



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:50 PM UTC

PDB ID : 6CH8 / pdb_00006ch8
Title : Crystal structure of a natively-glycosylated BG505 SOSIP.664 HIV-1 Envelope Trimer in complex with the broadly-neutralizing antibodies BG18 and 35O22
Authors : Barnes, C.O.; Bjorkman, P.J.
Deposited on : 2018-02-22
Resolution : 4.10 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

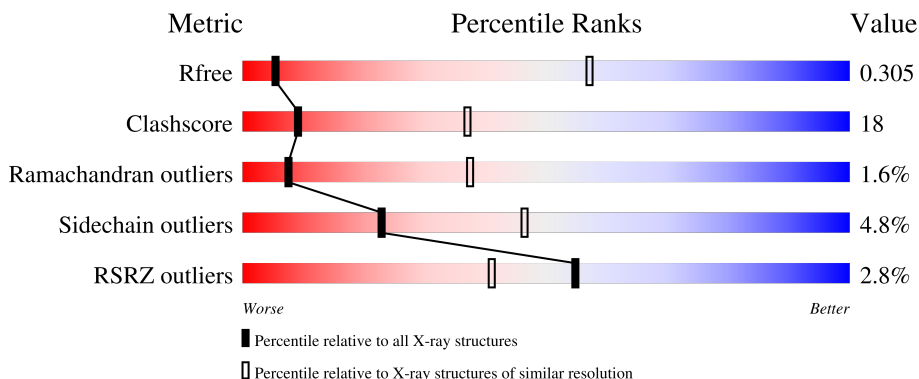
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.10 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.



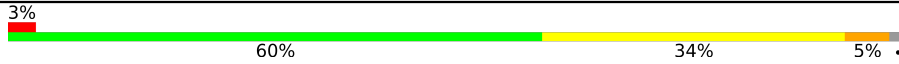

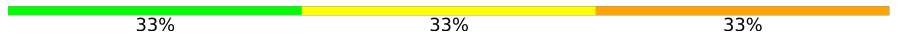


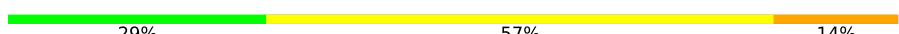
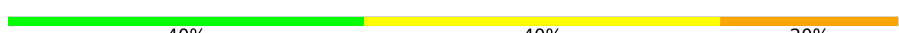







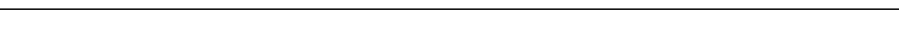
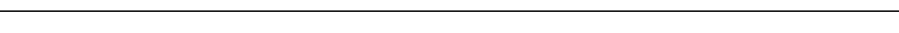
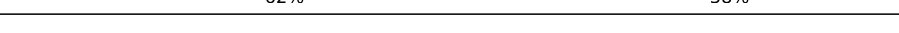
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1243 (4.40-3.80)
Clashscore	190562	1293 (4.40-3.80)
Ramachandran outliers	187476	1206 (4.40-3.80)
Sidechain outliers	187428	1193 (4.40-3.80)
RSRZ outliers	180081	1240 (4.40-3.80)

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	B	153	 3% 62% 25% 9%
2	D	243	 % 68% 26%
3	E	216	 4% 74% 23%
4	G	479	 3% 56% 33% 5% 6%
5	Q	241	 % 63% 27% 5%

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Mol	Chain	Length	Quality of chain
6	R	215	
7	A	3	
7	O	3	
8	C	5	
8	J	5	
9	F	7	
10	H	5	
10	U	5	
11	I	7	
12	K	4	
12	T	4	
13	L	4	
14	M	7	
15	N	8	
16	P	6	
17	S	8	
18	V	9	

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
17	NAG	S	1	-	-	X	-

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 12325 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 Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	139	1109	700	195	208	6	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	605	CYS	THR	engineered mutation	UNP Q2N0S7

- Molecule 2 is a protein called 35O22 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	235	1753	1110	295	340	8	0	0	0

- Molecule 3 is a protein called 35O22 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	210	1592	998	264	322	8	0	0	0

- Molecule 4 is a protein called Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	G	451	3537	2220	625	665	27	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	332	ASN	THR	conflict	UNP Q2N0S6
G	501	CYS	ALA	engineered mutation	UNP Q2N0S6

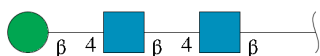
- Molecule 5 is a protein called BG18 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	Q	228	1678	1055	286	329	8	0	0	0

- Molecule 6 is a protein called BG18 Light Chain.

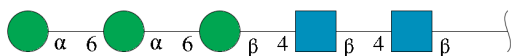
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	R	211	1514	947	253	308	6	0	0	0

- Molecule 7 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.



