



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 9, 2024 – 05:32 PM EST

PDB ID : 1HGG  
Title : BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY  
Authors : Sauter, N.K.; Hanson, J.E.; Glick, G.D.; Brown, J.H.; Crowther, R.L.; Park, S.-J.; Skehel, J.J.; Wiley, D.C.  
Deposited on : 1991-11-01  
Resolution : 2.90 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

<https://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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

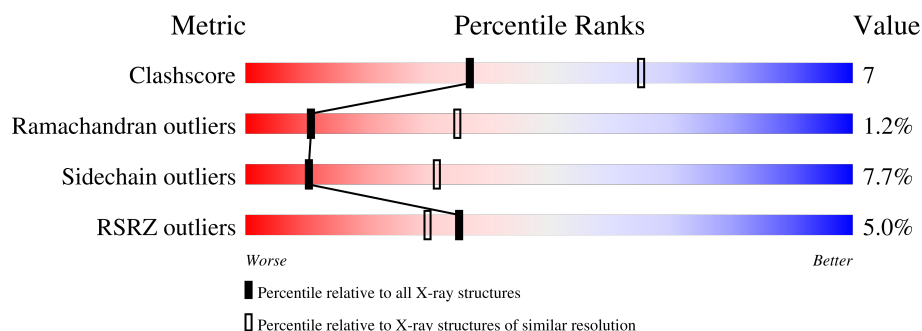
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
Clashscore	180529	2564 (2.90-2.90)
Ramachandran outliers	177936	2514 (2.90-2.90)
Sidechain outliers	177891	2516 (2.90-2.90)
RSRZ outliers	164620	2337 (2.90-2.90)

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	328	<div> <div>5%</div> <div> <div></div> <div>72%</div> <div>22%</div> <div>5%</div> </div> </div>
1	C	328	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div></div> </div> </div>
1	E	328	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>22%</div> <div></div> </div> </div>
2	B	175	<div> <div>3%</div> <div> <div></div> <div>75%</div> <div>22%</div> <div></div> </div> </div>
2	D	175	<div> <div>5%</div> <div> <div></div> <div>71%</div> <div>26%</div> <div></div> </div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	F	175	
3	G	3	
3	J	3	
3	M	3	
4	H	3	
4	I	3	
4	K	3	
4	L	3	
4	N	3	
4	O	3	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 15882 atoms, of which 3408 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.

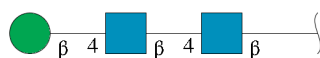
- Molecule 1 is a protein called HEMAGGLUTININ, CHAIN HA1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	328	Total	C	H	N	O	S	0	0	0
			3120	1581	588	445	493	13			
1	C	328	Total	C	H	N	O	S	0	0	0
			3120	1581	588	445	493	13			
1	E	328	Total	C	H	N	O	S	0	0	0
			3120	1581	588	445	493	13			

- Molecule 2 is a protein called HEMAGGLUTININ, CHAIN HA2.

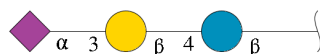
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	175	Total	C	H	N	O	S	0	0	0
			1752	882	331	250	283	6			
2	D	175	Total	C	H	N	O	S	0	0	0
			1752	882	331	250	283	6			
2	F	175	Total	C	H	N	O	S	0	0	0
			1752	882	331	250	283	6			

- Molecule 3 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.



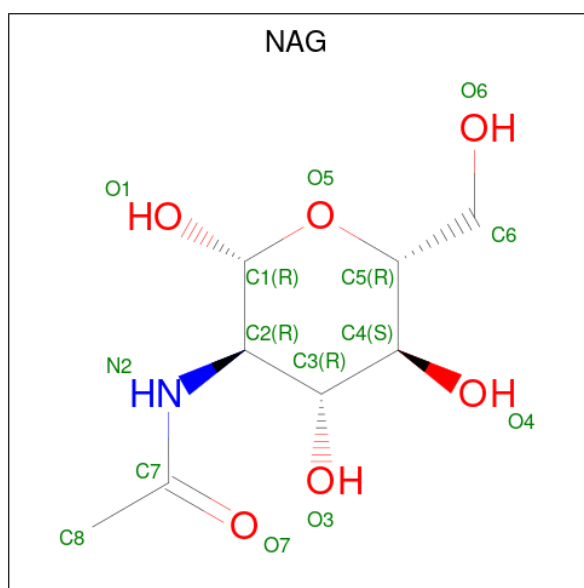
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	3	Total	C	H	N	O	0	0	0
			76	22	37	2	15			
3	J	3	Total	C	H	N	O	0	0	0
			76	22	37	2	15			
3	M	3	Total	C	H	N	O	0	0	0
			76	22	37	2	15			

- Molecule 4 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	3	Total	C	H	N	O	0	0	0
			81	23	38	1	19			
4	I	3	Total	C	H	N	O	0	0	0
			81	23	38	1	19			
4	K	3	Total	C	H	N	O	0	0	0
			81	23	38	1	19			
4	L	3	Total	C	H	N	O	0	0	0
			81	23	38	1	19			
4	N	3	Total	C	H	N	O	0	0	0
			81	23	38	1	19			
4	O	3	Total	C	H	N	O	0	0	0
			81	23	38	1	19			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

Continued on next page...

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	D	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
5	F	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

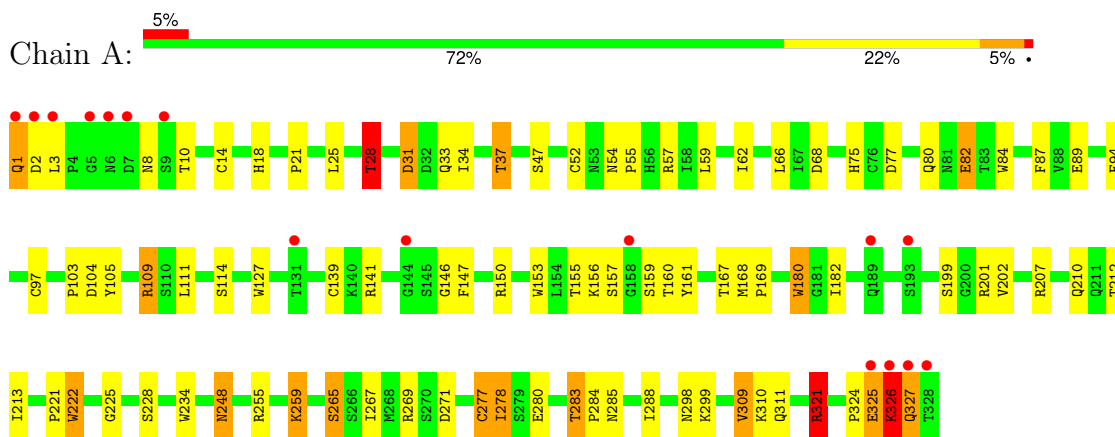
- Molecule 6 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	13	Total	H	O	0	0
			39	26	13		
6	B	11	Total	H	O	0	0
			33	22	11		
6	C	11	Total	H	O	0	0
			33	22	11		
6	D	13	Total	H	O	0	0
			39	26	13		
6	E	12	Total	H	O	0	0
			36	24	12		
6	F	12	Total	H	O	0	0
			36	24	12		

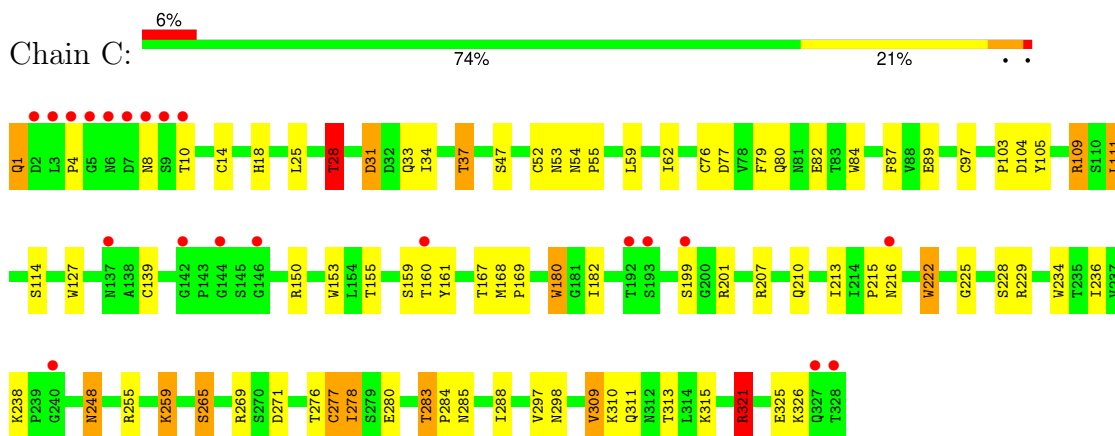
### 3 Residue-property plots [i](#)

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.

