



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 03:43 AM BST

PDB ID : 3CIY  
Title : Mouse Toll-like receptor 3 ectodomain complexed with double-stranded RNA  
Authors : Liu, L.; Botos, I.; Wang, Y.; Leonard, J.N.; Shiloach, J.; Segal, D.M.; Davies, D.R.  
Deposited on : 2008-03-12  
Resolution : 3.41 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.

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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	:	2.13.1
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)	:	2.13.1

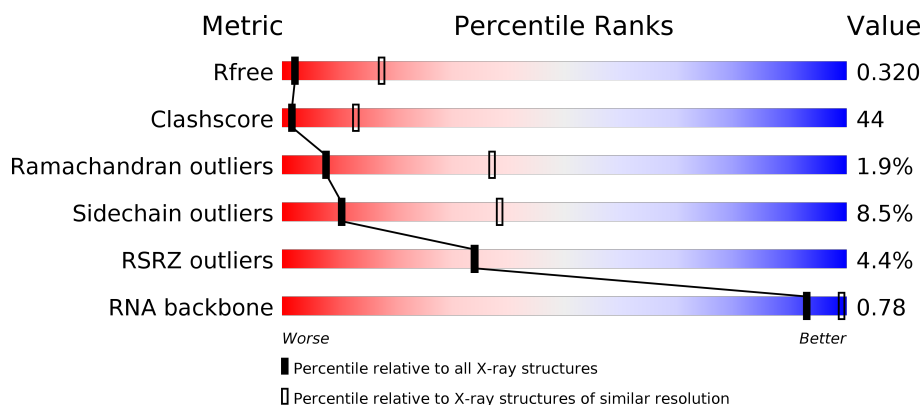
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.41 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.











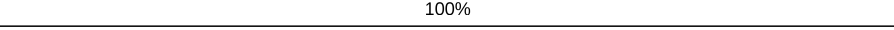


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1486 (3.50-3.34)
Clashscore	141614	1572 (3.50-3.34)
Ramachandran outliers	138981	1534 (3.50-3.34)
Sidechain outliers	138945	1535 (3.50-3.34)
RSRZ outliers	127900	1395 (3.50-3.34)
RNA backbone	3102	1012 (3.88-2.96)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	C	46	<div> <div>48%</div> <div>52%</div> </div>
2	D	46	<div> <div>37%</div> <div>63%</div> </div>
3	A	697	<div> <div>4%</div> <div>35%</div> <div>54%</div> <div>5%</div> <div>5%</div> </div>
3	B	697	<div> <div>5%</div> <div>34%</div> <div>56%</div> <div>6%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
4	E	2	
4	H	2	
4	L	2	
4	O	2	
5	F	3	
6	G	3	
7	I	5	
8	J	3	
8	Q	3	
9	K	2	
9	R	2	
10	M	3	
11	N	3	
12	P	5	

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
12	NAG	P	1	X	-	-	-
13	NAG	A	724	X	-	-	-
4	NAG	L	1	-	-	-	X
4	NDG	L	2	-	-	-	X
7	NAG	I	1	X	-	-	-
7	MAN	I	4	-	-	-	X
8	NAG	J	1	X	-	-	-
8	NAG	Q	1	X	-	-	-
9	NAG	K	1	X	-	-	-
9	NAG	R	1	X	-	-	-
9	NAG	R	2	-	-	-	X

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 13194 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 RNA chain called 46-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	46	Total	C	N	O	P	0	0	0
			978	439	176	318	45			

- Molecule 2 is a RNA chain called 46-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	46	Total	C	N	O	P	0	0	0
			968	435	166	322	45			

- Molecule 3 is a protein called Toll-like receptor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	661	Total	C	N	O	S	0	0	0
			5310	3392	905	999	14			
3	B	668	Total	C	N	O	S	0	0	0
			5360	3422	914	1010	14			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	704	ASN	-	expression tag	UNP Q99MB1
A	705	LEU	-	expression tag	UNP Q99MB1
A	706	TYR	-	expression tag	UNP Q99MB1
A	707	PHE	-	expression tag	UNP Q99MB1
A	708	GLN	-	expression tag	UNP Q99MB1
A	709	GLY	-	expression tag	UNP Q99MB1
A	710	HIS	-	expression tag	UNP Q99MB1
A	711	HIS	-	expression tag	UNP Q99MB1
A	712	HIS	-	expression tag	UNP Q99MB1
A	713	HIS	-	expression tag	UNP Q99MB1
A	714	HIS	-	expression tag	UNP Q99MB1
A	715	HIS	-	expression tag	UNP Q99MB1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	716	TRP	-	expression tag	UNP Q99MB1
A	717	SER	-	expression tag	UNP Q99MB1
A	718	HIS	-	expression tag	UNP Q99MB1
A	719	PRO	-	expression tag	UNP Q99MB1
A	720	GLN	-	expression tag	UNP Q99MB1
A	721	PHE	-	expression tag	UNP Q99MB1
A	722	GLU	-	expression tag	UNP Q99MB1
A	723	LYS	-	expression tag	UNP Q99MB1
B	704	ASN	-	expression tag	UNP Q99MB1
B	705	LEU	-	expression tag	UNP Q99MB1
B	706	TYR	-	expression tag	UNP Q99MB1
B	707	PHE	-	expression tag	UNP Q99MB1
B	708	GLN	-	expression tag	UNP Q99MB1
B	709	GLY	-	expression tag	UNP Q99MB1
B	710	HIS	-	expression tag	UNP Q99MB1
B	711	HIS	-	expression tag	UNP Q99MB1
B	712	HIS	-	expression tag	UNP Q99MB1
B	713	HIS	-	expression tag	UNP Q99MB1
B	714	HIS	-	expression tag	UNP Q99MB1
B	715	HIS	-	expression tag	UNP Q99MB1
B	716	TRP	-	expression tag	UNP Q99MB1
B	717	SER	-	expression tag	UNP Q99MB1
B	718	HIS	-	expression tag	UNP Q99MB1
B	719	PRO	-	expression tag	UNP Q99MB1
B	720	GLN	-	expression tag	UNP Q99MB1
B	721	PHE	-	expression tag	UNP Q99MB1
B	722	GLU	-	expression tag	UNP Q99MB1
B	723	LYS	-	expression tag	UNP Q99MB1

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



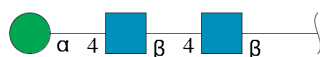
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

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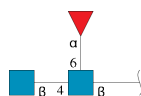
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

- 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.



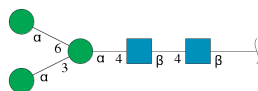
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



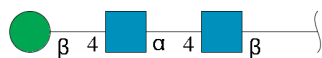
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	G	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



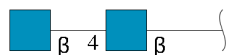
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	I	5	Total	C	N	O	0	0	0
			61	34	2	25			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
8	Q	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 9 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



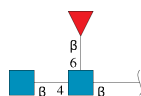
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
9	R	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 10 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.



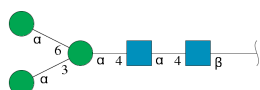
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	M	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 11 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-D-mannopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



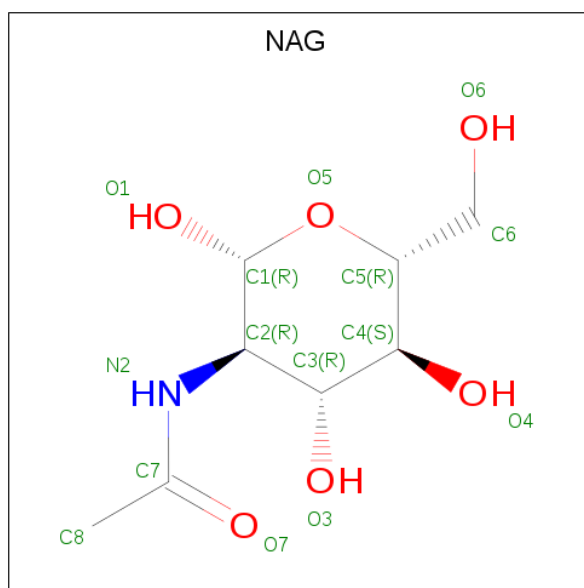
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	N	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 13 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
13	A	1	Total	C	N	O	0	0
			14	8	1	5		
13	A	1	Total	C	N	O	0	0
			14	8	1	5		
13	B	1	Total	C	N	O	0	0
			14	8	1	5		
13	B	1	Total	C	N	O	0	0
			14	8	1	5		

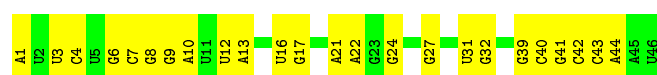


### 3 Residue-property plots [i](#)

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 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.

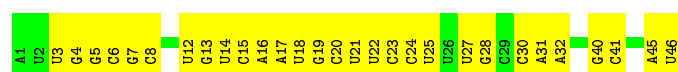
#### • Molecule 1: 46-MER

Chain C: 



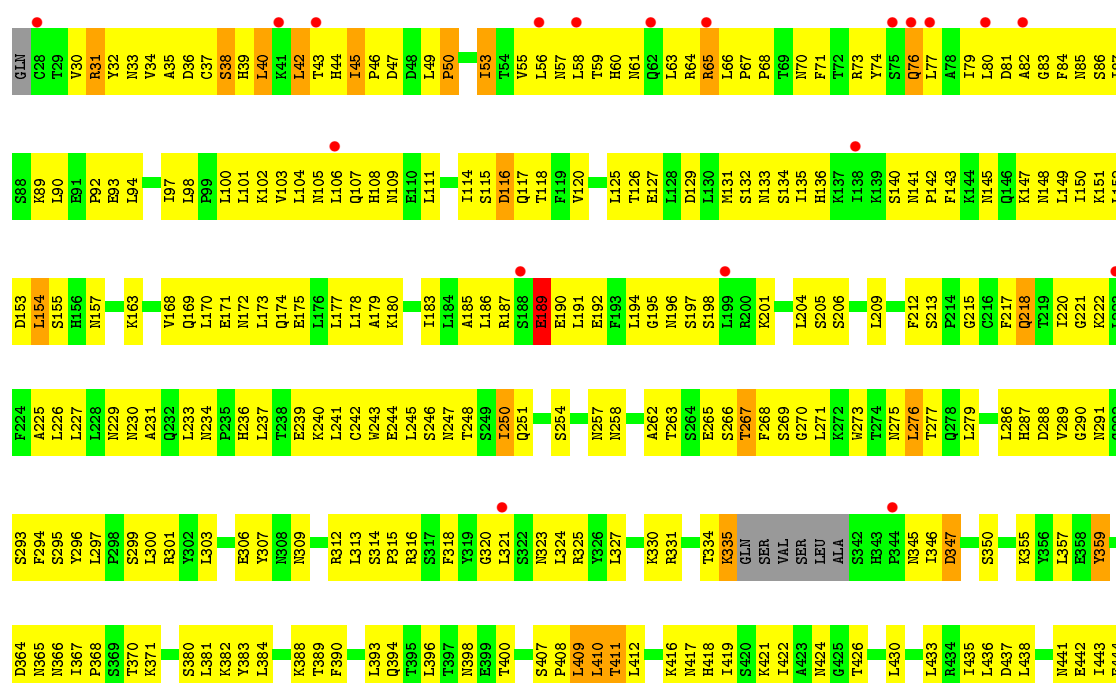
#### • Molecule 2: 46-MER

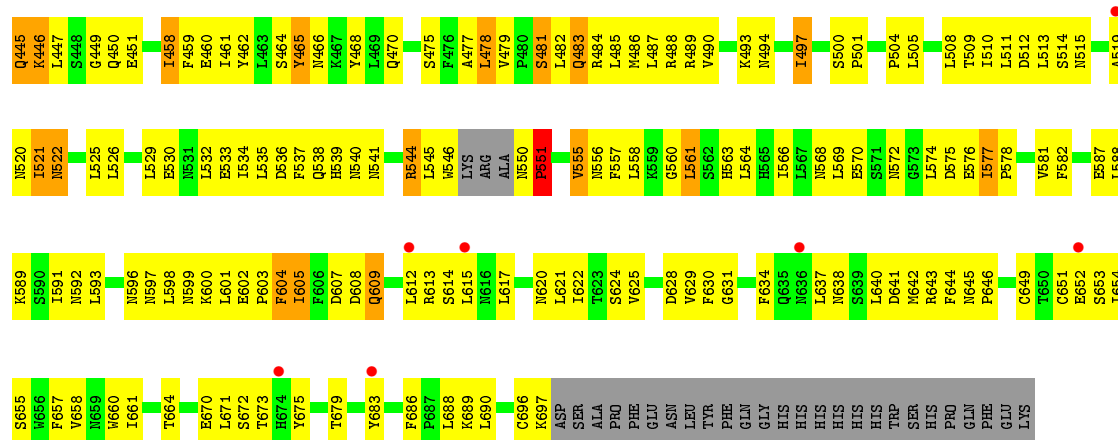
Chain D: 



