



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 21, 2024 – 04:10 PM EDT

PDB ID : 8W0Y  
Title : Crystal structure of broadly neutralizing antibody hcab17 in complex with Hepatitis C virus envelope glycoprotein E2 ectodomain  
Authors : Flyak, A.I.; Wilcox, X.E.  
Deposited on : 2024-02-14  
Resolution : 3.31 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36.1  
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) : 2.36.1

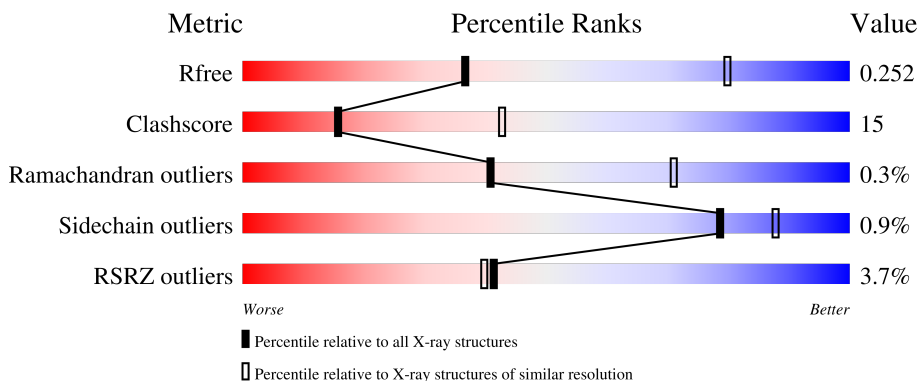
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.31 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



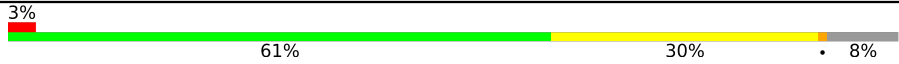


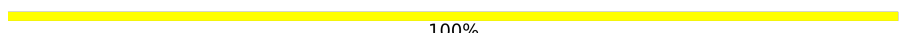


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1089 (3.36-3.28)
Clashscore	141614	1137 (3.36-3.28)
Ramachandran outliers	138981	1115 (3.36-3.28)
Sidechain outliers	138945	1114 (3.36-3.28)
RSRZ outliers	127900	1059 (3.36-3.28)

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	236	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 68%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 28%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: grey; margin-right: 2px;"></div> </div> <p style="margin-left: 20px;">2%      68%      28%      •</p>
1	H	236	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 69%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 25%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 5%; height: 10px; background-color: grey; margin-right: 2px;"></div> </div> <p style="margin-left: 20px;">3%      69%      25%      • 5%</p>
2	B	214	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 68%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 31%; height: 10px; background-color: yellow; margin-right: 2px;"></div> </div> <p style="margin-left: 20px;">3%      68%      31%</p>
2	L	214	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 67%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 32%; height: 10px; background-color: yellow; margin-right: 2px;"></div> </div> <p style="margin-left: 20px;">4%      67%      32%</p>
3	C	262	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 63%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 30%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 6%; height: 10px; background-color: grey; margin-right: 2px;"></div> </div> <p style="margin-left: 20px;">5%      63%      30%      • 6%</p>

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Mol	Chain	Length	Quality of chain
3	D	262	
4	E	2	
4	F	2	
4	I	2	
4	K	2	
4	M	2	
4	O	2	
4	P	2	
5	G	5	
6	J	3	
6	N	3	

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
4	NAG	K	2	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10803 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 hcab17 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	226	Total 1684	C 1057	N 288	O 333	S 6	0	0	0
1	H	225	Total 1678	C 1054	N 287	O 331	S 6	0	0	0

- Molecule 2 is a protein called hcab17 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	213	Total 1637	C 1025	N 279	O 327	S 6	0	0	0
2	L	213	Total 1644	C 1030	N 281	O 327	S 6	0	1	0

- Molecule 3 is a protein called Envelope glycoprotein E2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	247	Total 1924	C 1217	N 341	O 347	S 19	0	0	0
3	D	242	Total 1883	C 1187	N 336	O 341	S 19	0	0	0

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



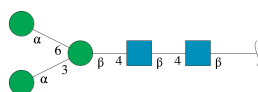
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	E	2	Total 28	C 16	N 2	O 10	0	0	0

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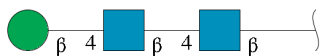
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	F	2	28	16	2	10	0	0	0
4	I	2	28	16	2	10	0	0	0
4	K	2	28	16	2	10	0	0	0
4	M	2	28	16	2	10	0	0	0
4	O	2	28	16	2	10	0	0	0
4	P	2	28	16	2	10	0	0	0

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 6 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
			Total	C	N	O			
6	J	3	39	22	2	15	0	0	0
6	N	3	39	22	2	15	0	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

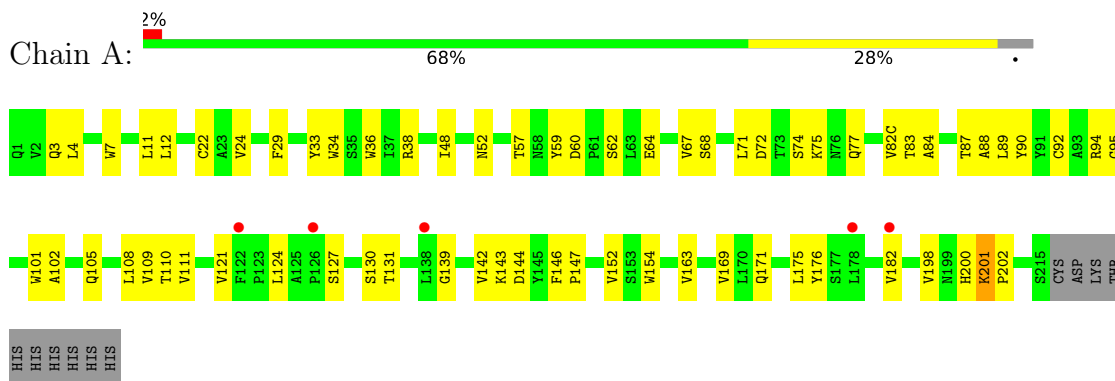
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	O	0	0
			1	1		
8	C	2	Total	O	0	0
			2	2		
8	D	1	Total	O	0	0
			1	1		

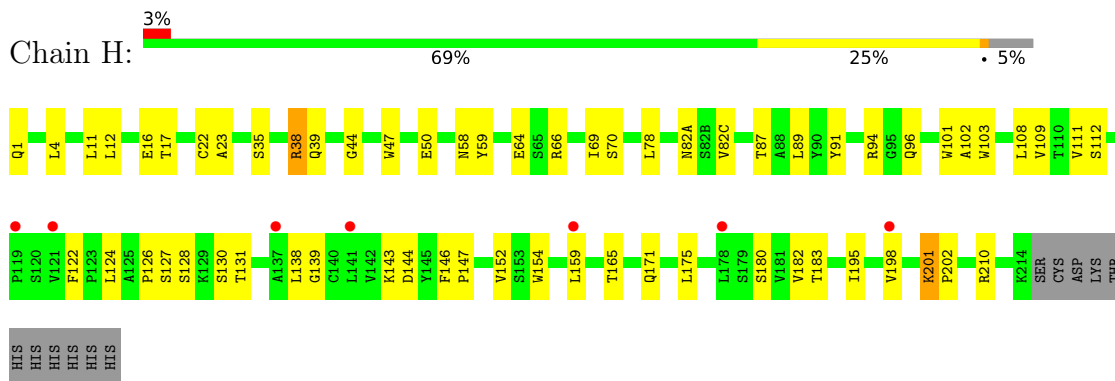
### 3 Residue-property plots [i](#)

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.