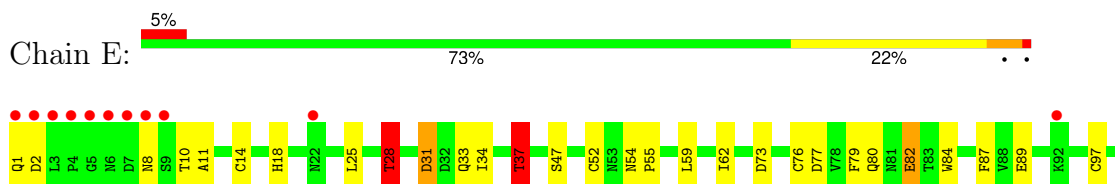
#### • Molecule 1: HEMAGGLUTININ, CHAIN HA1

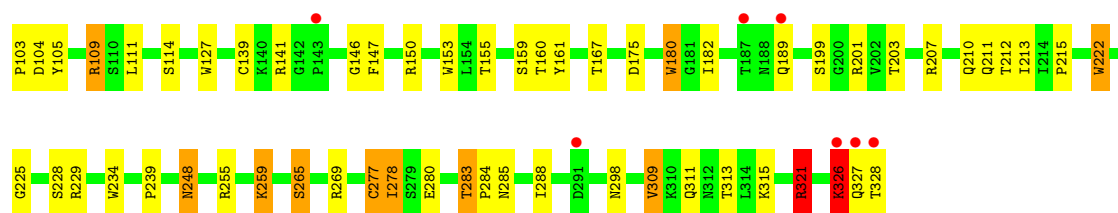


#### • Molecule 1: HEMAGGLUTININ, CHAIN HA1

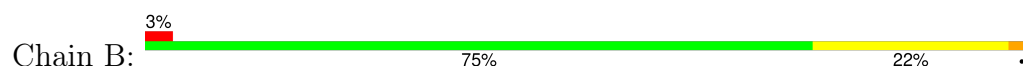


#### • Molecule 1: HEMAGGLUTININ, CHAIN HA1

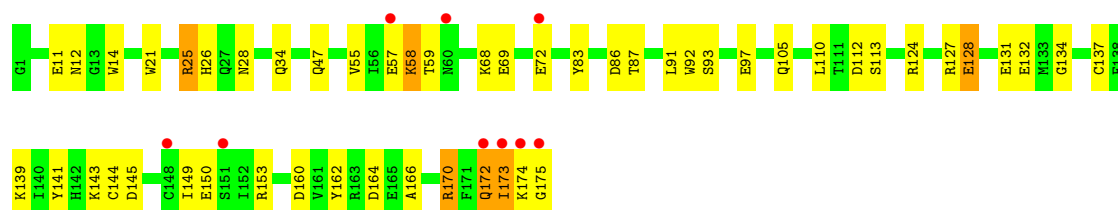




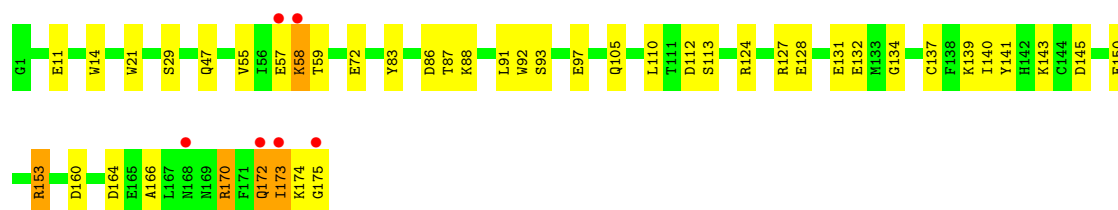
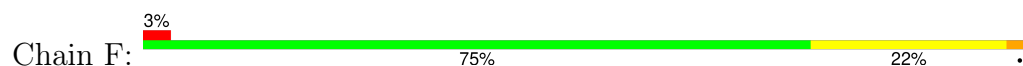
• Molecule 2: HEMAGGLUTININ, CHAIN HA2



• Molecule 2: HEMAGGLUTININ, CHAIN HA2



• Molecule 2: HEMAGGLUTININ, CHAIN HA2



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



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



Chain J:  67% 33%

BAG1  
BAG2  
BAG3

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

Chain M:  100%

BAG1  
BAG2  
BAG3

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain H:  100%

BGC1  
GAL2  
STAG

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain I:  33% 33% 33%

BGC1  
GAL2  
STAG

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain K:  100%

BGC1  
GAL2  
STAG

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain L:  33% 33% 33%

BGC1  
GAL2  
STAG

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain N:  100%

BGC1  
GAL2  
STAG

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain O:  33% 33% 33%

 33% 33% 33%

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.70Å 162.70Å 177.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 2.90 7.00 – 2.91	Depositor EDS
% Data completeness (in resolution range)	(Not available) (7.00-2.90) 63.6 (7.00-2.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 2.93Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.229 , (Not available) 0.238 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.5	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 52.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.039 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	15882	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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: BGC, SIA, NAG, GAL, BMA

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	0.91	2/2589 (0.1%)	1.47	38/3527 (1.1%)
1	C	0.89	1/2589 (0.0%)	1.45	33/3527 (0.9%)
1	E	0.92	1/2589 (0.0%)	1.48	36/3527 (1.0%)
2	B	0.92	0/1445	1.46	15/1939 (0.8%)
2	D	0.96	0/1445	1.49	20/1939 (1.0%)
2	F	0.95	0/1445	1.46	15/1939 (0.8%)
All	All	0.92	4/12102 (0.0%)	1.47	157/16398 (1.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	234	TRP	CG-CD2	-5.97	1.33	1.43
1	A	310	LYS	CD-CE	5.47	1.65	1.51
1	C	310	LYS	CD-CE	5.24	1.64	1.51
1	A	234	TRP	CG-CD2	-5.05	1.35	1.43

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	321	ARG	NE-CZ-NH2	-14.02	113.29	120.30
1	A	321	ARG	NE-CZ-NH2	-11.81	114.39	120.30
1	C	321	ARG	NE-CZ-NH2	-11.79	114.40	120.30
1	E	321	ARG	NE-CZ-NH1	10.92	125.76	120.30
1	C	321	ARG	NE-CZ-NH1	10.86	125.73	120.30

There are no chirality outliers.

There are no planarity outliers.

## 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	2532	588	2473	38	0
1	C	2532	588	2473	41	0
1	E	2532	588	2473	40	0
2	B	1421	331	1345	27	0
2	D	1421	331	1345	30	0
2	F	1421	331	1345	28	0
3	G	39	37	34	1	0
3	J	39	37	34	2	0
3	M	39	37	34	1	0
4	H	43	38	37	0	0
4	I	43	38	37	2	0
4	K	43	38	37	0	0
4	L	43	38	37	2	0
4	N	43	38	37	0	0
4	O	43	38	37	2	0
5	A	42	42	39	0	0
5	B	14	14	13	0	0
5	C	42	42	39	0	0
5	D	14	14	13	0	0
5	E	42	42	39	0	0
5	F	14	14	13	0	0
6	A	13	26	0	1	0
6	B	11	22	0	1	0
6	C	11	22	0	1	0
6	D	13	26	0	1	0
6	E	12	24	0	1	0
6	F	12	24	0	1	0
All	All	12474	3408	11934	170	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 7.

The worst 5 of 170 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ARG:HG2	1:A:321:ARG:HH11	1.45	0.81
1:E:321:ARG:HG2	1:E:321:ARG:HH11	1.43	0.81
1:C:321:ARG:HH11	1:C:321:ARG:HG2	1.46	0.79
2:B:83:TYR:O	2:B:87:THR:HG23	1.93	0.68
2:D:83:TYR:O	2:D:87:THR:HG23	1.95	0.67

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	326/328 (99%)	304 (93%)	17 (5%)	5 (2%)	8	29
1	C	326/328 (99%)	307 (94%)	16 (5%)	3 (1%)	14	43
1	E	326/328 (99%)	309 (95%)	16 (5%)	1 (0%)	37	66
2	B	173/175 (99%)	160 (92%)	10 (6%)	3 (2%)	7	27
2	D	173/175 (99%)	160 (92%)	10 (6%)	3 (2%)	7	27
2	F	173/175 (99%)	160 (92%)	10 (6%)	3 (2%)	7	27
All	All	1497/1509 (99%)	1400 (94%)	79 (5%)	18 (1%)	11	35

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	326	LYS
2	B	58	LYS
2	B	173	ILE
2	D	58	LYS

### 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	
1	A	289/289 (100%)	259 (90%)	30 (10%)	5	18
1	C	289/289 (100%)	264 (91%)	25 (9%)	8	27
1	E	289/289 (100%)	259 (90%)	30 (10%)	5	18
2	B	149/149 (100%)	144 (97%)	5 (3%)	32	67
2	D	149/149 (100%)	144 (97%)	5 (3%)	32	67
2	F	149/149 (100%)	143 (96%)	6 (4%)	27	61
All	All	1314/1314 (100%)	1213 (92%)	101 (8%)	10	31

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	283	THR
1	E	37	THR
2	F	170	ARG
1	C	321	ARG
1	E	2	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	12	ASN
2	D	49	ASN
1	E	171	ASN
1	E	8	ASN
1	E	132	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 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 ⓘ

27 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	$\# Z  > 2$
3	NAG	G	1	1,3	14,14,15	0.65	0	17,19,21	0.72	0
3	NAG	G	2	3	14,14,15	0.61	0	17,19,21	0.93	1 (5%)
3	BMA	G	3	3	11,11,12	0.35	0	15,15,17	1.03	2 (13%)
4	BGC	H	1	4	12,12,12	1.33	1 (8%)	17,17,17	1.01	1 (5%)
4	GAL	H	2	4	11,11,12	0.53	0	15,15,17	1.20	1 (6%)
4	SIA	H	3	4	20,20,21	0.93	2 (10%)	21,28,31	1.66	7 (33%)
4	BGC	I	1	4	12,12,12	0.52	0	17,17,17	0.81	0
4	GAL	I	2	4	11,11,12	0.59	0	15,15,17	1.18	2 (13%)
4	SIA	I	3	4	20,20,21	1.03	2 (10%)	21,28,31	1.63	7 (33%)
3	NAG	J	1	1,3	14,14,15	0.77	0	17,19,21	0.85	0
3	NAG	J	2	3	14,14,15	0.50	0	17,19,21	0.90	1 (5%)
3	BMA	J	3	3	11,11,12	0.81	0	15,15,17	1.47	2 (13%)
4	BGC	K	1	4	12,12,12	1.33	1 (8%)	17,17,17	0.94	1 (5%)
4	GAL	K	2	4	11,11,12	0.66	0	15,15,17	1.21	2 (13%)
4	SIA	K	3	4	20,20,21	0.88	1 (5%)	21,28,31	1.55	5 (23%)
4	BGC	L	1	4	12,12,12	0.56	0	17,17,17	0.73	0
4	GAL	L	2	4	11,11,12	0.64	0	15,15,17	1.20	2 (13%)
4	SIA	L	3	4	20,20,21	1.01	2 (10%)	21,28,31	1.60	6 (28%)
3	NAG	M	1	1,3	14,14,15	0.70	0	17,19,21	0.83	0
3	NAG	M	2	3	14,14,15	0.48	0	17,19,21	0.87	1 (5%)
3	BMA	M	3	3	11,11,12	0.91	0	15,15,17	1.07	1 (6%)
4	BGC	N	1	4	12,12,12	1.20	1 (8%)	17,17,17	0.99	1 (5%)
4	GAL	N	2	4	11,11,12	0.62	0	15,15,17	1.23	1 (6%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	SIA	N	3	4	20,20,21	0.93	1 (5%)	21,28,31	1.64	7 (33%)
4	BGC	O	1	4	12,12,12	0.48	0	17,17,17	0.69	0
4	GAL	O	2	4	11,11,12	0.67	0	15,15,17	1.20	2 (13%)
4	SIA	O	3	4	20,20,21	1.01	2 (10%)	21,28,31	1.67	7 (33%)