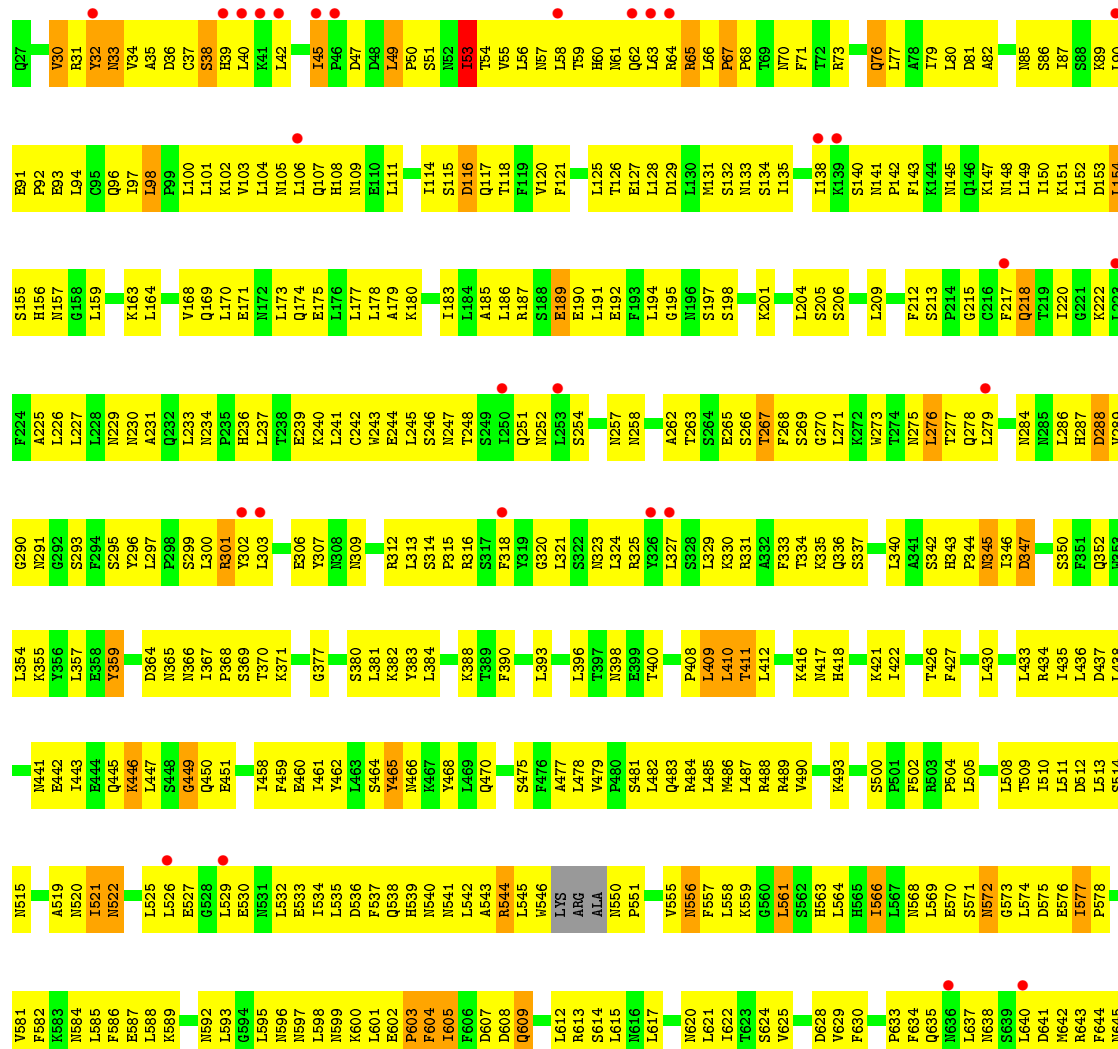
#### • Molecule 3: Toll-like receptor 3

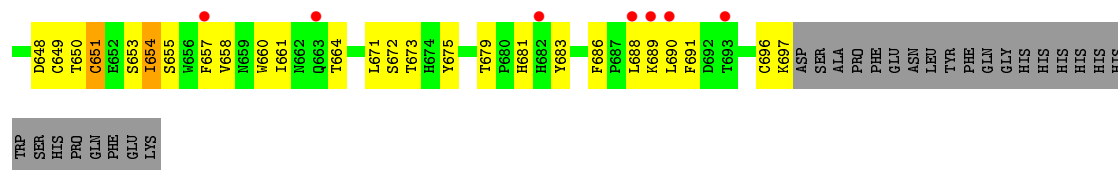
Chain A: 





### • Molecule 3: Toll-like receptor 3





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

Chain E: 50% 50%



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

Chain H: 100%



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

Chain L: 100%



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

Chain O: 50% 50%



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

Chain F: 33% 67%



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

Chain G: 67% 33%



- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:



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

Chain J:



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

Chain Q:



- Molecule 9: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:



- Molecule 9: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:



- Molecule 10: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

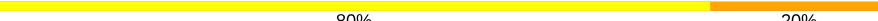


- Molecule 11: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  67% 33%

MAG1  
MAG2  
FUL3

- Molecule 12: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  80% 20%

MAG1  
MAG2  
MAN3  
MAN4  
MAN5

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.85Å 225.88Å 259.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.29 – 3.41 47.29 – 3.41	Depositor EDS
% Data completeness (in resolution range)	97.5 (47.29-3.41) 97.6 (47.29-3.41)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.00 (at 3.40Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.288 , 0.333 0.307 , 0.320	Depositor DCC
$R_{free}$ test set	2355 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	119.7	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 65.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	13194	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	154.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: BMA, NAG, NDG, FUC, FUL, 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	C	0.40	0/1094	0.70	0/1703
2	D	0.43	0/1080	0.70	0/1679
3	A	0.46	1/5421 (0.0%)	0.69	1/7360 (0.0%)
3	B	0.48	1/5472 (0.0%)	0.70	0/7431
All	All	0.46	2/13067 (0.0%)	0.70	1/18173 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	53	ILE	CA-CB	5.48	1.67	1.54
3	A	189	GLU	N-CA	5.34	1.57	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	560	GLY	N-CA-C	5.09	125.83	113.10

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	C	978	0	496	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	968	0	494	33	0
3	A	5310	0	5311	511	0
3	B	5360	0	5363	522	0
4	E	28	0	24	4	0
4	H	28	0	24	5	0
4	L	28	0	24	5	0
4	O	28	0	24	3	0
5	F	39	0	34	6	0
6	G	38	0	34	4	0
7	I	61	0	52	6	0
8	J	39	0	33	5	0
8	Q	39	0	33	6	0
9	K	28	0	25	3	0
9	R	28	0	25	2	0
10	M	39	0	34	3	0
11	N	38	0	34	1	0
12	P	61	0	51	1	0
13	A	28	0	26	2	0
13	B	28	0	26	1	0
All	All	13194	0	12167	1109	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 44.

The worst 5 of 1109 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)
3:B:650:THR:O	3:B:654:ILE:HD12	1.41	1.21
3:A:605:ILE:HD11	3:A:629:VAL:HG13	1.19	1.13
3:B:450:GLN:HG3	8:Q:1:NAG:H62	1.29	1.12
3:A:536:ASP:HB3	3:A:538:GLN:HE22	1.20	1.06
3:B:108:HIS:HA	3:B:132:SER:HB2	1.32	1.06

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	655/697 (94%)	527 (80%)	117 (18%)	11 (2%)	9	40
3	B	664/697 (95%)	537 (81%)	113 (17%)	14 (2%)	7	35
All	All	1319/1394 (95%)	1064 (81%)	230 (17%)	25 (2%)	8	37

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	551	PRO
3	A	247	ASN
3	A	290	GLY
3	A	38	SER
3	A	267	THR

### 5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	619/651 (95%)	564 (91%)	55 (9%)	9	37
3	B	625/651 (96%)	574 (92%)	51 (8%)	11	40
All	All	1244/1302 (96%)	1138 (92%)	106 (8%)	10	38

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	608	ASP

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Mol	Chain	Res	Type
3	B	65	ARG
3	B	609	GLN
3	A	628	ASP
3	A	679	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	674	HIS
3	B	113	GLN
3	B	618	GLN
3	B	33	ASN
3	B	85	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	45/46 (97%)	0	0
2	D	45/46 (97%)	0	0
All	All	90/92 (97%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

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

## 5.5 Carbohydrates ⓘ

40 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
4	NAG	E	1	3,4	14,14,15	1.00	1 (7%)	17,19,21	0.88	0
4	NDG	E	2	4	14,14,15	0.92	1 (7%)	17,19,21	0.89	1 (5%)
5	NAG	F	1	3,5	14,14,15	0.88	0	17,19,21	1.01	1 (5%)
5	NAG	F	2	5	14,14,15	0.82	1 (7%)	17,19,21	0.66	0
5	MAN	F	3	5	11,11,12	0.89	0	15,15,17	0.80	1 (6%)
6	NAG	G	1	3,6	14,14,15	0.92	0	17,19,21	0.84	0
6	NAG	G	2	6	14,14,15	0.89	1 (7%)	17,19,21	0.57	0
6	FUC	G	3	6	10,10,11	0.82	0	14,14,16	0.52	0
4	NAG	H	1	3,4	14,14,15	1.09	1 (7%)	17,19,21	0.84	0
4	NDG	H	2	4	14,14,15	0.99	1 (7%)	17,19,21	0.88	1 (5%)
7	NAG	I	1	3,7	14,14,15	0.52	0	17,19,21	1.18	2 (11%)
7	NAG	I	2	7	14,14,15	0.77	0	17,19,21	0.81	0
7	MAN	I	3	7	11,11,12	1.14	1 (9%)	15,15,17	0.89	0
7	MAN	I	4	7	11,11,12	0.90	0	15,15,17	0.78	1 (6%)
7	MAN	I	5	7	11,11,12	0.91	0	15,15,17	1.10	1 (6%)
8	NAG	J	1	8,3	14,14,15	0.99	1 (7%)	17,19,21	0.84	0
8	NDG	J	2	8	14,14,15	0.82	0	17,19,21	0.73	0
8	BMA	J	3	8	11,11,12	0.71	0	15,15,17	0.40	0
9	NAG	K	1	9,3	14,14,15	0.56	0	17,19,21	1.06	2 (11%)
9	NAG	K	2	9	14,14,15	0.82	0	17,19,21	0.87	0
4	NAG	L	1	3,4	14,14,15	1.09	1 (7%)	17,19,21	1.22	1 (5%)
4	NDG	L	2	4	14,14,15	1.03	1 (7%)	17,19,21	0.84	0
10	NAG	M	1	10,3	14,14,15	1.07	0	17,19,21	1.23	2 (11%)
10	NAG	M	2	10	14,14,15	0.82	0	17,19,21	0.56	0
10	BMA	M	3	10	11,11,12	0.96	0	15,15,17	0.91	1 (6%)
11	NAG	N	1	11,3	14,14,15	0.96	1 (7%)	17,19,21	0.75	0
11	NAG	N	2	11	14,14,15	0.92	0	17,19,21	1.01	1 (5%)
11	FUL	N	3	11	10,10,11	0.72	0	14,14,16	0.66	0
4	NAG	O	1	3,4	14,14,15	0.80	0	17,19,21	0.78	0
4	NDG	O	2	4	14,14,15	0.91	0	17,19,21	0.91	1 (5%)
12	NAG	P	1	3,12	14,14,15	0.72	0	17,19,21	1.03	1 (5%)
12	NDG	P	2	12	14,14,15	1.10	0	17,19,21	1.16	2 (11%)
12	MAN	P	3	12	11,11,12	1.27	2 (18%)	15,15,17	1.05	1 (6%)
12	MAN	P	4	12	11,11,12	0.86	0	15,15,17	0.83	1 (6%)
12	MAN	P	5	12	11,11,12	0.87	0	15,15,17	1.09	2 (13%)
8	NAG	Q	1	8,3	14,14,15	0.97	0	17,19,21	0.87	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	NDG	Q	2	8	14,14,15	1.08	1 (7%)	17,19,21	0.70	0
8	BMA	Q	3	8	11,11,12	0.91	0	15,15,17	0.35	0
9	NAG	R	1	9,3	14,14,15	1.28	1 (7%)	17,19,21	0.80	0
9	NAG	R	2	9	14,14,15	1.16	2 (14%)	17,19,21	1.15	1 (5%)

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
4	NAG	E	1	3,4	-	4/6/23/26	0/1/1/1
4	NDG	E	2	4	-	4/6/23/26	0/1/1/1
5	NAG	F	1	3,5	-	4/6/23/26	0/1/1/1
5	NAG	F	2	5	-	4/6/23/26	0/1/1/1
5	MAN	F	3	5	-	2/2/19/22	1/1/1/1
6	NAG	G	1	3,6	-	4/6/23/26	0/1/1/1
6	NAG	G	2	6	-	5/6/23/26	0/1/1/1
6	FUC	G	3	6	-	-	0/1/1/1
4	NAG	H	1	3,4	-	5/6/23/26	0/1/1/1
4	NDG	H	2	4	-	5/6/23/26	0/1/1/1
7	NAG	I	1	3,7	1/1/5/7	4/6/23/26	0/1/1/1
7	NAG	I	2	7	-	4/6/23/26	0/1/1/1
7	MAN	I	3	7	-	2/2/19/22	0/1/1/1
7	MAN	I	4	7	-	2/2/19/22	0/1/1/1
7	MAN	I	5	7	-	2/2/19/22	0/1/1/1
8	NAG	J	1	8,3	1/1/5/7	3/6/23/26	0/1/1/1
8	NDG	J	2	8	-	2/6/23/26	0/1/1/1
8	BMA	J	3	8	-	2/2/19/22	0/1/1/1
9	NAG	K	1	9,3	1/1/5/7	2/6/23/26	0/1/1/1
9	NAG	K	2	9	-	4/6/23/26	0/1/1/1
4	NAG	L	1	3,4	-	4/6/23/26	0/1/1/1
4	NDG	L	2	4	-	2/6/23/26	0/1/1/1
10	NAG	M	1	10,3	-	6/6/23/26	0/1/1/1
10	NAG	M	2	10	-	4/6/23/26	0/1/1/1
10	BMA	M	3	10	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	N	1	11,3	-	2/6/23/26	0/1/1/1
11	NAG	N	2	11	-	3/6/23/26	0/1/1/1
11	FUL	N	3	11	-	-	0/1/1/1
4	NAG	O	1	3,4	-	5/6/23/26	0/1/1/1
4	NDG	O	2	4	-	4/6/23/26	0/1/1/1
12	NAG	P	1	3,12	1/1/5/7	2/6/23/26	0/1/1/1
12	NDG	P	2	12	-	4/6/23/26	0/1/1/1
12	MAN	P	3	12	-	2/2/19/22	0/1/1/1
12	MAN	P	4	12	-	2/2/19/22	1/1/1/1
12	MAN	P	5	12	-	1/2/19/22	0/1/1/1
8	NAG	Q	1	8,3	1/1/5/7	6/6/23/26	0/1/1/1
8	NDG	Q	2	8	-	3/6/23/26	0/1/1/1
8	BMA	Q	3	8	-	2/2/19/22	0/1/1/1
9	NAG	R	1	9,3	1/1/5/7	2/6/23/26	0/1/1/1
9	NAG	R	2	9	-	6/6/23/26	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	R	2	NAG	C1-C2	2.95	1.56	1.52
8	J	1	NAG	C1-C2	2.89	1.56	1.52
4	H	1	NAG	C1-C2	2.77	1.56	1.52
11	N	1	NAG	C1-C2	2.71	1.56	1.52
7	I	3	MAN	C2-C3	2.57	1.56	1.52

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	I	5	MAN	C1-O5-C5	3.49	116.92	112.19
9	R	2	NAG	C1-O5-C5	3.47	116.89	112.19
12	P	3	MAN	C1-C2-C3	3.31	113.74	109.67
10	M	1	NAG	C3-C4-C5	3.28	116.09	110.24
12	P	1	NAG	C2-N2-C7	-3.17	118.38	122.90

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	K	1	NAG	C1
12	P	1	NAG	C1

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Mol	Chain	Res	Type	Atom
8	J	1	NAG	C1
8	Q	1	NAG	C1
7	I	1	NAG	C1

5 of 126 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	1	NAG	C3-C2-N2-C7
4	E	1	NAG	C8-C7-N2-C2
4	E	1	NAG	O7-C7-N2-C2
9	K	1	NAG	C8-C7-N2-C2
9	K	1	NAG	O7-C7-N2-C2

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	3	MAN	C1-C2-C3-C4-C5-O5
12	P	4	MAN	C1-C2-C3-C4-C5-O5

29 monomers are involved in 54 short contacts:

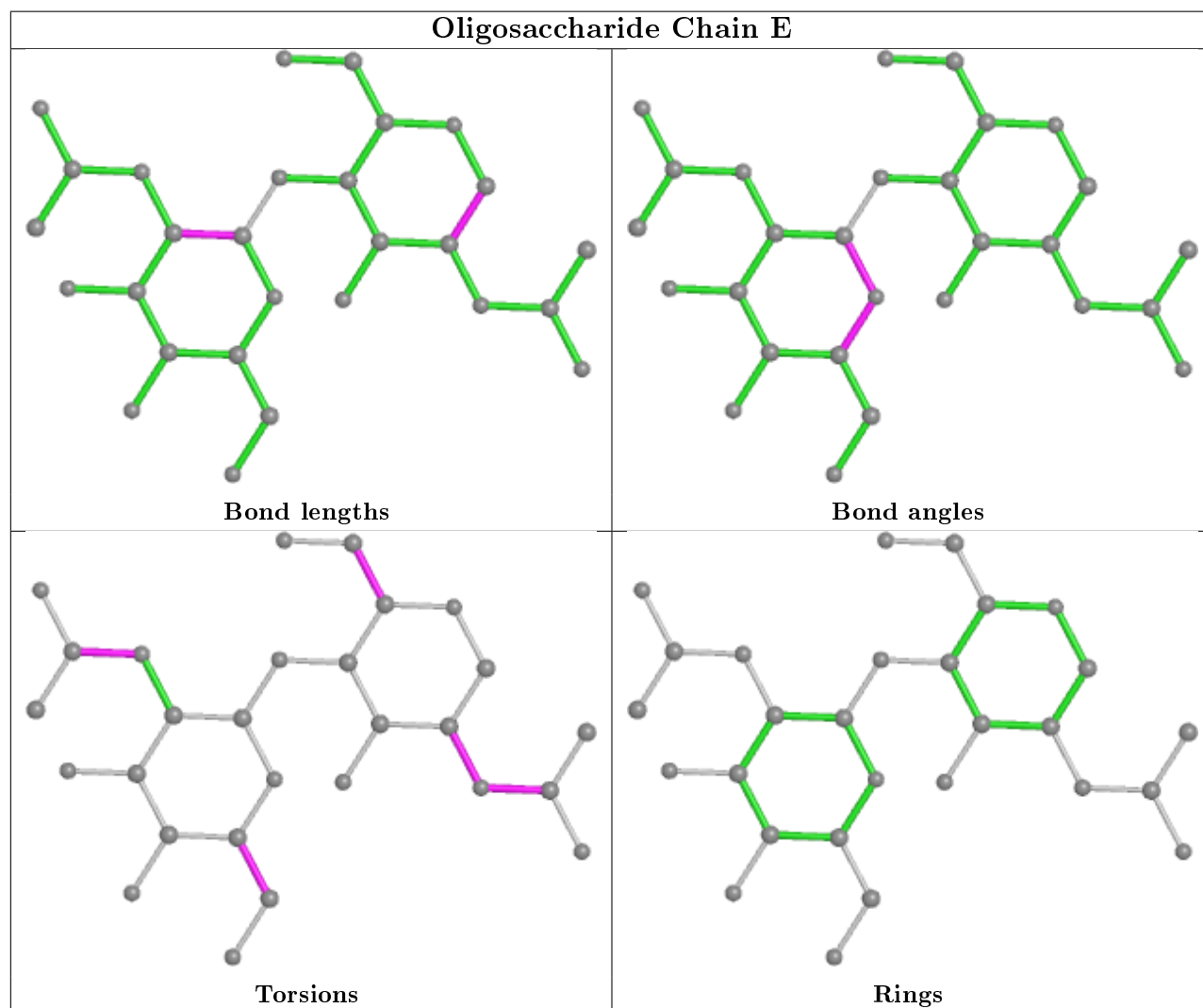
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1	NAG	4	0
9	K	1	NAG	3	0
8	J	3	BMA	1	0
10	M	1	NAG	3	0
8	Q	2	NDG	3	0
7	I	5	MAN	3	0
5	F	1	NAG	6	0
11	N	2	NAG	1	0
6	G	2	NAG	2	0
4	H	1	NAG	3	0
8	J	1	NAG	4	0
4	H	2	NDG	2	0
8	J	2	NDG	2	0
7	I	2	NAG	3	0
8	Q	1	NAG	5	0
11	N	3	FUL	1	0
7	I	1	NAG	3	0
4	O	1	NAG	3	0
9	R	1	NAG	1	0
8	Q	3	BMA	1	0

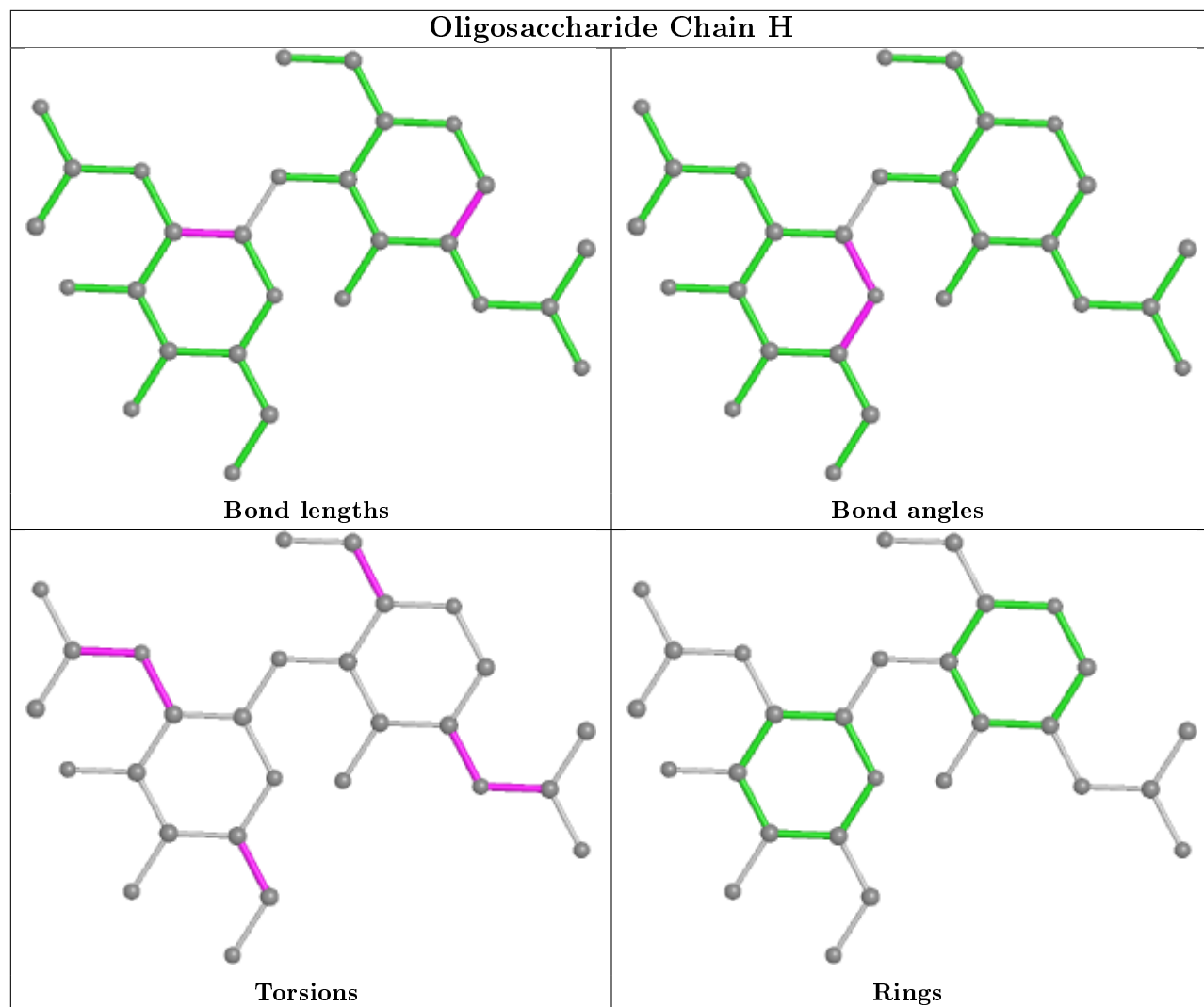
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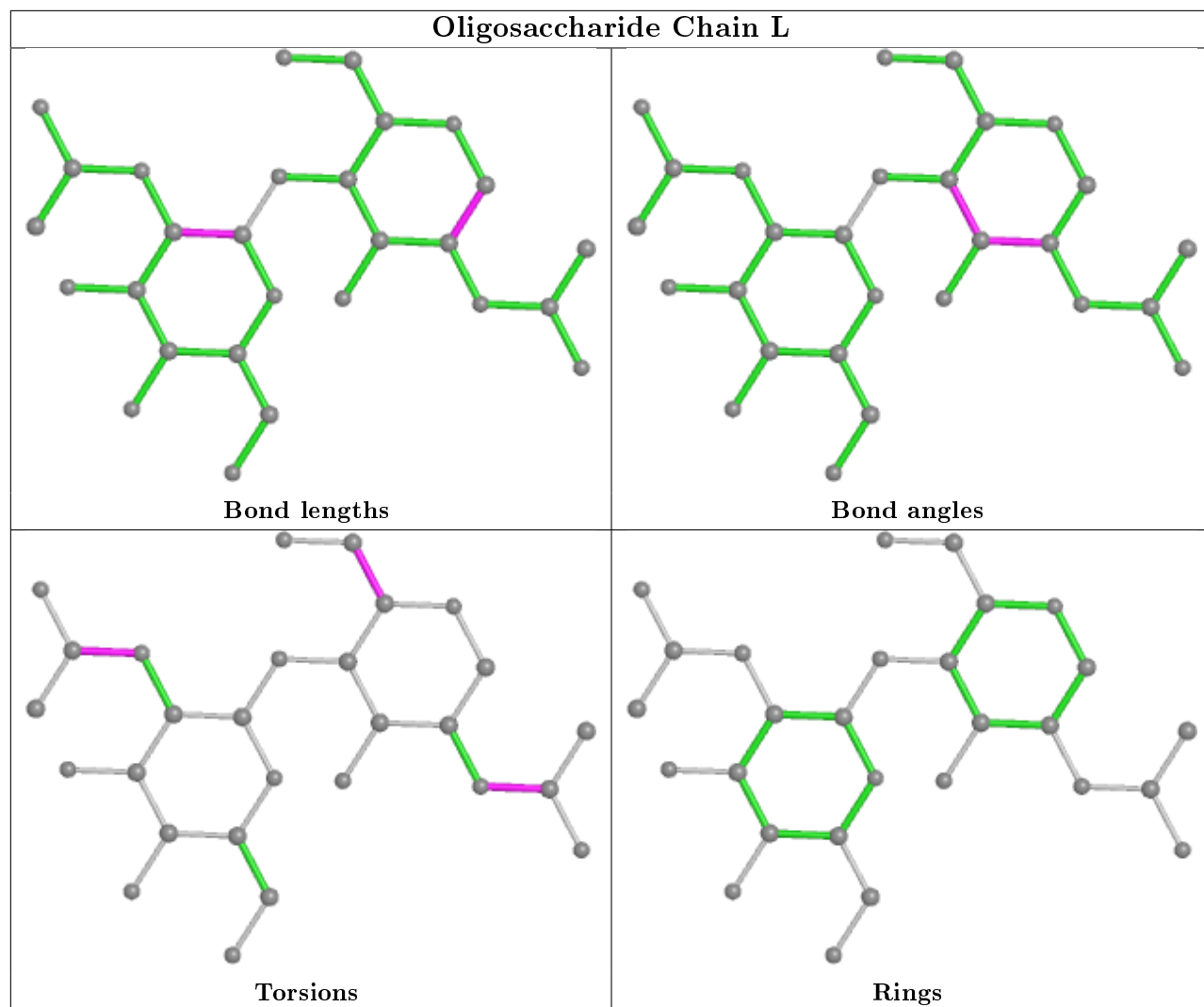
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	2	NAG	2	0
6	G	3	FUC	1	0
4	L	1	NAG	4	0
12	P	5	MAN	1	0
6	G	1	NAG	3	0
4	L	2	NDG	1	0
9	R	2	NAG	2	0
4	O	2	NDG	1	0
9	K	2	NAG	1	0

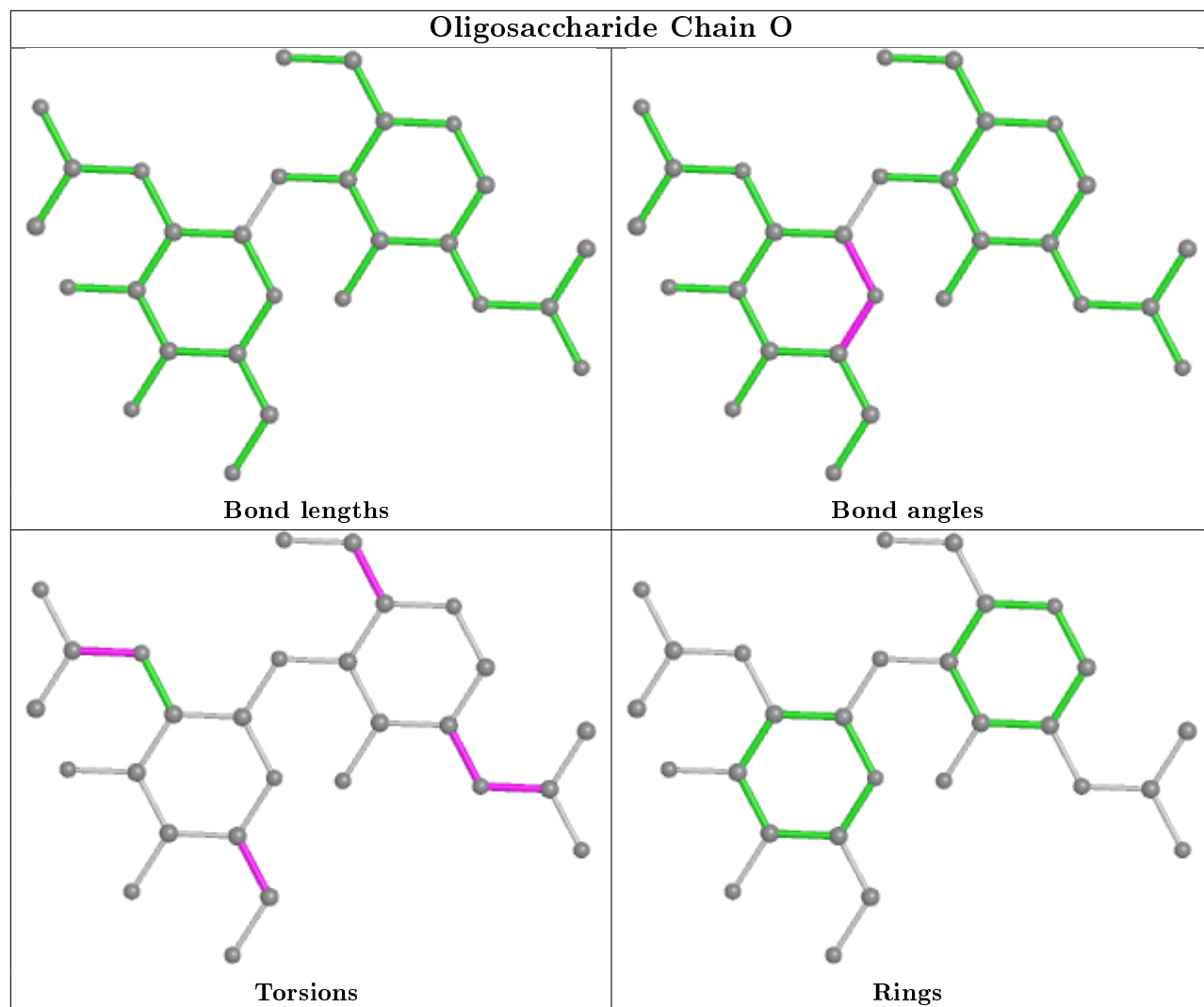
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

