



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 22, 2024 – 11:38 PM EDT

PDB ID : 4MC5
Title : Crystal structure of a subtype H18 hemagglutinin homologue from A/flat-faced bat/Peru/033/2010 (H18N11)
Authors : Yang, H.; Carney, P.J.; Chang, J.C.; Guo, Z.; Stevens, J.
Deposited on : 2013-08-21
Resolution : 2.24 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-467
Mogul	:	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)
Validation Pipeline (wwPDB-VP)	:	2.39

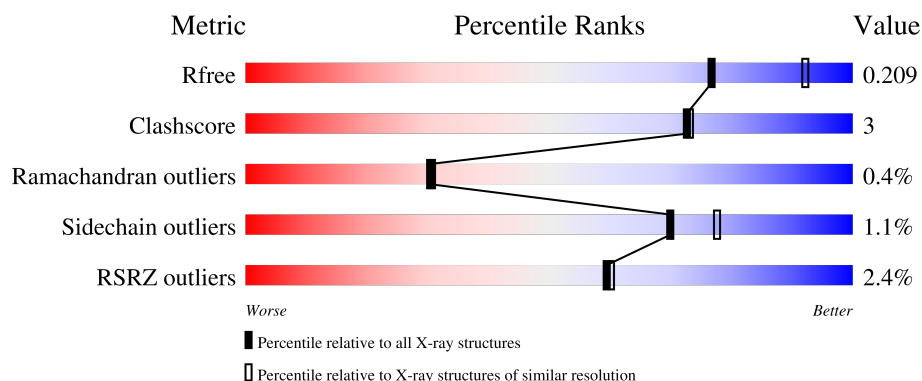
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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}	164625	3139 (2.26-2.22)
Clashscore	180529	3381 (2.26-2.22)
Ramachandran outliers	177936	3334 (2.26-2.22)
Sidechain outliers	177891	3335 (2.26-2.22)
RSRZ outliers	164620	3138 (2.26-2.22)

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 ≥ 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	510	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>5%</div> <div></div> </div> </div>
1	B	510	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div></div> </div> </div>
1	C	510	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div></div> </div> </div>
2	D	4	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
3	E	7	<div> <div></div> <div> <div>43%</div> <div>14%</div> <div>43%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	G	7	
4	F	2	
4	H	2	
4	J	2	
5	I	4	

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
7	NAG	A	616	X	-	-	-
7	NAG	B	612	X	-	-	-
7	NAG	C	610	X	-	-	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 13219 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 Hemagglutinin.

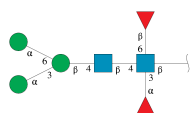
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	0	0	0
			3914	2459	660	777	18			
1	B	494	Total	C	N	O	S	0	0	0
			3914	2459	660	777	18			
1	C	497	Total	C	N	O	S	0	0	0
			3938	2476	664	780	18			

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



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

- Molecule 3 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)-[alpha-L-fucopyranose-(1-3)][beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	0	0	0
			81	46	2	33			

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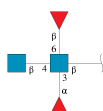
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	7	Total	C	N	O	0	0	0
			81	46	2	33			

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



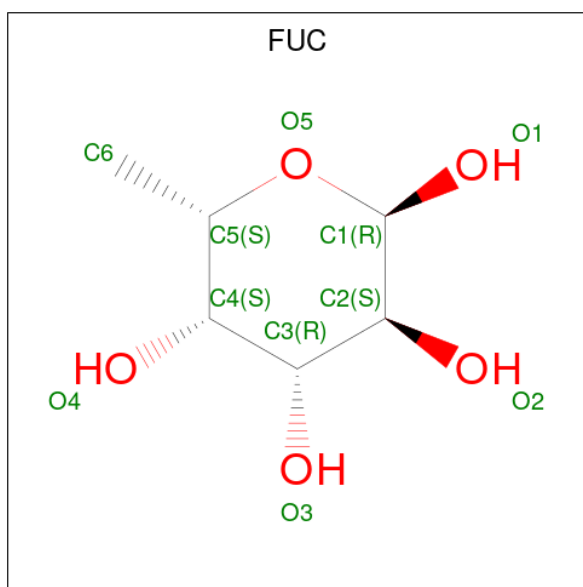
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	I	4	Total	C	N	O	0	0	0
			48	28	2	18			

- Molecule 6 is alpha-L-fucopyranose (three-letter code: FUC) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		
6	B	1	Total	C	O	0	0
			10	6	4		
6	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

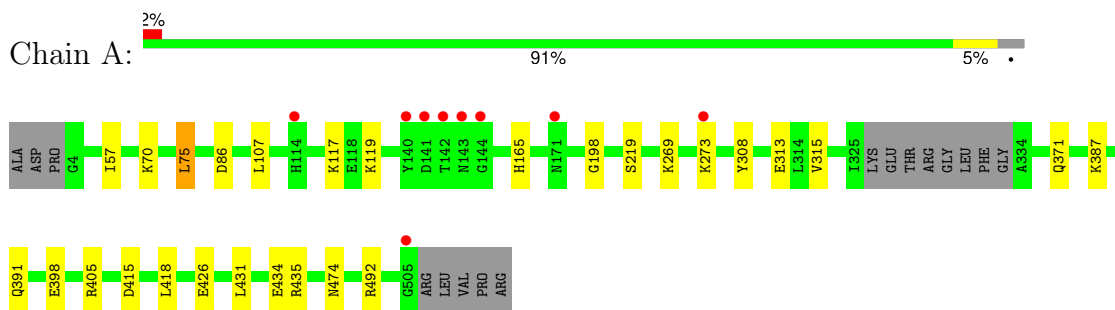
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	292	Total	O	0	0
			292	292		
8	B	343	Total	O	0	0
			343	343		
8	C	332	Total	O	0	0
			332	332		

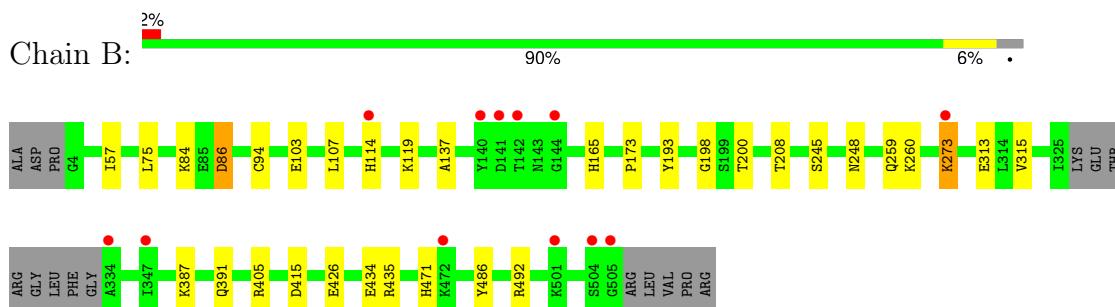
3 Residue-property plots [i](#)

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.

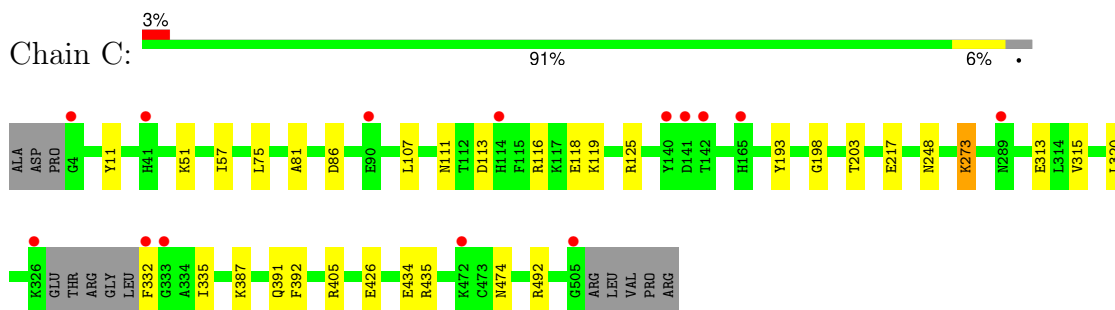
- Molecule 1: Hemagglutinin



- Molecule 1: Hemagglutinin



- Molecule 1: Hemagglutinin



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





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



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



- 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



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



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	239.09Å 239.09Å 161.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.02 – 2.24 48.02 – 2.24	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.02-2.24) 95.7 (48.02-2.24)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 2.24Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.175 , 0.204 0.180 , 0.209	Depositor DCC
R_{free} test set	5563 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13219	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: FUL, NAG, BMA, MAN, FUC

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	0.30	0/3998	0.46	0/5425
1	B	0.31	0/3998	0.47	0/5425
1	C	0.30	0/4023	0.46	0/5457
All	All	0.30	0/12019	0.46	0/16307

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3914	0	3734	27	0
1	B	3914	0	3733	26	1
1	C	3938	0	3758	26	0
2	D	50	0	43	0	0
3	E	81	0	70	2	1
3	G	81	0	70	2	1
4	F	28	0	25	0	0
4	H	28	0	25	0	0
4	J	28	0	25	3	0
5	I	48	0	43	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	10	0	10	2	0
6	B	10	0	10	1	0
6	C	10	0	10	3	0
7	A	28	0	26	0	0
7	B	42	0	39	1	0
7	C	42	0	39	0	0
8	A	292	0	0	12	0
8	B	343	0	0	7	1
8	C	332	0	0	12	0
All	All	13219	0	11660	74	2

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 3.