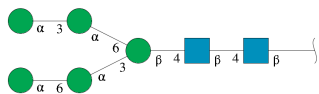
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
7	A	3	39	22	2	15	0	0	0
7	O	3	39	22	2	15	0	0	0

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



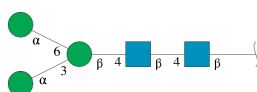
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
8	C	5	61	34	2	25	0	0	0
8	J	5	61	34	2	25	0	0	0

- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



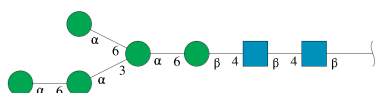
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	F	7	83	46	2	35	0	0	0

- Molecule 10 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.



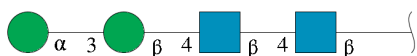
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
10	H	5	61	34	2	25	0	0	0
10	U	5	61	34	2	25	0	0	0

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
11	I	7	83	46	2	35	0	0	0

- Molecule 12 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.



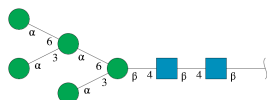
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
12	K	4	50	28	2	20	0	0	0
12	T	4	50	28	2	20	0	0	0

- Molecule 13 is an oligosaccharide called 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.



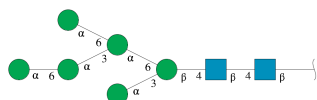
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
13	L	4	50	28	2	20	0	0	0

- Molecule 14 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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.



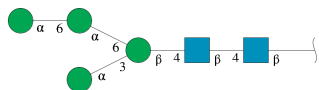
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
14	M	7	83	46	2	35	0	0	0

- Molecule 15 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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.



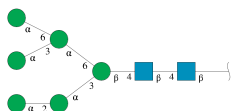
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
15	N	8	94	52	2	40	0	0	0

- Molecule 16 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[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.



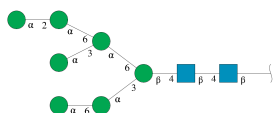
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
16	P	6	72	40	2	30	0	0	0

- Molecule 17 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
17	S	8	94	52	2	40	0	0	0

- Molecule 18 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-6)-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
			Total	C	N	O			
18	V	9	105	58	2	45	0	0	0

- Molecule 19 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

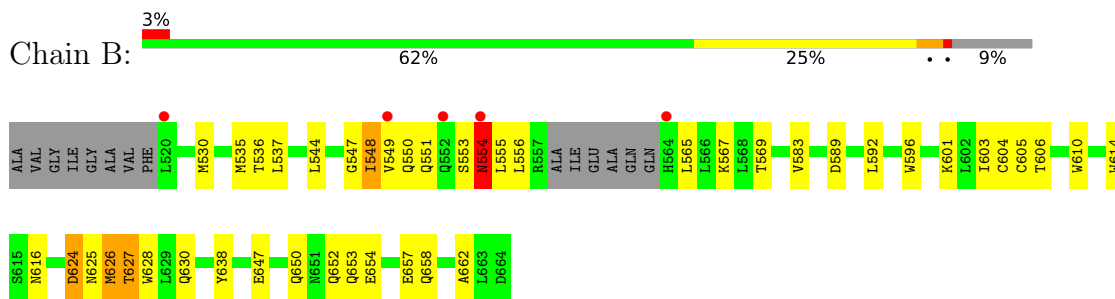


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
19	B	1	Total 14	8	1	5	0	0
19	G	1	Total 14	8	1	5	0	0
19	G	1	Total 14	8	1	5	0	0
19	G	1	Total 14	8	1	5	0	0