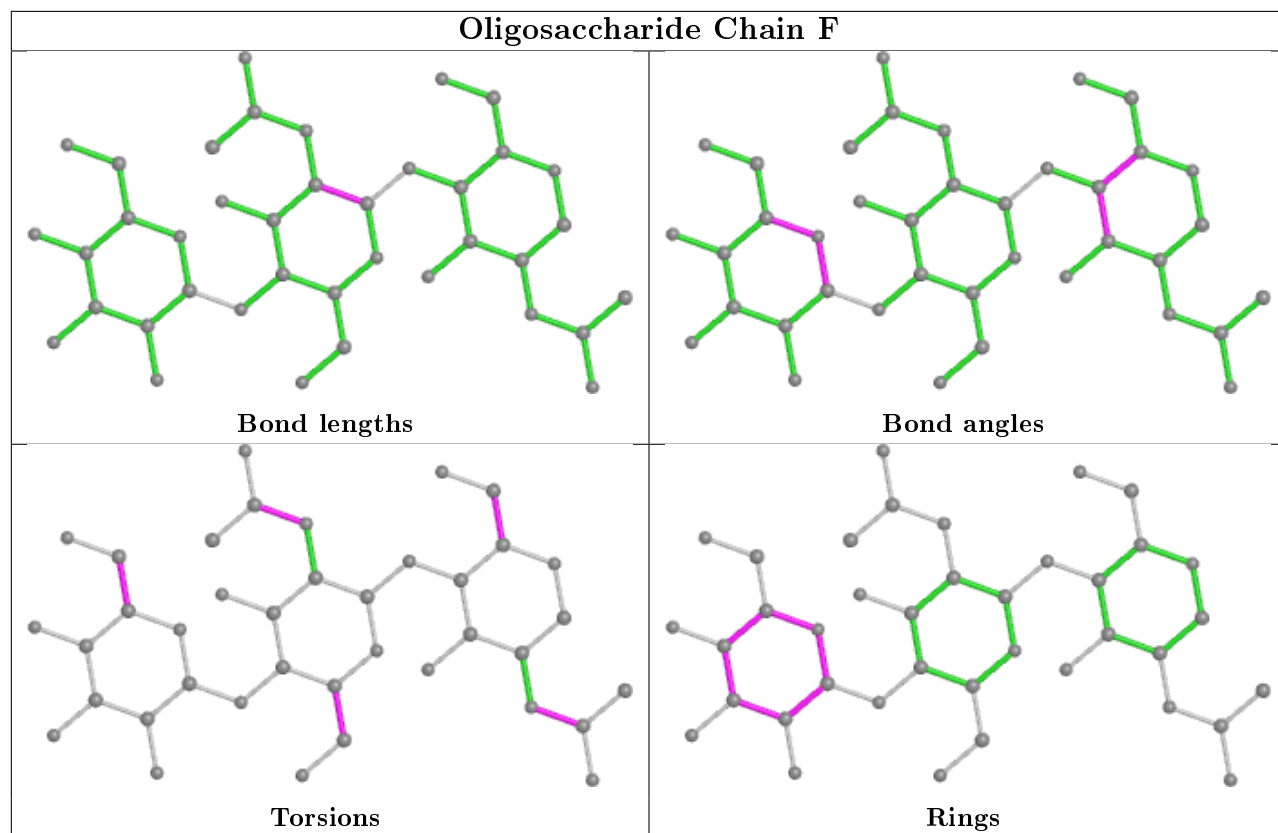


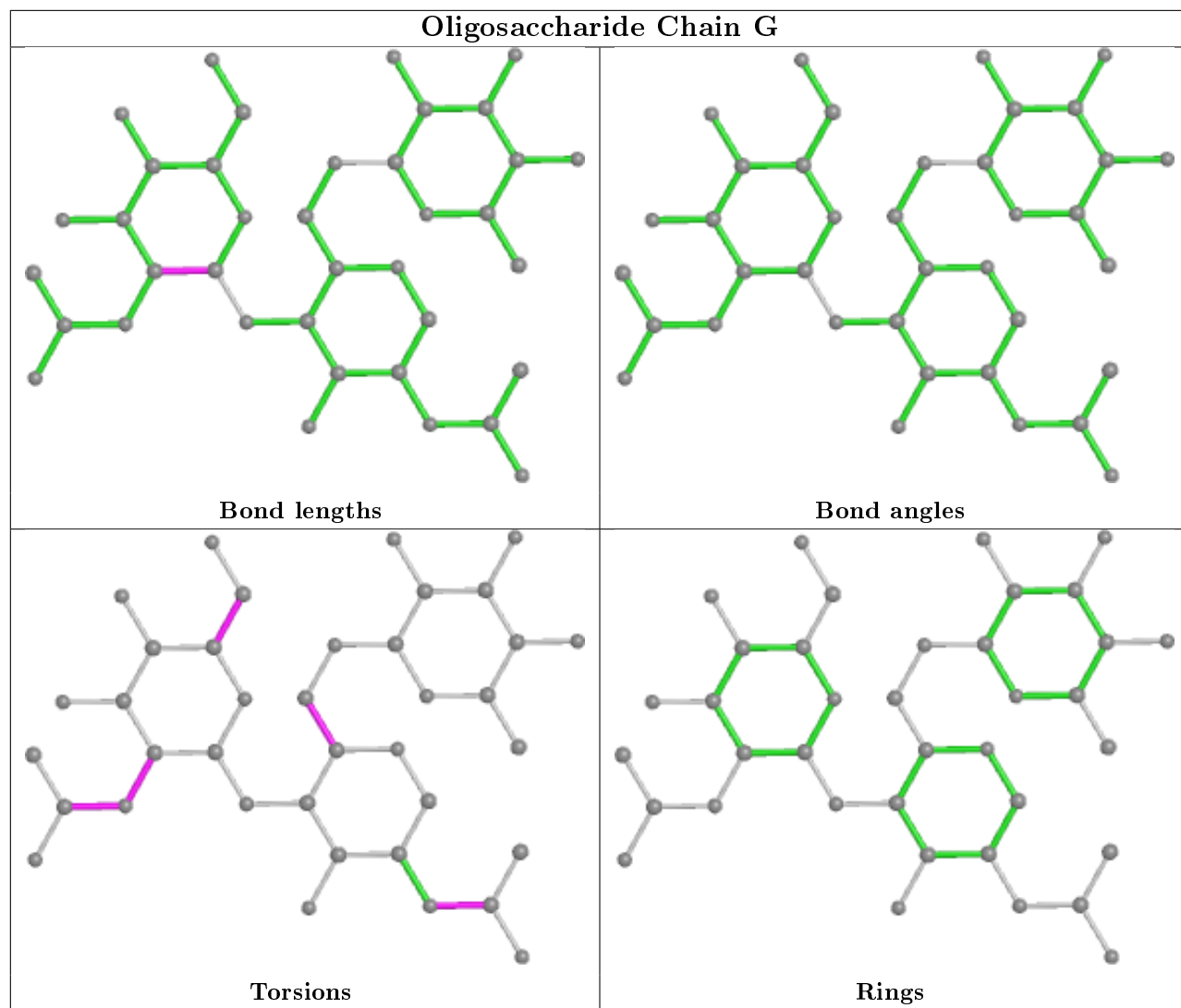


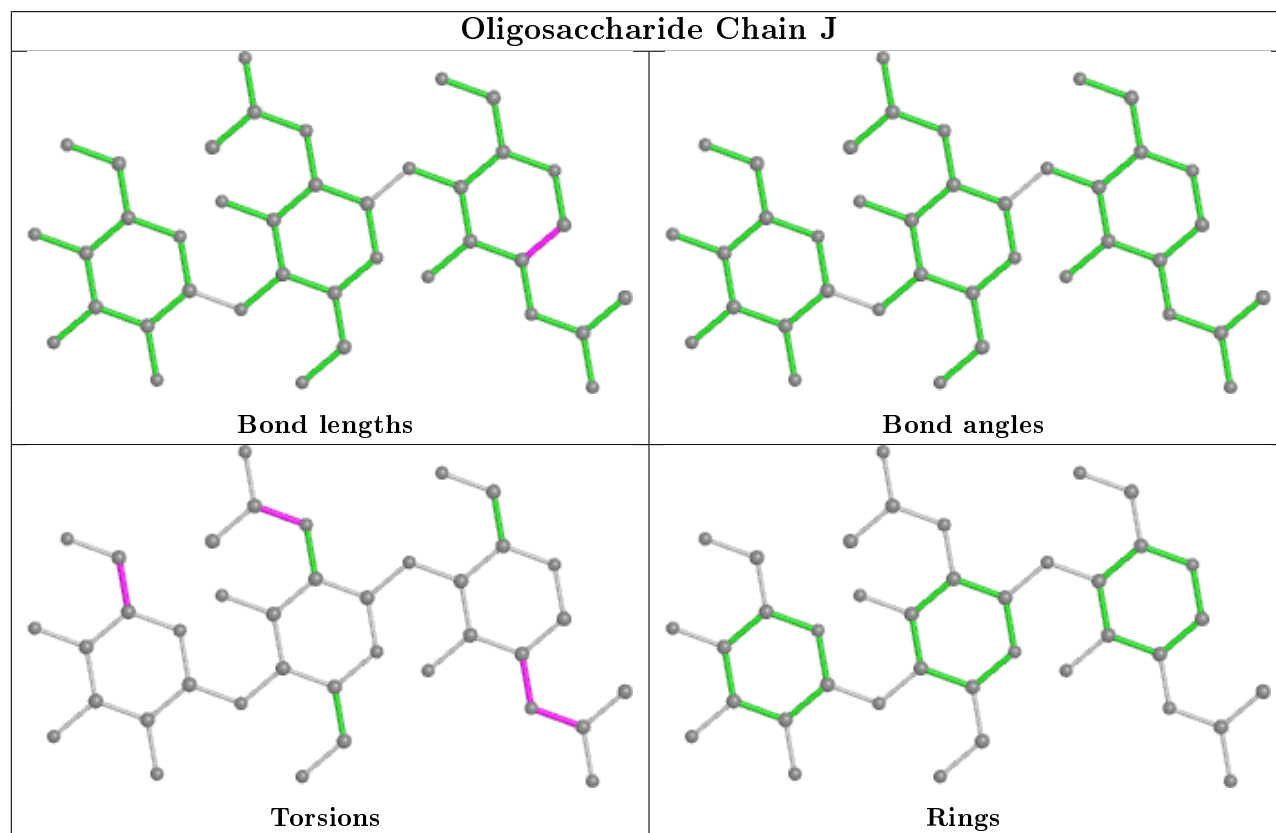
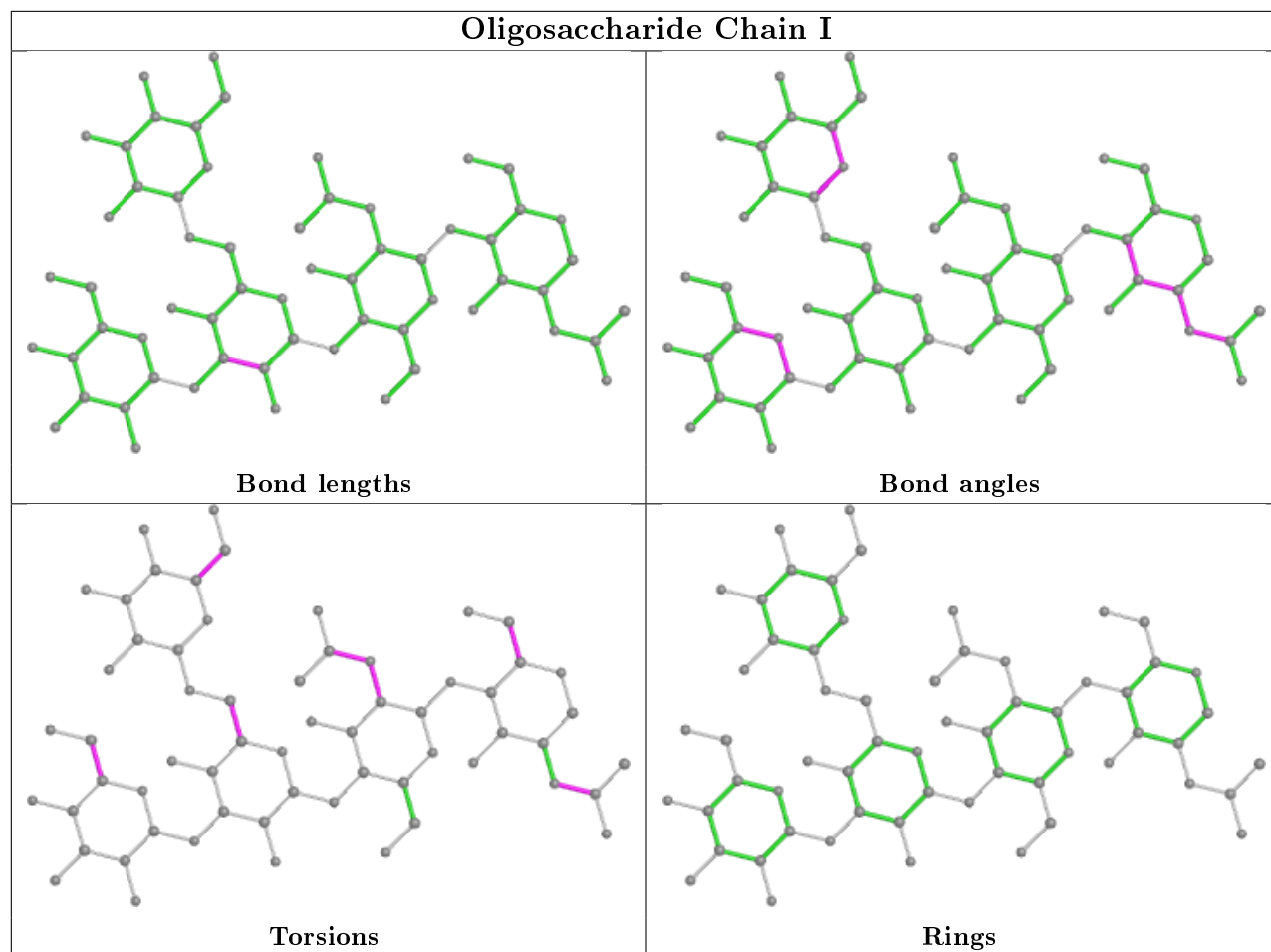


