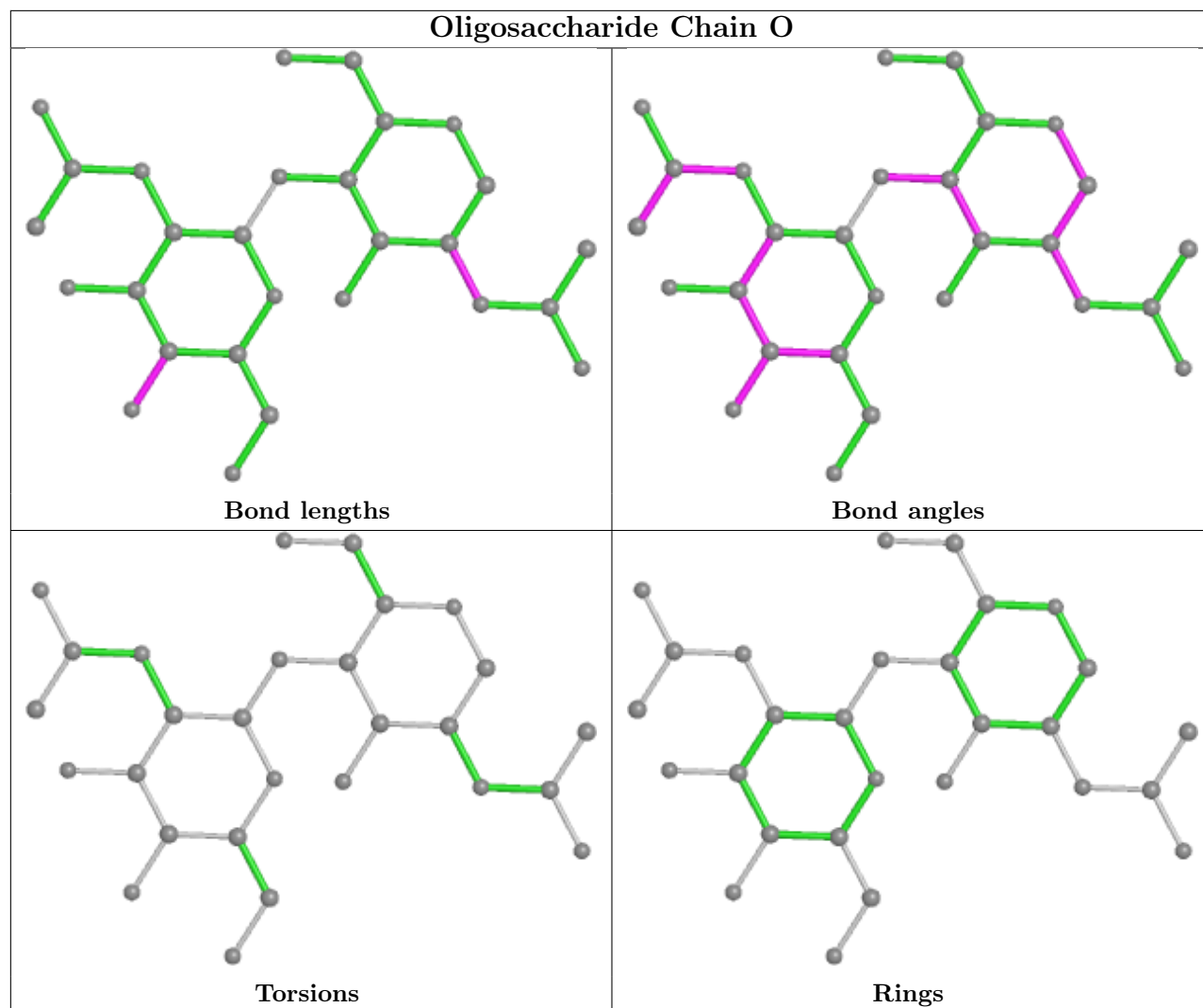
## Oligosaccharide Chain K

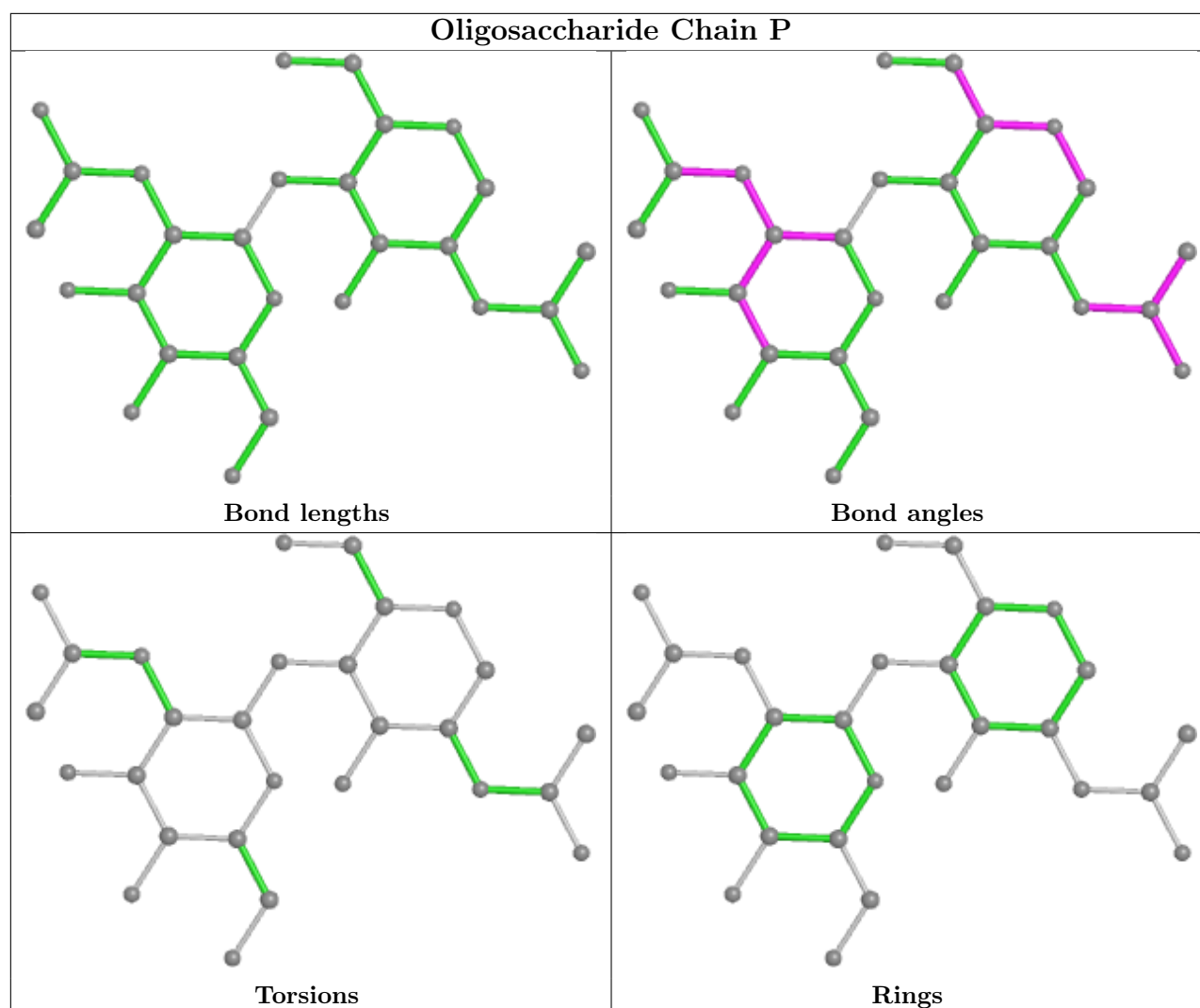












## 5.6 Ligand geometry [i](#)

22 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
9	NAG	A	901	1	13,13,15	1.44	2 (15%)	14,17,21	2.56	5 (35%)
9	NAG	B	903	1	14,14,15	0.50	0	17,19,21	1.56	2 (11%)
9	NAG	D	903	1	14,14,15	0.83	0	17,19,21	1.55	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	NAG	C	901	1	14,14,15	0.56	0	17,19,21	1.39	4 (23%)
13	MAN	B	909	-	12,12,12	0.46	0	17,17,17	0.53	0
9	NAG	A	905	1	14,14,15	0.48	0	17,19,21	1.41	1 (5%)
9	NAG	A	903	1	14,14,15	0.72	0	17,19,21	1.56	4 (23%)
13	MAN	B	907	-	11,11,12	0.86	0	15,15,17	2.24	5 (33%)
11	XYL	A	907	-	7,8,9	1.03	0	7,10,11	5.16	4 (57%)
9	NAG	B	904	1	14,14,15	0.78	0	17,19,21	1.61	4 (23%)
14	BMA	B	908	-	11,11,12	0.27	0	15,15,17	0.64	0
9	NAG	C	902	1	14,14,15	0.43	0	17,19,21	1.64	3 (17%)
9	NAG	B	901	1	14,14,15	0.64	0	17,19,21	1.31	3 (17%)
10	BKR	B	905	-	65,65,65	1.51	5 (7%)	101,101,101	1.56	15 (14%)
9	NAG	B	902	1	14,14,15	0.62	0	17,19,21	1.85	4 (23%)
9	NAG	D	902	1	14,14,15	0.41	0	17,19,21	1.43	3 (17%)
10	BKR	A	906	-	65,65,65	1.36	3 (4%)	101,101,101	1.48	14 (13%)
9	NAG	D	901	1	14,14,15	1.24	1 (7%)	17,19,21	1.22	1 (5%)
9	NAG	C	903	1	14,14,15	0.42	0	17,19,21	1.31	2 (11%)
9	NAG	A	904	1	14,14,15	0.55	0	17,19,21	1.53	4 (23%)
12	XYZ	B	906	-	10,10,10	1.17	2 (20%)	13,14,14	2.07	5 (38%)
9	NAG	A	902	1	14,14,15	0.66	1 (7%)	17,19,21	0.58	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
9	NAG	A	901	1	-	2/6/19/26	0/1/1/1
9	NAG	B	903	1	-	0/6/23/26	0/1/1/1