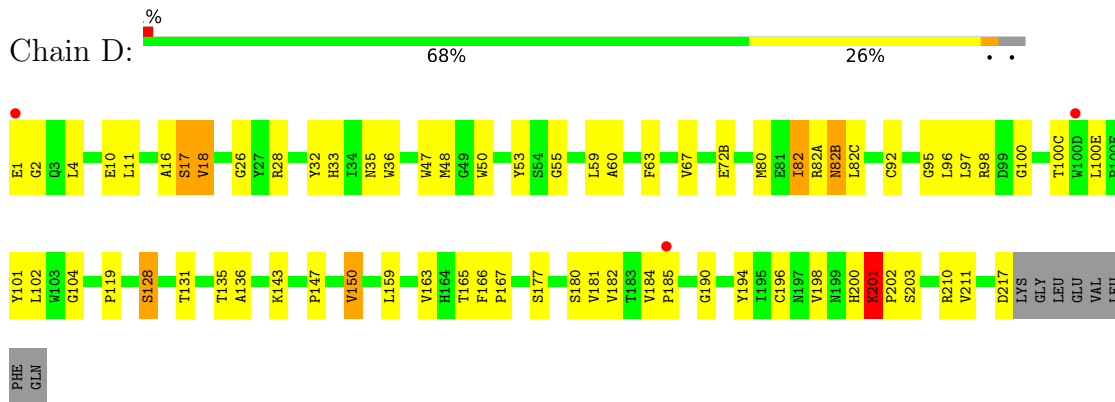
3 Residue-property plots i

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

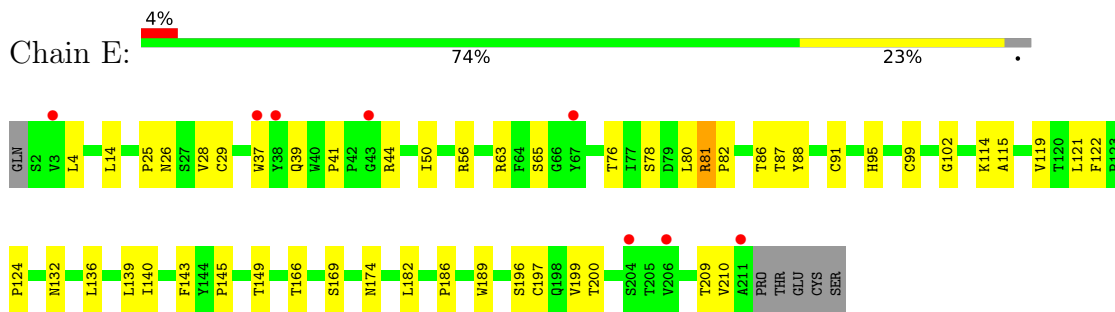
- Molecule 1: Envelope glycoprotein gp41



- Molecule 2: 35O22 Heavy Chain



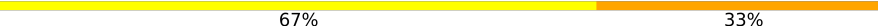
- Molecule 3: 35O22 Light Chain



- Molecule 4: Envelope glycoprotein gp120

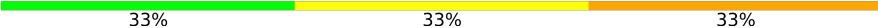


- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain A:  67% 33%



- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  33% 33% 33%



- Molecule 8: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  60% 20% 20%



- Molecule 8: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  60% 20% 20%



- Molecule 9: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  29% 57% 14%



- Molecule 10: 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 H:  40% 40% 20%



- Molecule 10: 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 U: 




- Molecule 11: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I: 



- Molecule 12: 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

Chain K: 



- Molecule 12: 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

Chain T: 

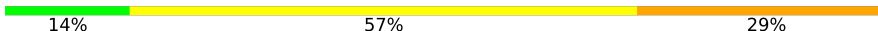


- Molecule 13: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L: 

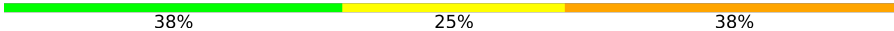


- Molecule 14: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M: 



- Molecule 15: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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

Chain N: 



- Molecule 16: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[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

Chain P: 




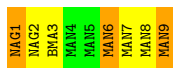
- Molecule 17: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S: 



- Molecule 18: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-6)-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

Chain V: 



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	239.22Å 239.22Å 355.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.51 – 4.10 39.51 – 4.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.51-4.10) 99.7 (39.51-4.10)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 4.13Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.229 , 0.274 0.261 , 0.305	Depositor DCC
R_{free} test set	1551 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	163.4	Xtrriage
Anisotropy	0.427	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 189.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	12325	wwPDB-VP
Average B, all atoms (Å ²)	226.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% 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: NAG, BMA, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.29	0/1127	0.75	5/1527 (0.3%)
2	D	0.20	0/1798	0.52	2/2450 (0.1%)
3	E	0.14	0/1635	0.32	0/2235
4	G	0.24	0/3610	0.76	15/4901 (0.3%)
5	Q	0.18	0/1721	0.48	0/2353
6	R	0.24	0/1552	0.62	4/2129 (0.2%)
All	All	0.22	0/11443	0.62	26/15595 (0.2%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	219	ALA	CA-C-N	19.29	139.21	120.31
4	G	219	ALA	C-N-CA	19.29	139.21	120.31
4	G	464	THR	N-CA-C	14.82	127.51	111.36
4	G	279	ASN	N-CA-C	-10.24	95.27	109.71
2	D	203	SER	N-CA-C	10.19	124.79	111.75

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	B	1109	0	1103	47	1
2	D	1753	0	1713	66	0
3	E	1592	0	1530	35	0
4	G	3537	0	3469	166	0
5	Q	1678	0	1590	58	0
6	R	1514	0	1411	83	0
7	A	39	0	34	2	0
7	O	39	0	34	2	0
8	C	61	0	52	1	0
8	J	61	0	52	1	0
9	F	83	0	70	3	0
10	H	61	0	52	2	0
10	U	61	0	52	3	0
11	I	83	0	70	5	0
12	K	50	0	43	3	0
12	T	50	0	43	0	0
13	L	50	0	43	0	0
14	M	83	0	69	3	0
15	N	94	0	79	3	0
16	P	72	0	61	0	0
17	S	94	0	79	15	0
18	V	105	0	87	4	0
19	B	14	0	13	0	0
19	G	42	0	39	0	0
All	All	12325	0	11788	442	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 18.