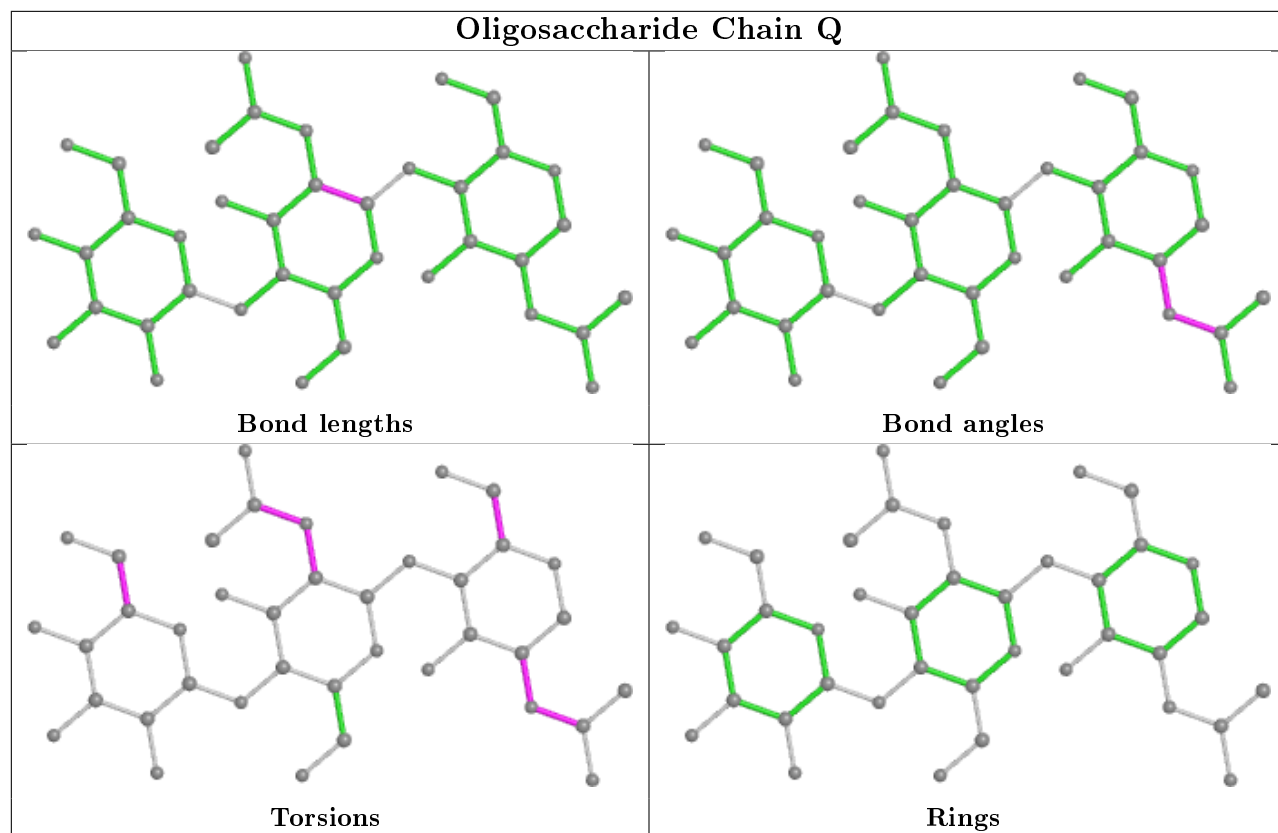


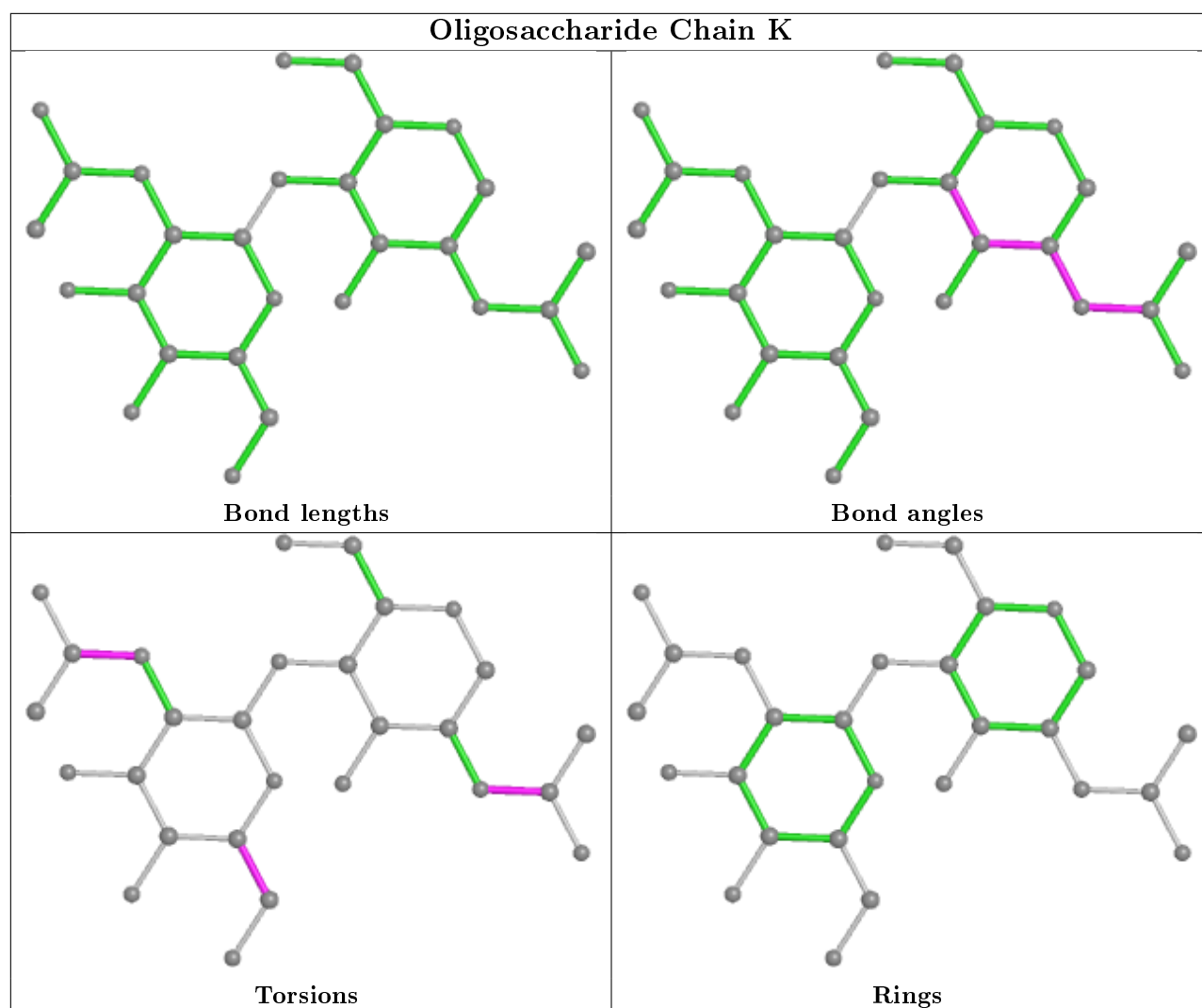


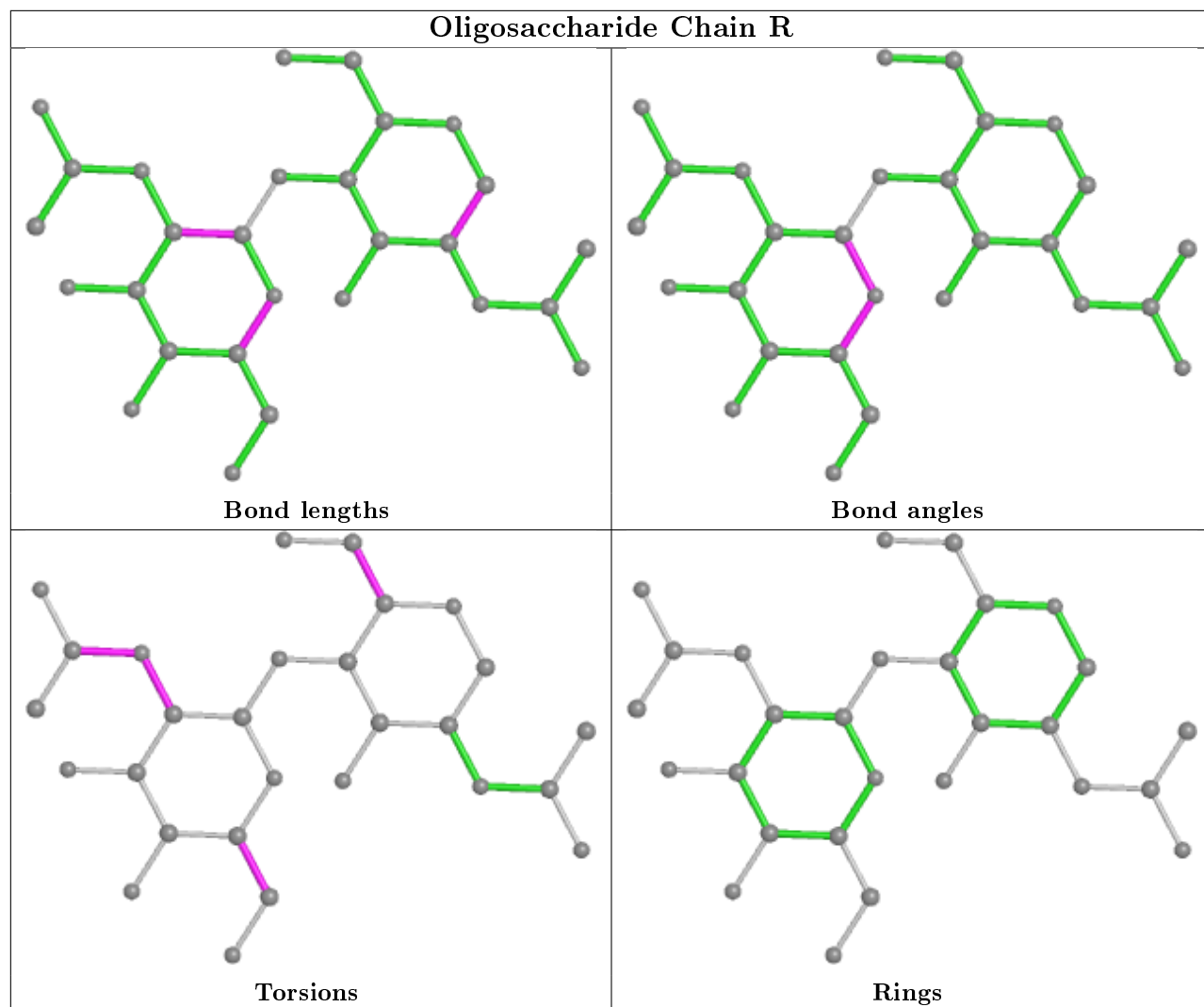




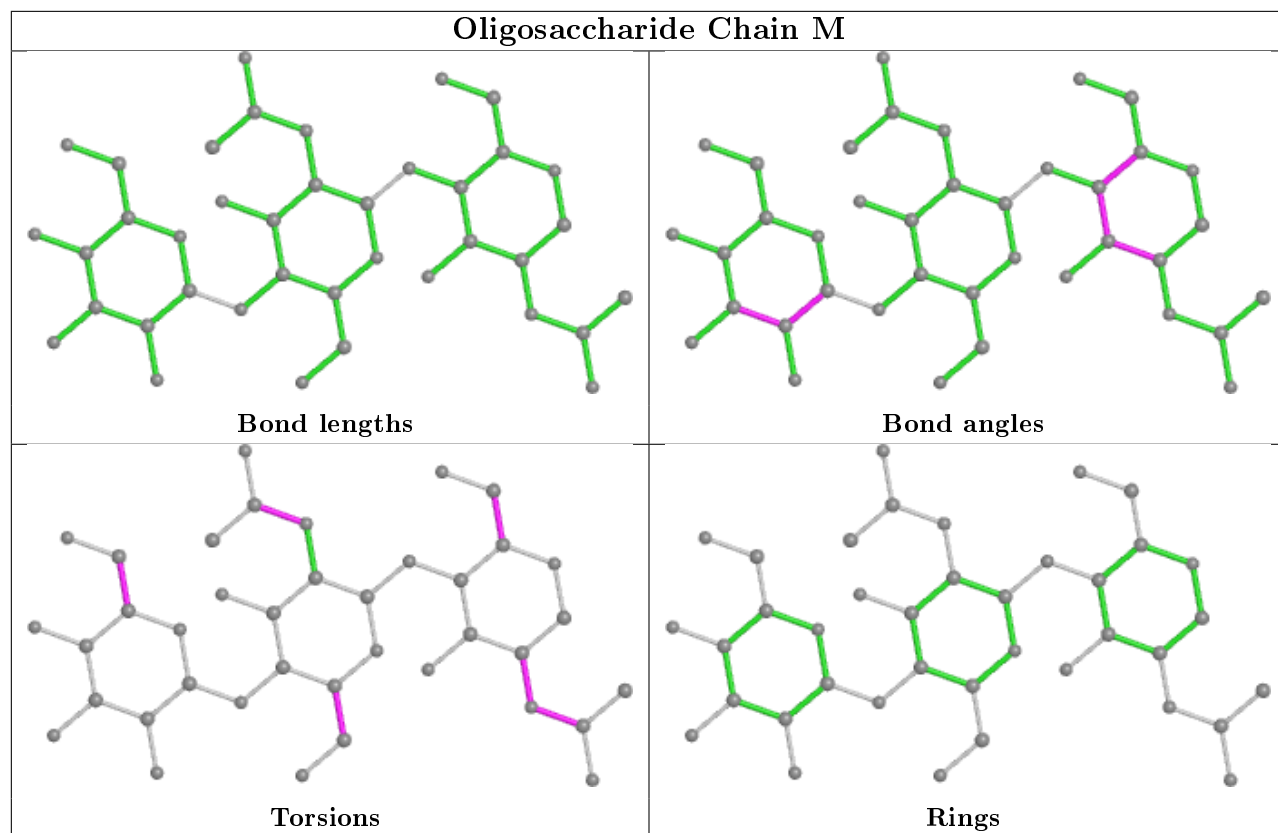


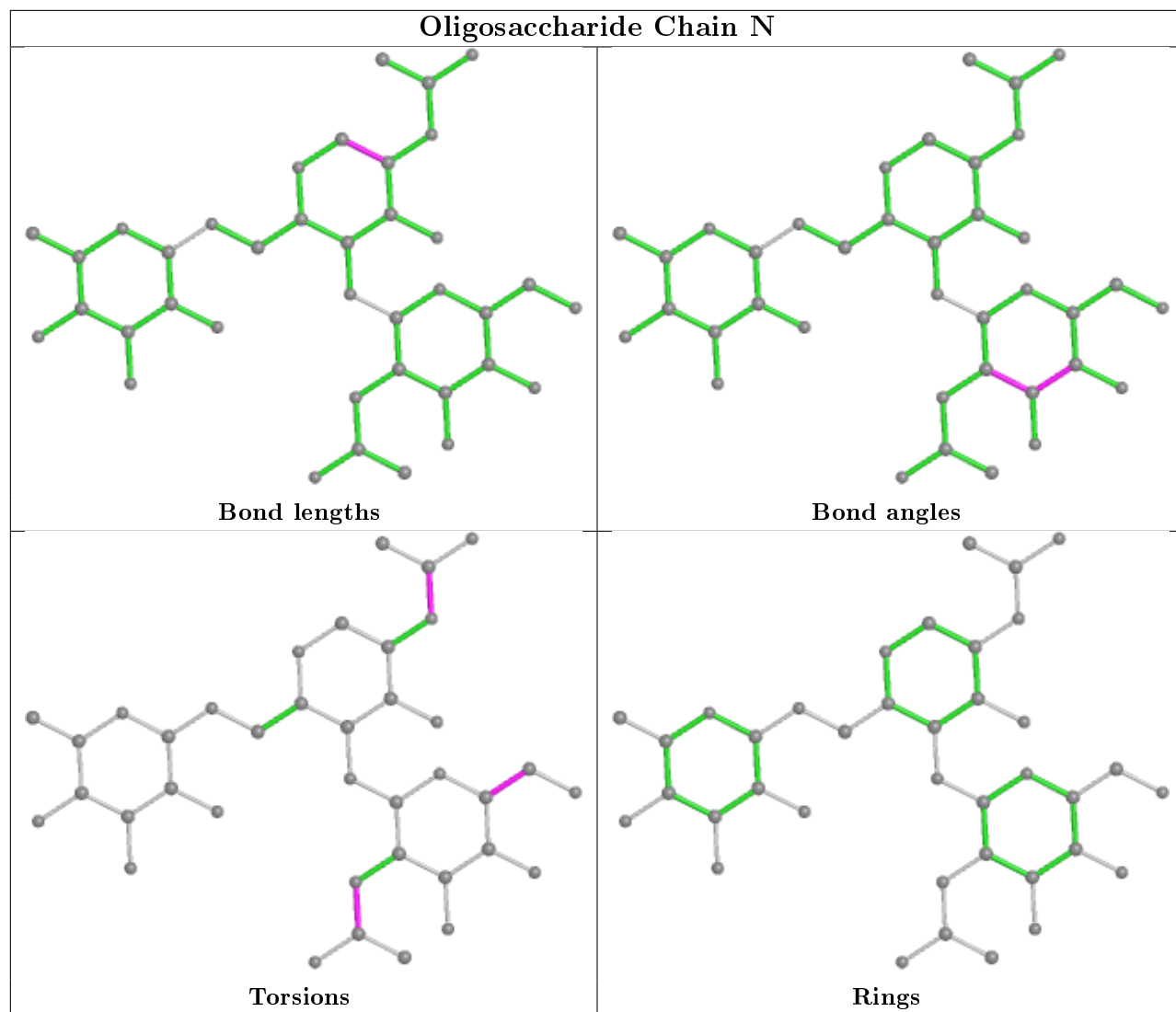


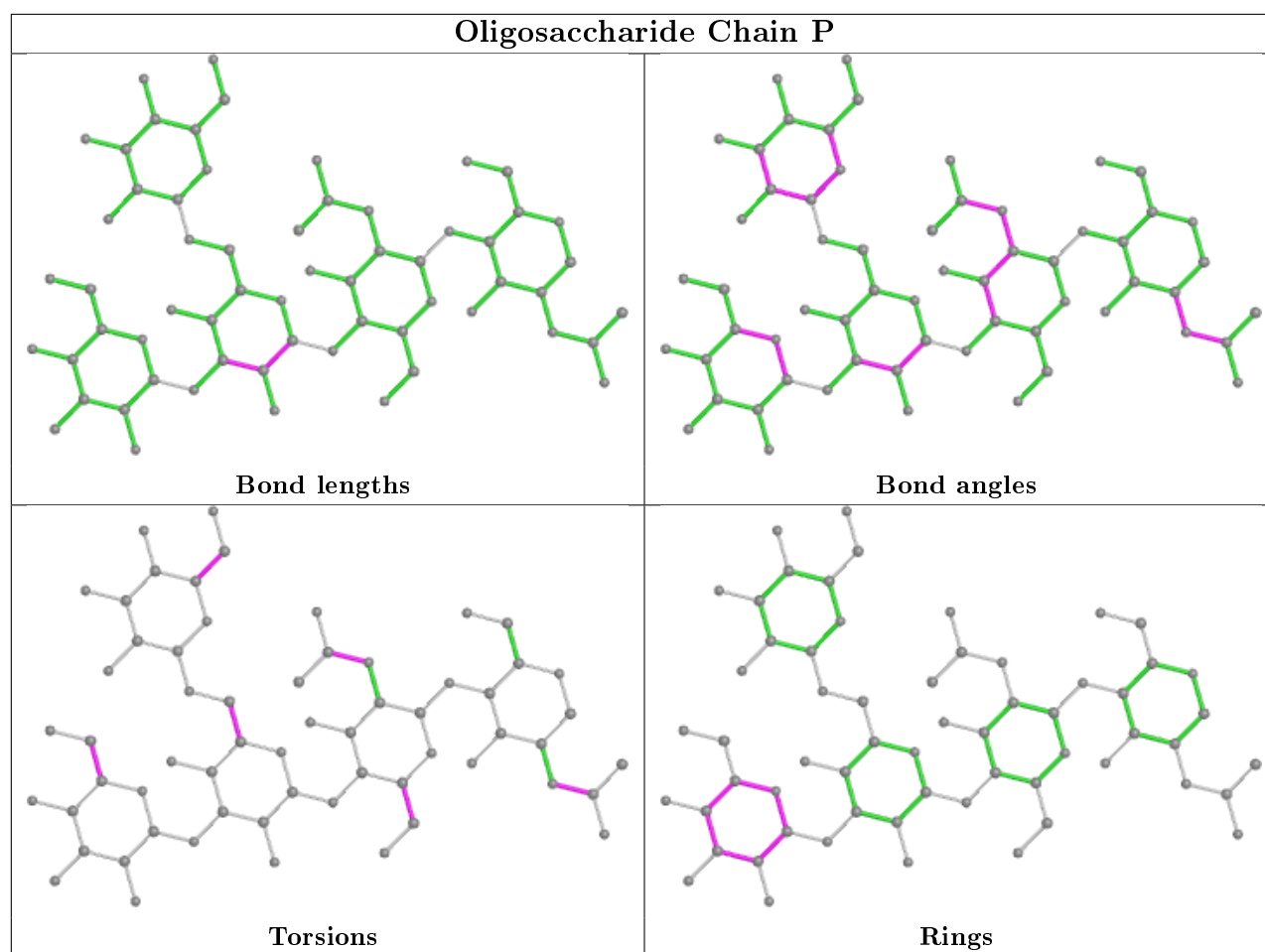












## 5.6 Ligand geometry [i](#)

4 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	$\# Z  > 2$
13	NAG	B	724	3	14,14,15	0.83	1 (7%)	17,19,21	0.62	0
13	NAG	B	1961	3	14,14,15	1.19	1 (7%)	17,19,21	0.83	1 (5%)
13	NAG	A	1961	3	14,14,15	1.00	0	17,19,21	0.93	1 (5%)
13	NAG	A	724	3	14,14,15	0.88	1 (7%)	17,19,21	0.81	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
13	NAG	B	724	3	-	5/6/23/26	0/1/1/1
13	NAG	B	1961	3	-	4/6/23/26	0/1/1/1
13	NAG	A	1961	3	-	2/6/23/26	0/1/1/1
13	NAG	A	724	3	1/1/5/7	4/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	B	1961	NAG	C1-C2	3.30	1.57	1.52
13	B	724	NAG	C1-C2	2.28	1.55	1.52
13	A	724	NAG	C1-C2	2.14	1.55	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	1961	NAG	C1-O5-C5	2.71	115.87	112.19
13	B	1961	NAG	C1-O5-C5	2.30	115.31	112.19

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
13	A	724	NAG	C1

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	B	724	NAG	C8-C7-N2-C2
13	B	724	NAG	O7-C7-N2-C2
13	B	1961	NAG	C8-C7-N2-C2
13	B	1961	NAG	O7-C7-N2-C2
13	A	1961	NAG	C8-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	B	724	NAG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	A	1961	NAG	1	0
13	A	724	NAG	1	0

## 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	C	46/46 (100%)	0.22	0 100 100	167, 194, 197, 197	0
2	D	46/46 (100%)	0.19	0 100 100	164, 193, 197, 197	0
3	A	661/697 (94%)	0.33	26 (3%) 39 39	108, 144, 182, 191	0
3	B	668/697 (95%)	0.30	36 (5%) 25 27	109, 144, 179, 189	0
All	All	1421/1486 (95%)	0.31	62 (4%) 34 34	108, 145, 188, 197	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	62	GLN	6.8
3	B	663	GLN	5.9
3	B	302	TYR	5.2
3	A	41	LYS	4.3
3	B	42	LEU	4.1

### 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
7	MAN	I	5	11/12	0.55	0.23	186,187,187,188	0