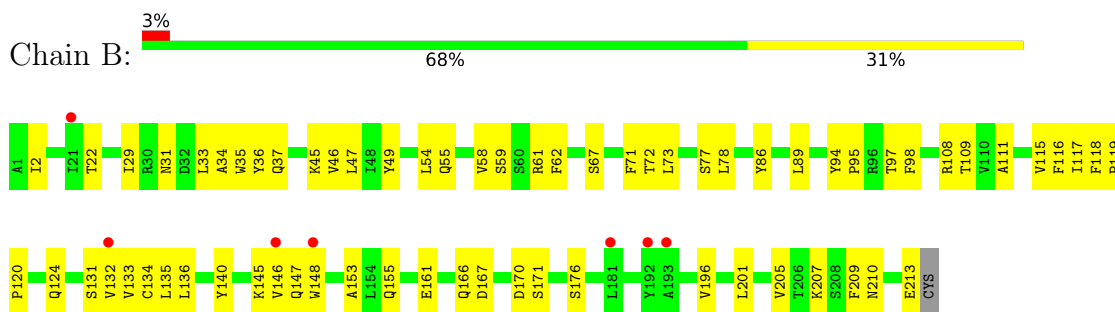
- Molecule 1: hcab17 Fab Heavy Chain



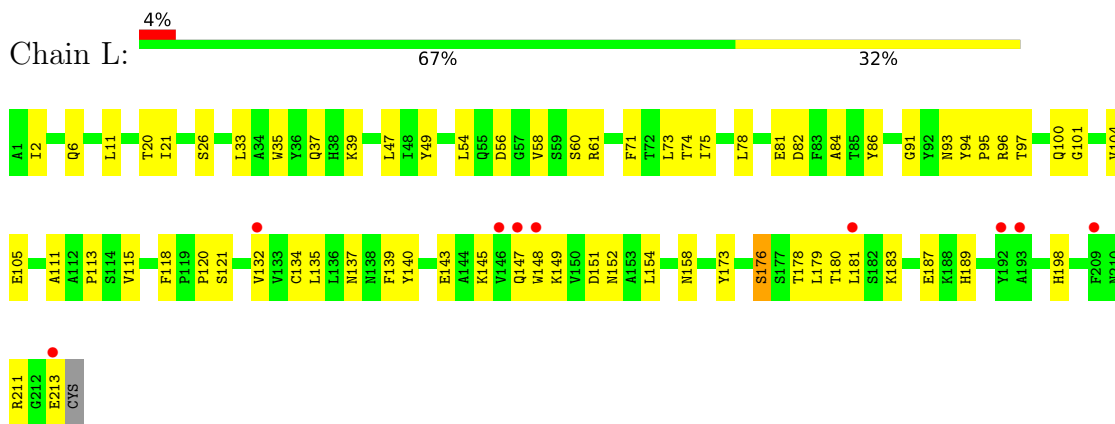
- Molecule 1: hcab17 Fab Heavy Chain



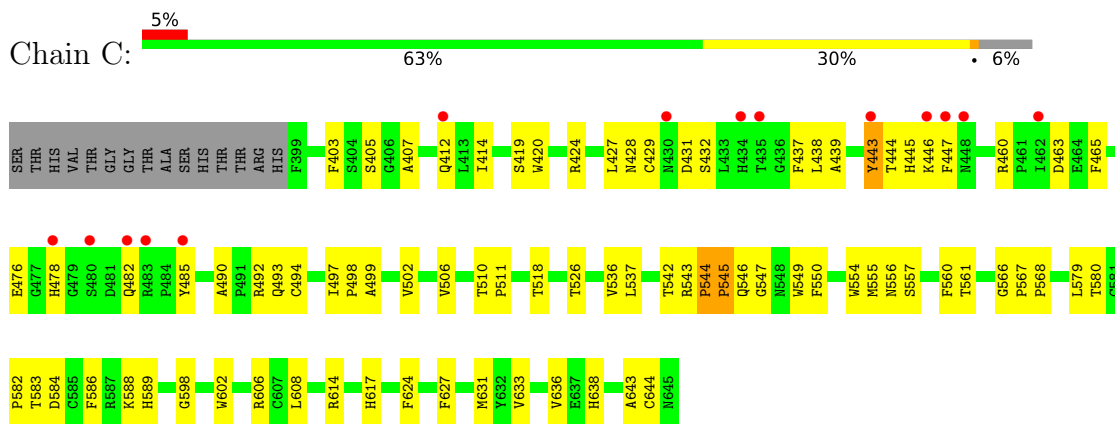
- Molecule 2: hcab17 Fab Light Chain



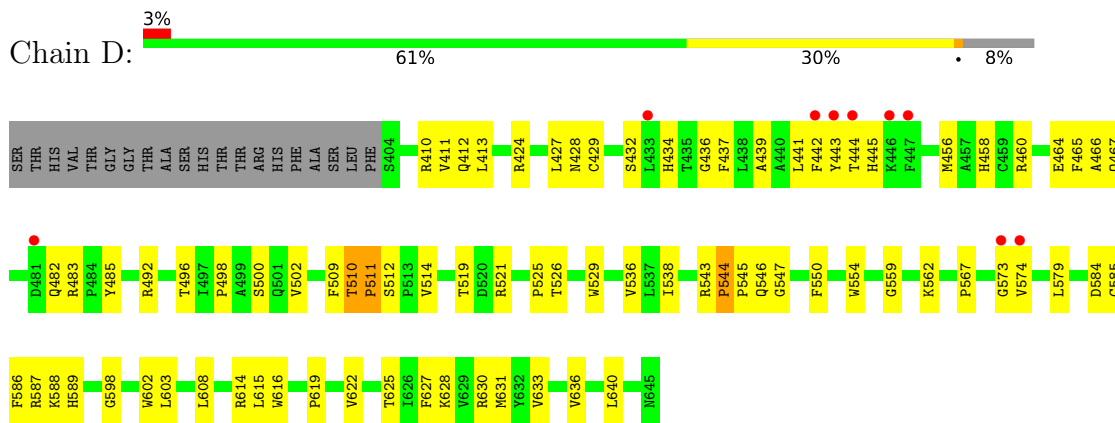
- Molecule 2: hcab17 Fab Light Chain



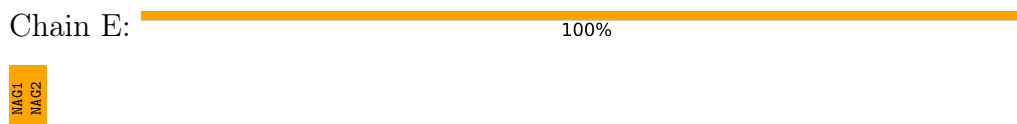
• Molecule 3: Envelope glycoprotein E2



• Molecule 3: Envelope glycoprotein E2




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




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



Chain F:  100%


MAG1  
MAG2

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

Chain I:  50% 50%

MAG1  
MAG2

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

Chain K:  100%


MAG1  
MAG2

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

Chain M:  50% 50%

MAG1  
MAG2

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

Chain O:  50% 50%

MAG1  
MAG2

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

Chain P:  100%

MAG1  
MAG2

- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  40% 60%



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

Chain J:  100%



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

Chain N:  100%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	179.41Å 179.41Å 168.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	77.69 – 3.31 89.71 – 3.31	Depositor EDS
% Data completeness (in resolution range)	99.8 (77.69-3.31) 99.8 (89.71-3.31)	Depositor EDS
$R_{merge}$	0.48	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.36 (at 3.33Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.209 , 0.253 0.210 , 0.252	Depositor DCC
$R_{free}$ test set	2249 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	94.1	Xtrriage
Anisotropy	0.152	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 87.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.039 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	10803	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	101.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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: MAN, BMA, 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	0.39	0/1726	0.64	0/2358
1	H	0.45	0/1720	0.67	0/2350
2	B	0.39	0/1673	0.65	0/2270
2	L	0.41	0/1684	0.66	0/2285
3	C	0.43	0/1992	0.66	0/2726
3	D	0.42	0/1949	0.65	0/2668
All	All	0.42	0/10744	0.65	0/14657

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	H	0	2
3	C	0	2
3	D	0	3
All	All	0	7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	544	PRO	Peptide
3	C	555	MET	Peptide
3	D	509	PHE	Peptide
3	D	510	THR	Peptide

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Mol	Chain	Res	Type	Group
3	D	544	PRO	Peptide

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1684	0	1641	53	1
1	H	1678	0	1636	49	0
2	B	1637	0	1591	49	1
2	L	1644	0	1598	55	0
3	C	1924	0	1778	63	0
3	D	1883	0	1740	61	0
4	E	28	0	25	3	0
4	F	28	0	25	0	0
4	I	28	0	25	1	0
4	K	28	0	25	0	0
4	M	28	0	25	0	0
4	O	28	0	25	1	0
4	P	28	0	25	0	0
5	G	61	0	52	0	0
6	J	39	0	34	0	0
6	N	39	0	34	2	0
7	C	14	0	13	1	0
8	A	1	0	0	0	0
8	C	2	0	0	0	0
8	D	1	0	0	0	0
All	All	10803	0	10292	310	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

The worst 5 of 310 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)
4:E:1:NAG:H61	4:E:2:NAG:HN2	1.36	0.90
2:L:94:TYR:CG	2:L:95:PRO:HD3	2.08	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:GLN:H	6:N:1:NAG:H81	1.43	0.81
1:A:60:ASP:OD2	1:A:62:SER:HB3	1.82	0.80
3:C:431:ASP:HB2	3:C:444:THR:HG21	1.64	0.80

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:THR:OG1	2:B:94:TYR:OH[3_665]	2.19	0.01

## 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	224/236 (95%)	217 (97%)	7 (3%)	0	100	100
1	H	223/236 (94%)	212 (95%)	11 (5%)	0	100	100
2	B	211/214 (99%)	197 (93%)	14 (7%)	0	100	100
2	L	212/214 (99%)	197 (93%)	15 (7%)	0	100	100
3	C	245/262 (94%)	203 (83%)	40 (16%)	2 (1%)	19	51
3	D	240/262 (92%)	206 (86%)	32 (13%)	2 (1%)	19	51
All	All	1355/1424 (95%)	1232 (91%)	119 (9%)	4 (0%)	41	71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	403	PHE
3	D	511	PRO
3	C	545	PRO
3	D	545	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/200 (95%)	188 (99%)	2 (1%)	73	85
1	H	189/200 (94%)	187 (99%)	2 (1%)	73	85
2	B	184/185 (100%)	184 (100%)	0	100	100
2	L	185/185 (100%)	184 (100%)	1 (0%)	88	93
3	C	207/219 (94%)	204 (99%)	3 (1%)	67	82
3	D	203/219 (93%)	201 (99%)	2 (1%)	76	86
All	All	1158/1208 (96%)	1148 (99%)	10 (1%)	78	88

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	22	CYS
1	H	201	LYS
2	L	176	SER
3	C	482	GLN
3	C	485	TYR

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

Mol	Chain	Res	Type
2	L	137	ASN
2	L	189	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates i