The worst 5 of 442 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:G:386:ASN:HD21	17:S:1:NAG:C2	1.24	1.48
4:G:386:ASN:ND2	17:S:1:NAG:C1	1.75	1.45
1:B:626:MET:O	1:B:627:THR:CG2	1.79	1.30
1:B:624:ASP:O	2:D:98:ARG:HG3	1.35	1.22
4:G:386:ASN:ND2	17:S:1:NAG:N2	1.86	1.21

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:B:535:MET:O	1:B:652:GLN:NE2[2_545]	2.11	0.09

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	B	135/153 (88%)	124 (92%)	10 (7%)	1 (1%)	18	55
2	D	233/243 (96%)	205 (88%)	25 (11%)	3 (1%)	9	41
3	E	208/216 (96%)	185 (89%)	23 (11%)	0	100	100
4	G	443/479 (92%)	386 (87%)	54 (12%)	3 (1%)	18	55
5	Q	226/241 (94%)	184 (81%)	35 (16%)	7 (3%)	3	25
6	R	209/215 (97%)	143 (68%)	57 (27%)	9 (4%)	2	20
All	All	1454/1547 (94%)	1227 (84%)	204 (14%)	23 (2%)	7	37

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	554	ASN
2	D	201	LYS
5	Q	50	GLY
6	R	62	ARG
6	R	212	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	B	121/129 (94%)	114 (94%)	7 (6%)	18	42
2	D	194/206 (94%)	185 (95%)	9 (5%)	24	47
3	E	183/189 (97%)	181 (99%)	2 (1%)	65	74
4	G	400/426 (94%)	374 (94%)	26 (6%)	15	40
5	Q	181/208 (87%)	172 (95%)	9 (5%)	22	45
6	R	161/182 (88%)	154 (96%)	7 (4%)	26	49
All	All	1240/1340 (92%)	1180 (95%)	60 (5%)	23	46

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	G	274	SER
6	R	82	ASP
4	G	322	ILE
6	R	54	GLN
6	R	171	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
5	Q	99	ASN
5	Q	114	HIS
6	R	39	GLN
4	G	386	ASN
4	G	422	GLN

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](#)