9	NAG	D	903	1	-	2/6/23/26	0/1/1/1
9	NAG	C	901	1	-	2/6/23/26	0/1/1/1
13	MAN	B	909	-	-	2/2/22/22	0/1/1/1
9	NAG	A	905	1	-	2/6/23/26	0/1/1/1
9	NAG	A	903	1	-	0/6/23/26	0/1/1/1
13	MAN	B	907	-	-	2/2/19/22	0/1/1/1
11	XYL	A	907	-	-	2/10/10/12	-
9	NAG	B	904	1	-	2/6/23/26	0/1/1/1
14	BMA	B	908	-	-	2/2/19/22	0/1/1/1

Continued on next page...

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	C	902	1	-	2/6/23/26	0/1/1/1
9	NAG	B	901	1	-	2/6/23/26	0/1/1/1
10	BKR	B	905	-	-	6/37/123/123	0/7/7/7
9	NAG	B	902	1	-	2/6/23/26	0/1/1/1
9	NAG	D	902	1	-	2/6/23/26	0/1/1/1
10	BKR	A	906	-	-	9/37/123/123	0/7/7/7
9	NAG	D	901	1	-	1/6/23/26	0/1/1/1
9	NAG	C	903	1	-	0/6/23/26	0/1/1/1
9	NAG	A	904	1	-	0/6/23/26	0/1/1/1
12	XYZ	B	906	-	-	0/2/18/18	0/1/1/1
9	NAG	A	902	1	-	0/6/23/26	0/1/1/1

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	905	BKR	O11-C27	5.98	1.48	1.34
10	B	905	BKR	O2-C3	5.84	1.46	1.34
10	A	906	BKR	O11-C27	5.37	1.46	1.34
10	A	906	BKR	O2-C3	5.30	1.45	1.34
9	A	901	NAG	O5-C1	-3.98	1.37	1.43

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	907	XYL	C4-C3-C2	7.92	124.89	112.47
11	A	907	XYL	O4-C4-C3	-6.86	92.43	109.10
11	A	907	XYL	C5-C4-C3	6.84	127.25	112.41
10	A	906	BKR	C45-C24-C21	6.44	126.26	119.52
9	A	901	NAG	C1-C2-N2	-5.10	101.78	110.49

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

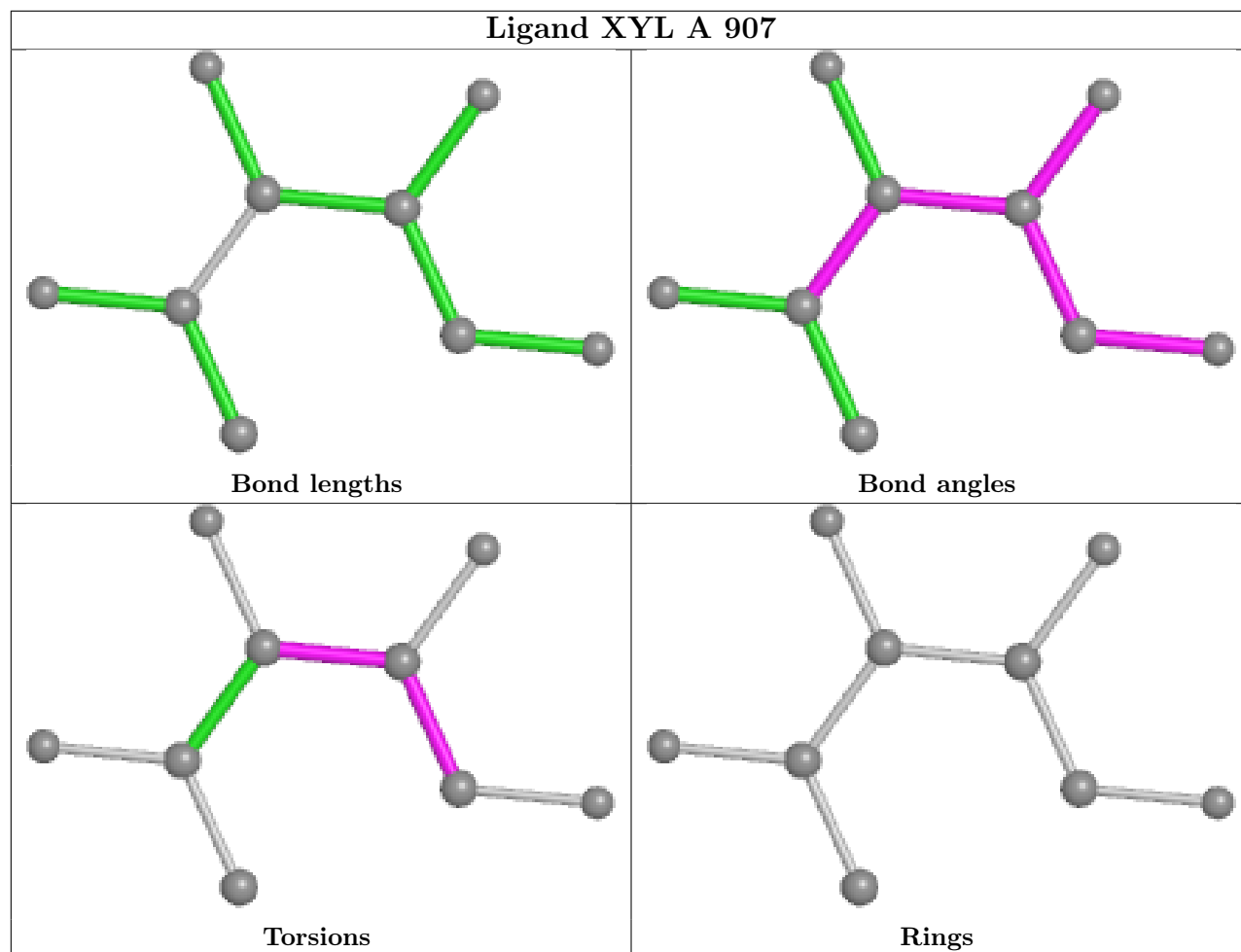
Mol	Chain	Res	Type	Atoms
9	A	901	NAG	C4-C5-C6-O6
9	A	901	NAG	O5-C5-C6-O6
9	C	902	NAG	O5-C5-C6-O6
9	D	903	NAG	O5-C5-C6-O6
9	D	902	NAG	O5-C5-C6-O6

There are no ring outliers.