25 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	4,3	14,14,15	0.40	0	17,19,21	1.43	3 (17%)
4	NAG	E	2	4	14,14,15	0.55	0	17,19,21	1.42	2 (11%)
4	NAG	F	1	4,3	14,14,15	0.59	0	17,19,21	0.80	1 (5%)
4	NAG	F	2	4	14,14,15	0.54	0	17,19,21	0.98	2 (11%)
5	NAG	G	1	5,3	14,14,15	0.39	0	17,19,21	0.89	0
5	NAG	G	2	5	14,14,15	0.40	0	17,19,21	1.08	2 (11%)
5	BMA	G	3	5	11,11,12	1.20	0	15,15,17	0.95	0
5	MAN	G	4	5	11,11,12	1.48	4 (36%)	15,15,17	1.57	1 (6%)
5	MAN	G	5	5	11,11,12	1.39	2 (18%)	15,15,17	1.15	1 (6%)
4	NAG	I	1	4,3	14,14,15	0.32	0	17,19,21	0.98	2 (11%)
4	NAG	I	2	4	14,14,15	0.46	0	17,19,21	0.86	0
6	NAG	J	1	3,6	14,14,15	0.51	0	17,19,21	1.55	4 (23%)
6	NAG	J	2	6	14,14,15	0.81	0	17,19,21	1.39	1 (5%)
6	BMA	J	3	6	11,11,12	2.05	3 (27%)	15,15,17	1.28	2 (13%)
4	NAG	K	1	4,3	14,14,15	0.45	0	17,19,21	1.18	2 (11%)
4	NAG	K	2	4	14,14,15	0.65	0	17,19,21	0.99	1 (5%)
4	NAG	M	1	4,3	14,14,15	0.52	0	17,19,21	1.16	2 (11%)
4	NAG	M	2	4	14,14,15	0.52	0	17,19,21	0.91	0
6	NAG	N	1	3,6	14,14,15	0.34	0	17,19,21	0.65	0
6	NAG	N	2	6	14,14,15	0.38	0	17,19,21	0.78	1 (5%)
6	BMA	N	3	6	11,11,12	1.28	1 (9%)	15,15,17	0.78	0
4	NAG	O	1	4,3	14,14,15	0.36	0	17,19,21	1.54	3 (17%)
4	NAG	O	2	4	14,14,15	0.55	0	17,19,21	0.88	1 (5%)
4	NAG	P	1	4,3	14,14,15	0.60	0	17,19,21	1.97	5 (29%)
4	NAG	P	2	4	14,14,15	0.37	0	17,19,21	0.92	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	4,3	-	4/6/23/26	0/1/1/1
4	NAG	E	2	4	-	3/6/23/26	0/1/1/1
4	NAG	F	1	4,3	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
5	NAG	G	1	5,3	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	0/1/1/1
5	MAN	G	5	5	-	0/2/19/22	0/1/1/1
4	NAG	I	1	4,3	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
6	NAG	J	1	3,6	-	3/6/23/26	0/1/1/1
6	NAG	J	2	6	-	3/6/23/26	0/1/1/1
6	BMA	J	3	6	-	1/2/19/22	0/1/1/1
4	NAG	K	1	4,3	-	3/6/23/26	0/1/1/1
4	NAG	K	2	4	-	4/6/23/26	0/1/1/1
4	NAG	M	1	4,3	-	3/6/23/26	0/1/1/1
4	NAG	M	2	4	-	3/6/23/26	0/1/1/1
6	NAG	N	1	3,6	-	4/6/23/26	0/1/1/1
6	NAG	N	2	6	-	1/6/23/26	0/1/1/1
6	BMA	N	3	6	-	1/2/19/22	0/1/1/1
4	NAG	O	1	4,3	-	3/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	NAG	P	1	4,3	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	2/6/23/26	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	3	BMA	C2-C3	4.08	1.58	1.52
6	J	3	BMA	O5-C5	3.58	1.50	1.43
5	G	5	MAN	C1-C2	3.07	1.59	1.52
6	J	3	BMA	O5-C1	3.05	1.48	1.43
5	G	4	MAN	C1-C2	2.63	1.58	1.52

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	4	MAN	C1-O5-C5	5.07	119.06	112.19
6	J	2	NAG	O5-C1-C2	-4.44	104.28	111.29
4	P	1	NAG	O5-C1-C2	-4.34	104.44	111.29
4	E	2	NAG	C2-N2-C7	4.29	129.02	122.90
6	J	1	NAG	O4-C4-C5	-4.17	98.94	109.30

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

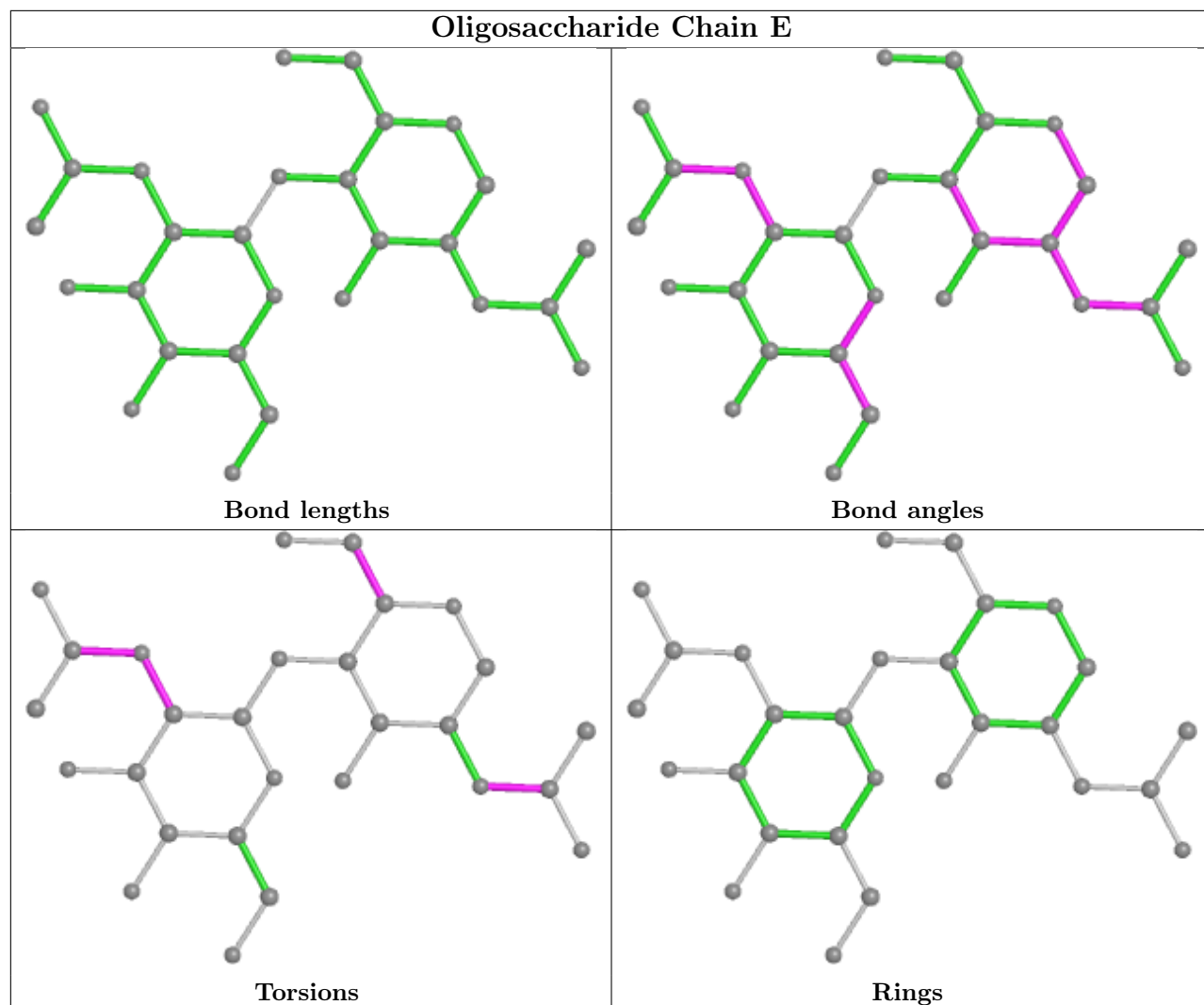
Mol	Chain	Res	Type	Atoms
4	E	2	NAG	C3-C2-N2-C7
4	E	2	NAG	C8-C7-N2-C2
4	E	2	NAG	O7-C7-N2-C2
4	F	1	NAG	O7-C7-N2-C2
4	F	2	NAG	C8-C7-N2-C2

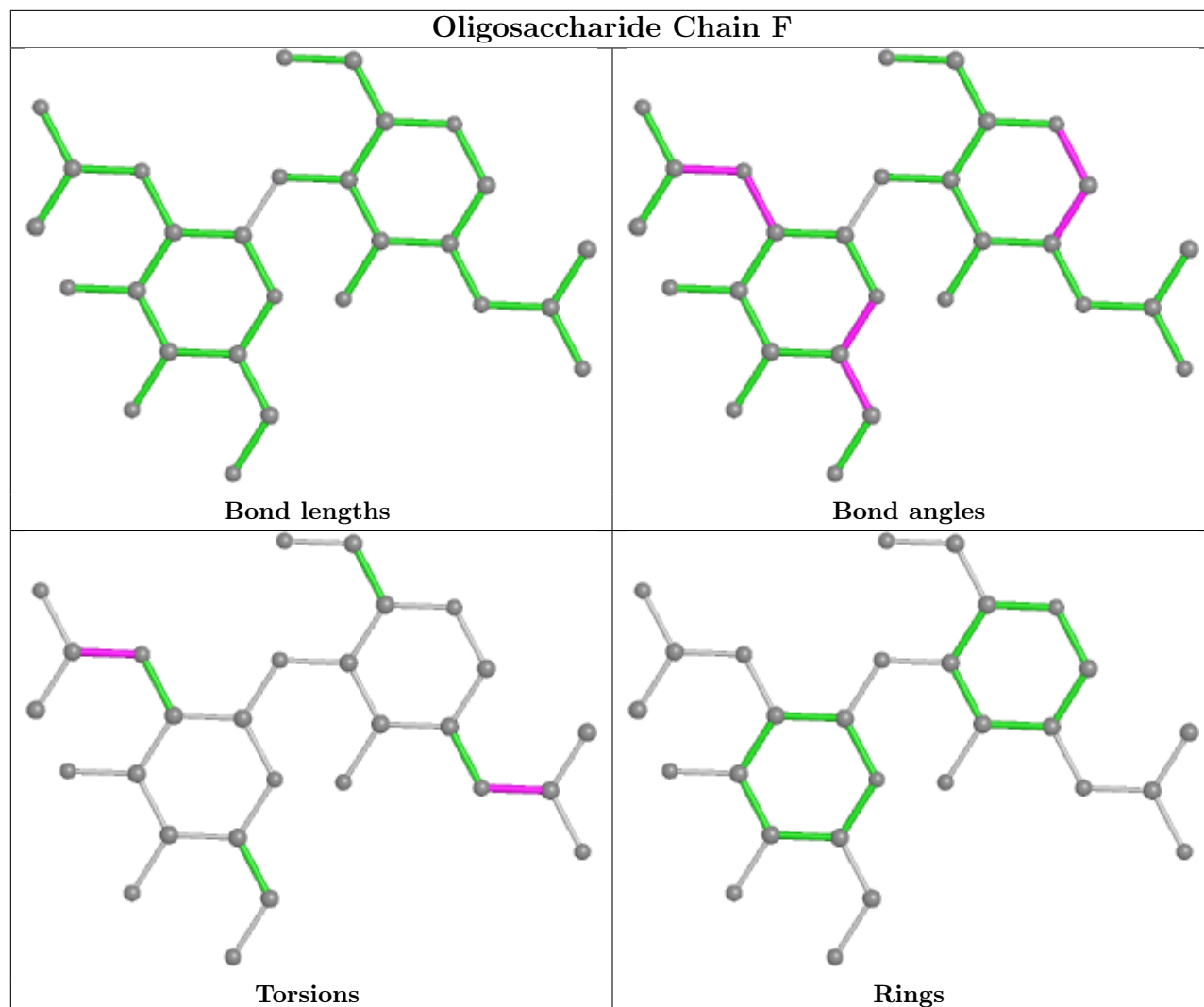
There are no ring outliers.