90 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	$\# Z > 2$
7	NAG	A	1	1,7	14,14,15	0.27	0	17,19,21	1.38	1 (5%)
7	NAG	A	2	7	14,14,15	0.35	0	17,19,21	0.68	0
7	BMA	A	3	7	11,11,12	0.24	0	15,15,17	0.79	0
8	NAG	C	1	1,8	14,14,15	0.29	0	17,19,21	0.83	0
8	NAG	C	2	8	14,14,15	0.32	0	17,19,21	1.15	2 (11%)
8	BMA	C	3	8	11,11,12	0.44	0	15,15,17	0.94	0
8	MAN	C	4	8	11,11,12	0.35	0	15,15,17	0.99	0
8	MAN	C	5	8	11,11,12	0.22	0	15,15,17	0.61	0
9	NAG	F	1	9,4	14,14,15	0.29	0	17,19,21	1.92	6 (35%)
9	NAG	F	2	9	14,14,15	0.26	0	17,19,21	1.65	2 (11%)
9	BMA	F	3	9	11,11,12	0.37	0	15,15,17	1.15	0
9	MAN	F	4	9	11,11,12	0.31	0	15,15,17	0.91	1 (6%)
9	MAN	F	5	9	11,11,12	0.25	0	15,15,17	0.71	0
9	MAN	F	6	9	11,11,12	0.45	0	15,15,17	0.88	0
9	MAN	F	7	9	11,11,12	0.26	0	15,15,17	0.73	0
10	NAG	H	1	10,4	14,14,15	0.28	0	17,19,21	0.90	0
10	NAG	H	2	10	14,14,15	0.31	0	17,19,21	0.59	0
10	BMA	H	3	10	11,11,12	0.31	0	15,15,17	0.82	0
10	MAN	H	4	10	11,11,12	0.94	1 (9%)	15,15,17	1.79	3 (20%)
10	MAN	H	5	10	11,11,12	0.25	0	15,15,17	0.62	0
11	NAG	I	1	11,4	14,14,15	0.28	0	17,19,21	0.92	1 (5%)
11	NAG	I	2	11	14,14,15	0.30	0	17,19,21	0.67	0
11	BMA	I	3	11	11,11,12	0.32	0	15,15,17	0.82	1 (6%)
11	MAN	I	4	11	11,11,12	0.79	0	15,15,17	2.12	4 (26%)
11	MAN	I	5	11	11,11,12	0.49	0	15,15,17	1.09	2 (13%)
11	MAN	I	6	11	11,11,12	0.30	0	15,15,17	0.75	0
11	MAN	I	7	11	11,11,12	0.43	0	15,15,17	0.94	0
8	NAG	J	1	8,4	14,14,15	0.69	0	17,19,21	0.86	1 (5%)
8	NAG	J	2	8	14,14,15	0.42	0	17,19,21	1.06	1 (5%)
8	BMA	J	3	8	11,11,12	0.30	0	15,15,17	0.82	0
8	MAN	J	4	8	11,11,12	0.25	0	15,15,17	0.58	0
8	MAN	J	5	8	11,11,12	0.26	0	15,15,17	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	NAG	K	1	12,4	14,14,15	0.47	0	17,19,21	2.25	6 (35%)
12	NAG	K	2	12	14,14,15	0.37	0	17,19,21	0.92	1 (5%)
12	BMA	K	3	12	11,11,12	0.31	0	15,15,17	1.06	0
12	MAN	K	4	12	11,11,12	0.26	0	15,15,17	0.82	1 (6%)
13	NAG	L	1	13,4	14,14,15	0.28	0	17,19,21	0.92	0
13	NAG	L	2	13	14,14,15	0.39	0	17,19,21	1.06	1 (5%)
13	BMA	L	3	13	11,11,12	0.30	0	15,15,17	0.71	0
13	MAN	L	4	13	11,11,12	0.26	0	15,15,17	0.56	0
14	NAG	M	1	14,4	14,14,15	0.31	0	17,19,21	0.90	1 (5%)
14	NAG	M	2	14	14,14,15	0.42	0	17,19,21	0.87	1 (5%)
14	BMA	M	3	14	11,11,12	0.73	0	15,15,17	1.28	2 (13%)
14	MAN	M	4	14	11,11,12	0.36	0	15,15,17	1.82	4 (26%)
14	MAN	M	5	14	11,11,12	0.45	0	15,15,17	1.19	2 (13%)