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
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
4	BGC	H	1	4	-	2/2/22/22	0/1/1/1
4	GAL	H	2	4	-	1/2/19/22	0/1/1/1
4	SIA	H	3	4	-	1/18/34/38	0/1/1/1
4	BGC	I	1	4	-	0/2/22/22	0/1/1/1
4	GAL	I	2	4	-	1/2/19/22	0/1/1/1
4	SIA	I	3	4	-	0/18/34/38	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
3	BMA	J	3	3	-	0/2/19/22	0/1/1/1
4	BGC	K	1	4	-	2/2/22/22	0/1/1/1
4	GAL	K	2	4	-	1/2/19/22	0/1/1/1
4	SIA	K	3	4	-	1/18/34/38	0/1/1/1
4	BGC	L	1	4	-	0/2/22/22	0/1/1/1
4	GAL	L	2	4	-	1/2/19/22	0/1/1/1
4	SIA	L	3	4	-	0/18/34/38	0/1/1/1
3	NAG	M	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	0/6/23/26	0/1/1/1
3	BMA	M	3	3	-	0/2/19/22	0/1/1/1
4	BGC	N	1	4	-	2/2/22/22	0/1/1/1
4	GAL	N	2	4	-	1/2/19/22	0/1/1/1
4	SIA	N	3	4	-	1/18/34/38	0/1/1/1
4	BGC	O	1	4	-	0/2/22/22	0/1/1/1
4	GAL	O	2	4	-	1/2/19/22	0/1/1/1
4	SIA	O	3	4	-	0/18/34/38	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	3	SIA	C2-C1	3.13	1.56	1.52
4	H	1	BGC	C4-C5	3.06	1.59	1.53
4	K	1	BGC	C4-C5	2.95	1.59	1.53
4	O	3	SIA	C2-C1	2.92	1.55	1.52
4	N	1	BGC	C4-C5	2.80	1.59	1.53

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	3	BMA	C1-O5-C5	4.17	117.78	112.19
4	L	2	GAL	C1-O5-C5	3.75	117.21	112.19
4	O	2	GAL	C1-O5-C5	3.75	117.21	112.19
4	I	2	GAL	C1-O5-C5	3.62	117.03	112.19
4	H	2	GAL	C1-O5-C5	3.09	116.33	112.19

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

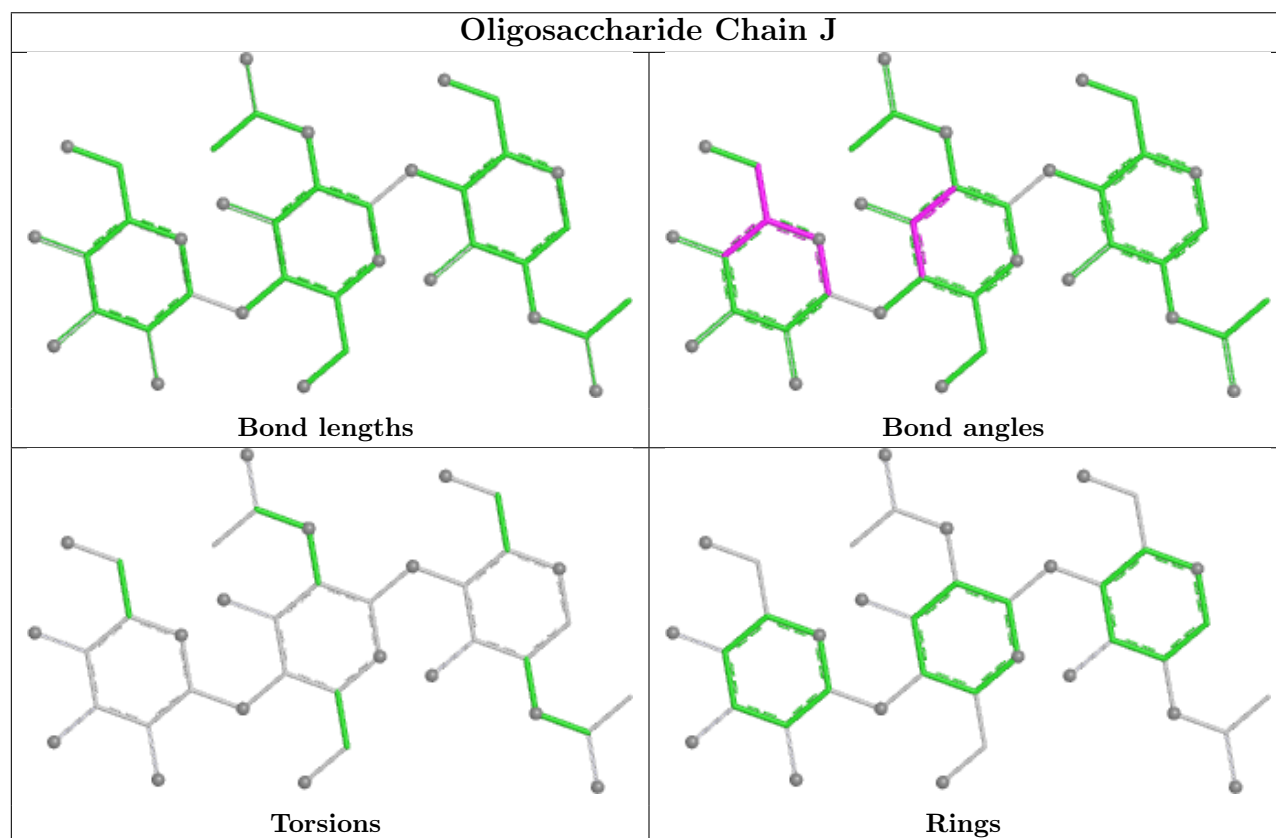
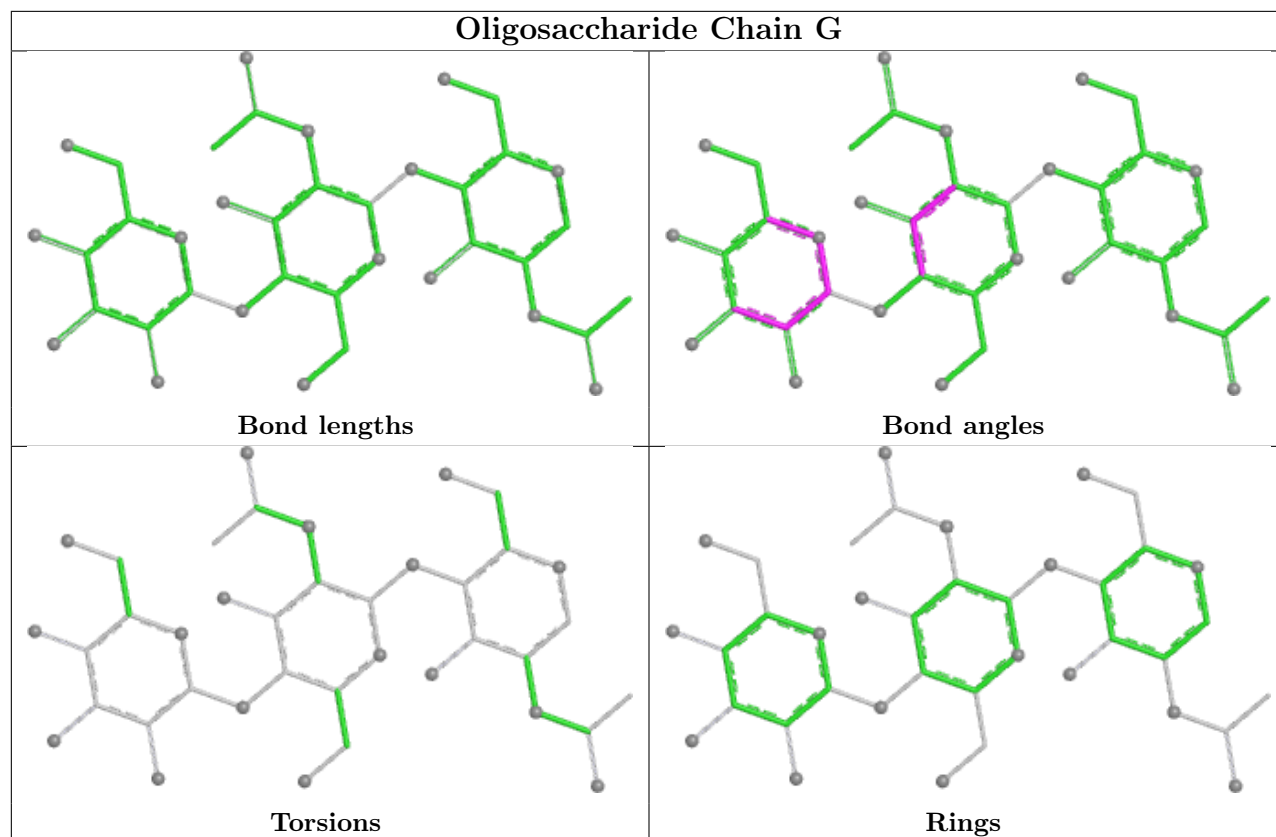
Mol	Chain	Res	Type	Atoms
4	N	1	BGC	O5-C5-C6-O6
4	H	1	BGC	O5-C5-C6-O6
4	K	1	BGC	O5-C5-C6-O6
4	L	2	GAL	O5-C5-C6-O6
4	I	2	GAL	O5-C5-C6-O6