The worst 5 of 74 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:C:125:ARG:NH2	8:C:980:HOH:O	2.01	0.91
8:C:997:HOH:O	4:J:2:NAG:O4	1.91	0.87
1:C:113:ASP:OD2	8:C:927:HOH:O	1.96	0.82
1:C:474:ASN:OD1	8:C:811:HOH:O	1.99	0.80
1:A:474:ASN:OD1	8:A:812:HOH:O	2.01	0.78

All (2) 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)
3:E:4:MAN:O4	3:G:1:NAG:O7[3_755]	2.16	0.04
1:B:273:LYS:NZ	8:B:969:HOH:O[6_575]	2.18	0.02

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	490/510 (96%)	480 (98%)	8 (2%)	2 (0%)	30	31
1	B	490/510 (96%)	479 (98%)	9 (2%)	2 (0%)	30	31
1	C	493/510 (97%)	482 (98%)	9 (2%)	2 (0%)	30	31
All	All	1473/1530 (96%)	1441 (98%)	26 (2%)	6 (0%)	30	31

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	ILE
1	A	198	GLY
1	B	57	ILE
1	C	57	ILE
1	C	198	GLY

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	437/450 (97%)	433 (99%)	4 (1%)	75	82
1	B	437/450 (97%)	433 (99%)	4 (1%)	75	82
1	C	439/450 (98%)	433 (99%)	6 (1%)	62	71
All	All	1313/1350 (97%)	1299 (99%)	14 (1%)	70	77

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	492	ARG
1	C	75	LEU
1	C	492	ARG
1	C	332	PHE
1	C	335	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	165	HIS
1	C	133	ASN
1	C	161	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 ⓘ

28 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	D	1	2,1	14,14,15	0.47	0	17,19,21	1.58	2 (11%)
2	NAG	D	2	2	14,14,15	0.55	0	17,19,21	0.92	0
2	BMA	D	3	2	11,11,12	0.62	0	15,15,17	0.84	1 (6%)
2	MAN	D	4	2	11,11,12	0.52	0	15,15,17	0.70	0
3	NAG	E	1	3,1	14,14,15	0.55	0	17,19,21	0.91	0
3	NAG	E	2	3	14,14,15	0.47	0	17,19,21	0.75	0
3	BMA	E	3	3	11,11,12	0.58	0	15,15,17	1.12	1 (6%)
3	MAN	E	4	3	11,11,12	0.60	0	15,15,17	0.94	1 (6%)
3	MAN	E	5	3	11,11,12	0.52	0	15,15,17	1.06	1 (6%)
3	FUC	E	6	3	10,10,11	0.84	0	14,14,16	0.69	0
3	FUL	E	7	3	10,10,11	1.09	1 (10%)	14,14,16	1.07	1 (7%)
4	NAG	F	1	4,1	14,14,15	0.44	0	17,19,21	1.21	2 (11%)
4	NAG	F	2	4	14,14,15	0.50	0	17,19,21	1.89	3 (17%)
3	NAG	G	1	3,1	14,14,15	0.53	0	17,19,21	1.27	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	2	3	14,14,15	0.52	0	17,19,21	0.92	1 (5%)
3	BMA	G	3	3	11,11,12	0.62	0	15,15,17	0.92	0
3	MAN	G	4	3	11,11,12	0.47	0	15,15,17	2.11	2 (13%)
3	MAN	G	5	3	11,11,12	0.56	0	15,15,17	1.68	3 (20%)
3	FUC	G	6	3	10,10,11	0.90	0	14,14,16	0.61	0
3	FUL	G	7	3	10,10,11	1.09	1 (10%)	14,14,16	1.14	1 (7%)
4	NAG	H	1	4,1	14,14,15	0.52	0	17,19,21	0.98	0
4	NAG	H	2	4	14,14,15	0.43	0	17,19,21	2.35	4 (23%)
5	NAG	I	1	5,1	14,14,15	0.40	0	17,19,21	1.20	3 (17%)
5	FUC	I	2	5	10,10,11	1.21	2 (20%)	14,14,16	1.29	2 (14%)
5	NAG	I	3	5	14,14,15	0.56	0	17,19,21	1.23	2 (11%)
5	FUL	I	4	5	10,10,11	1.06	0	14,14,16	0.88	0
4	NAG	J	1	4,1	14,14,15	0.46	0	17,19,21	0.96	1 (5%)
4	NAG	J	2	4	14,14,15	0.55	0	17,19,21	0.91	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
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	1/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	2/2/19/22	1/1/1/1
3	MAN	E	5	3	-	2/2/19/22	0/1/1/1
3	FUC	E	6	3	-	-	0/1/1/1
3	FUL	E	7	3	-	-	0/1/1/1
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
3	NAG	G	1	3,1	-	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
3	MAN	G	4	3	-	0/2/19/22	0/1/1/1
3	MAN	G	5	3	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FUC	G	6	3	-	-	0/1/1/1
3	FUL	G	7	3	-	-	0/1/1/1
4	NAG	H	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
5	NAG	I	1	5,1	-	4/6/23/26	0/1/1/1
5	FUC	I	2	5	-	-	0/1/1/1
5	NAG	I	3	5	-	2/6/23/26	0/1/1/1
5	FUL	I	4	5	-	-	0/1/1/1
4	NAG	J	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	J	2	4	-	3/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	2	FUC	O5-C5	2.23	1.48	1.43
3	E	7	FUL	C4-C5	2.21	1.57	1.52
5	I	2	FUC	C4-C5	2.19	1.57	1.52
3	G	7	FUL	O5-C1	-2.16	1.40	1.43

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	4	MAN	C1-O5-C5	7.39	122.09	112.19
4	H	2	NAG	C1-O5-C5	7.26	121.91	112.19
4	F	2	NAG	C1-O5-C5	5.39	119.41	112.19
2	D	1	NAG	C1-O5-C5	5.00	118.88	112.19
3	G	5	MAN	C1-O5-C5	4.52	118.25	112.19

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	I	3	NAG	C8-C7-N2-C2
5	I	3	NAG	O7-C7-N2-C2
4	F	2	NAG	O5-C5-C6-O6
4	H	2	NAG	O5-C5-C6-O6
4	J	1	NAG	O5-C5-C6-O6