12	MAN	P	3	11/12	0.62	0.29	180,182,186,187	0

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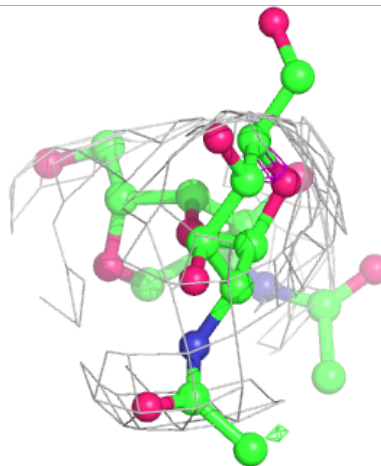
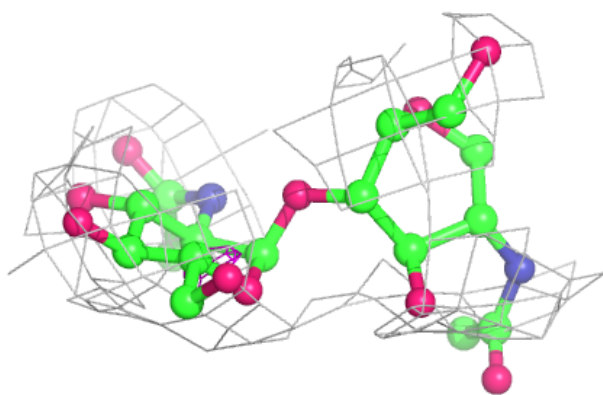
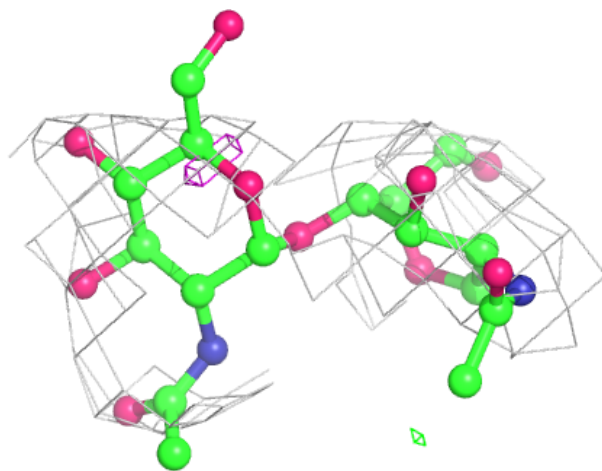
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
9	NAG	R	2	14/15	0.63	0.43	197,197,197,197	0
7	MAN	I	4	11/12	0.64	0.49	188,190,191,192	0
12	MAN	P	5	11/12	0.65	0.32	185,187,187,188	0
8	BMA	J	3	11/12	0.66	0.23	186,187,187,187	0
8	BMA	Q	3	11/12	0.68	0.25	190,191,192,192	0
4	NAG	L	1	14/15	0.74	0.42	173,177,179,183	0
12	MAN	P	4	11/12	0.75	0.28	188,189,190,190	0
4	NDG	L	2	14/15	0.76	1.02	186,188,188,188	0
6	FUC	G	3	10/11	0.77	0.32	189,190,191,191	0
6	NAG	G	1	14/15	0.78	0.20	172,176,178,178	0
4	NDG	E	2	14/15	0.79	0.29	181,182,182,183	0
10	BMA	M	3	11/12	0.82	0.37	191,193,193,194	0
4	NDG	H	2	14/15	0.82	0.30	184,185,187,188	0
8	NDG	J	2	14/15	0.82	0.43	180,182,184,186	0
9	NAG	K	2	14/15	0.82	0.23	170,172,174,174	0
8	NAG	Q	1	14/15	0.84	0.18	168,171,174,177	0
11	NAG	N	1	14/15	0.85	0.24	169,171,173,176	0
11	FUL	N	3	10/11	0.85	0.23	191,192,192,192	0
4	NDG	O	2	14/15	0.86	0.24	172,175,177,177	0
6	NAG	G	2	14/15	0.86	0.20	179,180,180,180	0
8	NAG	J	1	14/15	0.87	0.17	169,173,174,176	0
7	MAN	I	3	11/12	0.87	0.24	177,180,185,185	0
5	MAN	F	3	11/12	0.88	0.15	192,195,196,197	0
9	NAG	R	1	14/15	0.88	0.34	160,162,163,163	0
12	NDG	P	2	14/15	0.88	0.19	158,165,169,175	0
10	NAG	M	2	14/15	0.90	0.21	183,184,188,190	0
4	NAG	E	1	14/15	0.90	0.17	171,175,177,179	0
7	NAG	I	2	14/15	0.90	0.22	159,162,167,172	0
11	NAG	N	2	14/15	0.90	0.38	176,179,180,180	0
10	NAG	M	1	14/15	0.91	0.23	173,176,179,182	0
8	NDG	Q	2	14/15	0.91	0.22	177,181,184,188	0
12	NAG	P	1	14/15	0.91	0.24	141,144,149,155	0
5	NAG	F	1	14/15	0.91	0.27	167,172,176,180	0
5	NAG	F	2	14/15	0.93	0.26	183,185,188,191	0
4	NAG	H	1	14/15	0.93	0.22	168,171,176,180	0
9	NAG	K	1	14/15	0.94	0.15	160,164,165,168	0
4	NAG	O	1	14/15	0.94	0.14	163,167,168,171	0
7	NAG	I	1	14/15	0.97	0.23	140,145,147,152	0