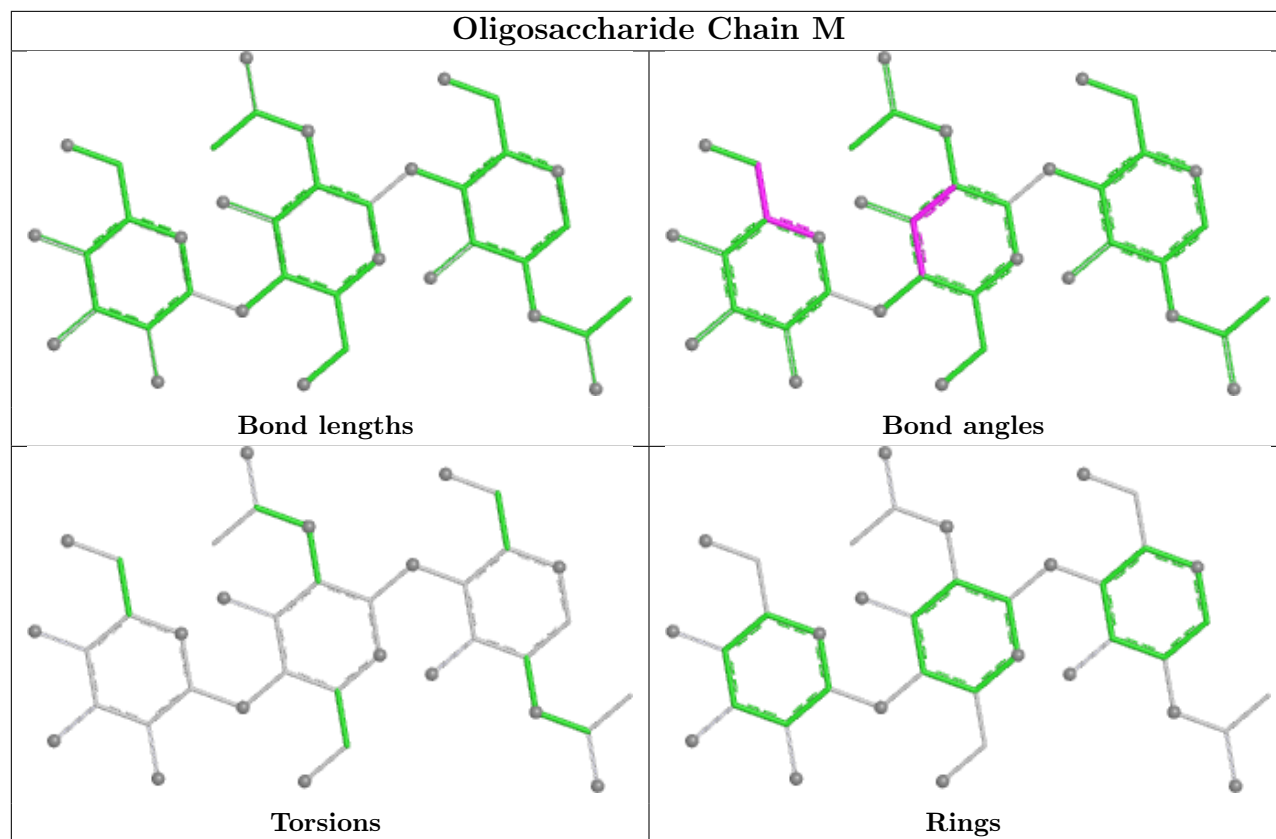
There are no ring outliers.

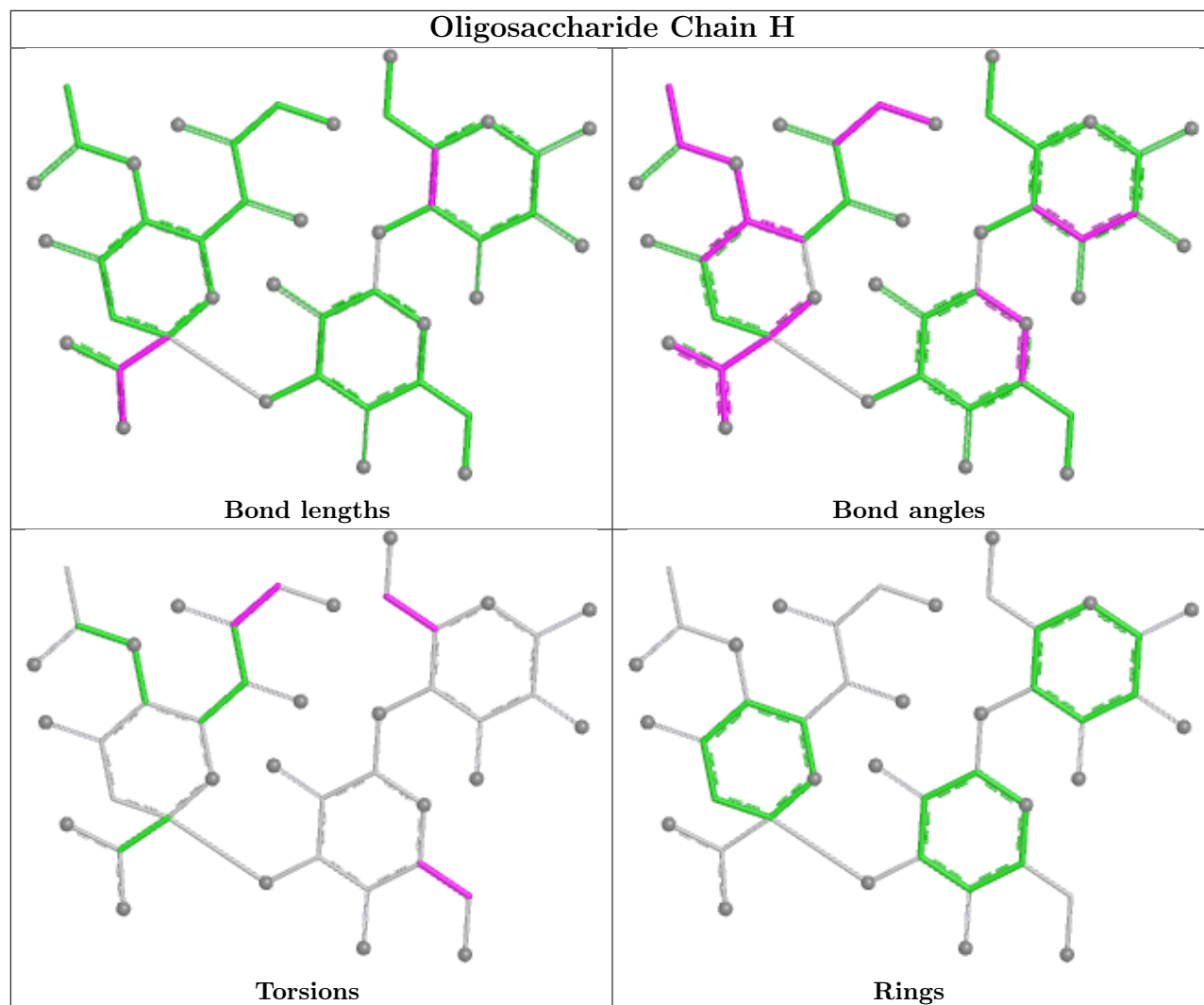
7 monomers are involved in 10 short contacts:

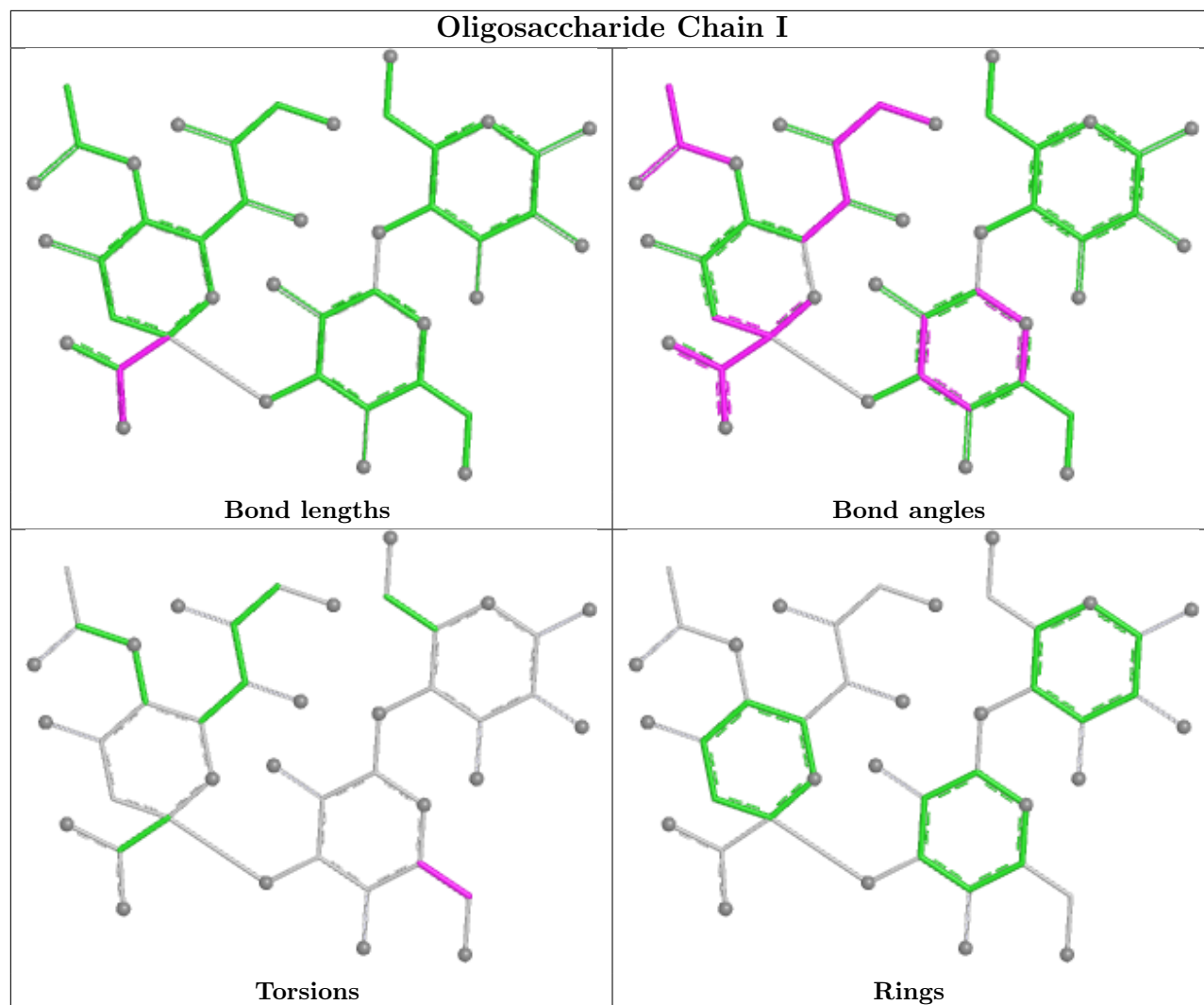
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	O	3	SIA	2	0
3	G	1	NAG	1	0
3	J	1	NAG	1	0
4	L	3	SIA	2	0
4	I	3	SIA	2	0
3	M	1	NAG	1	0
3	J	2	NAG	1	0