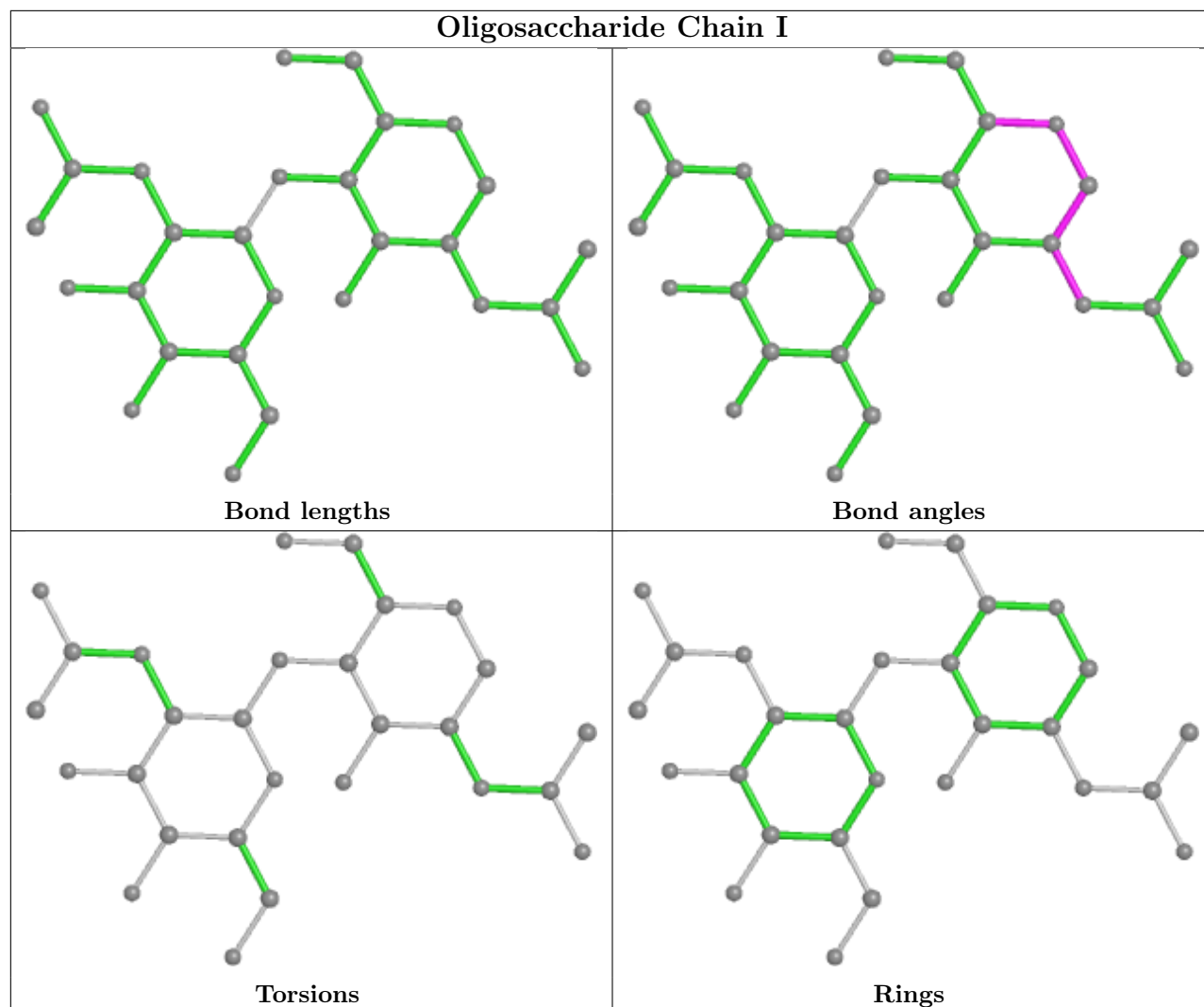
6 monomers are involved in 7 short contacts:

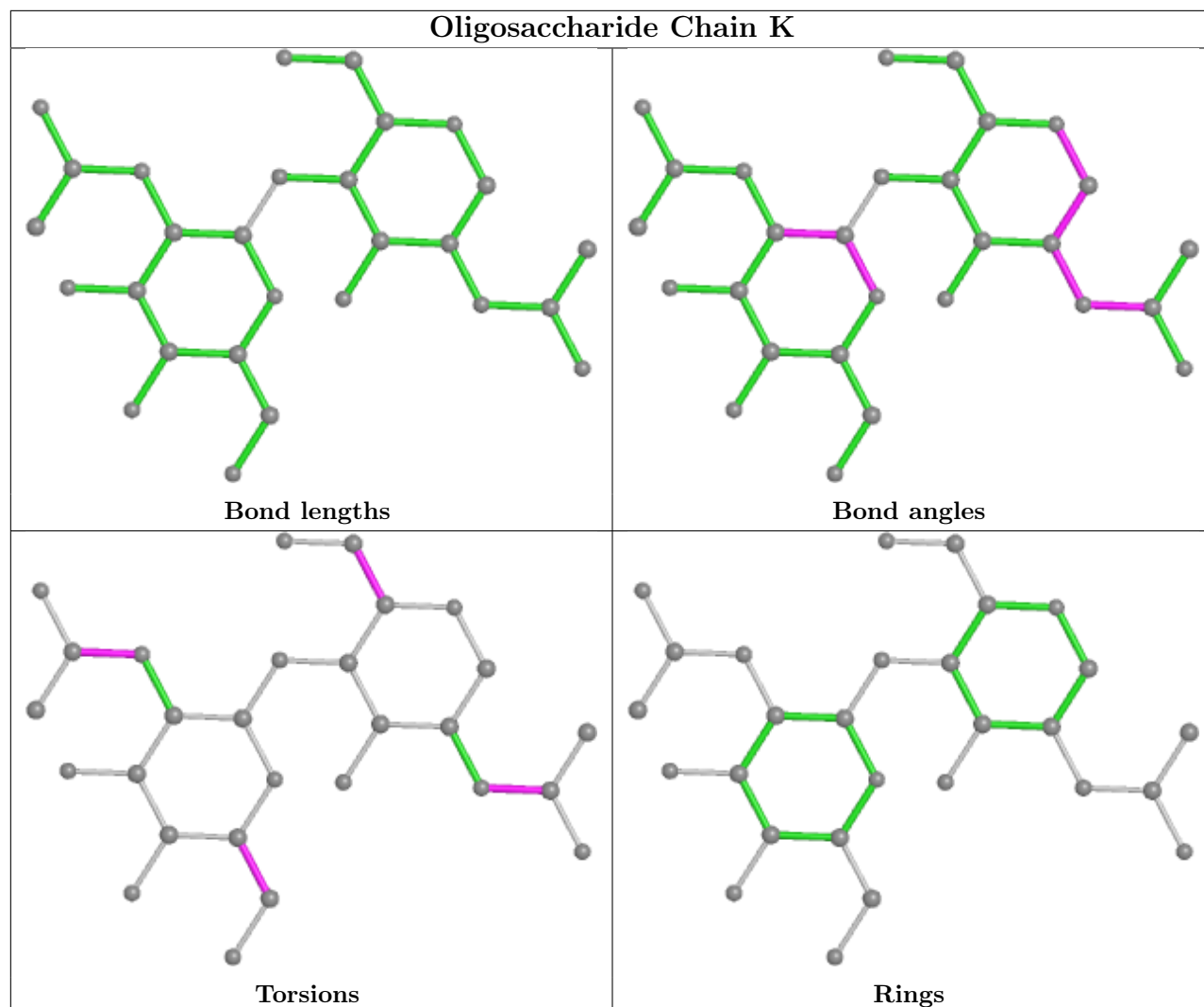
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	1	NAG	1	0
6	N	1	NAG	2	0
4	I	2	NAG	1	0
4	E	2	NAG	2	0
4	E	1	NAG	3	0
4	O	1	NAG	1	0