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

**Electron density around Chain E:**

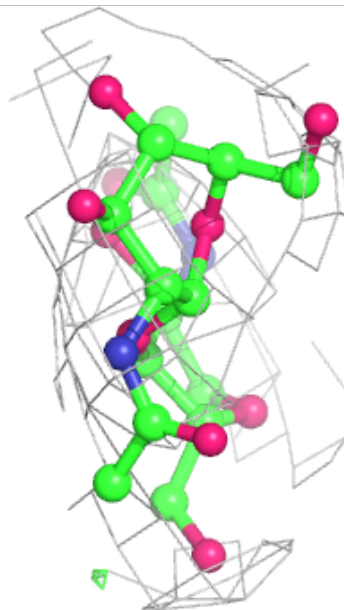
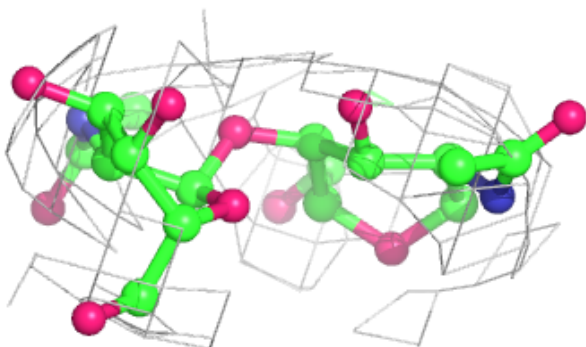
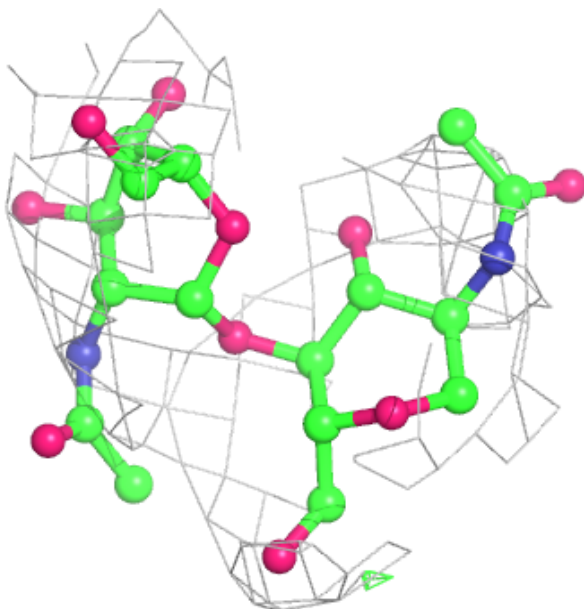
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





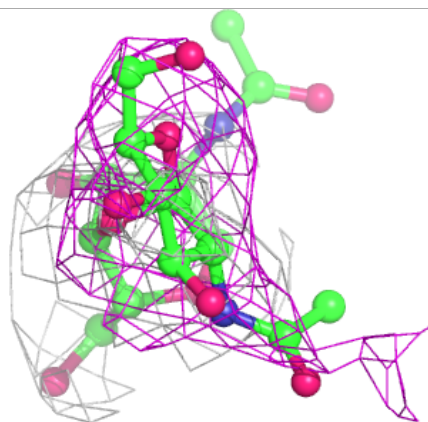
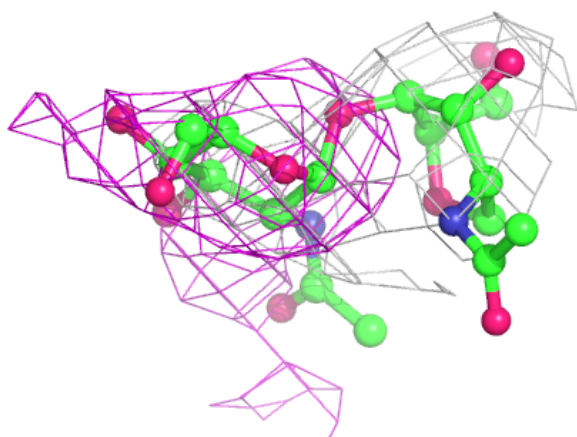
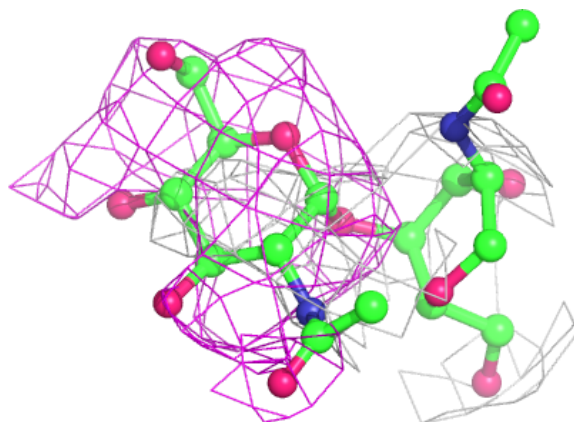
**Electron density around Chain H:**

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and green (positive)



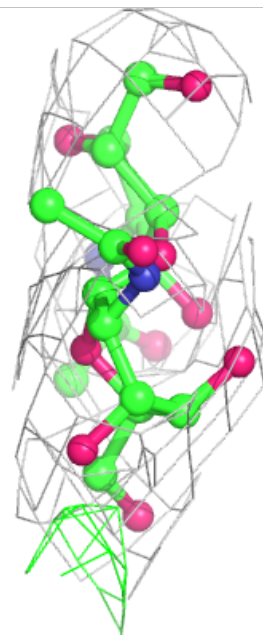
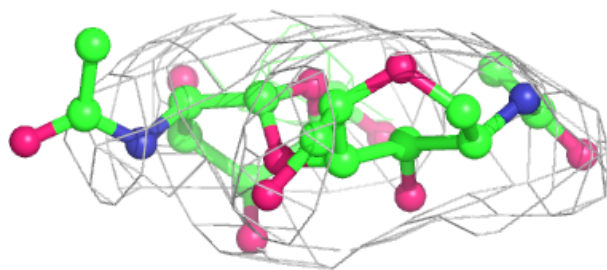
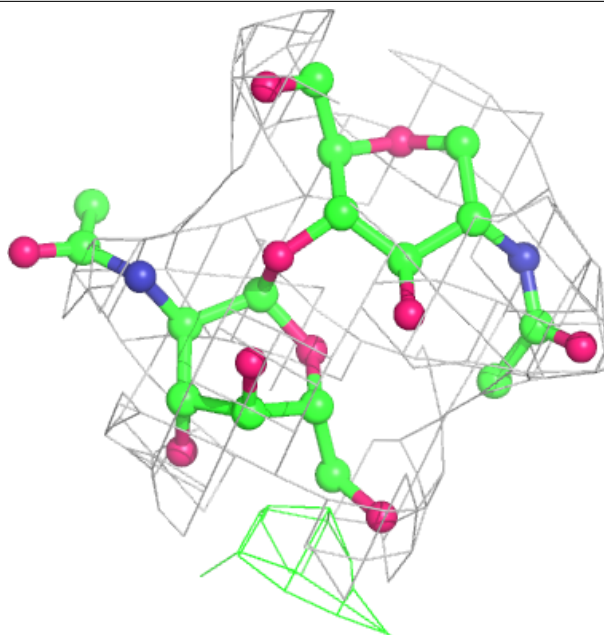
**Electron density around Chain L:**

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



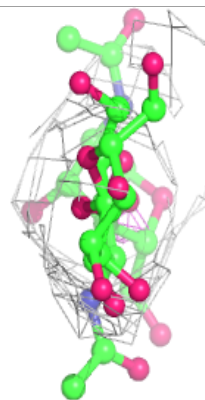
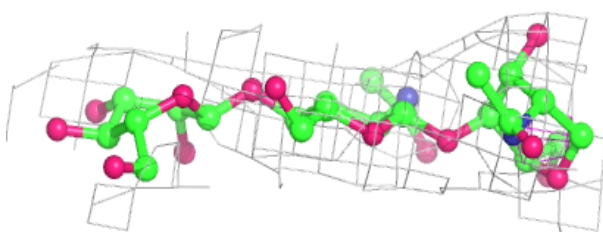
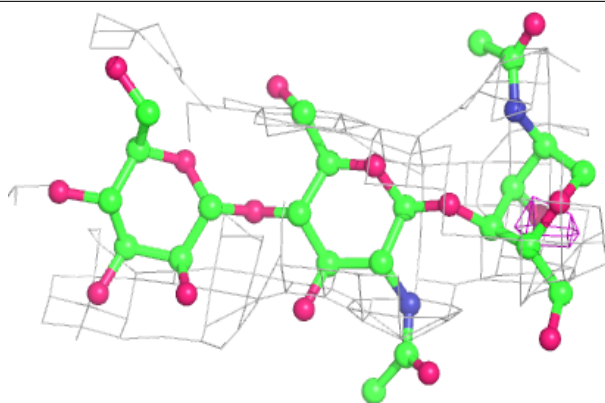
**Electron density around Chain O:**

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



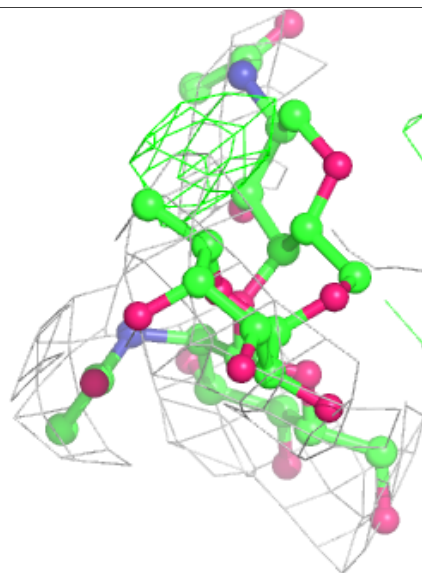
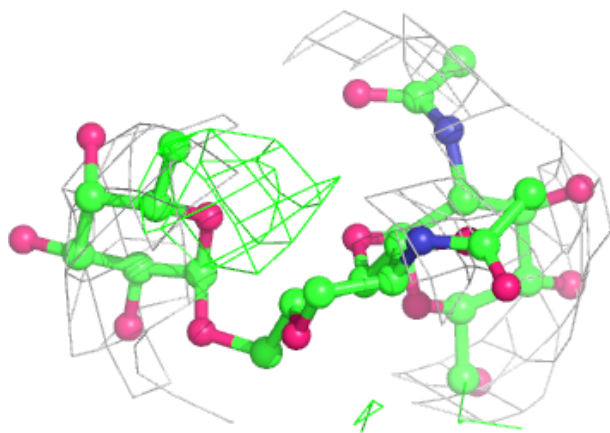
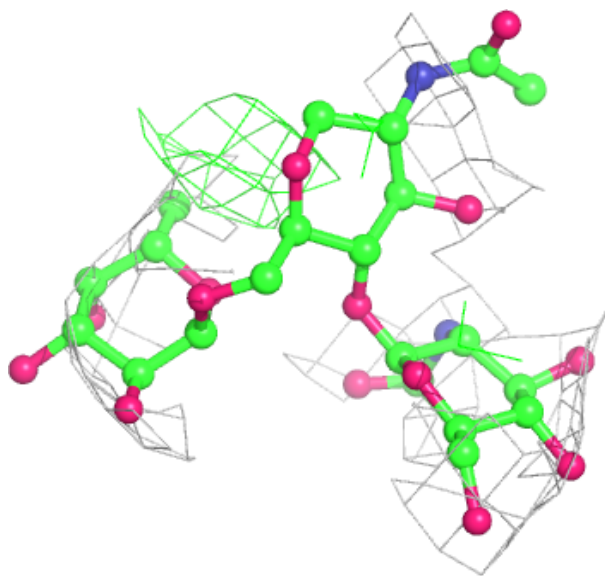
**Electron density around Chain F:**

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



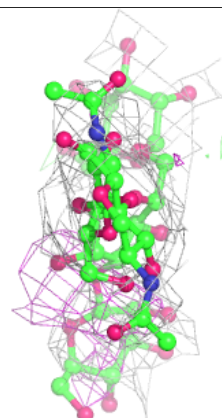
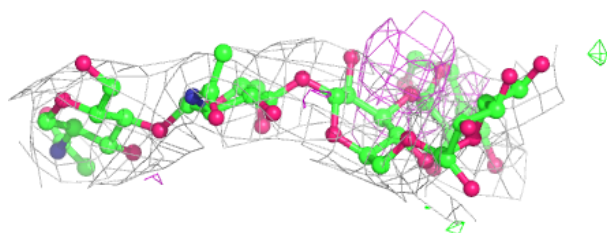
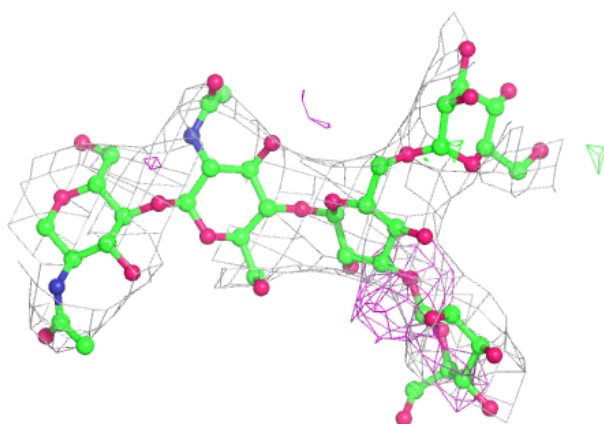
**Electron density around Chain G:**