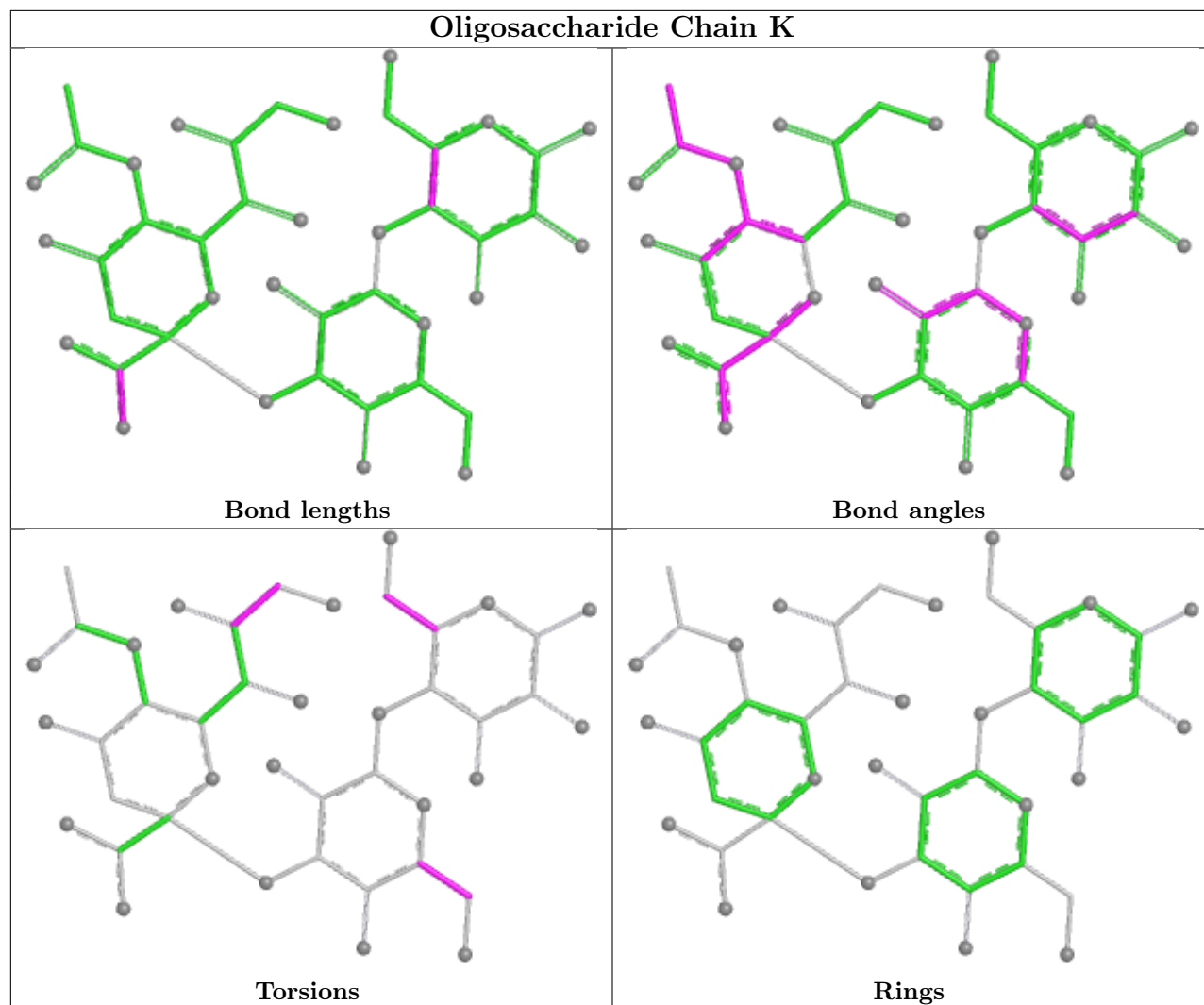
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