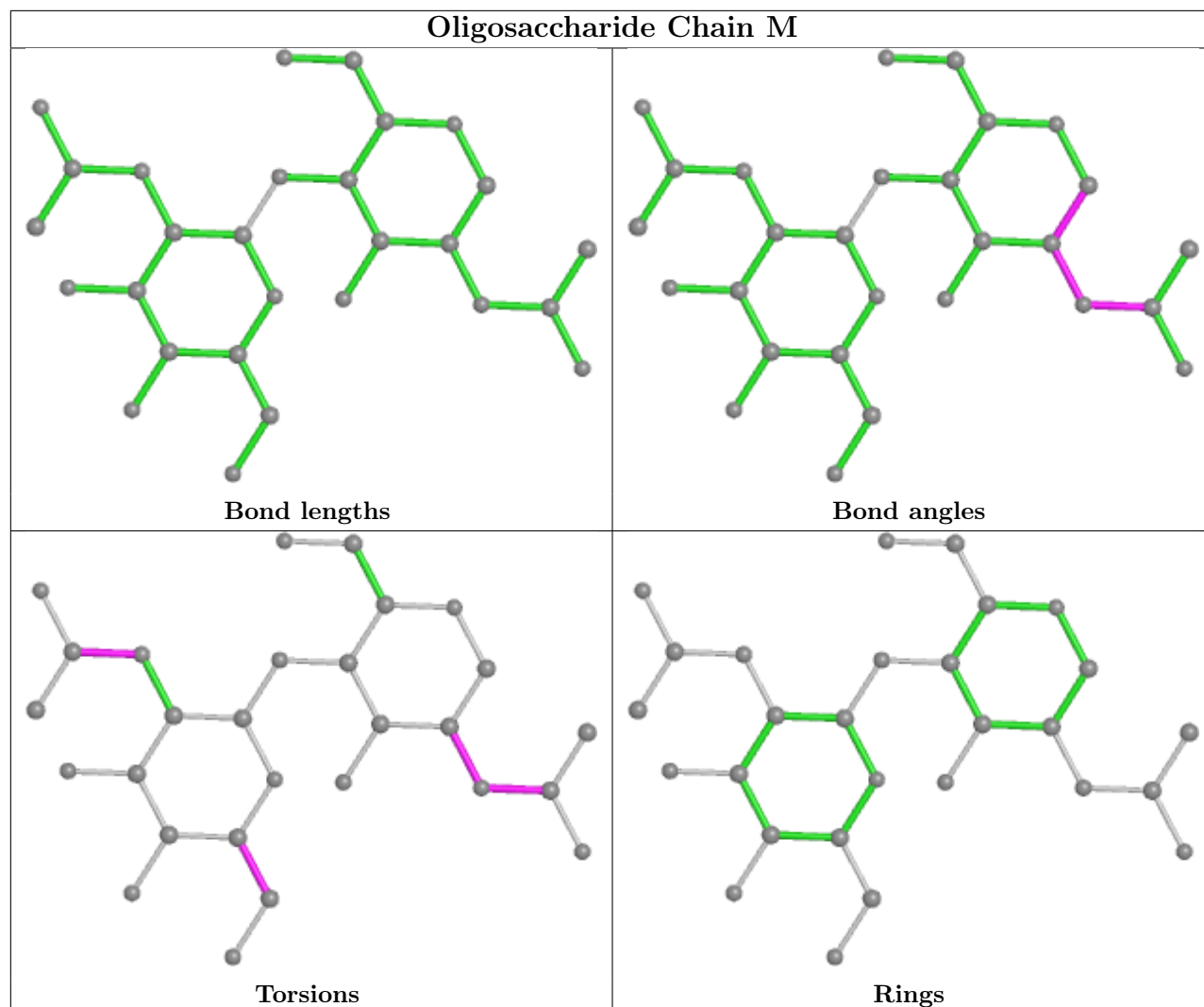
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