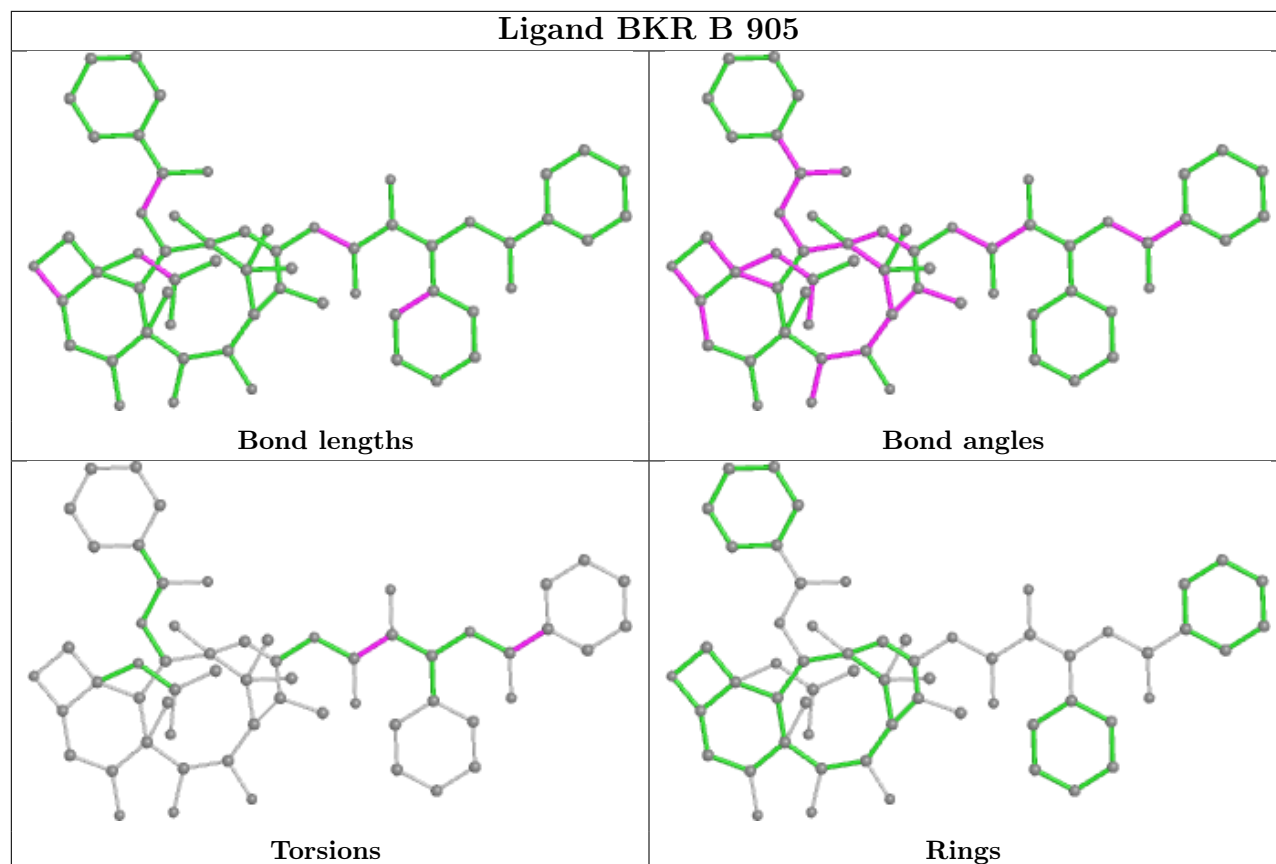
6 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	901	NAG	2	0
13	B	909	MAN	2	0
14	B	908	BMA	6	0
10	B	905	BKR	2	0
10	A	906	BKR	1	0
12	B	906	XYZ	2	0

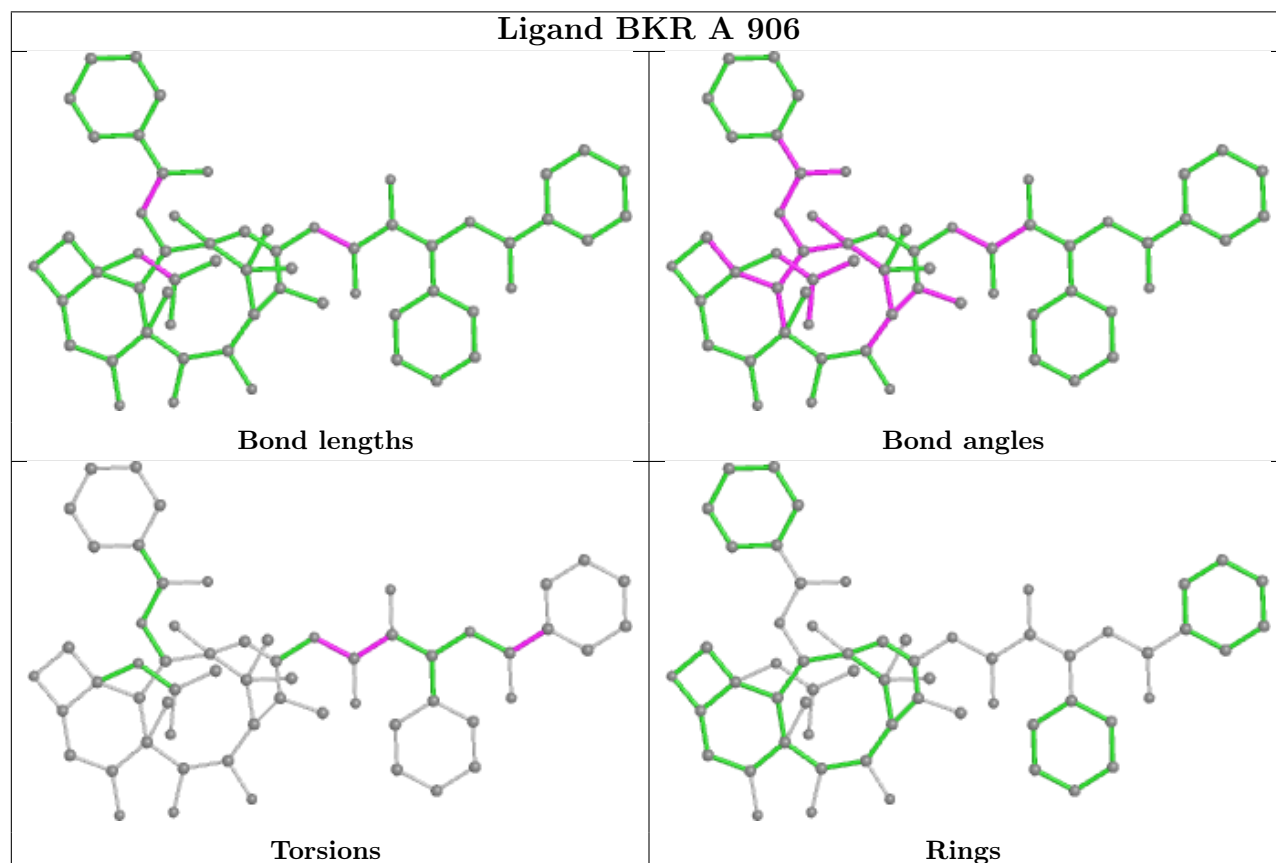
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

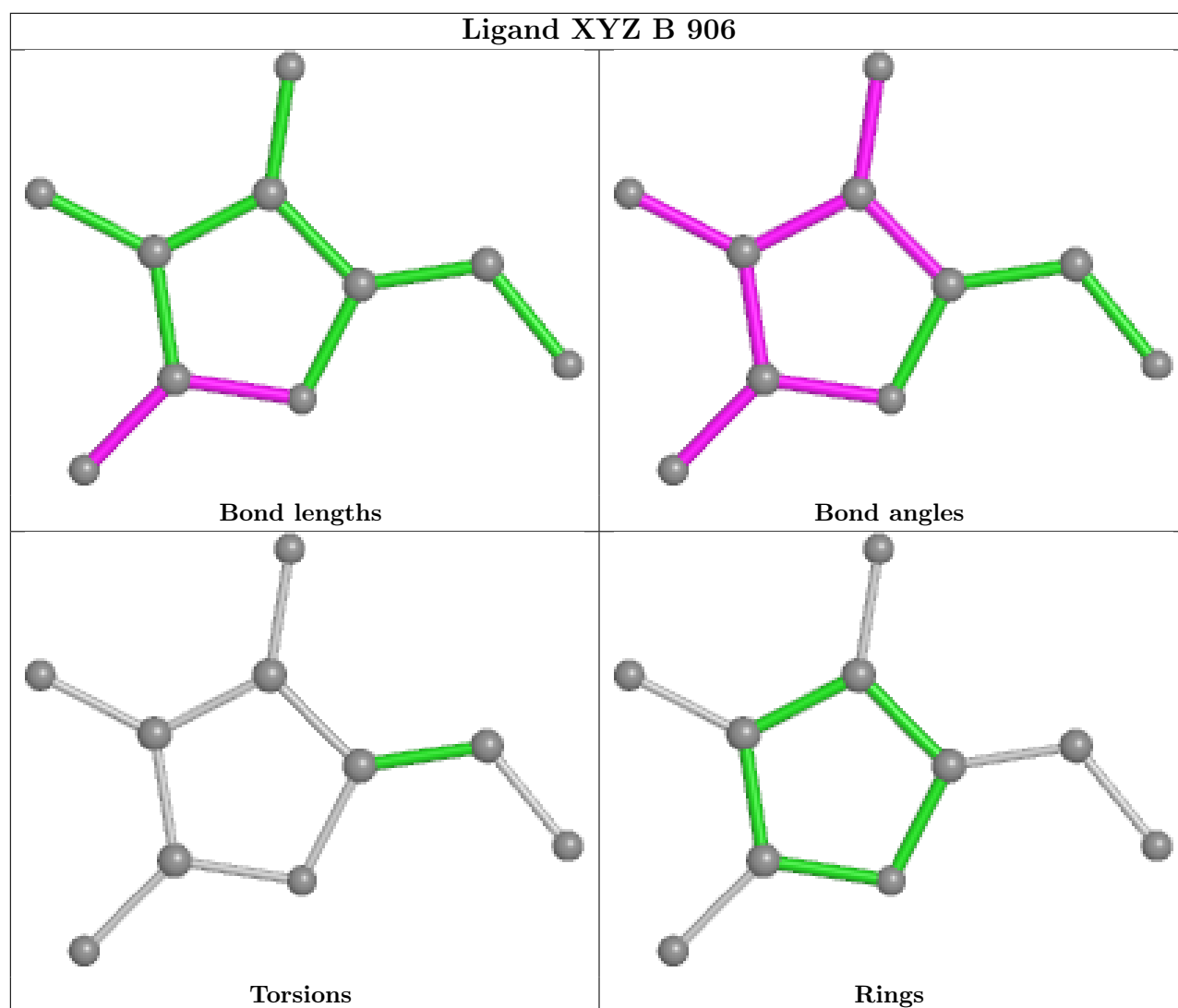


## Ligand BKR B 905



## Ligand BKR A 906





## 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	756/803 (94%)	-0.56	4 (0%) 91 91	20, 29, 48, 104	0
1	B	756/803 (94%)	-0.68	3 (0%) 92 92	18, 29, 44, 88	0
1	C	756/803 (94%)	-0.15	16 (2%) 63 60	26, 50, 77, 121	0
1	D	756/803 (94%)	-0.06	18 (2%) 59 54	27, 49, 74, 104	0
All	All	3024/3212 (94%)	-0.36	41 (1%) 75 73	18, 39, 70, 121	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	225	ASP	5.9
1	C	227	VAL	4.5
1	C	226	GLY	4.1
1	A	226	GLY	4.0
1	D	699	THR	3.5