14	MAN	M	6	14	11,11,12	0.26	0	15,15,17	0.66	0
14	MAN	M	7	14	11,11,12	0.56	0	15,15,17	1.07	2 (13%)
15	NAG	N	1	15	14,14,15	0.94	1 (7%)	17,19,21	3.14	5 (29%)
15	NAG	N	2	15	14,14,15	0.28	0	17,19,21	0.81	1 (5%)
15	BMA	N	3	15	11,11,12	0.31	0	15,15,17	1.37	1 (6%)
15	MAN	N	4	15	11,11,12	0.28	0	15,15,17	0.70	0
15	MAN	N	5	15	11,11,12	0.26	0	15,15,17	0.78	0
15	MAN	N	6	15	11,11,12	0.23	0	15,15,17	0.71	0
15	MAN	N	7	15	11,11,12	0.25	0	15,15,17	0.64	0
15	MAN	N	8	15	11,11,12	0.56	0	15,15,17	1.23	2 (13%)
7	NAG	O	1	7,4	14,14,15	0.31	0	17,19,21	2.31	4 (23%)
7	NAG	O	2	7	14,14,15	0.29	0	17,19,21	0.96	1 (5%)
7	BMA	O	3	7	11,11,12	0.22	0	15,15,17	0.65	0
16	NAG	P	1	16,4	14,14,15	0.26	0	17,19,21	1.12	1 (5%)
16	NAG	P	2	16	14,14,15	0.44	0	17,19,21	1.41	2 (11%)
16	BMA	P	3	16	11,11,12	0.50	0	15,15,17	1.07	1 (6%)
16	MAN	P	4	16	11,11,12	0.31	0	15,15,17	0.62	0
16	MAN	P	5	16	11,11,12	0.27	0	15,15,17	0.73	0
16	MAN	P	6	16	11,11,12	0.27	0	15,15,17	0.70	0
17	NAG	S	1	17	14,14,15	0.27	0	17,19,21	1.54	3 (17%)
17	NAG	S	2	17	14,14,15	0.51	0	17,19,21	1.27	1 (5%)
17	BMA	S	3	17	11,11,12	0.51	0	15,15,17	1.07	1 (6%)
17	MAN	S	4	17	11,11,12	0.34	0	15,15,17	0.64	0
17	MAN	S	5	17	11,11,12	0.24	0	15,15,17	0.60	0
17	MAN	S	6	17	11,11,12	0.30	0	15,15,17	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	MAN	S	7	17	11,11,12	0.26	0	15,15,17	0.66	0
17	MAN	S	8	17	11,11,12	0.24	0	15,15,17	0.64	0
12	NAG	T	1	12,4	14,14,15	0.33	0	17,19,21	0.71	0
12	NAG	T	2	12	14,14,15	0.35	0	17,19,21	0.93	1 (5%)
12	BMA	T	3	12	11,11,12	0.25	0	15,15,17	0.78	0
12	MAN	T	4	12	11,11,12	0.32	0	15,15,17	0.84	0
10	NAG	U	1	10,4	14,14,15	0.27	0	17,19,21	1.08	2 (11%)
10	NAG	U	2	10	14,14,15	0.42	0	17,19,21	1.92	4 (23%)
10	BMA	U	3	10	11,11,12	0.46	0	15,15,17	1.83	4 (26%)
10	MAN	U	4	10	11,11,12	1.04	1 (9%)	15,15,17	1.74	3 (20%)
10	MAN	U	5	10	11,11,12	0.90	1 (9%)	15,15,17	1.87	3 (20%)
18	NAG	V	1	18,4	14,14,15	0.28	0	17,19,21	0.96	1 (5%)
18	NAG	V	2	18	14,14,15	0.30	0	17,19,21	0.61	0
18	BMA	V	3	18	11,11,12	0.29	0	15,15,17	1.12	1 (6%)
18	MAN	V	4	18	11,11,12	0.25	0	15,15,17	0.93	0
18	MAN	V	5	18	11,11,12	0.23	0	15,15,17	0.87	0
18	MAN	V	6	18	11,11,12	0.23	0	15,15,17	0.84	1 (6%)
18	MAN	V	7	18	11,11,12	0.54	0	15,15,17	1.16	1 (6%)
18	MAN	V	8	18	11,11,12	0.50	0	15,15,17	1.04	1 (6%)
18	MAN	V	9	18	11,11,12	0.57	0	15,15,17	1.17	2 (13%)