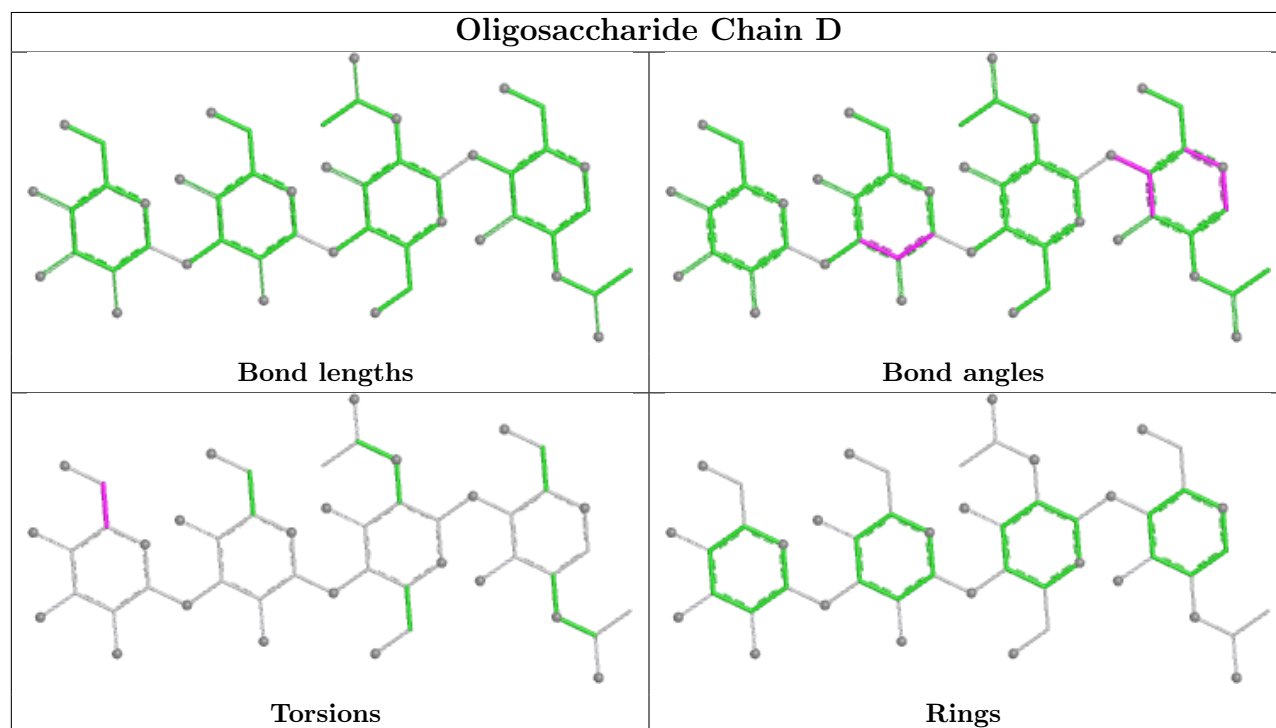
All (1) ring outliers are listed below:

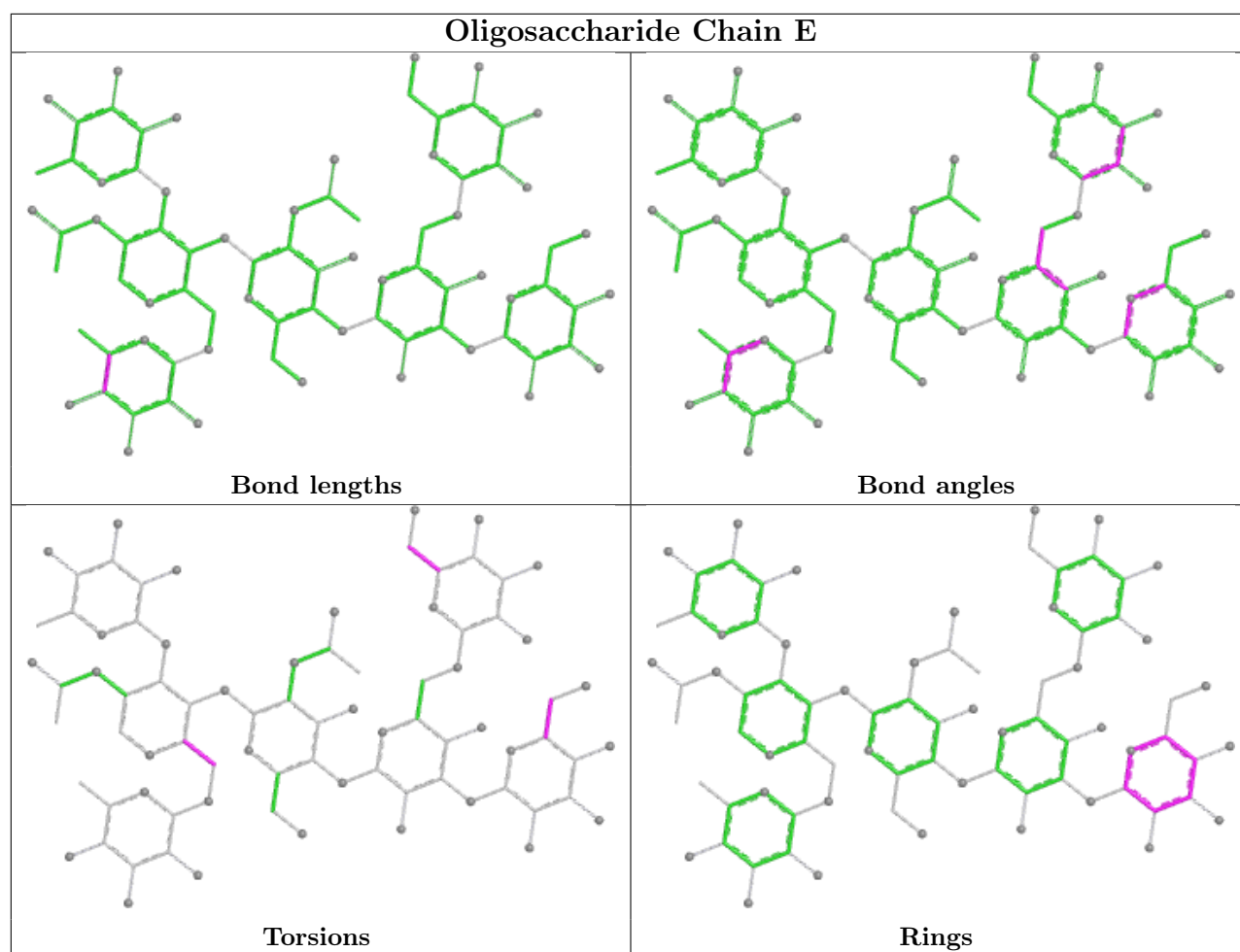
Mol	Chain	Res	Type	Atoms
3	E	4	MAN	C1-C2-C3-C4-C5-O5

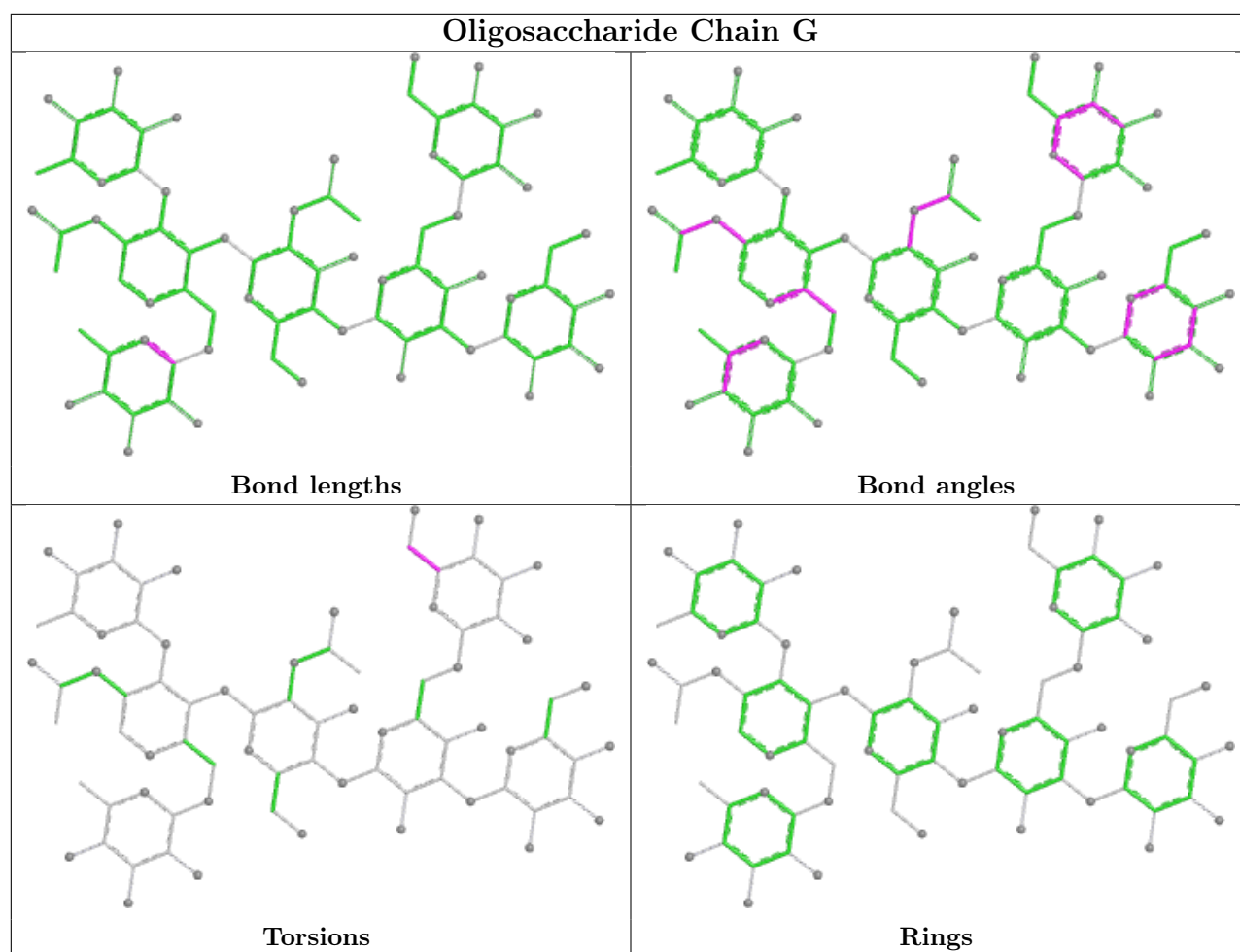
9 monomers are involved in 9 short contacts:

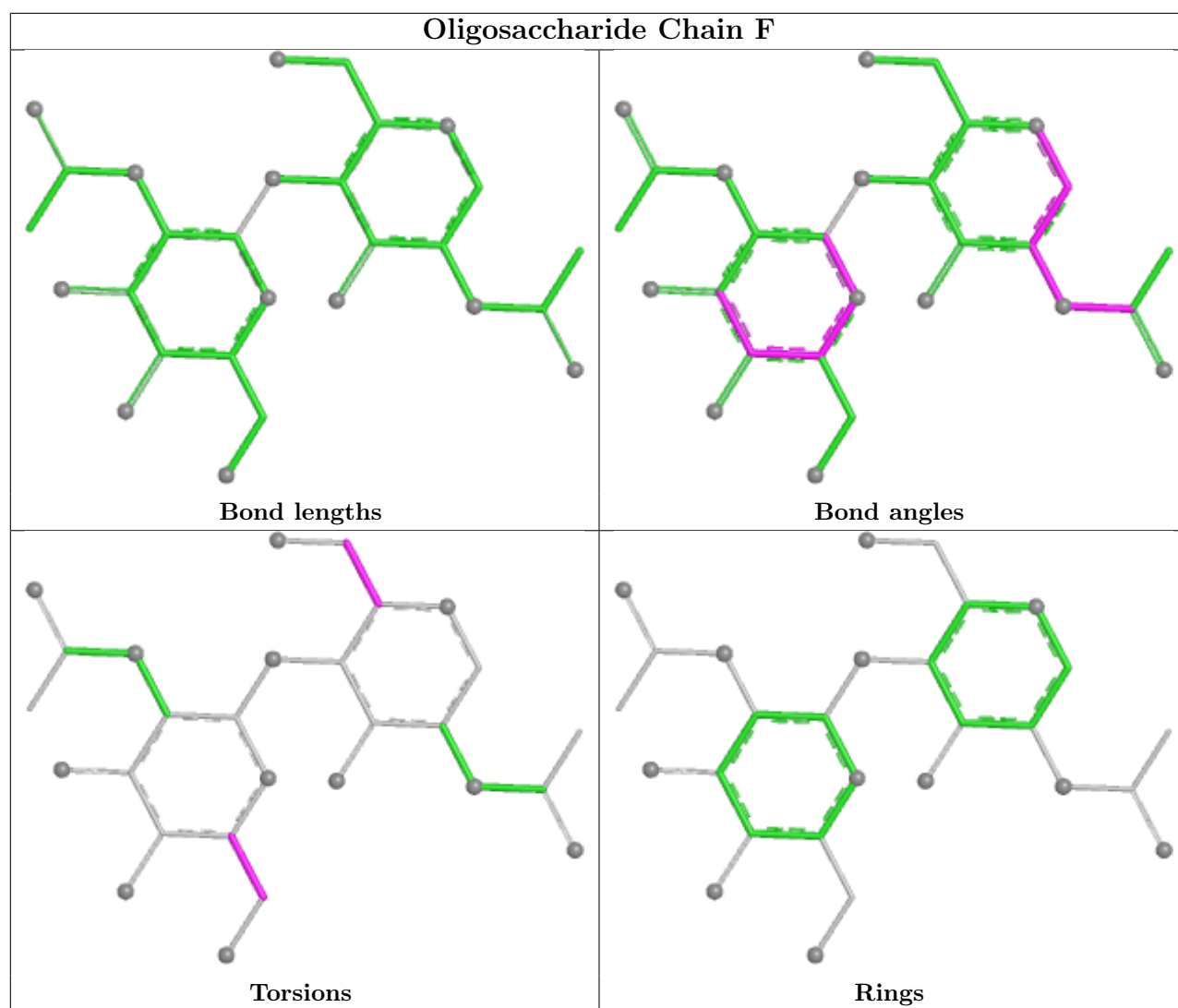
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	2	NAG	2	0
3	E	3	BMA	1	0
4	J	1	NAG	1	0
5	I	3	NAG	1	0
5	I	2	FUC	1	0
3	G	1	NAG	0	1
3	G	7	FUL	2	0
3	E	7	FUL	1	0
3	E	4	MAN	0	1

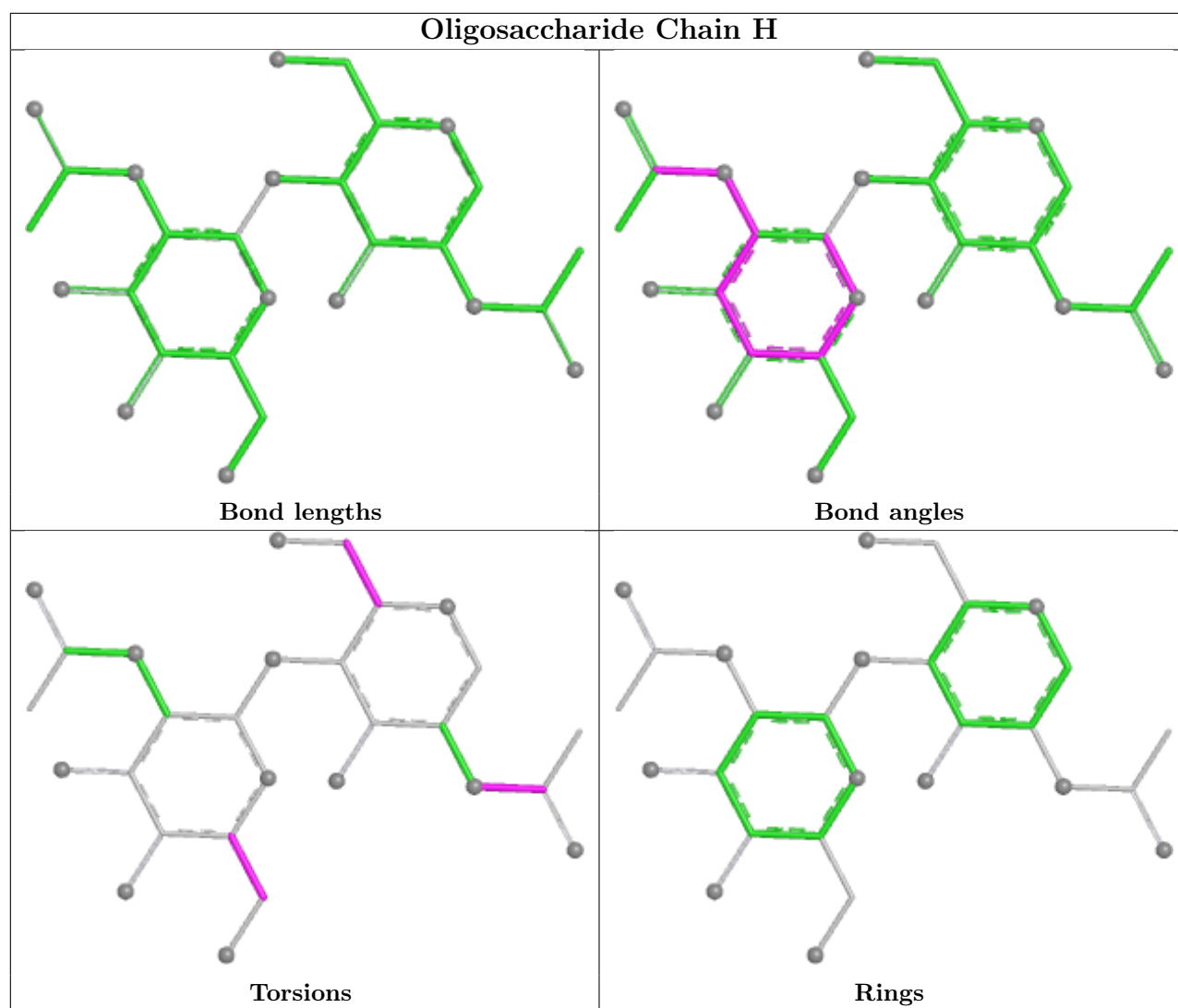
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