### 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
6	BMA	I	8	11/12	0.60	0.24	67,87,90,91	0
5	MAN	L	3	11/12	0.65	0.33	83,95,98,101	0

*Continued on next page...*

*Continued from previous page...*

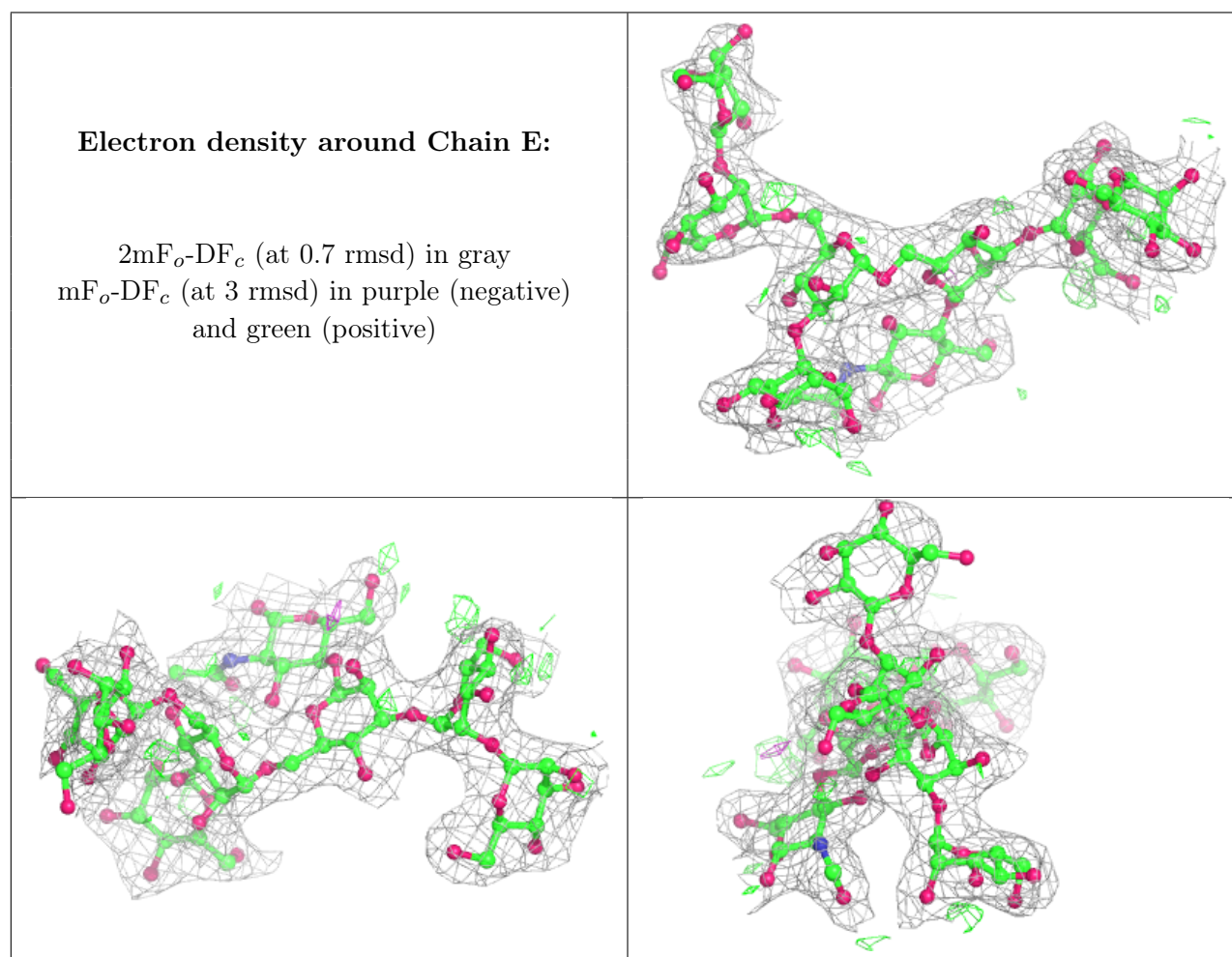
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	F	4	14/15	0.71	0.24	53,66,79,89	0
7	MAN	K	8	12/12	0.73	0.24	71,85,97,102	0
5	MAN	J	3	11/12	0.79	0.19	54,64,72,75	0
4	BMA	G	8	11/12	0.79	0.28	42,49,54,55	0
4	BMA	G	5	11/12	0.81	0.40	57,66,71,87	0
7	MAN	K	4	11/12	0.81	0.22	60,70,77,77	0
6	MAN	I	5	11/12	0.81	0.16	55,65,83,85	0
7	MAN	K	5	11/12	0.83	0.18	69,75,78,79	0
8	NAG	P	2	14/15	0.83	0.23	66,91,95,97	0
4	MAN	G	6	11/12	0.84	0.43	90,102,111,111	0
8	NAG	O	2	14/15	0.85	0.20	63,73,82,83	0
6	NAG	I	2	14/15	0.85	0.17	57,69,77,78	0
5	NAG	L	2	14/15	0.86	0.17	52,66,82,92	0
8	NAG	P	1	14/15	0.86	0.28	20,20,20,20	0
2	MAN	E	5	11/12	0.86	0.39	79,91,101,103	0
6	NAG	I	1	14/15	0.87	0.28	20,20,20,20	0
2	BMA	E	4	11/12	0.88	0.33	67,74,86,93	0
8	NAG	O	1	14/15	0.89	0.30	20,20,20,20	0
6	MAN	I	6	11/12	0.90	0.18	60,69,86,86	0
6	MAN	I	4	11/12	0.90	0.23	69,84,89,92	0
7	MAN	K	6	11/12	0.90	0.21	53,66,76,78	0
7	NAG	K	1	14/15	0.90	0.30	20,20,20,20	0
4	MAN	G	9	11/12	0.92	0.15	48,49,56,57	0
5	MAN	H	3	11/12	0.92	0.11	29,37,46,47	0
2	BMA	E	2	11/12	0.92	0.13	33,41,45,47	0
2	MAN	E	8	11/12	0.92	0.13	45,55,60,61	0
5	NAG	J	2	14/15	0.93	0.14	35,37,45,55	0
6	MAN	I	7	11/12	0.93	0.14	54,69,79,82	0
3	MAN	F	3	11/12	0.93	0.24	20,20,20,20	0
5	NAG	L	1	14/15	0.93	0.11	39,43,49,63	0
8	NAG	N	2	14/15	0.94	0.16	41,50,56,59	0
2	MAN	E	7	11/12	0.94	0.14	48,56,58,60	0
6	BMA	I	3	11/12	0.94	0.15	61,62,69,72	0
7	NAG	K	2	14/15	0.94	0.12	43,46,48,52	0
7	BMA	K	3	11/12	0.94	0.11	41,44,47,51	0
7	MAN	K	7	11/12	0.95	0.12	55,60,68,71	0
2	MAN	E	3	11/12	0.95	0.13	40,45,50,61	0
8	NAG	M	2	14/15	0.95	0.12	34,39,41,44	0
4	BMA	G	3	11/12	0.95	0.10	26,30,36,37	0
8	NAG	N	1	14/15	0.96	0.10	26,28,31,45	0
2	MAN	E	6	11/12	0.96	0.13	43,45,46,47	0
2	NAG	E	1	15/15	0.96	0.14	36,38,39,40	0