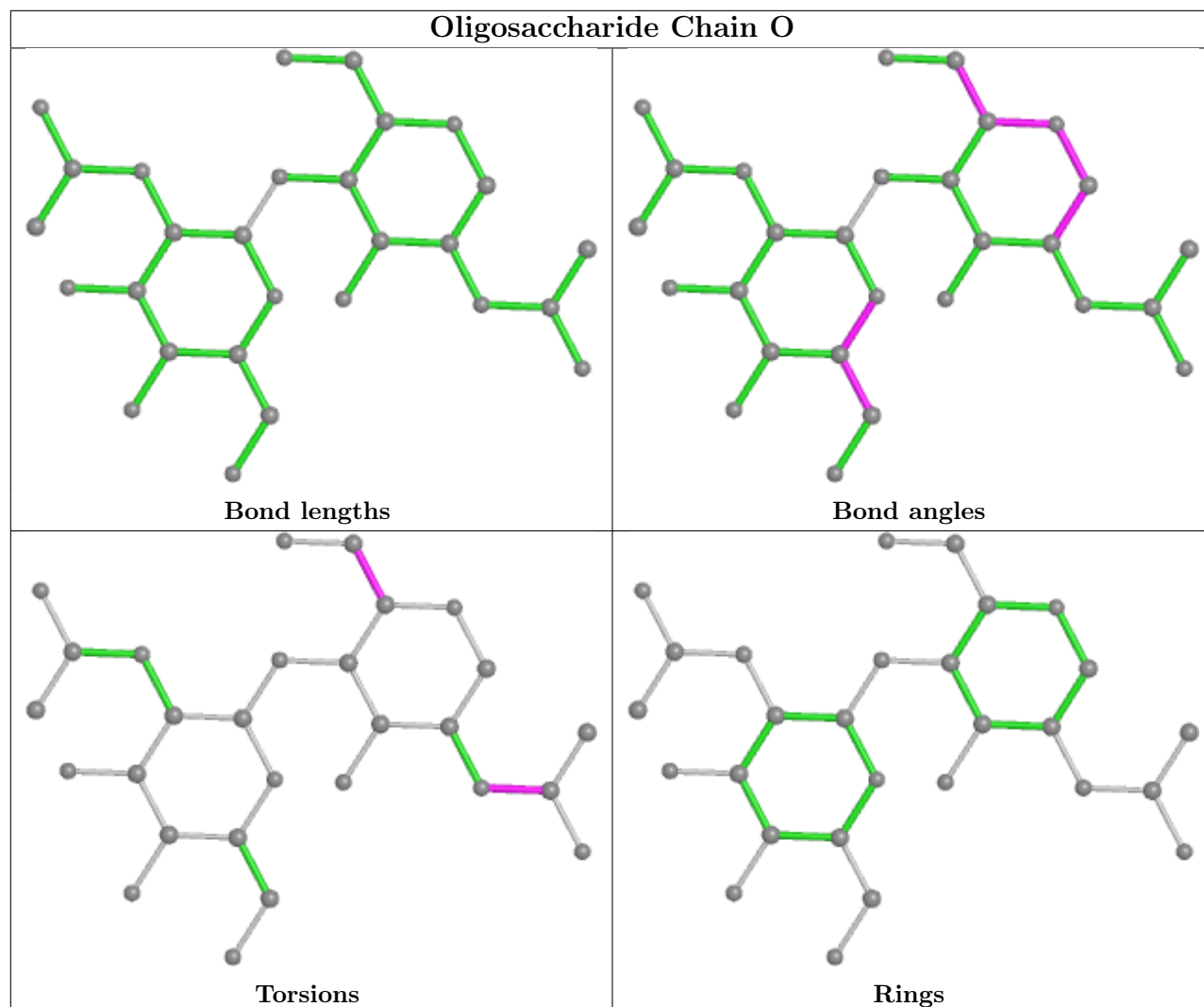




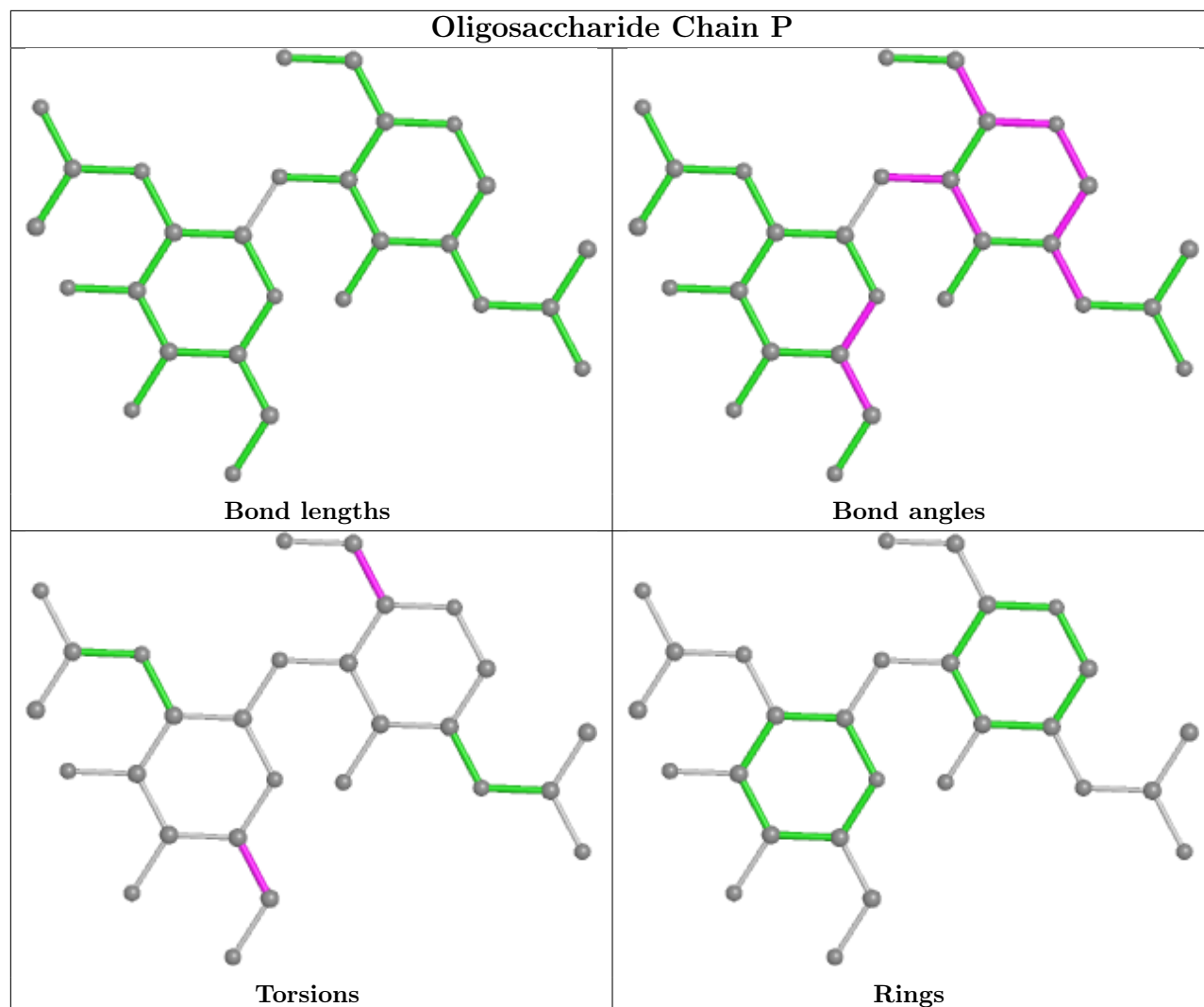


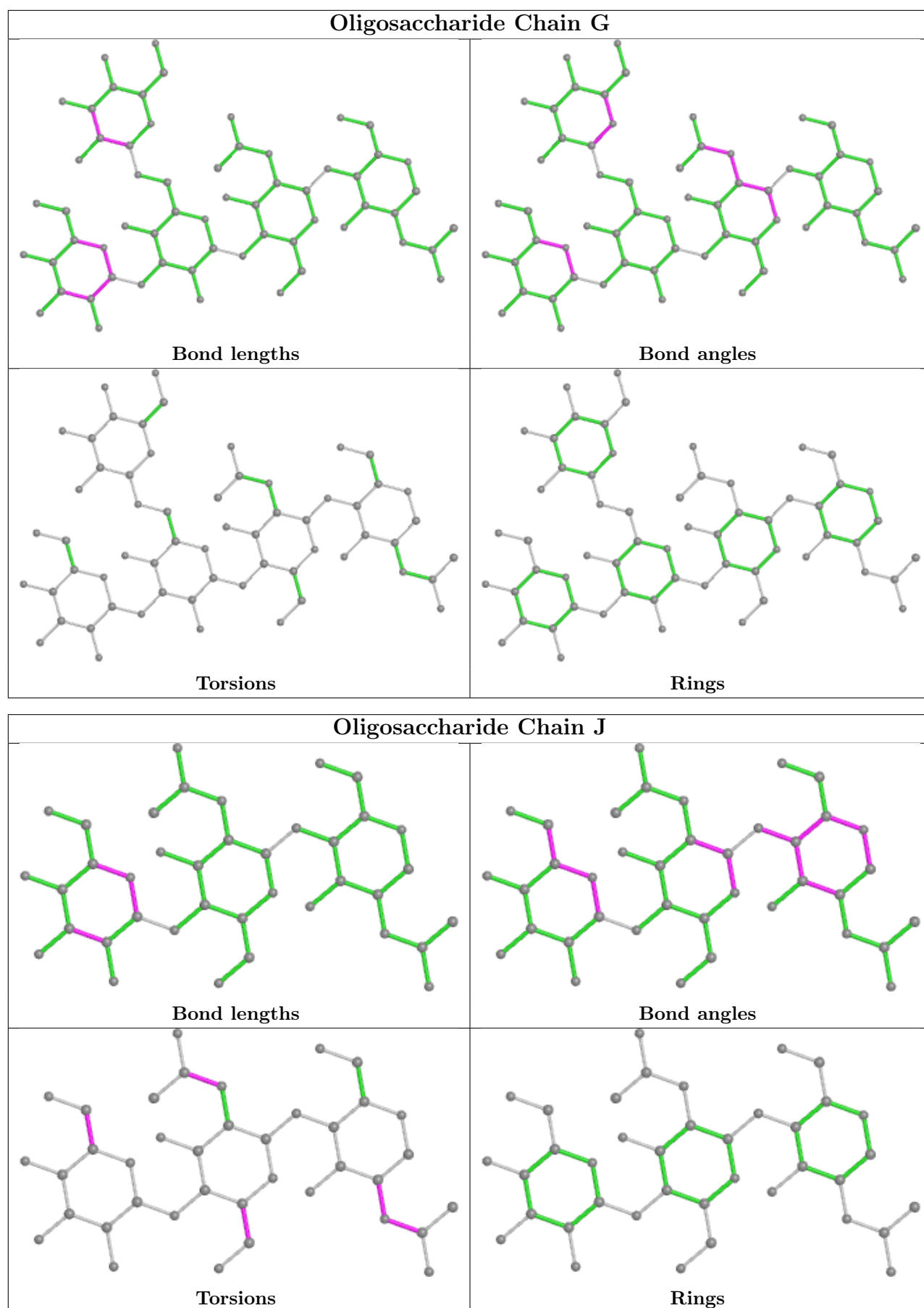


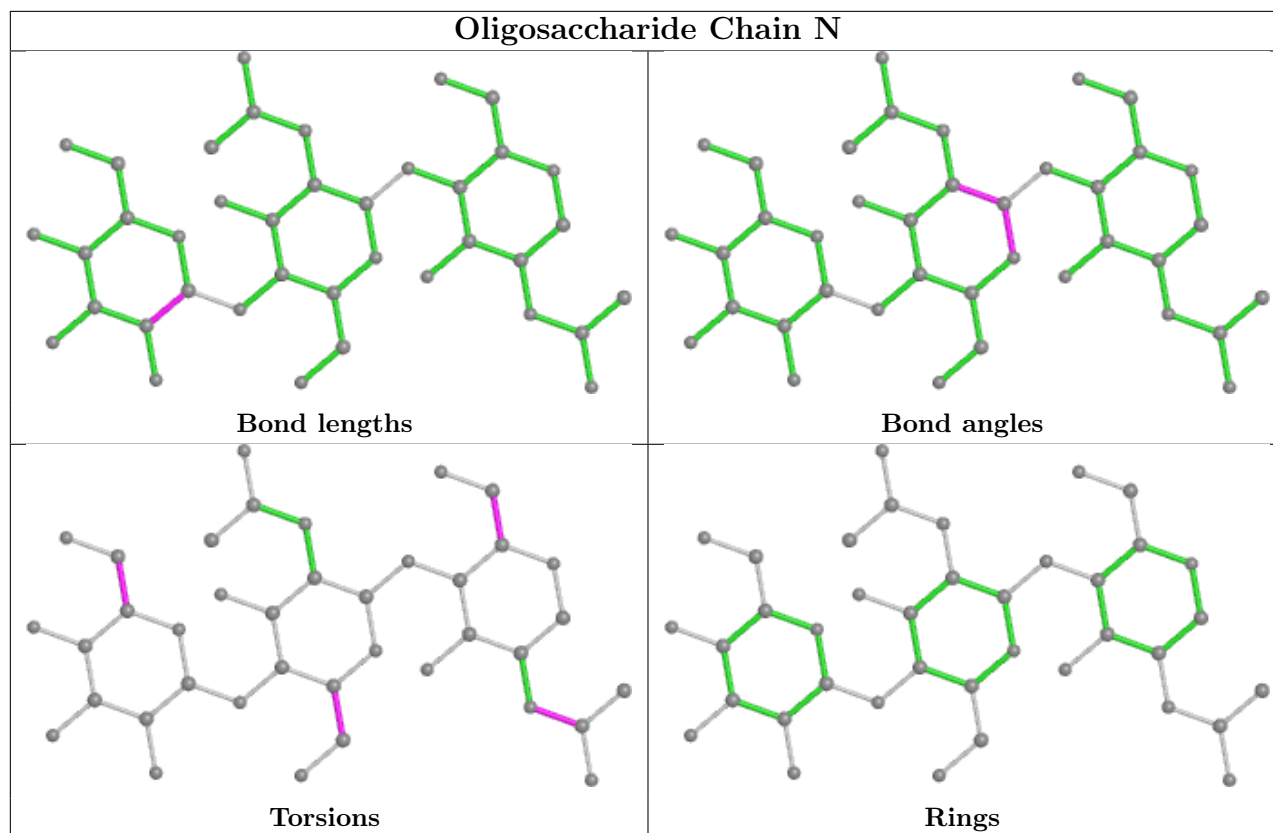












## 5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
7	NAG	C	701	3	14,14,15	0.54	0	17,19,21	0.92	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
7	NAG	C	701	3	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
7	C	701	NAG	O5-C5-C6	2.84	111.66	107.20

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	701	NAG	C8-C7-N2-C2
7	C	701	NAG	C4-C5-C6-O6
7	C	701	NAG	O7-C7-N2-C2
7	C	701	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	701	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	A	226/236 (95%)	0.39	5 (2%) 62 60	71, 92, 121, 170	0
1	H	225/236 (95%)	0.43	7 (3%) 49 48	59, 85, 134, 198	0
2	B	213/214 (99%)	0.49	7 (3%) 46 44	68, 95, 140, 191	0
2	L	213/214 (99%)	0.44	9 (4%) 36 35	62, 95, 146, 174	0
3	C	247/262 (94%)	0.51	14 (5%) 23 24	69, 95, 168, 228	0
3	D	242/262 (92%)	0.56	9 (3%) 41 40	71, 100, 172, 205	0
All	All	1366/1424 (95%)	0.47	51 (3%) 41 40	59, 94, 152, 228	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	446	LYS	5.0
3	D	443	TYR	4.8
3	D	447	PHE	4.3
3	D	481	ASP	4.2
3	C	434	HIS	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](#)