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	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	A	2	7	-	3/6/23/26	0/1/1/1
7	BMA	A	3	7	-	1/2/19/22	0/1/1/1
8	NAG	C	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	C	2	8	-	5/6/23/26	0/1/1/1
8	BMA	C	3	8	-	0/2/19/22	0/1/1/1
8	MAN	C	4	8	-	2/2/19/22	0/1/1/1
8	MAN	C	5	8	-	1/2/19/22	0/1/1/1
9	NAG	F	1	9,4	-	3/6/23/26	0/1/1/1
9	NAG	F	2	9	-	4/6/23/26	0/1/1/1
9	BMA	F	3	9	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	MAN	F	4	9	-	2/2/19/22	0/1/1/1
9	MAN	F	5	9	-	0/2/19/22	0/1/1/1
9	MAN	F	6	9	-	1/2/19/22	0/1/1/1
9	MAN	F	7	9	-	0/2/19/22	0/1/1/1
10	NAG	H	1	10,4	-	0/6/23/26	0/1/1/1
10	NAG	H	2	10	-	5/6/23/26	0/1/1/1
10	BMA	H	3	10	-	0/2/19/22	0/1/1/1
10	MAN	H	4	10	-	0/2/19/22	0/1/1/1
10	MAN	H	5	10	-	0/2/19/22	0/1/1/1
11	NAG	I	1	11,4	-	4/6/23/26	0/1/1/1
11	NAG	I	2	11	-	3/6/23/26	0/1/1/1
11	BMA	I	3	11	-	0/2/19/22	0/1/1/1
11	MAN	I	4	11	-	2/2/19/22	0/1/1/1
11	MAN	I	5	11	-	1/2/19/22	0/1/1/1
11	MAN	I	6	11	-	0/2/19/22	0/1/1/1
11	MAN	I	7	11	-	1/2/19/22	0/1/1/1
8	NAG	J	1	8,4	-	3/6/23/26	0/1/1/1
8	NAG	J	2	8	-	4/6/23/26	0/1/1/1
8	BMA	J	3	8	-	2/2/19/22	0/1/1/1
8	MAN	J	4	8	-	0/2/19/22	0/1/1/1
8	MAN	J	5	8	-	1/2/19/22	0/1/1/1
12	NAG	K	1	12,4	-	2/6/23/26	0/1/1/1
12	NAG	K	2	12	-	3/6/23/26	0/1/1/1
12	BMA	K	3	12	-	0/2/19/22	0/1/1/1
12	MAN	K	4	12	-	1/2/19/22	0/1/1/1
13	NAG	L	1	13,4	-	2/6/23/26	0/1/1/1
13	NAG	L	2	13	-	3/6/23/26	0/1/1/1
13	BMA	L	3	13	-	2/2/19/22	0/1/1/1
13	MAN	L	4	13	-	0/2/19/22	0/1/1/1
14	NAG	M	1	14,4	-	3/6/23/26	0/1/1/1
14	NAG	M	2	14	-	3/6/23/26	0/1/1/1
14	BMA	M	3	14	-	0/2/19/22	0/1/1/1
14	MAN	M	4	14	-	1/2/19/22	0/1/1/1
14	MAN	M	5	14	-	0/2/19/22	0/1/1/1
14	MAN	M	6	14	-	0/2/19/22	0/1/1/1
14	MAN	M	7	14	-	2/2/19/22	0/1/1/1
15	NAG	N	1	15	-	5/6/23/26	0/1/1/1
15	NAG	N	2	15	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BMA	N	3	15	-	2/2/19/22	0/1/1/1
15	MAN	N	4	15	-	2/2/19/22	0/1/1/1
15	MAN	N	5	15	-	2/2/19/22	0/1/1/1
15	MAN	N	6	15	-	0/2/19/22	0/1/1/1
15	MAN	N	7	15	-	2/2/19/22	0/1/1/1
15	MAN	N	8	15	-	0/2/19/22	0/1/1/1
7	NAG	O	1	7,4	-	2/6/23/26	0/1/1/1
7	NAG	O	2	7	-	3/6/23/26	0/1/1/1
7	BMA	O	3	7	-	0/2/19/22	0/1/1/1
16	NAG	P	1	16,4	-	2/6/23/26	0/1/1/1
16	NAG	P	2	16	-	1/6/23/26	0/1/1/1
16	BMA	P	3	16	-	1/2/19/22	0/1/1/1
16	MAN	P	4	16	-	2/2/19/22	0/1/1/1
16	MAN	P	5	16	-	0/2/19/22	0/1/1/1
16	MAN	P	6	16	-	0/2/19/22	0/1/1/1
17	NAG	S	1	17	-	5/6/23/26	0/1/1/1
17	NAG	S	2	17	-	4/6/23/26	0/1/1/1
17	BMA	S	3	17	-	2/2/19/22	0/1/1/1
17	MAN	S	4	17	-	1/2/19/22	0/1/1/1
17	MAN	S	5	17	-	1/2/19/22	0/1/1/1
17	MAN	S	6	17	-	2/2/19/22	0/1/1/1
17	MAN	S	7	17	-	1/2/19/22	0/1/1/1
17	MAN	S	8	17	-	1/2/19/22	0/1/1/1
12	NAG	T	1	12,4	-	2/6/23/26	0/1/1/1
12	NAG	T	2	12	-	2/6/23/26	0/1/1/1
12	BMA	T	3	12	-	0/2/19/22	0/1/1/1
12	MAN	T	4	12	-	0/2/19/22	0/1/1/1
10	NAG	U	1	10,4	-	2/6/23/26	0/1/1/1
10	NAG	U	2	10	-	4/6/23/26	0/1/1/1
10	BMA	U	3	10	-	2/2/19/22	0/1/1/1
10	MAN	U	4	10	-	2/2/19/22	0/1/1/1
10	MAN	U	5	10	-	0/2/19/22	0/1/1/1
18	NAG	V	1	18,4	-	4/6/23/26	0/1/1/1
18	NAG	V	2	18	-	0/6/23/26	0/1/1/1
18	BMA	V	3	18	-	0/2/19/22	0/1/1/1
18	MAN	V	4	18	-	2/2/19/22	0/1/1/1
18	MAN	V	5	18	-	0/2/19/22	0/1/1/1
18	MAN	V	6	18	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	MAN	V	7	18	-	0/2/19/22	0/1/1/1
18	MAN	V	8	18	-	2/2/19/22	0/1/1/1
18	MAN	V	9	18	-	2/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	N	1	NAG	O5-C1	-2.87	1.38	1.43
10	U	4	MAN	O5-C1	2.73	1.48	1.43
10	H	4	MAN	O5-C1	2.35	1.47	1.43
10	U	5	MAN	O5-C1	2.15	1.47	1.43