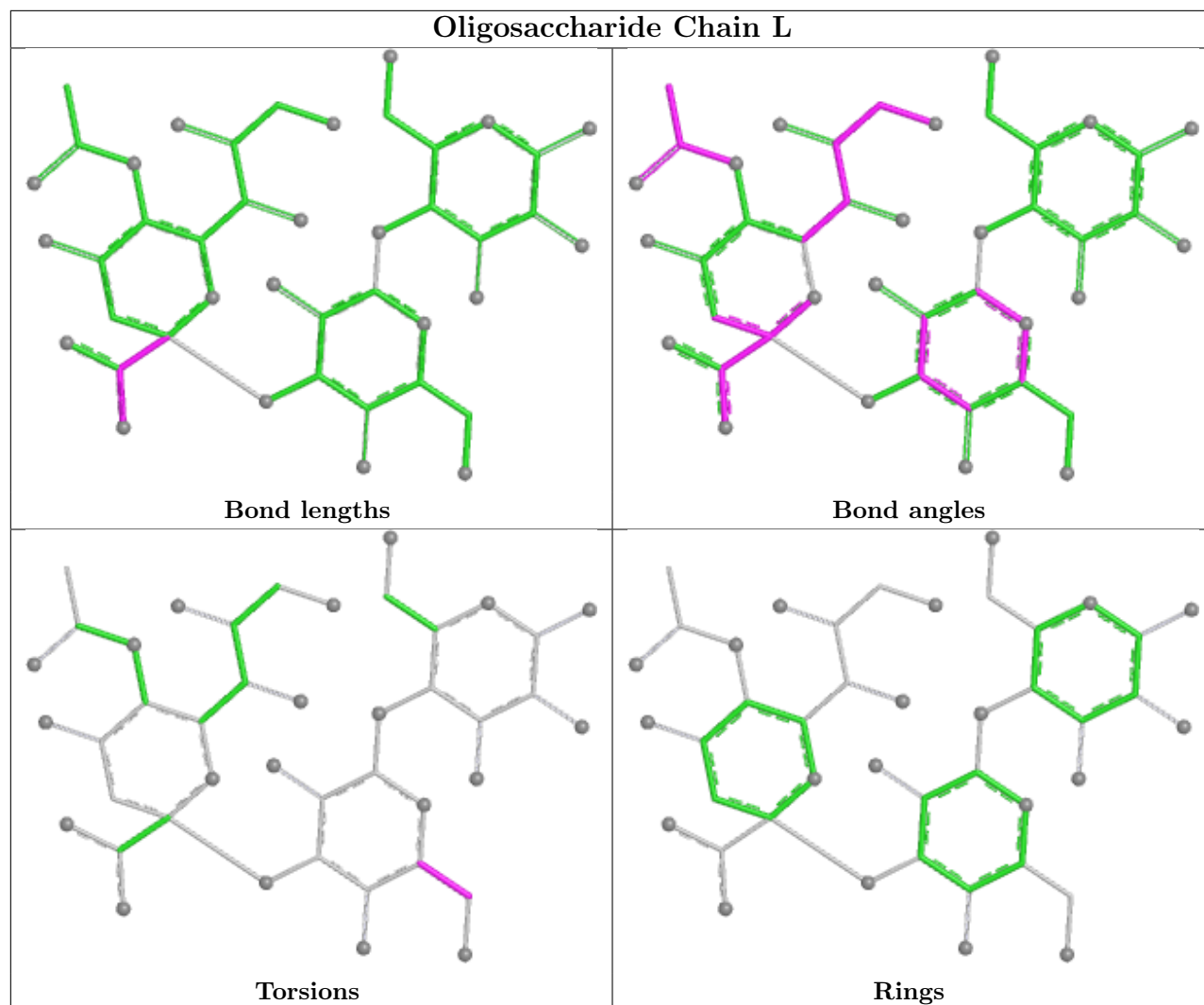




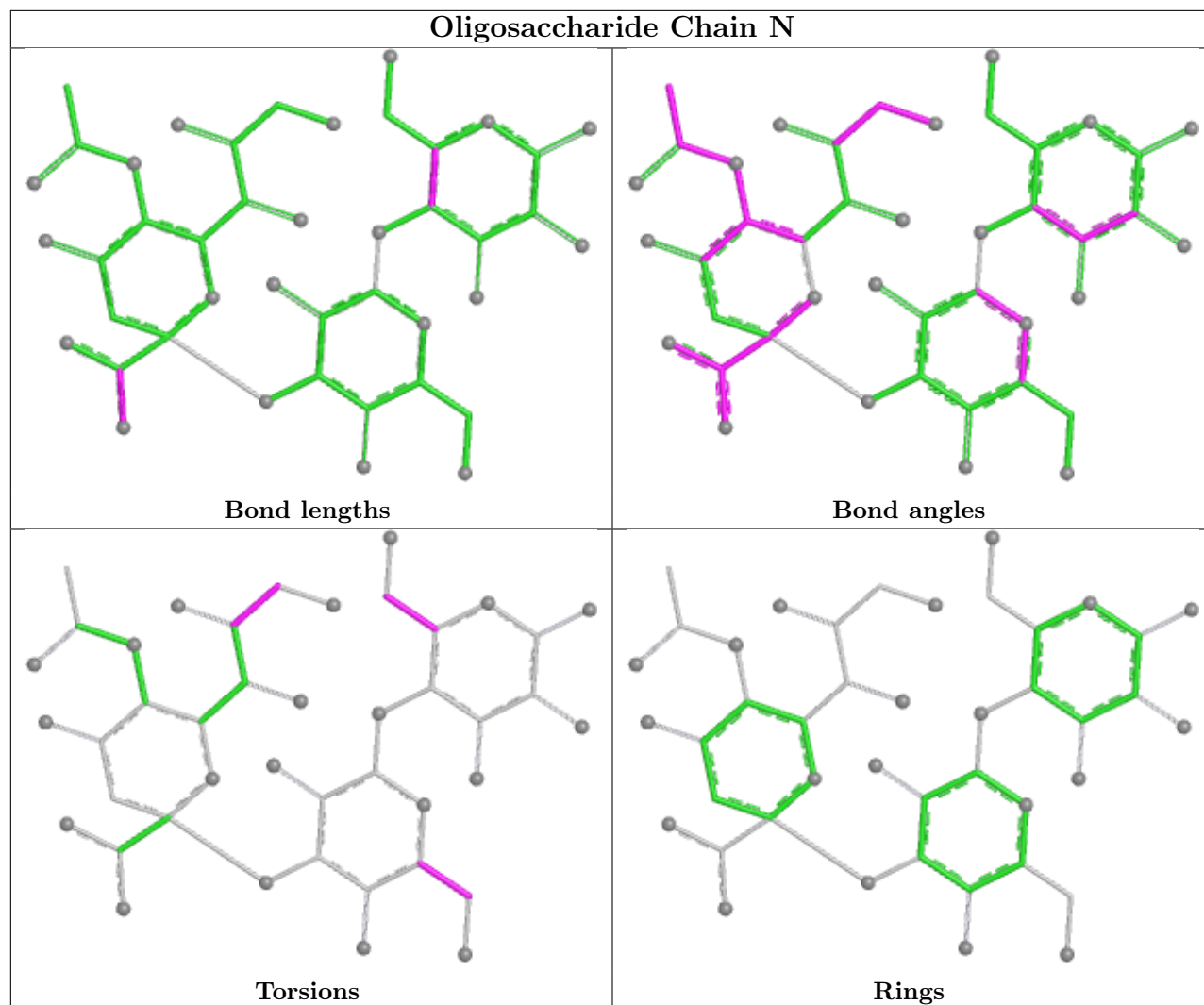


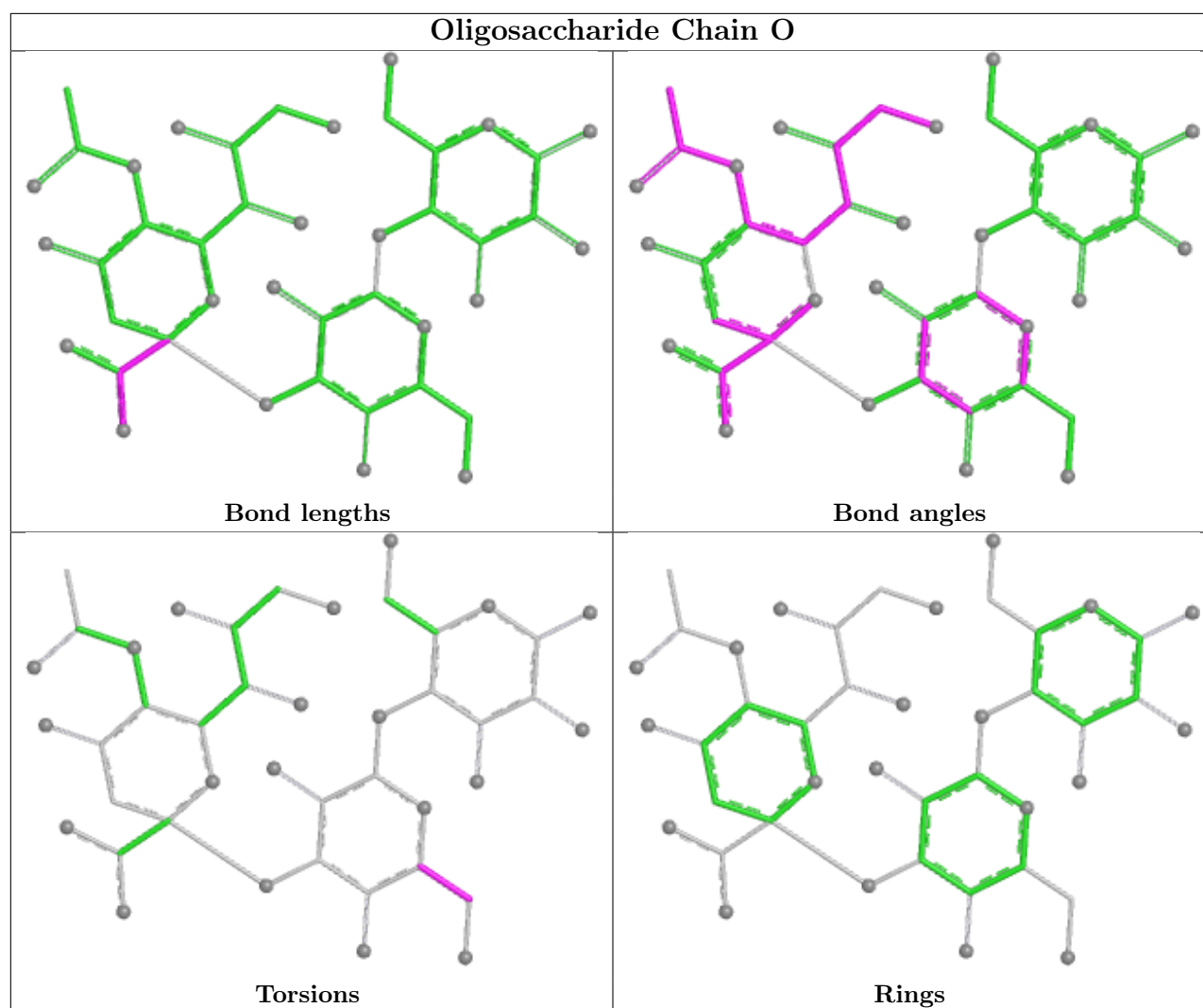












## 5.6 Ligand geometry [i](#)

12 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	$\# Z  > 2$
5	NAG	C	329	1	14,14,15	0.70	0	17,19,21	1.11	1 (5%)
5	NAG	E	329	1	14,14,15	0.85	0	17,19,21	1.07	1 (5%)
5	NAG	E	334	1	14,14,15	0.79	0	17,19,21	1.38	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	F	401	2	14,14,15	0.91	1 (7%)	17,19,21	1.33	1 (5%)
5	NAG	A	329	1	14,14,15	0.87	1 (7%)	17,19,21	1.11	1 (5%)
5	NAG	A	334	1	14,14,15	0.71	0	17,19,21	1.36	2 (11%)
5	NAG	B	401	2	14,14,15	0.86	0	17,19,21	1.28	1 (5%)
5	NAG	C	348	1	14,14,15	0.69	0	17,19,21	1.58	4 (23%)
5	NAG	E	348	1	14,14,15	0.80	0	17,19,21	1.53	4 (23%)
5	NAG	C	334	1	14,14,15	0.82	0	17,19,21	1.42	1 (5%)
5	NAG	A	348	1	14,14,15	0.92	1 (7%)	17,19,21	1.45	4 (23%)
5	NAG	D	401	2	14,14,15	0.87	0	17,19,21	1.34	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
5	NAG	C	329	1	-	0/6/23/26	0/1/1/1
5	NAG	E	329	1	-	0/6/23/26	0/1/1/1
5	NAG	E	334	1	-	0/6/23/26	0/1/1/1
5	NAG	F	401	2	-	0/6/23/26	0/1/1/1
5	NAG	A	329	1	-	0/6/23/26	0/1/1/1
5	NAG	A	334	1	-	0/6/23/26	0/1/1/1
5	NAG	B	401	2	-	0/6/23/26	0/1/1/1
5	NAG	C	348	1	-	2/6/23/26	0/1/1/1
5	NAG	E	348	1	-	2/6/23/26	0/1/1/1
5	NAG	C	334	1	-	0/6/23/26	0/1/1/1
5	NAG	A	348	1	-	2/6/23/26	0/1/1/1
5	NAG	D	401	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	348	NAG	C1-C2	2.24	1.55	1.52
5	F	401	NAG	C4-C5	2.12	1.57	1.53
5	A	329	NAG	C4-C5	2.08	1.57	1.53

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
5	F	401	NAG	C1-O5-C5	3.77	117.23	112.19
5	D	401	NAG	C1-O5-C5	3.60	117.01	112.19
5	C	348	NAG	C1-O5-C5	3.48	116.85	112.19
5	B	401	NAG	C1-O5-C5	3.41	116.75	112.19
5	A	348	NAG	C1-O5-C5	3.21	116.49	112.19

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	348	NAG	O5-C5-C6-O6
5	C	348	NAG	O5-C5-C6-O6
5	E	348	NAG	O5-C5-C6-O6
5	A	348	NAG	C4-C5-C6-O6
5	C	348	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data [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	328/328 (100%)	-0.21	16 (4%) 36 30	5, 21, 42, 135	0
1	C	328/328 (100%)	-0.16	21 (6%) 27 22	5, 21, 41, 141	0
1	E	328/328 (100%)	-0.27	18 (5%) 32 27	5, 21, 41, 138	0
2	B	175/175 (100%)	-0.32	6 (3%) 48 42	2, 16, 39, 88	0
2	D	175/175 (100%)	-0.30	9 (5%) 34 29	2, 16, 38, 88	0
2	F	175/175 (100%)	-0.45	6 (3%) 48 42	2, 16, 38, 88	0
All	All	1509/1509 (100%)	-0.26	76 (5%) 35 30	2, 20, 41, 141	0

The worst 5 of 76 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	8	ASN	7.6
1	C	7	ASP	6.1
1	C	5	GLY	5.9
1	A	328	THR	5.4
1	E	6	ASN	5.2