*Continued on next page...*

*Continued from previous page...*

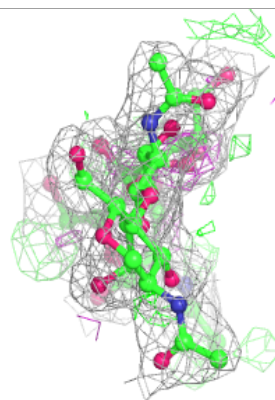
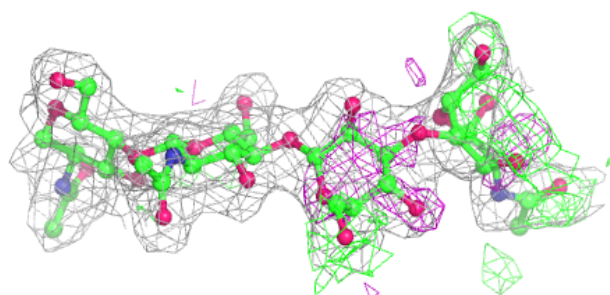
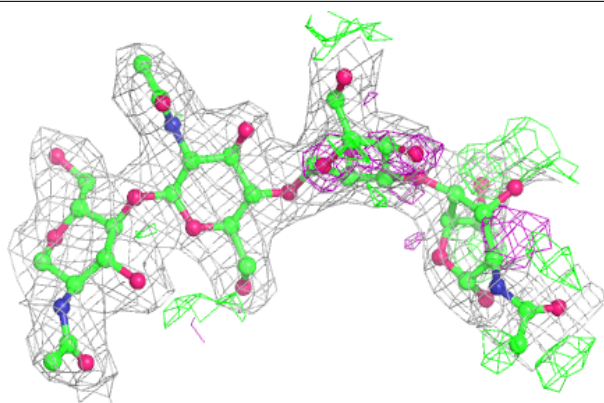
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NAG	J	1	14/15	0.96	0.09	32,34,36,36	0
4	MAN	G	7	11/12	0.96	0.13	34,40,44,47	0
4	MAN	G	4	11/12	0.96	0.11	37,41,58,64	0
5	NAG	H	2	14/15	0.97	0.09	28,29,34,35	0
3	NAG	F	2	14/15	0.97	0.09	25,31,34,36	0
4	NAG	G	2	14/15	0.97	0.10	27,29,32,34	0
3	NAG	F	1	14/15	0.97	0.08	24,26,29,29	0
8	NAG	M	1	14/15	0.97	0.09	22,23,24,35	0
5	NAG	H	1	14/15	0.97	0.08	22,23,26,29	0
4	NAG	G	1	14/15	0.98	0.09	24,26,32,32	0

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



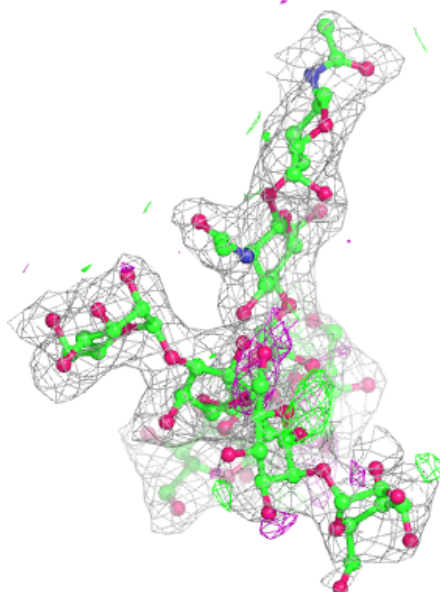
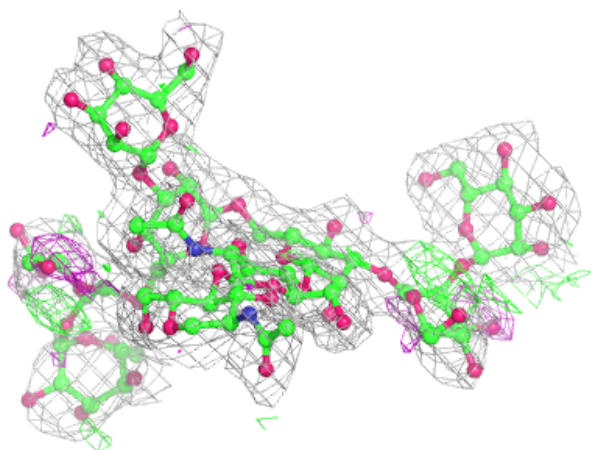
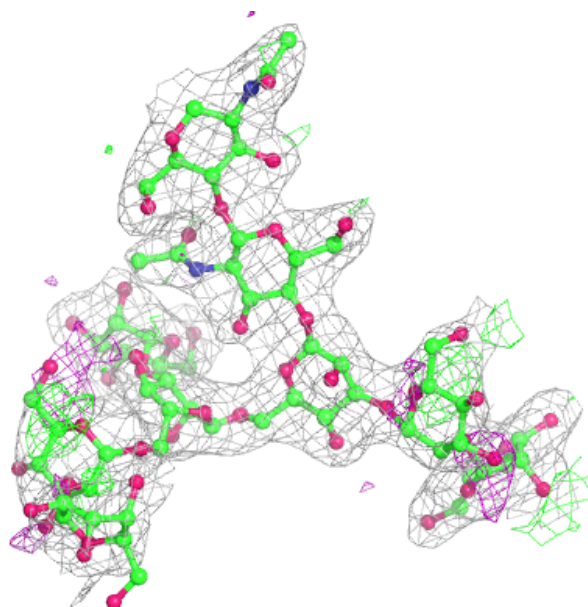
**Electron density around Chain F:**

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



**Electron density around Chain G:**

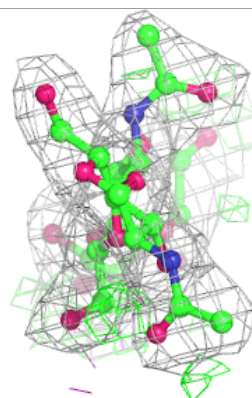
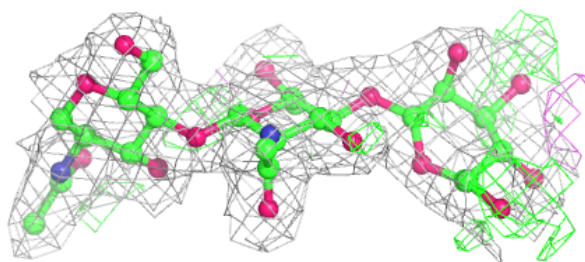
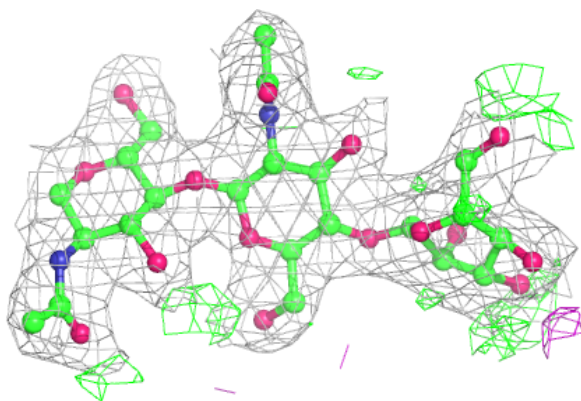
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



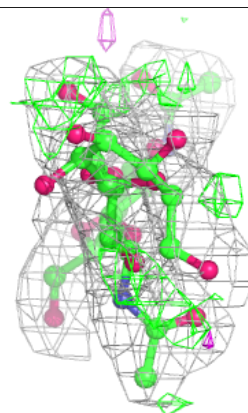
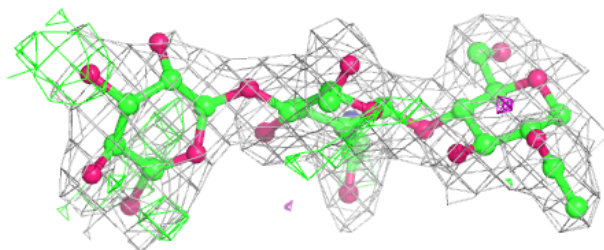
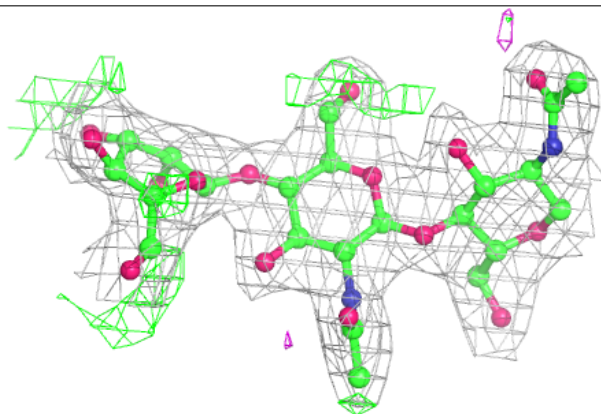