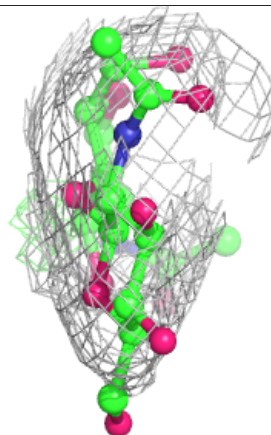
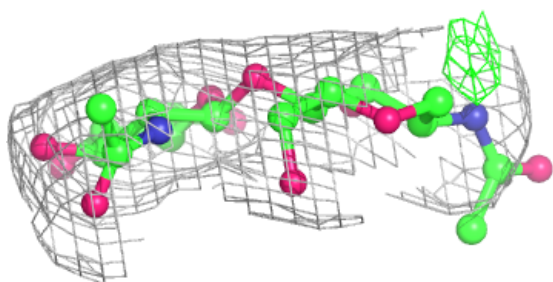
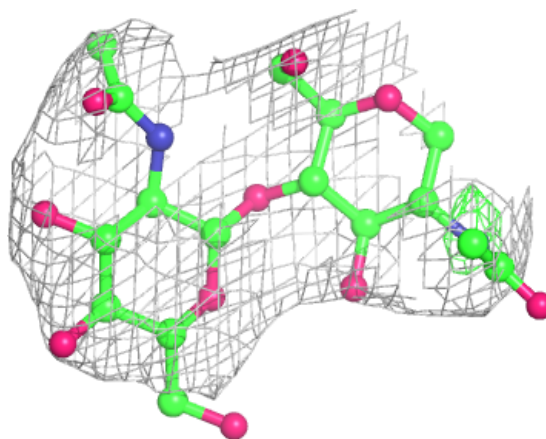
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	BMA	J	3	11/12	0.56	0.35	142,158,164,164	0
5	MAN	G	4	11/12	0.67	0.27	165,169,174,174	0
4	NAG	K	2	14/15	0.69	0.47	152,167,173,176	0
5	BMA	G	3	11/12	0.73	0.28	166,169,175,185	0
6	NAG	J	2	14/15	0.80	0.37	140,152,157,158	0
4	NAG	E	2	14/15	0.80	0.22	129,140,142,144	0
4	NAG	M	2	14/15	0.83	0.25	149,158,162,164	0
6	BMA	N	3	11/12	0.84	0.17	146,148,153,154	0
4	NAG	O	2	14/15	0.85	0.30	116,122,132,135	0
4	NAG	E	1	14/15	0.85	0.23	116,125,136,142	0
5	MAN	G	5	11/12	0.86	0.23	148,158,163,165	0
4	NAG	K	1	14/15	0.87	0.24	111,135,153,160	0
4	NAG	P	1	14/15	0.88	0.29	105,126,132,139	0
4	NAG	P	2	14/15	0.89	0.20	134,139,150,153	0
5	NAG	G	2	14/15	0.89	0.17	109,122,144,158	0
4	NAG	M	1	14/15	0.89	0.22	124,132,138,145	0
4	NAG	F	2	14/15	0.89	0.42	146,150,156,156	0
6	NAG	J	1	14/15	0.90	0.40	131,137,148,152	0
4	NAG	O	1	14/15	0.92	0.22	105,108,112,116	0
4	NAG	I	1	14/15	0.92	0.18	105,112,120,121	0
6	NAG	N	2	14/15	0.92	0.15	109,121,134,140	0
4	NAG	I	2	14/15	0.92	0.23	119,126,137,140	0
4	NAG	F	1	14/15	0.94	0.18	116,125,137,144	0
5	NAG	G	1	14/15	0.95	0.20	72,89,102,114	0
6	NAG	N	1	14/15	0.95	0.16	81,96,107,115	0

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

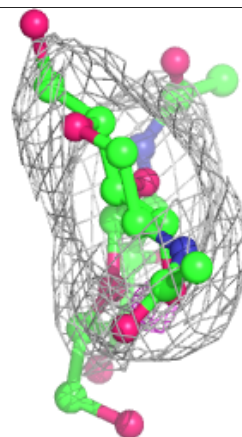
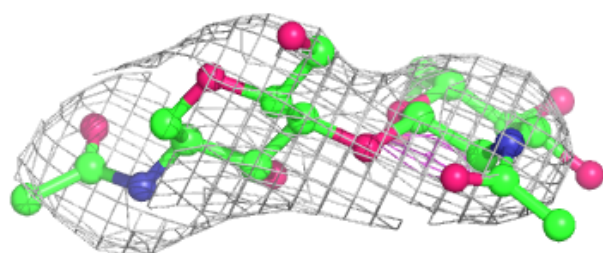
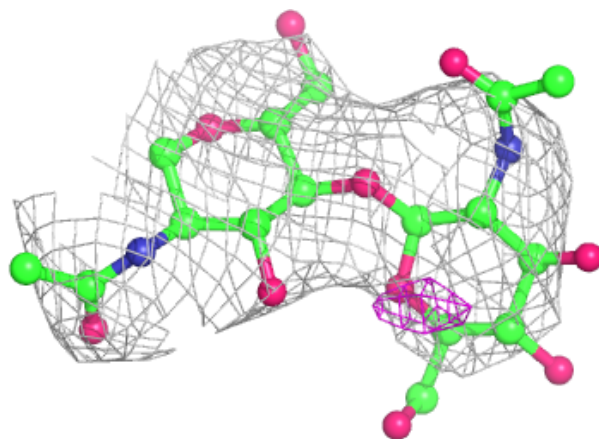
**Electron density around Chain E:**

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

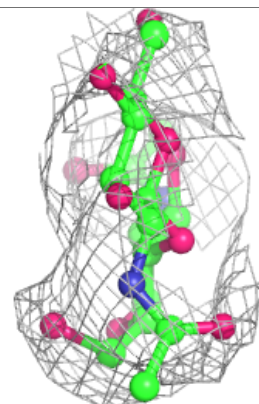
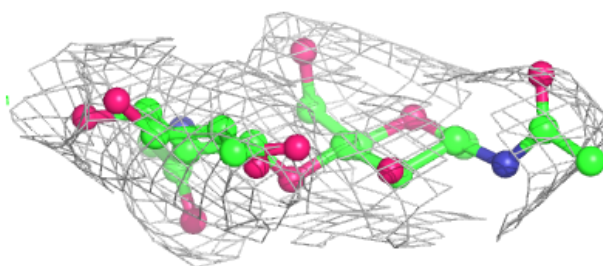
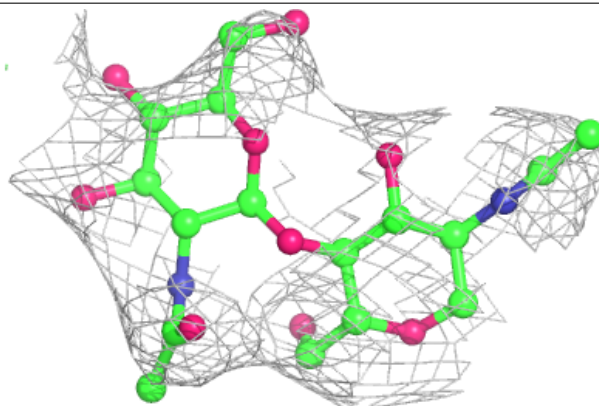


**Electron density around Chain F:**

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

**Electron density around Chain I:**

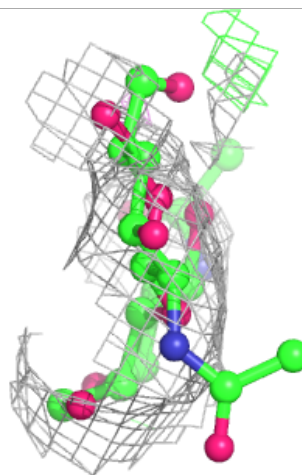
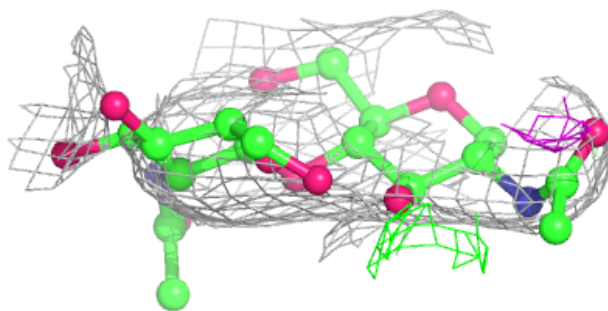
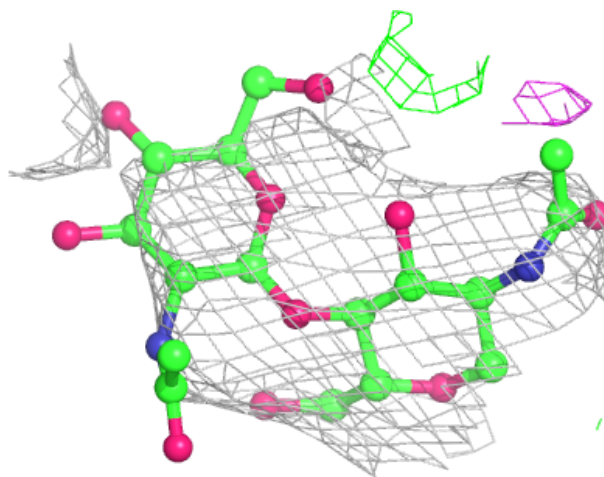
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





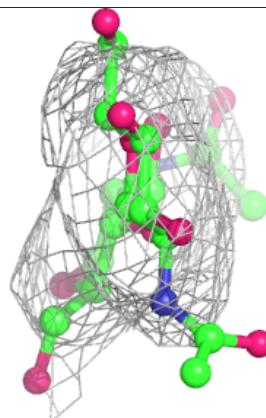
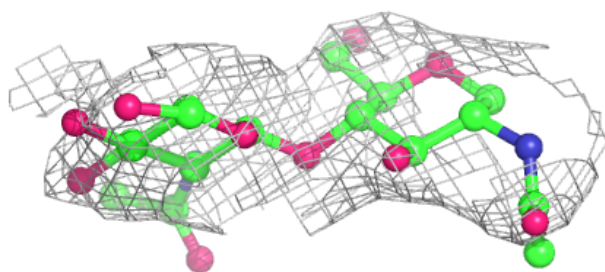
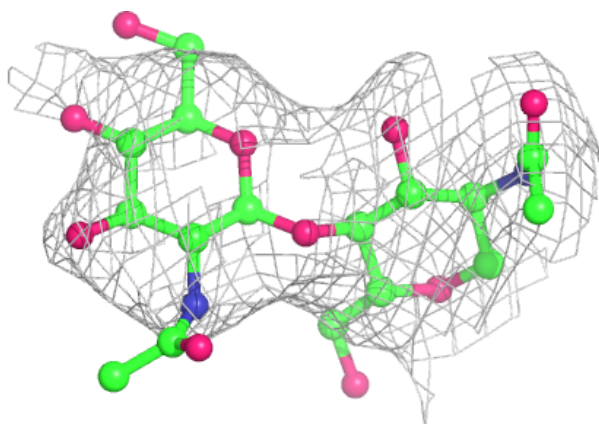
**Electron density around Chain K:**