### 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](#)

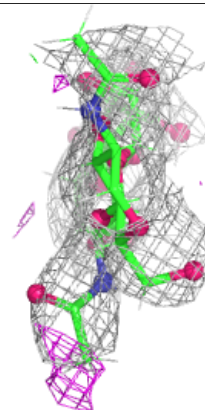
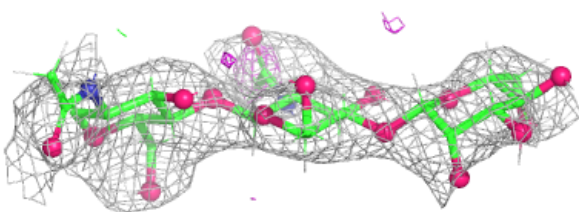
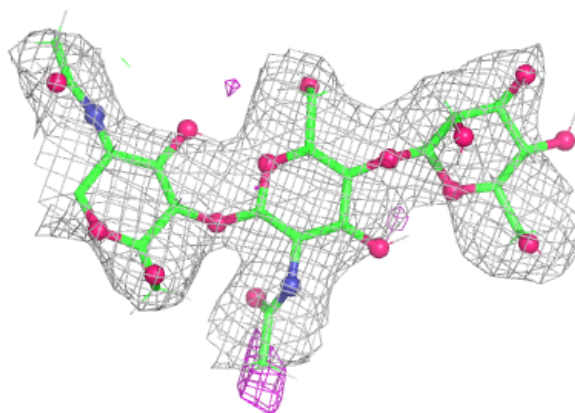
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 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
4	BGC	K	1	12/12	0.53	0.25	0,0,67,68	23
4	BGC	H	1	12/12	0.57	0.30	0,0,67,68	23
4	GAL	I	2	11/12	0.65	0.17	0,0,47,48	21
3	BMA	G	3	11/12	0.68	0.14	0,0,64,65	0
4	BGC	N	1	12/12	0.73	0.28	0,0,67,68	23
4	BGC	O	1	12/12	0.73	0.24	0,0,49,50	23
3	BMA	M	3	11/12	0.76	0.14	0,0,65,68	0
4	SIA	L	3	20/21	0.78	0.25	0,41,44,44	37
4	GAL	L	2	11/12	0.79	0.13	0,0,47,48	21
4	BGC	I	1	12/12	0.79	0.19	0,0,49,50	23
3	NAG	J	2	14/15	0.80	0.13	0,0,57,60	0
4	BGC	L	1	12/12	0.80	0.22	0,0,49,50	23
3	BMA	J	3	11/12	0.80	0.15	0,0,70,72	0
3	NAG	G	2	14/15	0.81	0.12	0,0,57,59	0
3	NAG	J	1	14/15	0.81	0.11	0,0,45,48	0
4	SIA	I	3	20/21	0.82	0.24	0,41,44,44	37
4	SIA	K	3	20/21	0.86	0.14	0,35,41,42	37
3	NAG	G	1	14/15	0.86	0.10	0,0,45,48	0
3	NAG	M	1	14/15	0.86	0.11	0,0,44,48	0
4	GAL	O	2	11/12	0.86	0.14	0,0,47,48	21
4	SIA	N	3	20/21	0.88	0.14	0,35,41,42	37
4	GAL	H	2	11/12	0.88	0.15	0,0,51,53	21
4	GAL	N	2	11/12	0.88	0.14	0,0,51,53	21
4	GAL	K	2	11/12	0.89	0.13	0,0,51,53	21
3	NAG	M	2	14/15	0.89	0.11	0,0,57,59	0
4	SIA	H	3	20/21	0.90	0.12	0,35,41,42	37
4	SIA	O	3	20/21	0.90	0.20	0,42,44,44	37

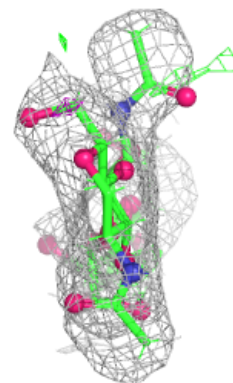
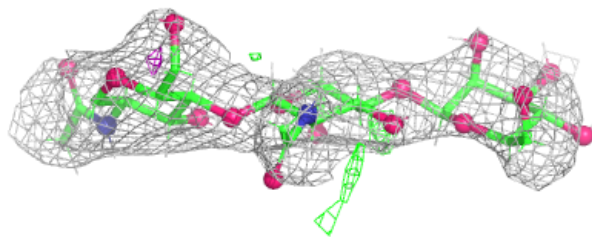
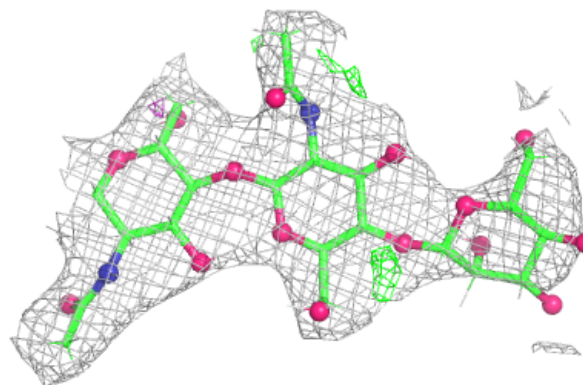
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain G:**

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

**Electron density around Chain J:**

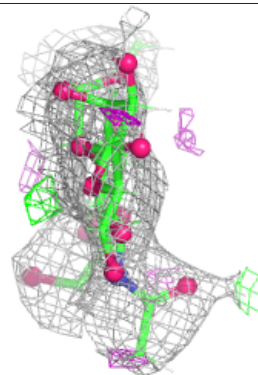
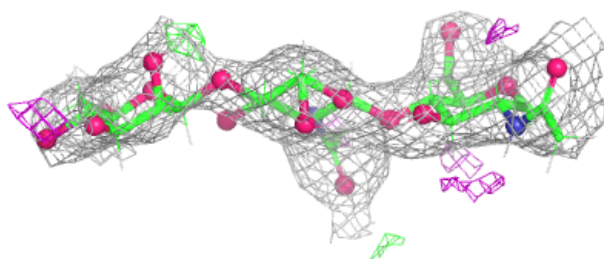
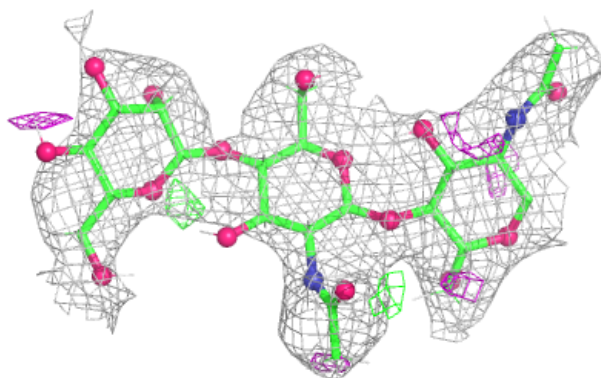
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



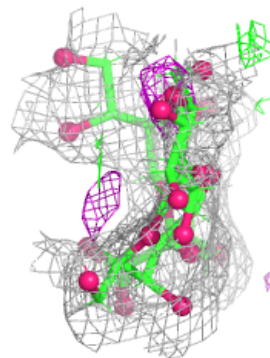
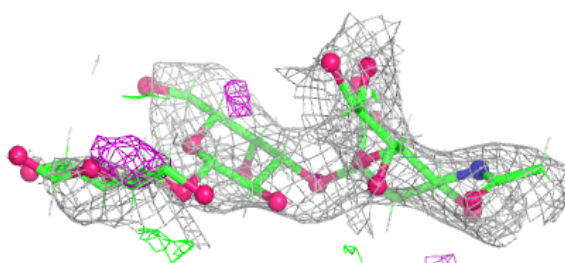
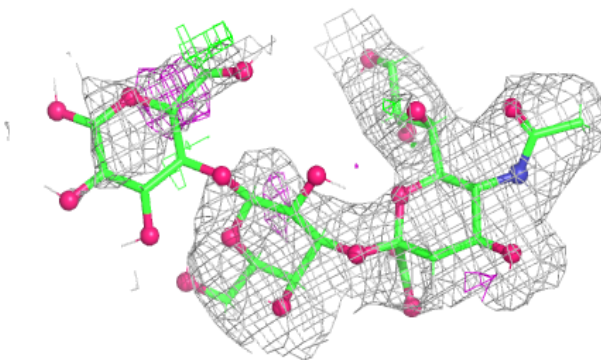


**Electron density around Chain M:**

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

**Electron density around Chain H:**

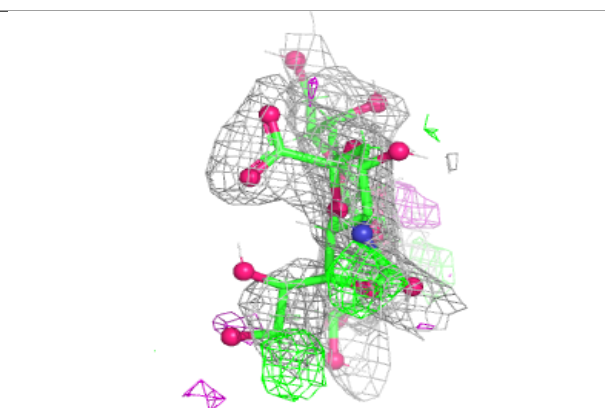
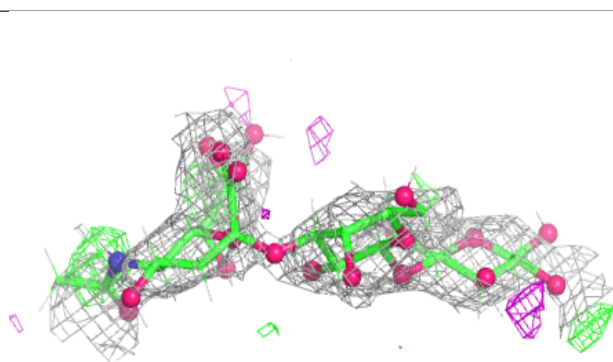
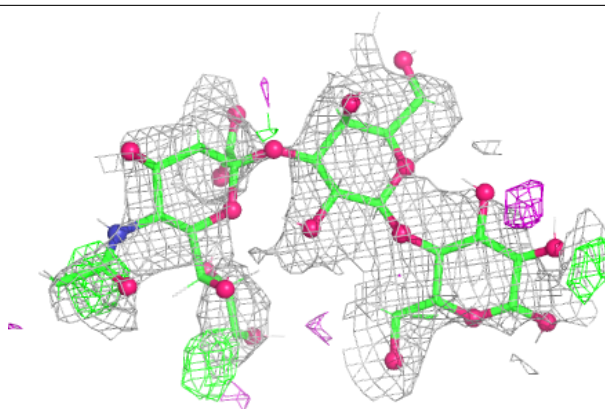
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