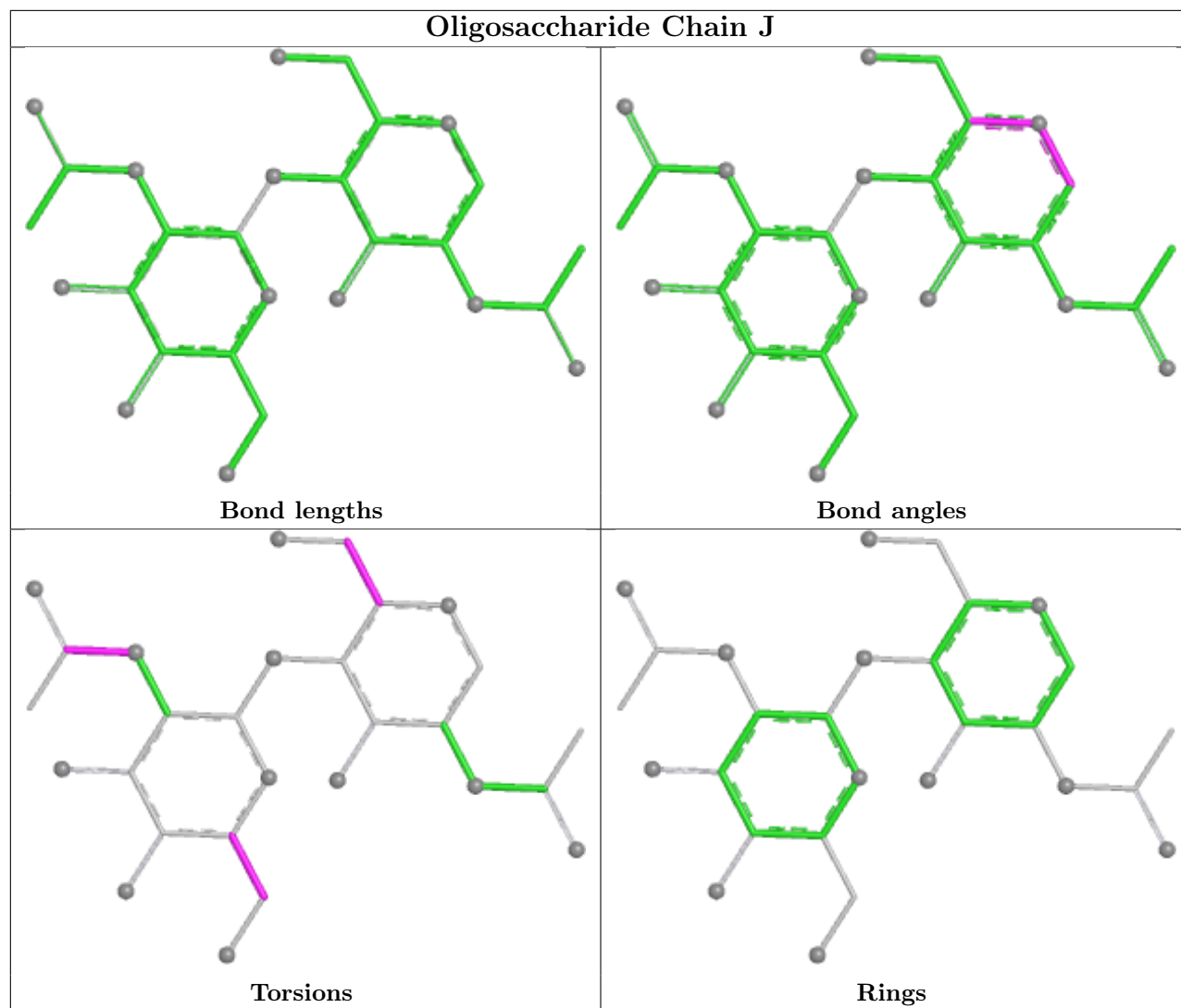


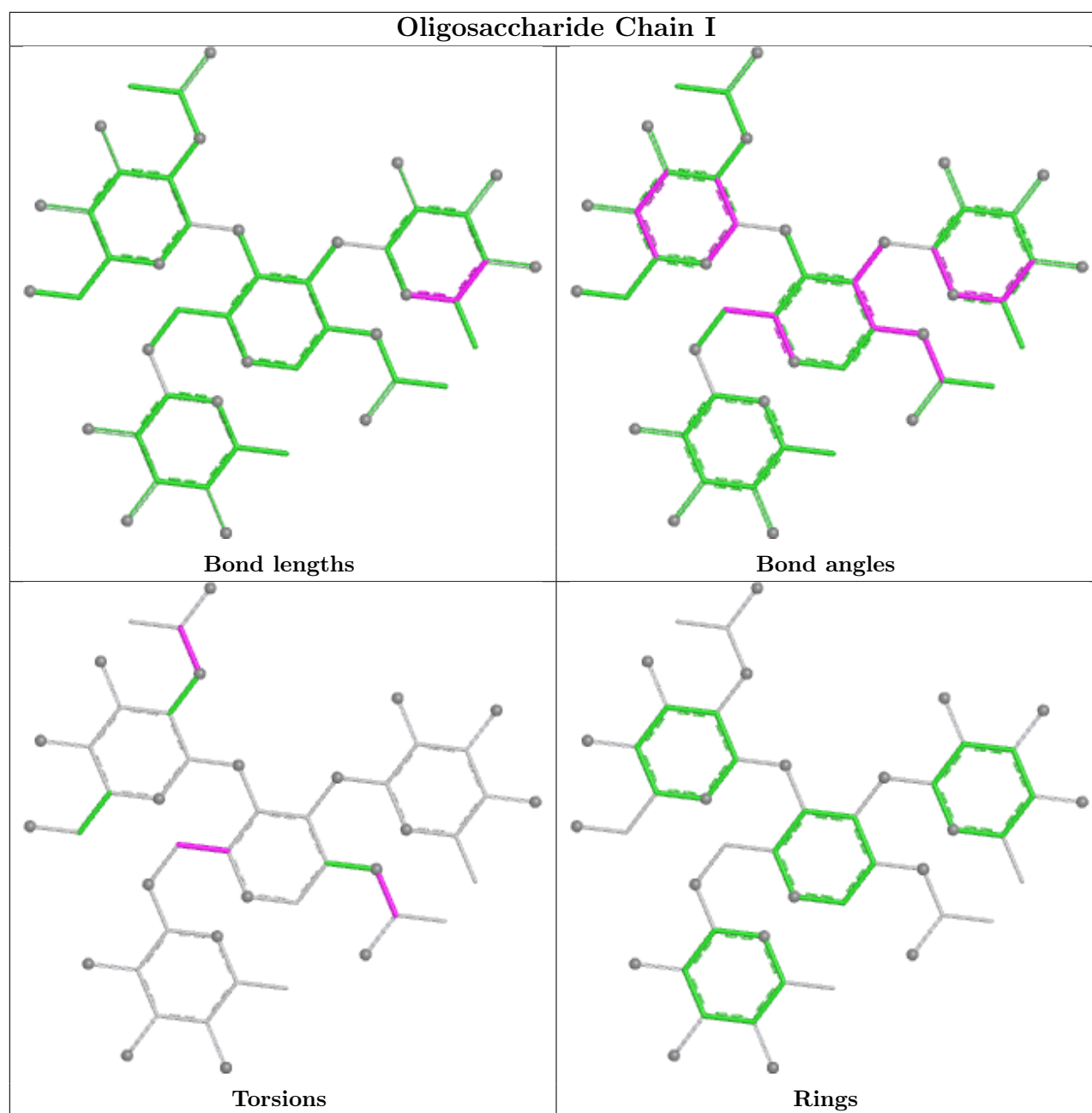












5.6 Ligand geometry [i](#)

11 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
7	NAG	A	616	1	14,14,15	0.50	0	17,19,21	0.96	1 (5%)
7	NAG	A	615	1	14,14,15	0.54	0	17,19,21	0.89	1 (5%)
7	NAG	C	601	1	14,14,15	0.38	0	17,19,21	2.11	4 (23%)
6	FUC	A	614	-	10,10,11	1.11	1 (10%)	14,14,16	1.71	3 (21%)
7	NAG	B	611	1	14,14,15	0.56	0	17,19,21	0.83	0
7	NAG	B	613	1	14,14,15	0.47	0	17,19,21	0.97	1 (5%)
7	NAG	C	609	1	14,14,15	0.57	0	17,19,21	0.72	1 (5%)
7	NAG	C	610	1	14,14,15	0.56	0	17,19,21	0.89	0
7	NAG	B	612	1	14,14,15	0.46	0	17,19,21	0.93	1 (5%)
6	FUC	B	610	-	10,10,11	1.09	1 (10%)	14,14,16	1.69	4 (28%)
6	FUC	C	608	-	10,10,11	0.98	1 (10%)	14,14,16	1.83	3 (21%)