**Electron density around Chain H:**

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

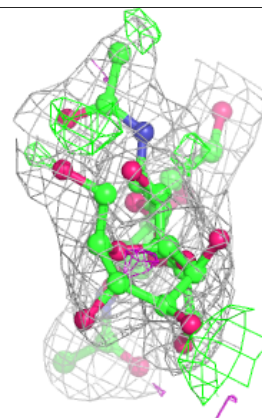
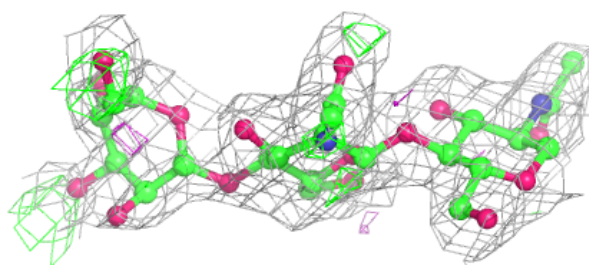
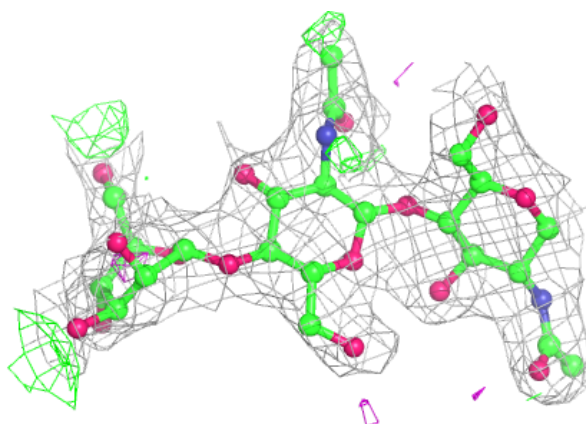
**Electron density around Chain J:**

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



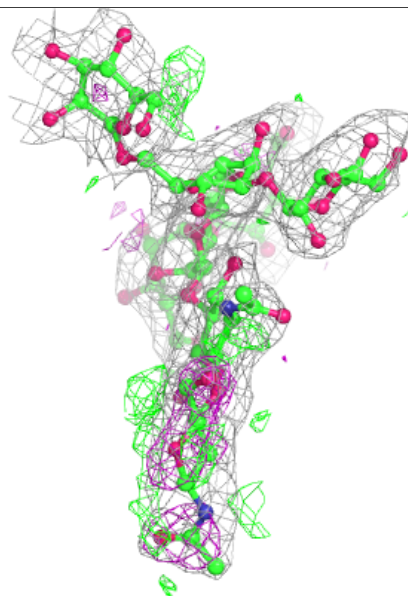
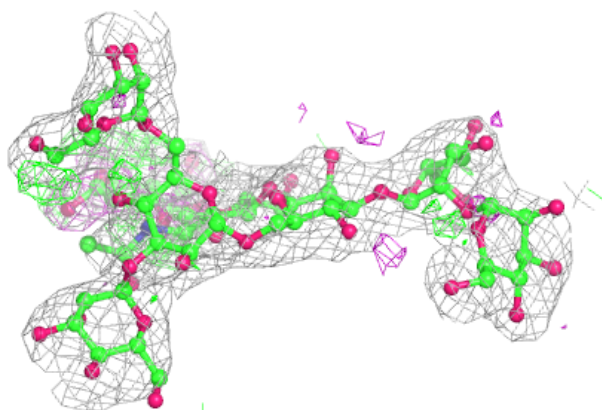
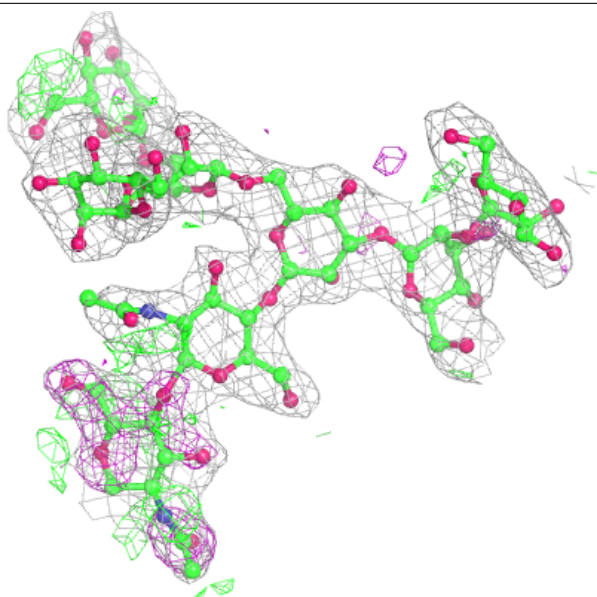
**Electron density around Chain L:**

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



**Electron density around Chain I:**

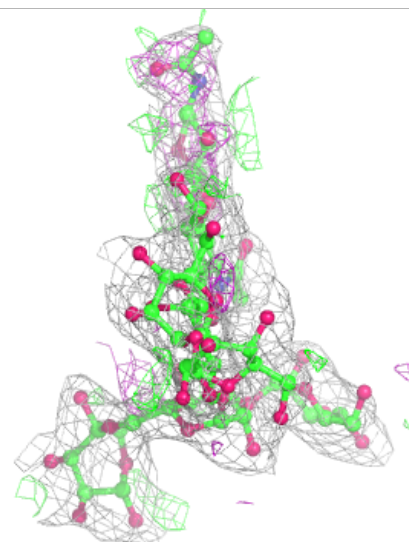
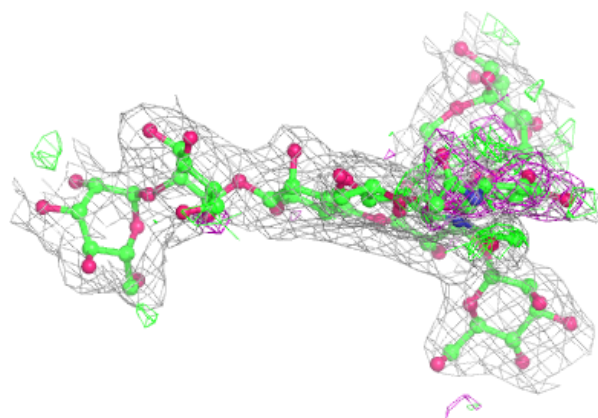
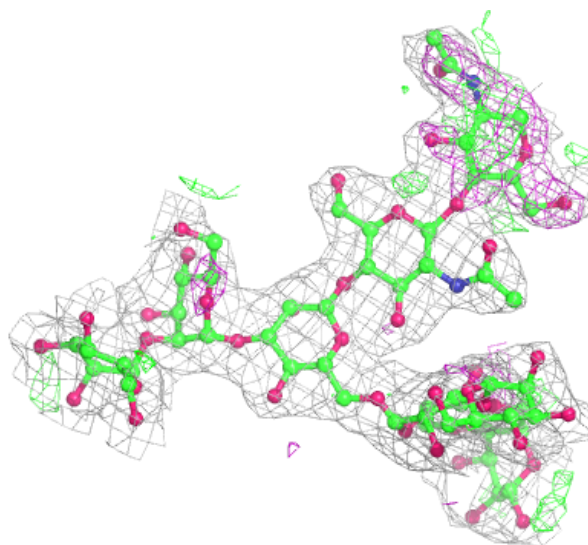
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





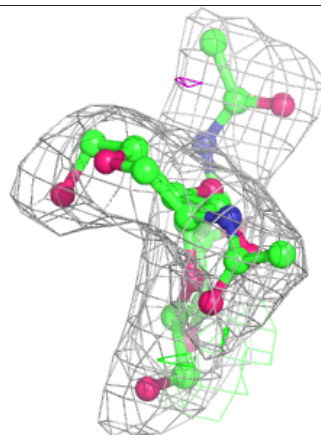
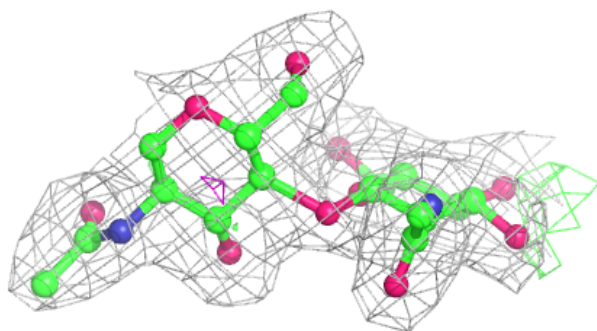
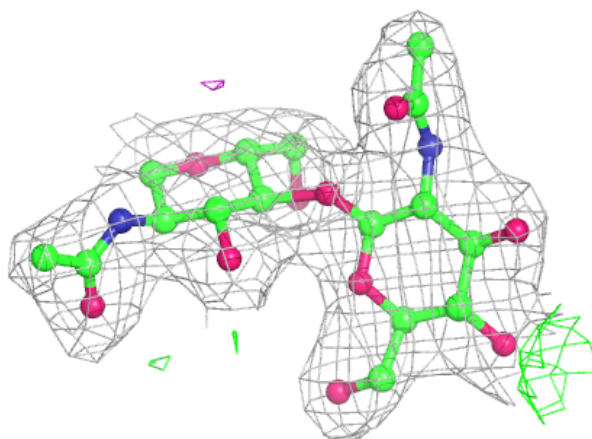
**Electron density around Chain K:**