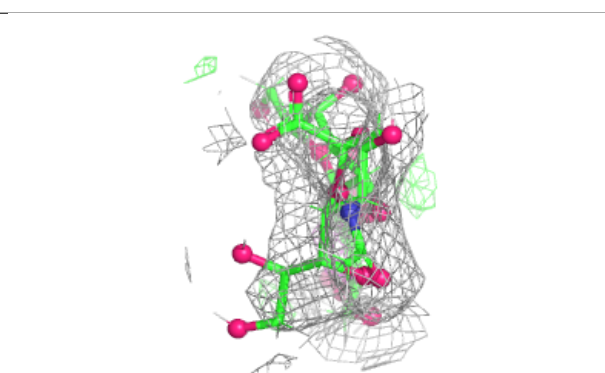
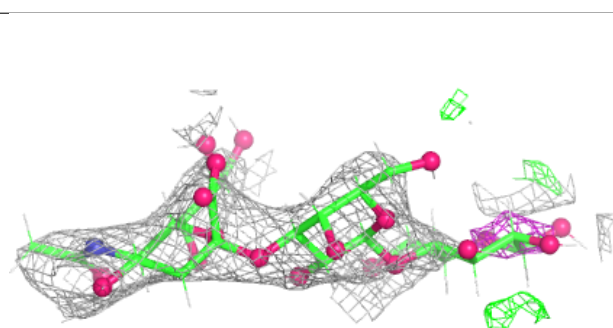
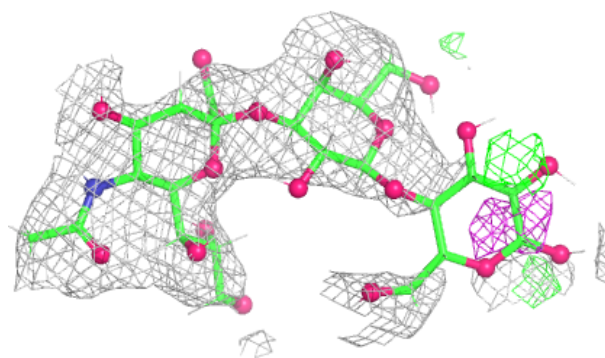


**Electron density around Chain I:**

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

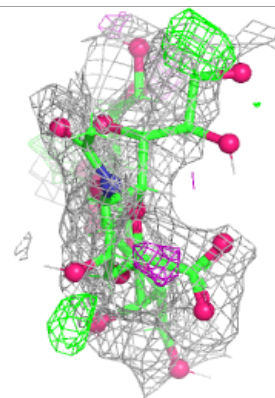
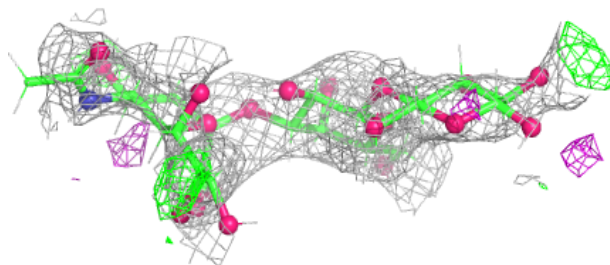
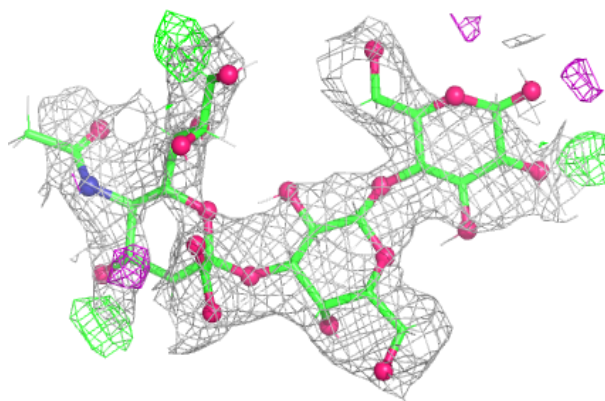
**Electron density around Chain K:**

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

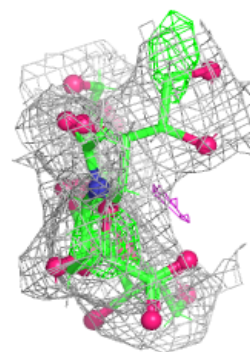
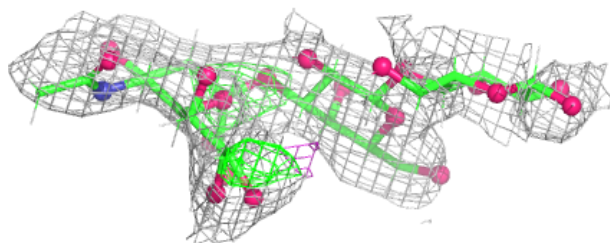
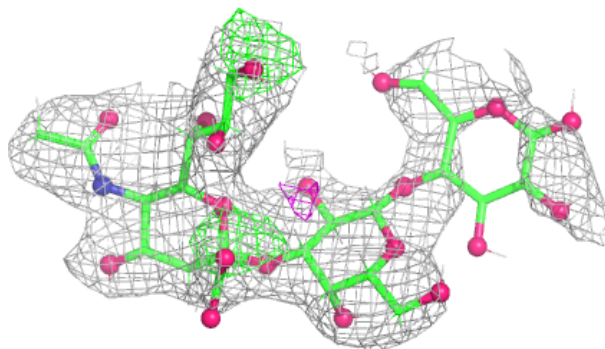


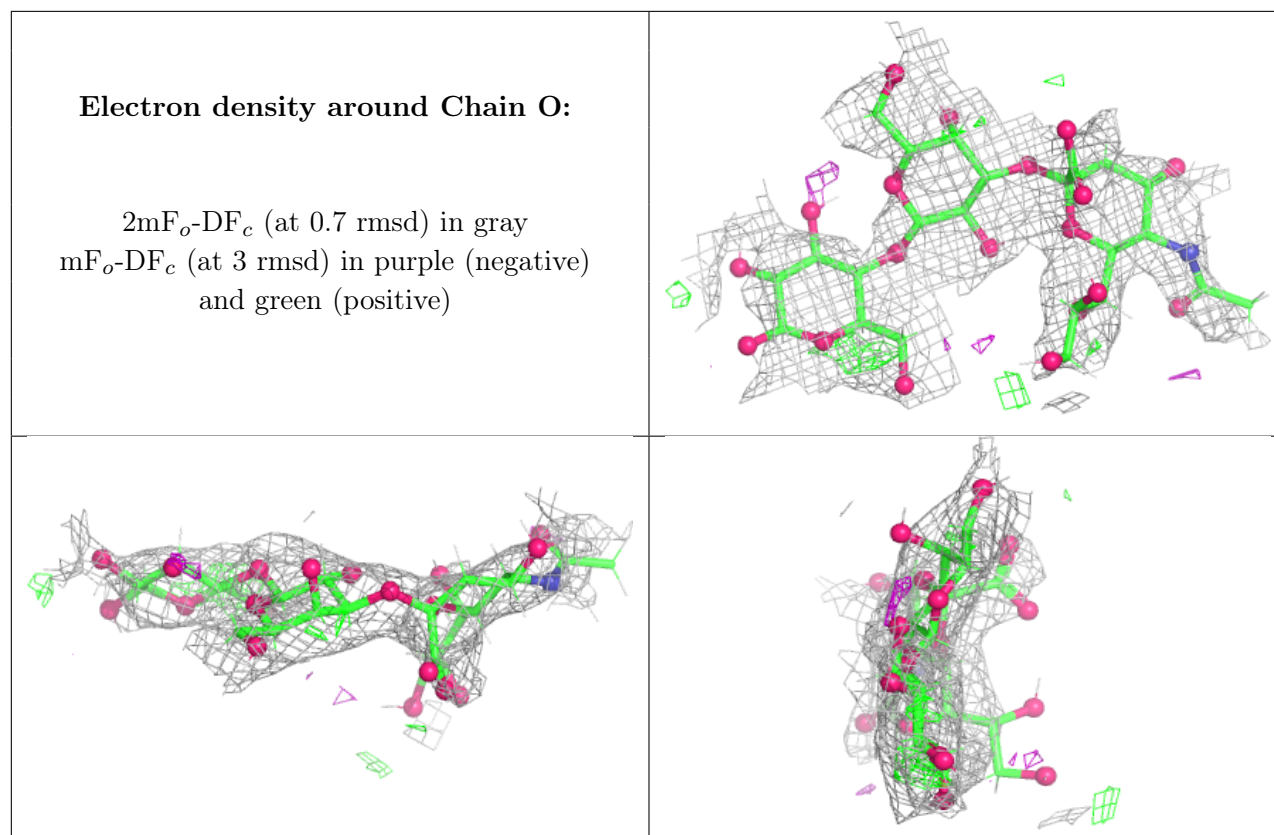
**Electron density around Chain L:**

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

**Electron density around Chain 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 ⓘ

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
5	NAG	E	348	14/15	0.75	0.16	0,0,49,50	0
5	NAG	F	401	14/15	0.75	0.18	0,0,61,61	0
5	NAG	E	329	14/15	0.76	0.18	0,0,50,50	0
5	NAG	B	401	14/15	0.78	0.20	0,0,61,61	0
5	NAG	D	401	14/15	0.79	0.19	0,0,61,62	0
5	NAG	C	348	14/15	0.79	0.15	0,0,49,51	0
5	NAG	C	334	14/15	0.80	0.15	0,0,44,46	0
5	NAG	A	334	14/15	0.81	0.09	0,0,44,45	0
5	NAG	A	329	14/15	0.82	0.19	0,0,49,50	0
5	NAG	A	348	14/15	0.84	0.14	0,0,50,51	0
5	NAG	C	329	14/15	0.90	0.13	0,0,49,50	0
5	NAG	E	334	14/15	0.90	0.09	0,0,44,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.