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	A	616	1	1/1/5/7	2/6/23/26	0/1/1/1
6	FUC	B	610	-	-	-	0/1/1/1
7	NAG	A	615	1	-	2/6/23/26	0/1/1/1
7	NAG	C	601	1	-	2/6/23/26	0/1/1/1
7	NAG	B	613	1	-	2/6/23/26	0/1/1/1
7	NAG	B	611	1	-	4/6/23/26	0/1/1/1
7	NAG	C	609	1	-	2/6/23/26	0/1/1/1
6	FUC	A	614	-	-	-	0/1/1/1
7	NAG	B	612	1	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	C	610	1	1/1/5/7	4/6/23/26	0/1/1/1
6	FUC	C	608	-	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	610	FUC	O5-C5	3.24	1.50	1.43
6	A	614	FUC	O5-C5	3.14	1.49	1.43
6	C	608	FUC	O5-C5	2.87	1.49	1.43

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	601	NAG	C1-O5-C5	6.78	121.27	112.19
6	C	608	FUC	O5-C1-C2	4.51	121.54	110.79
6	A	614	FUC	O5-C1-C2	4.09	120.53	110.79
6	B	610	FUC	O5-C1-C2	4.06	120.46	110.79
7	C	601	NAG	C4-C3-C2	-3.66	105.66	111.02

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	616	NAG	C1
7	B	612	NAG	C1
7	C	610	NAG	C1

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	610	NAG	C4-C5-C6-O6
7	B	613	NAG	O5-C5-C6-O6
7	C	601	NAG	O5-C5-C6-O6
7	C	610	NAG	O5-C5-C6-O6
7	B	611	NAG	C8-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	614	FUC	2	0
7	B	611	NAG	1	0
6	B	610	FUC	1	0
6	C	608	FUC	3	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, 95th 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 ²)	Q<0.9
1	A	494/510 (96%)	-0.25	9 (1%) 67 68	23, 39, 59, 110	0
1	B	494/510 (96%)	-0.38	12 (2%) 59 60	21, 34, 56, 86	0
1	C	497/510 (97%)	-0.37	14 (2%) 55 55	22, 36, 56, 82	0
All	All	1485/1530 (97%)	-0.34	35 (2%) 59 60	21, 37, 57, 110	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	505	GLY	6.4
1	C	505	GLY	5.3
1	A	142	THR	5.2
1	B	140	TYR	5.0
1	C	140	TYR	4.9

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, 95th 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 ²)	Q<0.9
5	NAG	I	3	14/15	0.34	0.21	104,114,120,120	0
5	FUL	I	4	10/11	0.47	0.21	93,106,135,135	0
5	FUC	I	2	10/11	0.54	0.20	102,104,105,106	0

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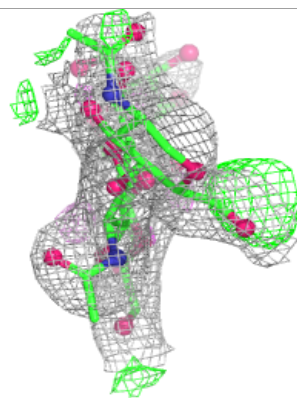
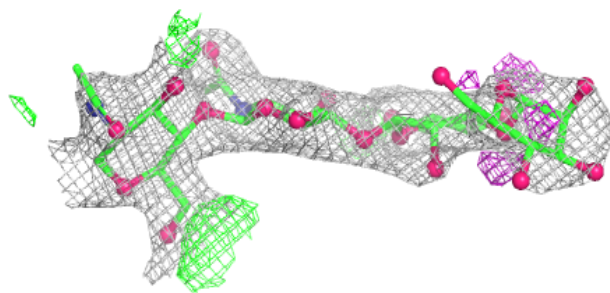
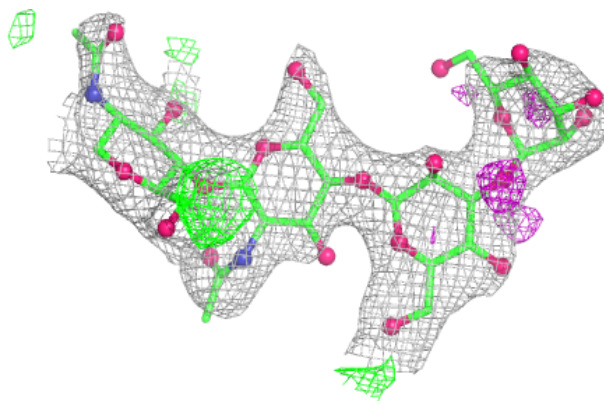
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	D	1	14/15	0.59	0.17	73,79,85,85	0
3	MAN	E	5	11/12	0.60	0.22	67,76,86,87	0
3	MAN	G	4	11/12	0.61	0.26	103,109,114,114	0
4	NAG	J	2	14/15	0.67	0.19	73,84,90,90	0
3	BMA	G	3	11/12	0.71	0.20	74,82,89,92	0
4	NAG	F	2	14/15	0.73	0.17	72,74,80,81	0
4	NAG	H	2	14/15	0.73	0.18	66,73,86,86	0
3	MAN	G	5	11/12	0.75	0.20	84,90,96,96	0
2	MAN	D	4	11/12	0.76	0.15	82,87,91,91	0
3	MAN	E	4	11/12	0.76	0.18	82,88,94,94	0
3	FUL	G	7	10/11	0.78	0.18	63,73,84,85	0
4	NAG	H	1	14/15	0.80	0.17	57,65,76,82	0
4	NAG	F	1	14/15	0.80	0.17	61,69,75,81	0
5	NAG	I	1	14/15	0.81	0.14	80,87,100,108	0
4	NAG	J	1	14/15	0.81	0.15	55,64,76,79	0
2	NAG	D	2	14/15	0.82	0.13	78,80,82,83	0
3	FUL	E	7	10/11	0.82	0.17	58,68,71,72	0
3	FUC	E	6	10/11	0.84	0.13	52,58,63,65	0
2	BMA	D	3	11/12	0.84	0.13	66,72,77,80	0
3	NAG	E	2	14/15	0.87	0.12	53,58,63,65	0
3	BMA	E	3	11/12	0.87	0.11	65,69,75,75	0
3	NAG	G	2	14/15	0.90	0.11	52,59,63,63	0
3	FUC	G	6	10/11	0.91	0.09	52,55,59,60	0
3	NAG	G	1	14/15	0.91	0.09	37,47,57,66	0
3	NAG	E	1	14/15	0.92	0.08	42,52,62,69	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.