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

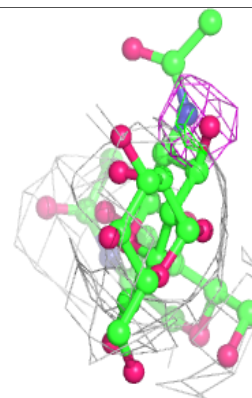
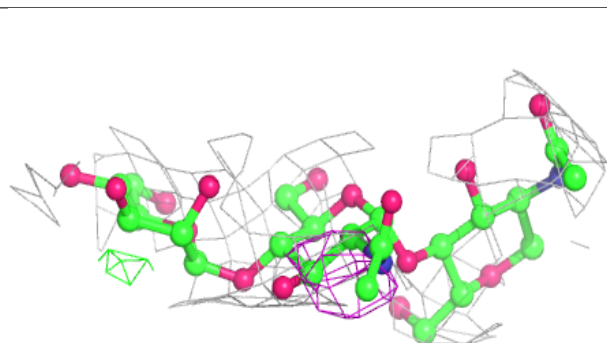
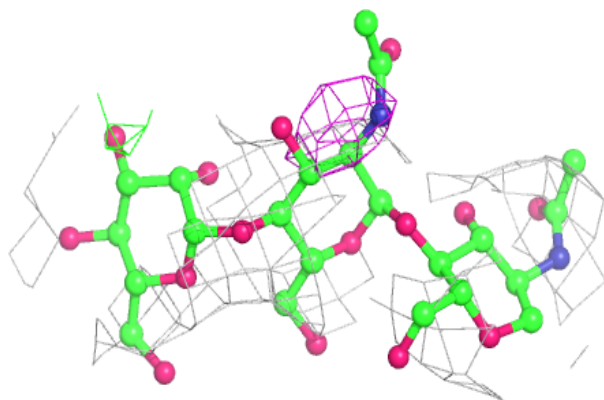


**Electron density around Chain I:**

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

**Electron density around Chain J:**

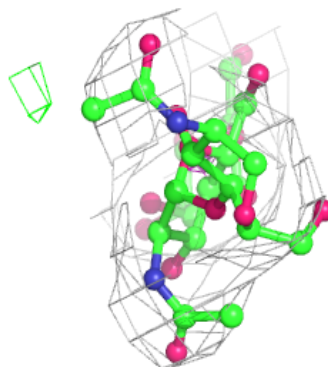
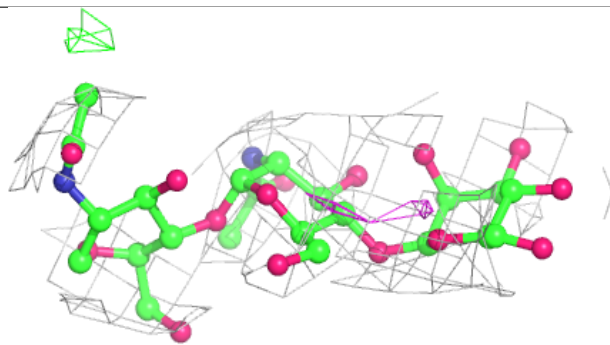
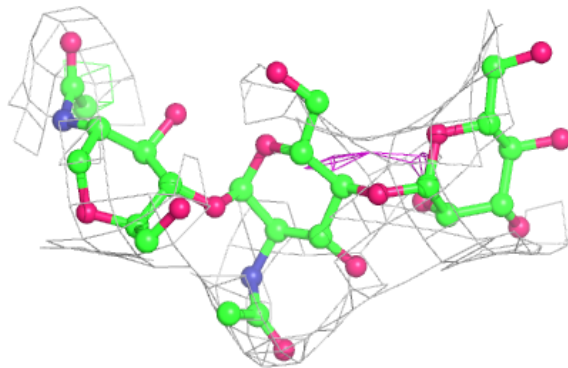
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



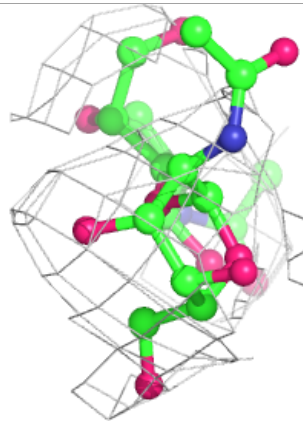
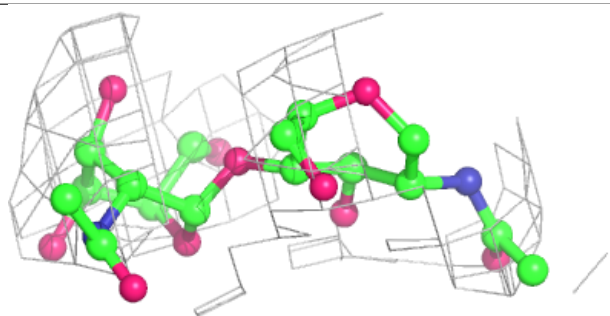
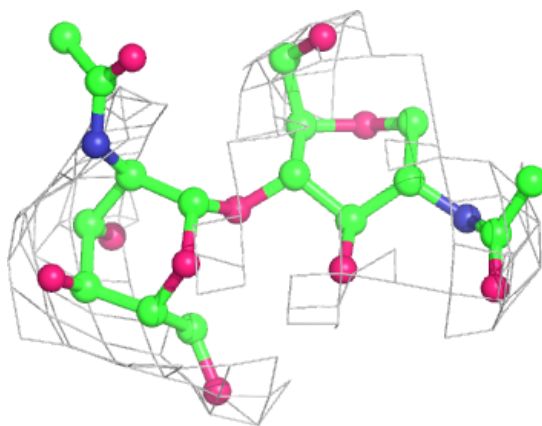


**Electron density around Chain Q:**

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

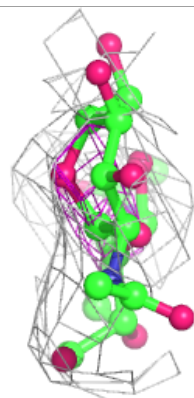
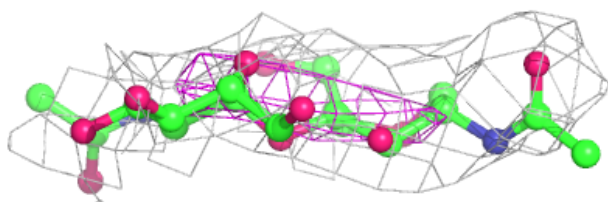
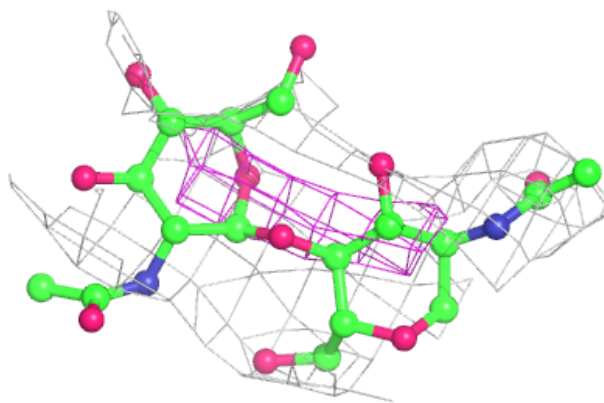
**Electron density around Chain K:**

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

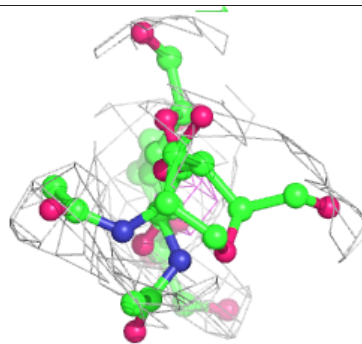
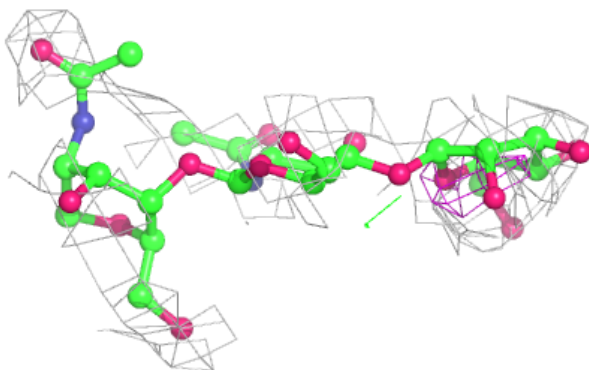
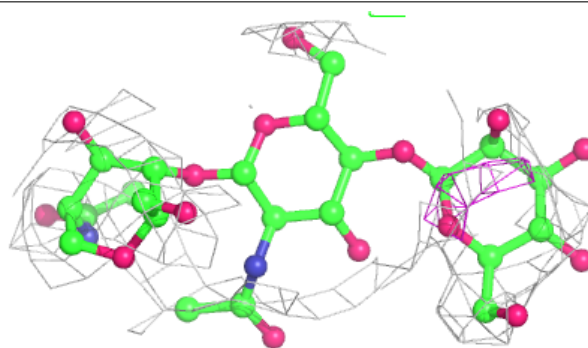


**Electron density around Chain R:**

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

**Electron density around Chain M:**

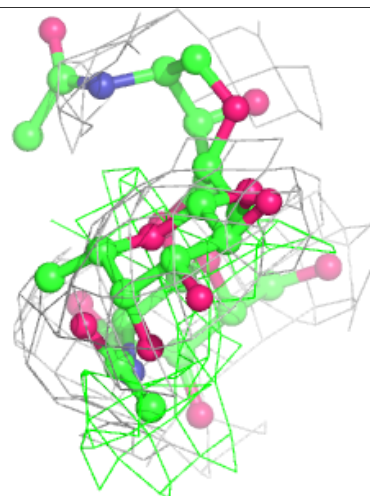
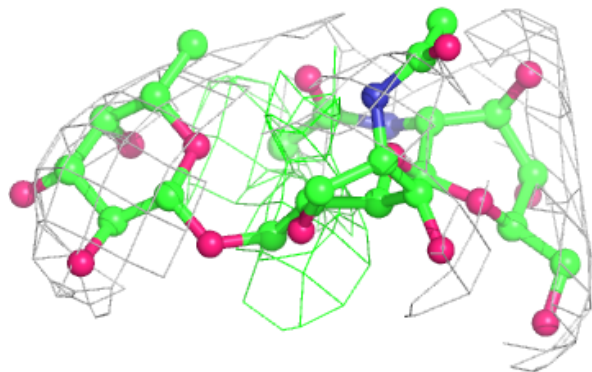
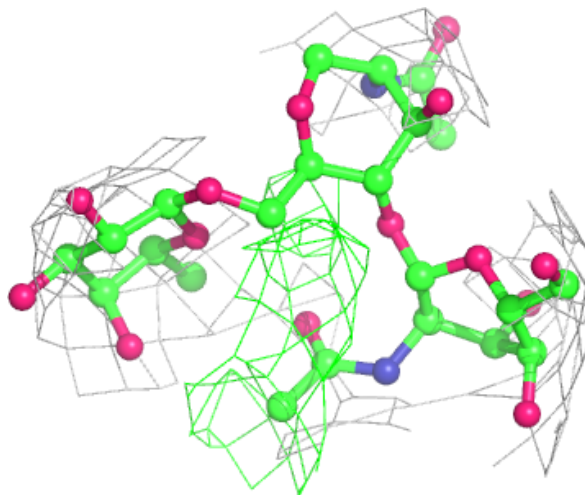
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

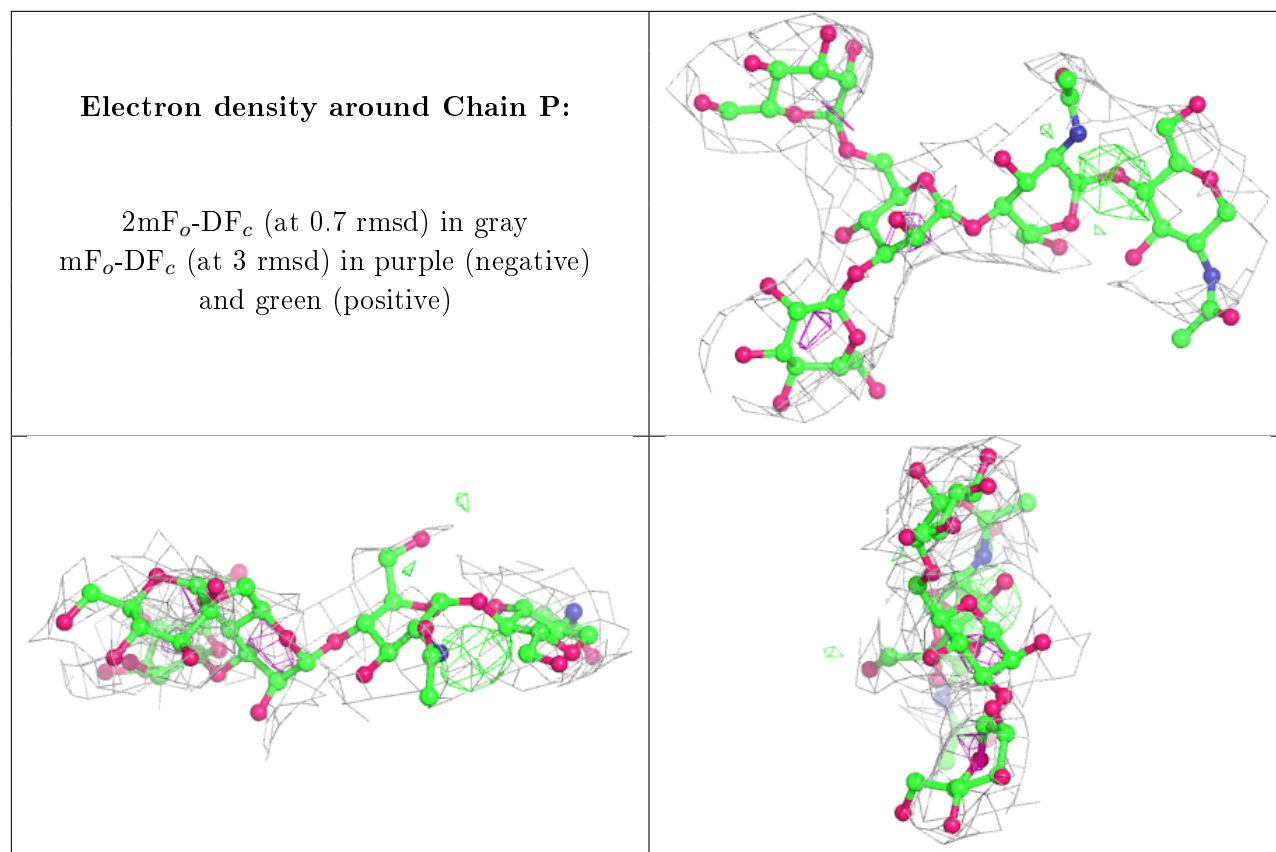




**Electron density around Chain N:**

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





## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
13	NAG	A	1961	14/15	0.67	0.30	182,186,187,187	0
13	NAG	A	724	14/15	0.77	0.26	196,197,197,197	0
13	NAG	B	724	14/15	0.78	0.31	189,190,190,190	0
13	NAG	B	1961	14/15	0.86	0.20	181,183,184,184	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.