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

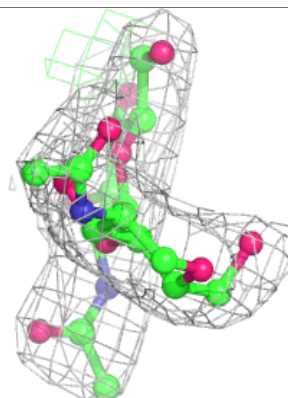
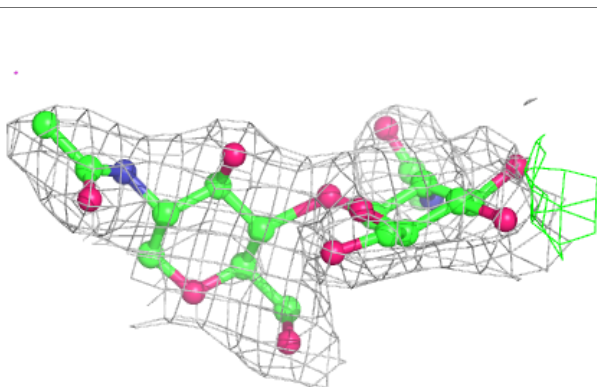
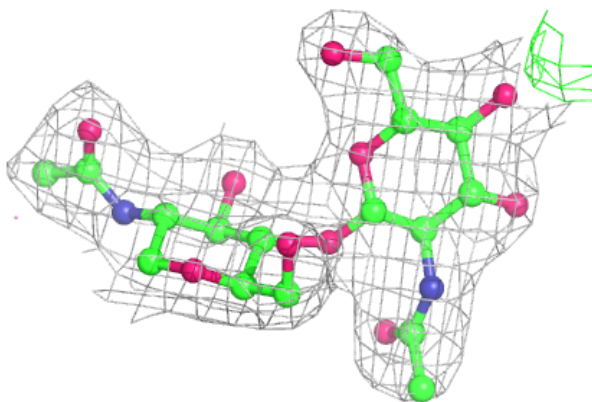


**Electron density around Chain M:**

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

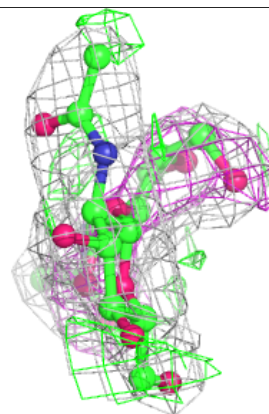
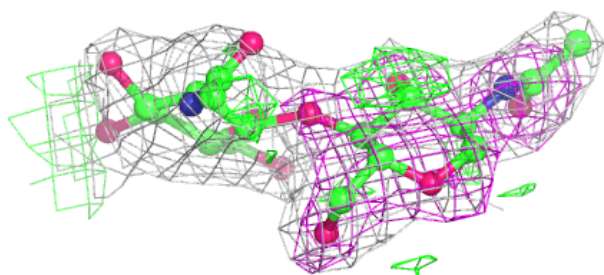
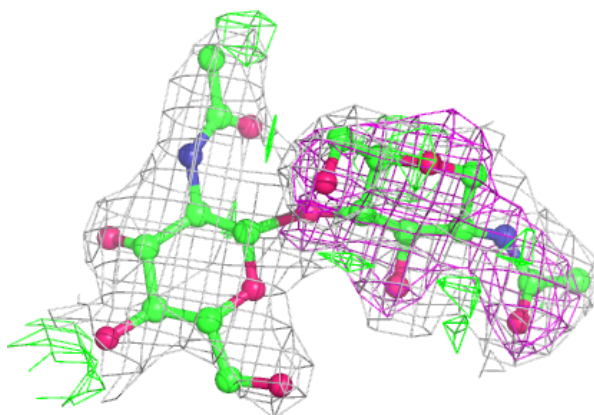
**Electron density around Chain N:**

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

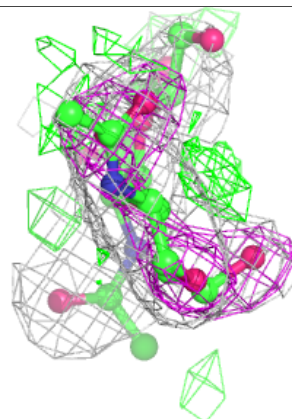
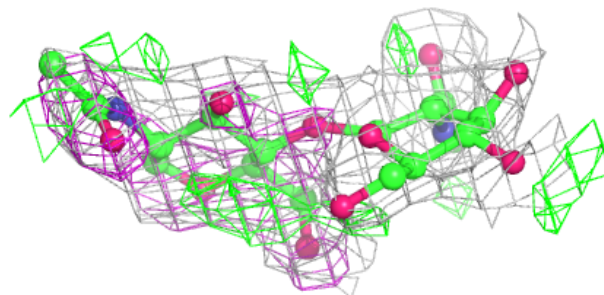
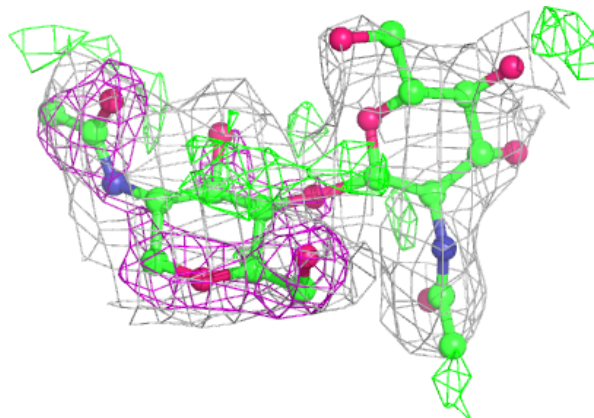


**Electron density around Chain O:**

$2mF_o-DF_c$  (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)



## 6.4 Ligands ⓘ

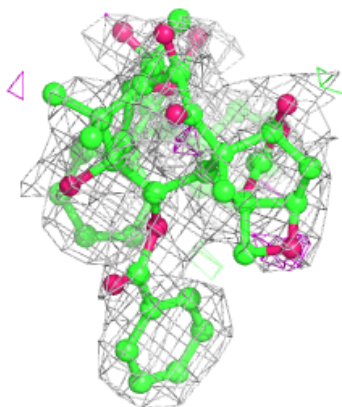
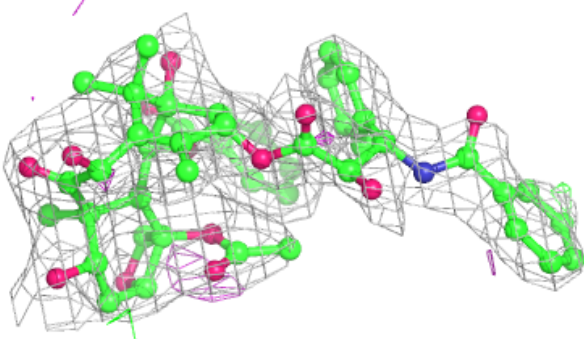
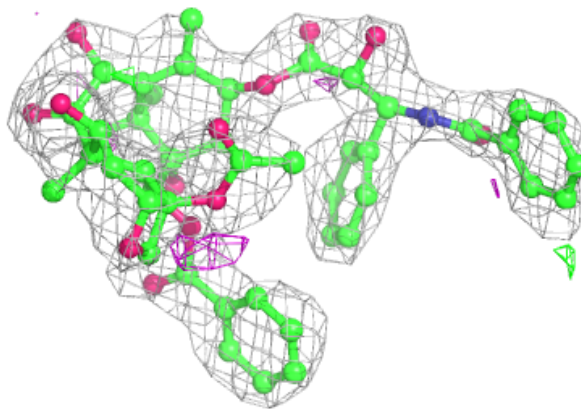
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
13	MAN	B	909	12/12	0.67	0.41	20,20,20,20	0
14	BMA	B	908	11/12	0.73	0.30	20,20,20,20	0
9	NAG	A	905	14/15	0.80	0.33	72,84,89,93	0
9	NAG	C	901	14/15	0.82	0.36	86,96,106,109	0
13	MAN	B	907	11/12	0.84	0.22	64,74,77,78	0
10	BKR	A	906	59/59	0.86	0.23	51,69,86,90	0
9	NAG	D	901	14/15	0.86	0.30	73,84,101,101	0
9	NAG	B	904	14/15	0.88	0.30	65,75,79,83	0
9	NAG	C	902	14/15	0.88	0.31	68,75,82,83	0
11	XYL	A	907	9/10	0.88	0.26	41,49,57,62	0
9	NAG	D	902	14/15	0.90	0.33	69,78,82,85	0
10	BKR	B	905	59/59	0.90	0.19	43,52,63,65	0
9	NAG	D	903	14/15	0.90	0.19	45,62,68,68	0
12	XYZ	B	906	10/10	0.92	0.21	38,53,65,72	0
9	NAG	A	903	14/15	0.94	0.24	43,47,52,53	0
9	NAG	A	902	14/15	0.95	0.18	38,48,55,56	0
9	NAG	B	901	14/15	0.95	0.14	39,42,48,51	0
9	NAG	B	902	14/15	0.95	0.22	40,44,49,49	0
9	NAG	A	904	14/15	0.95	0.13	32,37,40,41	0
9	NAG	A	901	13/15	0.96	0.09	27,29,36,37	0
9	NAG	C	903	14/15	0.96	0.11	41,43,45,46	0
9	NAG	B	903	14/15	0.96	0.10	35,40,43,44	0