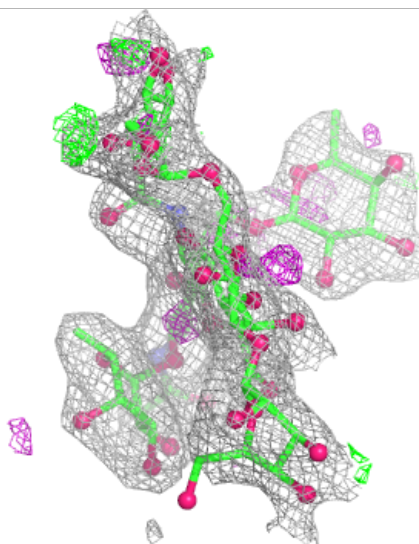
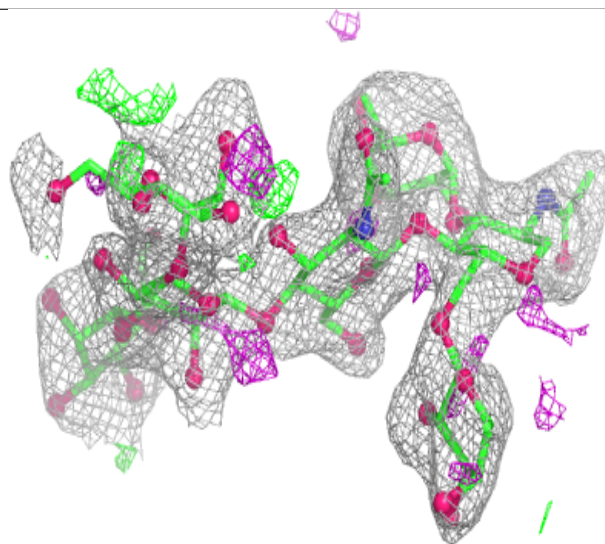
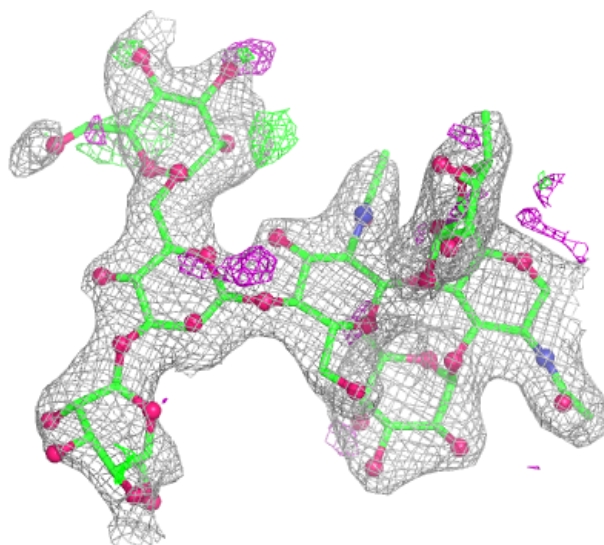
Electron density around Chain D:

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



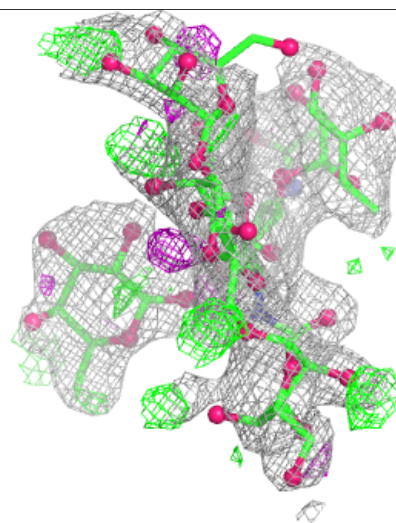
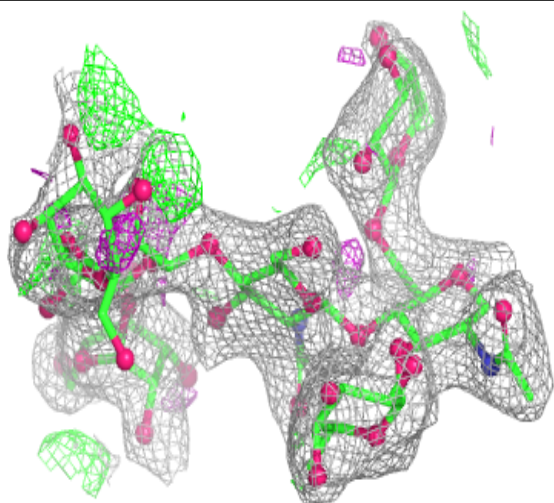
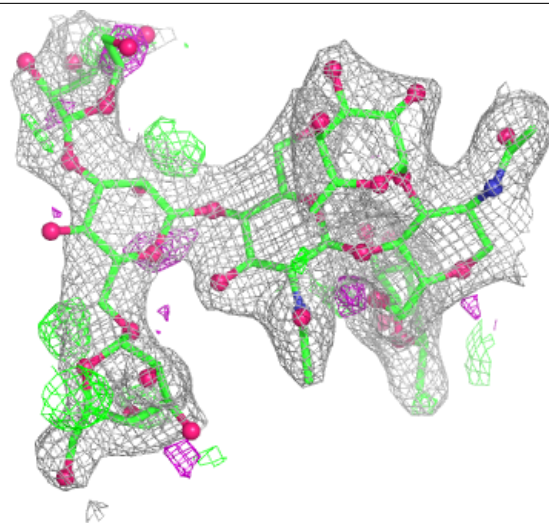
Electron density around Chain E:

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



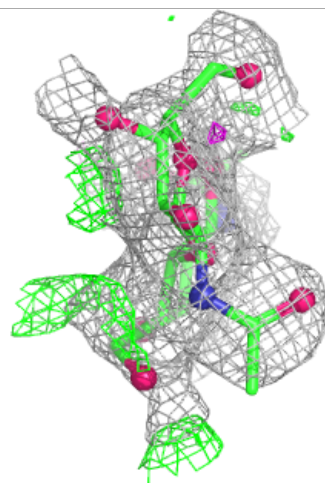
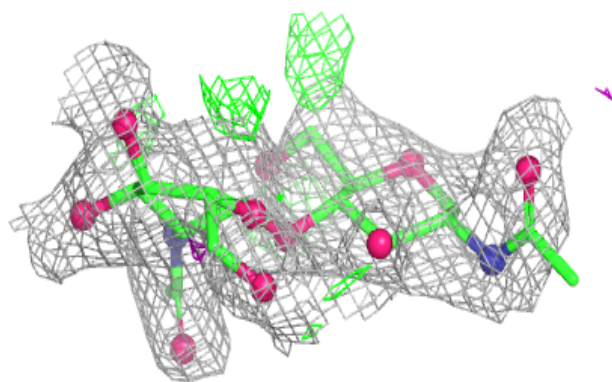
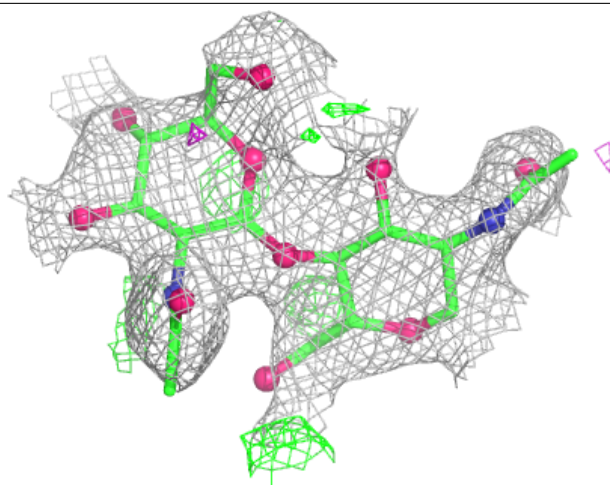
Electron density around Chain G:

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



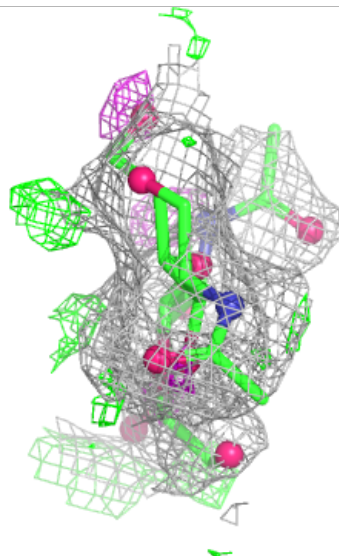
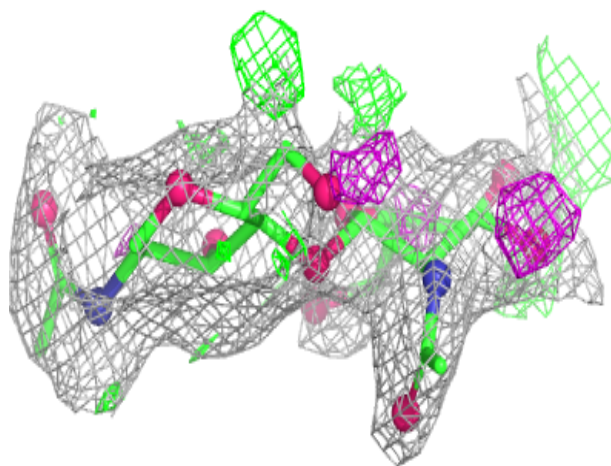
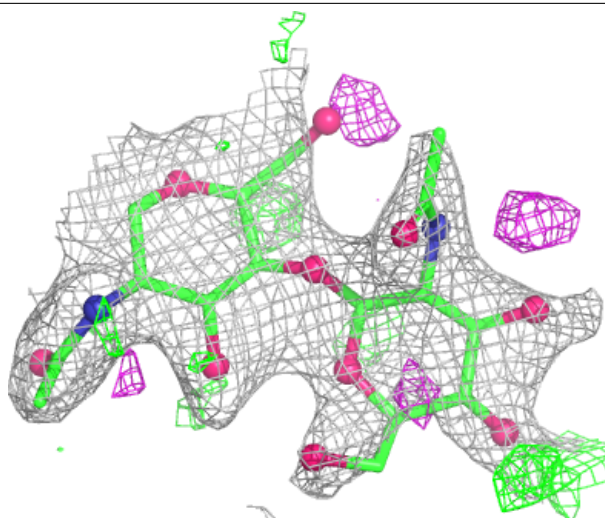
Electron density around Chain F:

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



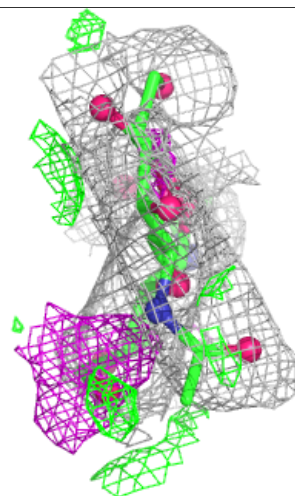
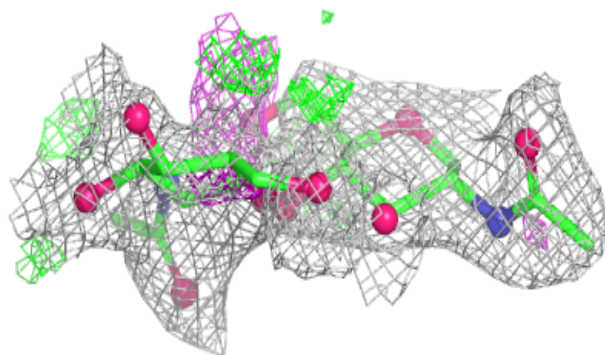
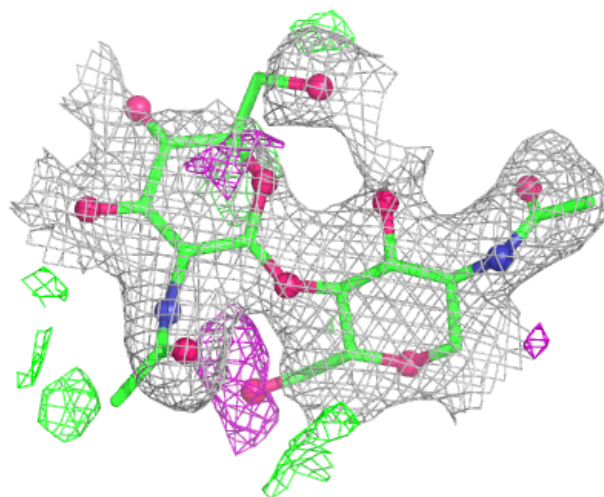
Electron density around Chain H:

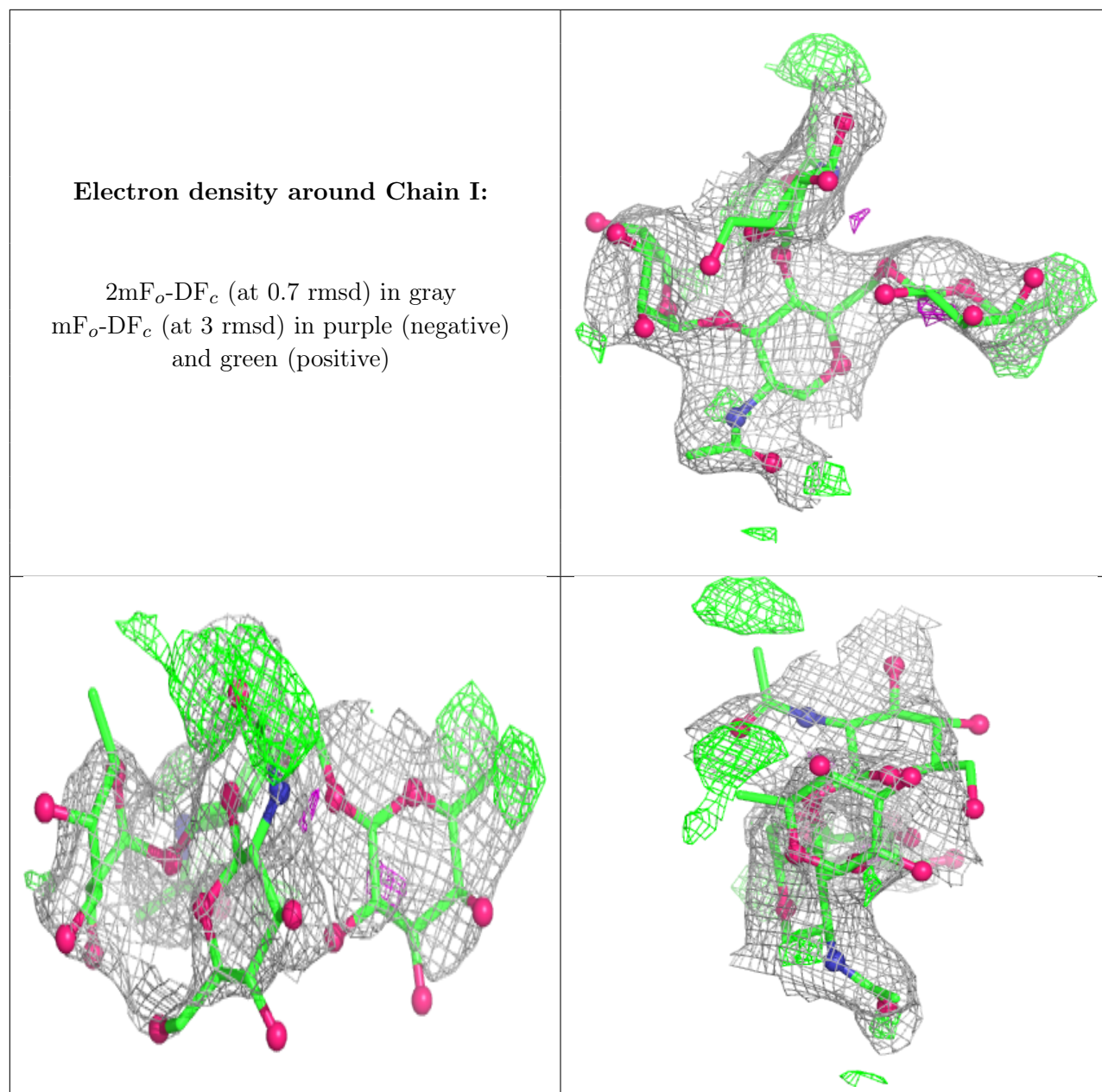
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain J:

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





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, 95th 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 ²)	Q<0.9
7	NAG	B	613	14/15	0.57	0.21	85,90,93,95	0
6	FUC	B	610	10/11	0.59	0.29	81,86,87,87	0
6	FUC	C	608	10/11	0.63	0.29	86,89,92,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	NAG	C	601	14/15	0.65	0.19	95,103,107,108	0
7	NAG	C	610	14/15	0.69	0.19	81,88,89,90	0
7	NAG	B	612	14/15	0.76	0.17	83,91,92,93	0
6	FUC	A	614	10/11	0.76	0.22	75,83,85,86	0
7	NAG	C	609	14/15	0.77	0.14	58,68,71,73	0
7	NAG	A	616	14/15	0.78	0.16	82,89,91,92	0
7	NAG	A	615	14/15	0.79	0.14	64,73,75,76	0
7	NAG	B	611	14/15	0.85	0.13	63,68,73,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.