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



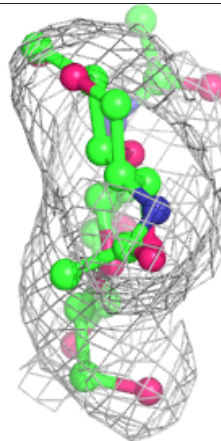
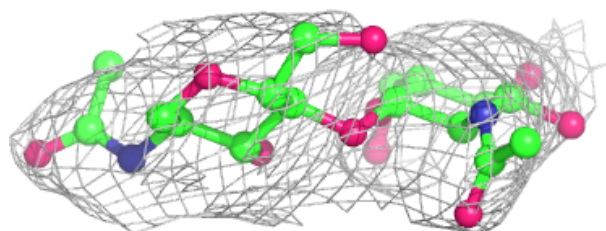
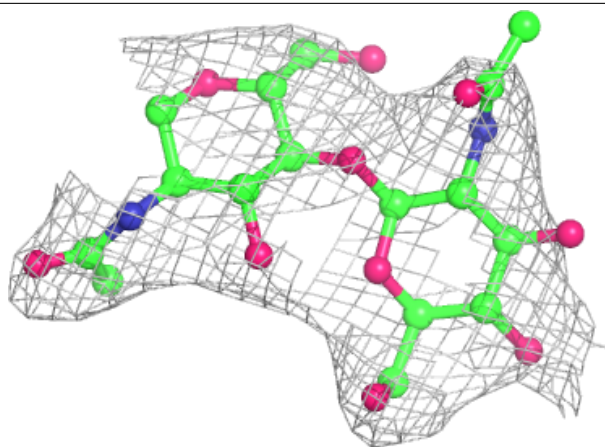
**Electron density around Chain M:**

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

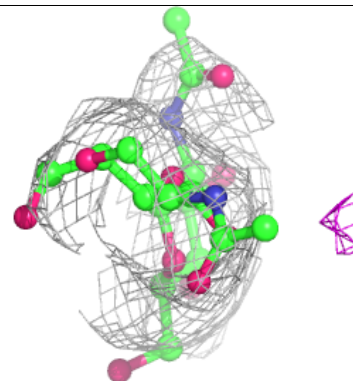
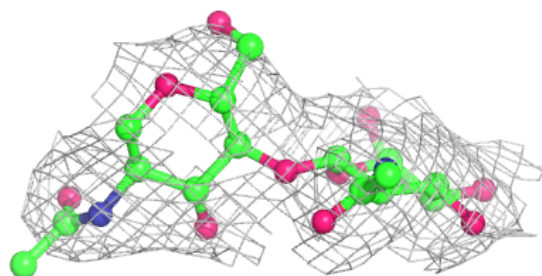
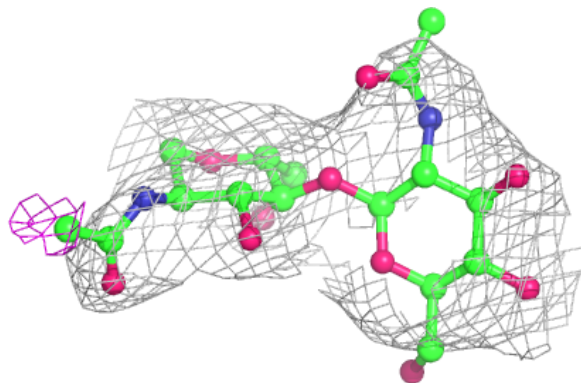


**Electron density around Chain O:**

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

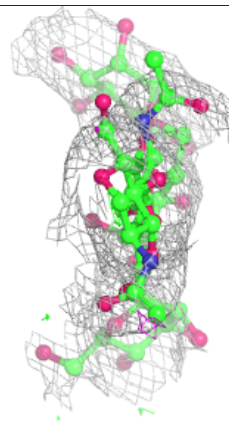
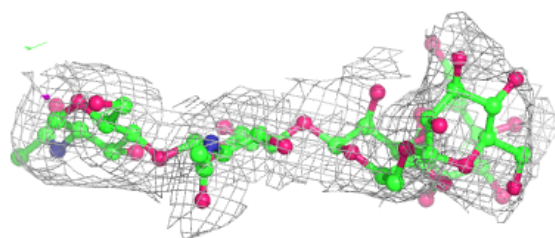
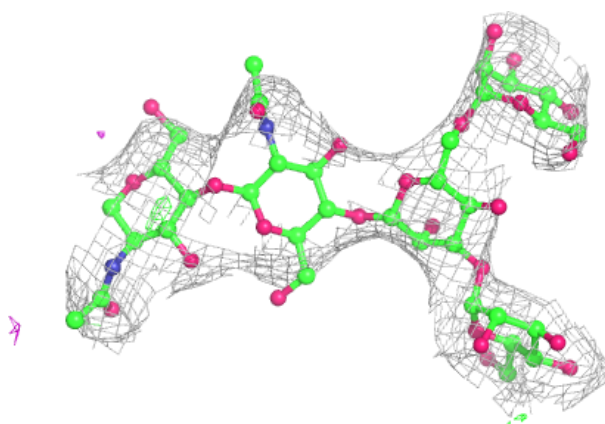
**Electron density around Chain P:**

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

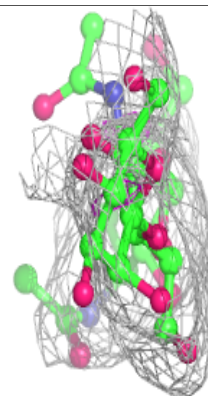
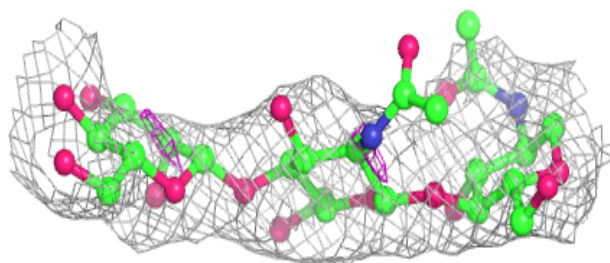
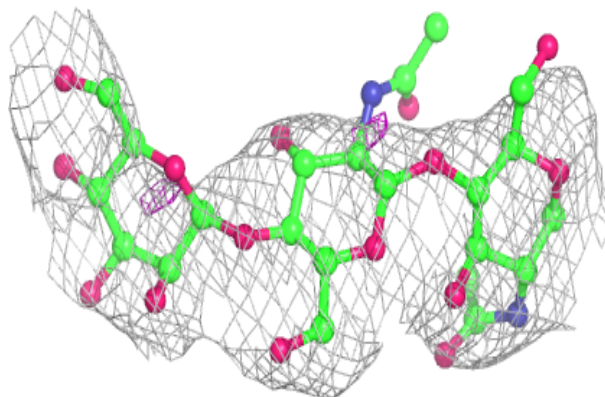


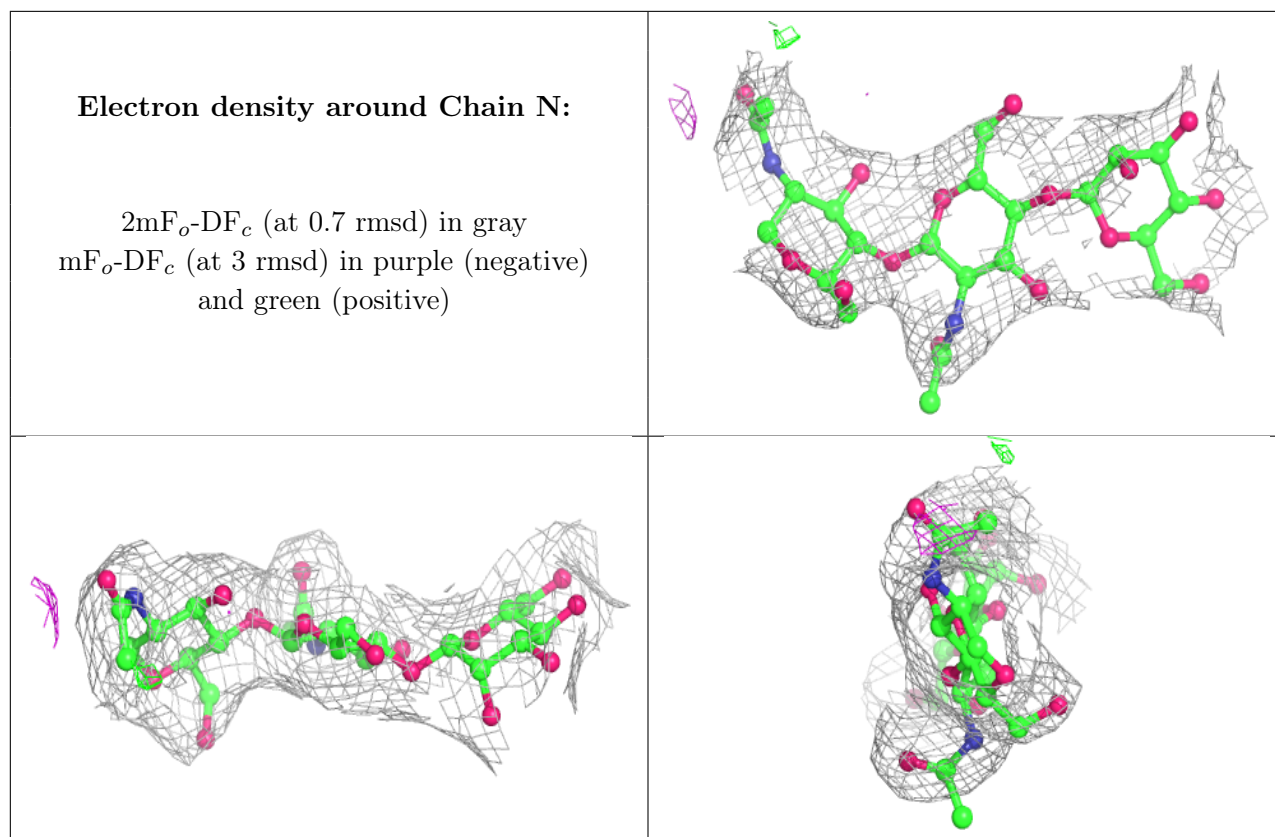
**Electron density around Chain G:**

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

**Electron density around Chain J:**

$2mF_o-DF_c$  (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( $\text{\AA}^2$ )	Q<0.9
7	NAG	C	701	14/15	0.69	0.36	147,155,162,163	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.