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

**Electron density around BKR A 906:**

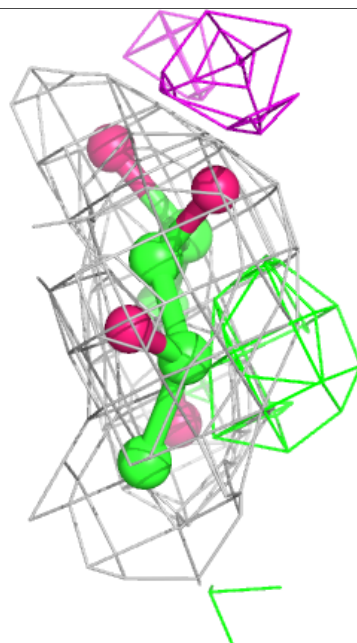
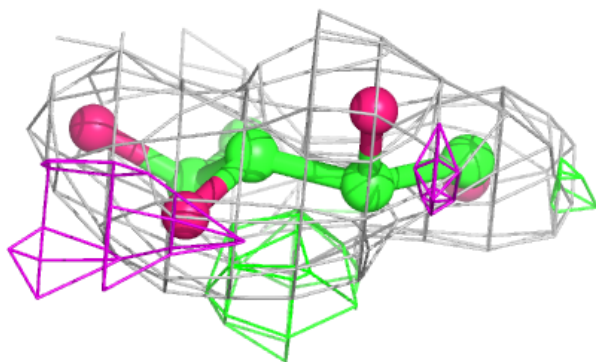
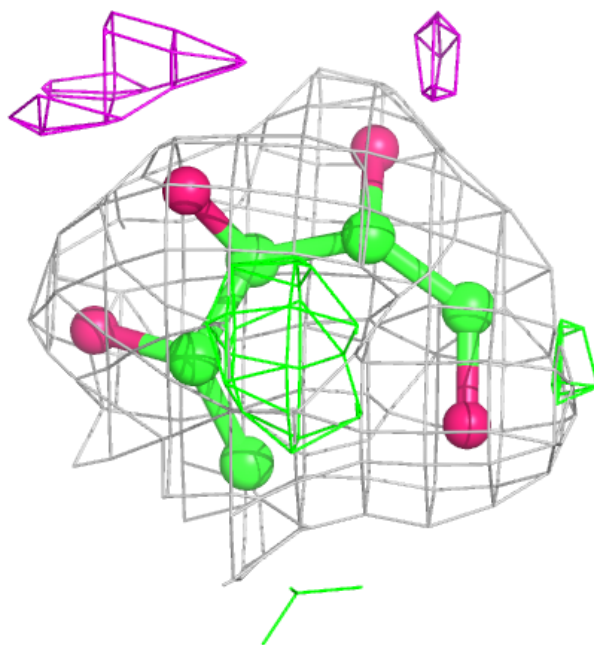
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





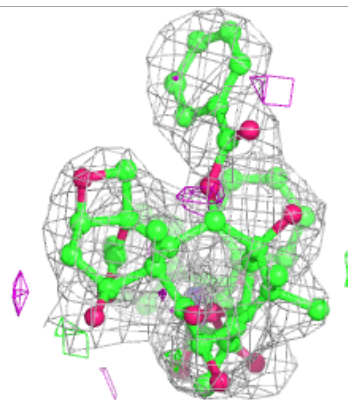
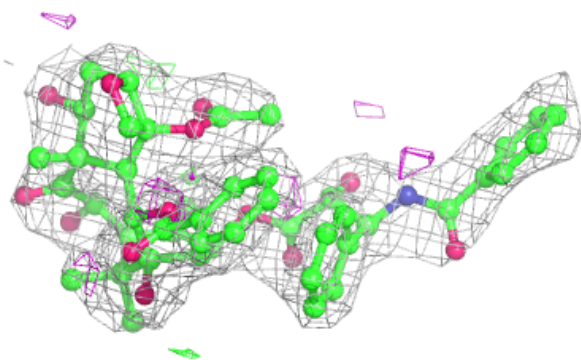
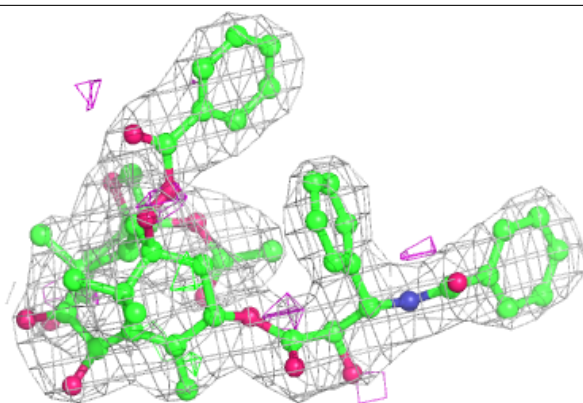
**Electron density around XYL A 907:**

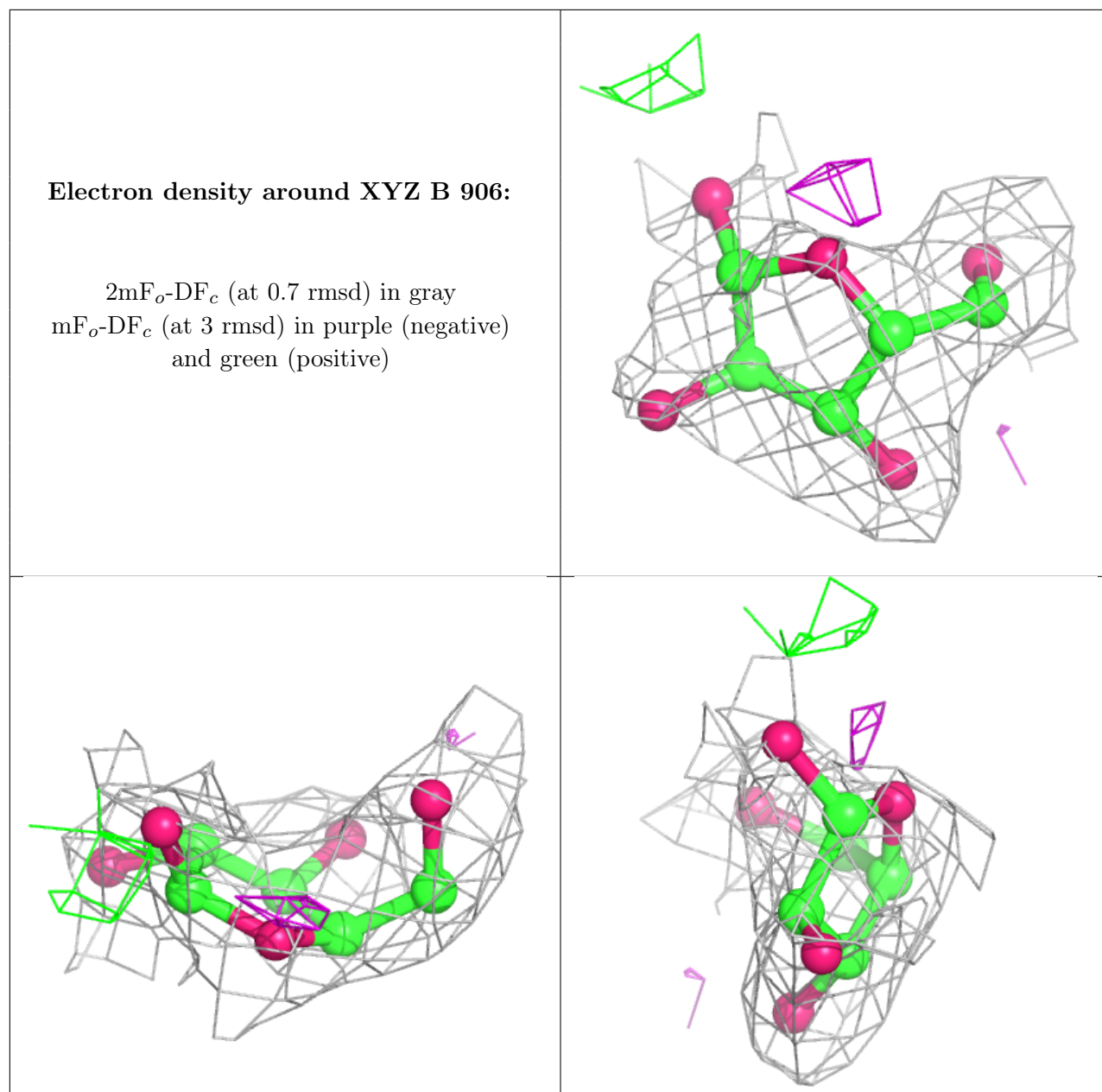
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around BKR B 905:**

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





## 6.5 Other polymers ⓘ

There are no such residues in this entry.