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	N	1	NAG	C1-O5-C5	-9.69	99.20	112.19
7	O	1	NAG	C1-O5-C5	-6.25	103.82	112.19
10	U	2	NAG	O4-C4-C5	-5.73	95.22	109.32
12	K	1	NAG	C1-O5-C5	-5.49	104.83	112.19
10	U	5	MAN	C1-O5-C5	5.24	119.21	112.19

There are no chirality outliers.

5 of 143 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1	NAG	C8-C7-N2-C2
7	A	1	NAG	O7-C7-N2-C2
7	A	2	NAG	C8-C7-N2-C2
7	A	2	NAG	O7-C7-N2-C2
8	C	2	NAG	C3-C2-N2-C7

There are no ring outliers.

36 monomers are involved in 47 short contacts:

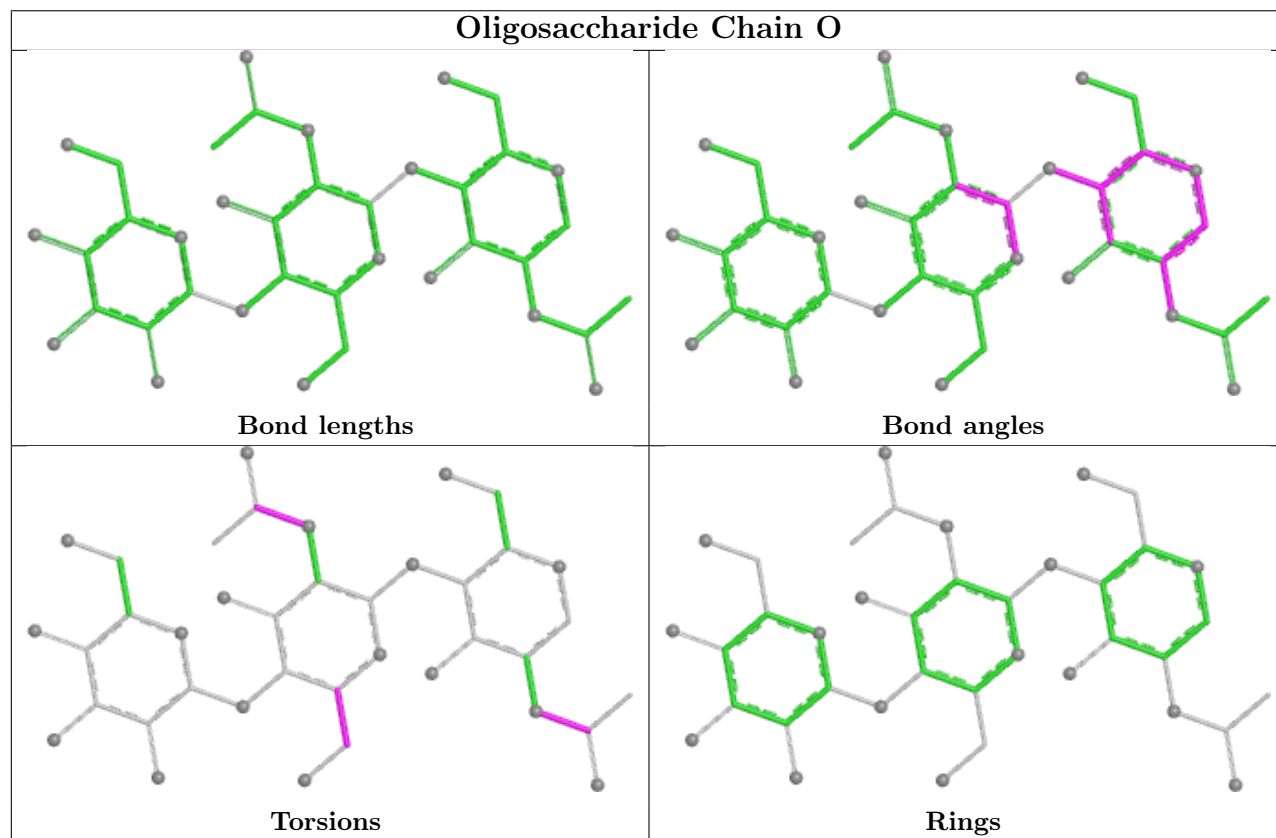
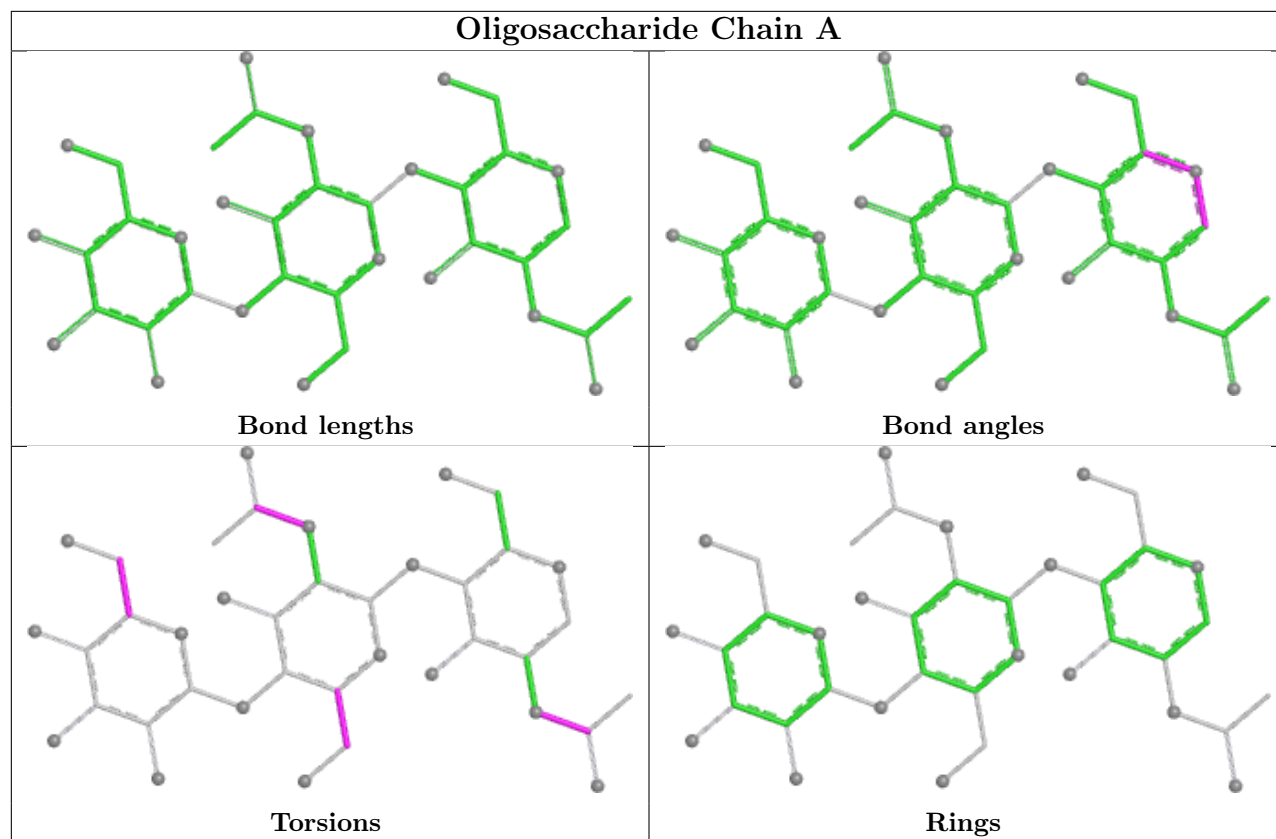
Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	N	6	MAN	1	0
10	H	4	MAN	1	0
7	A	1	NAG	1	0
11	I	2	NAG	1	0
15	N	1	NAG	1	0

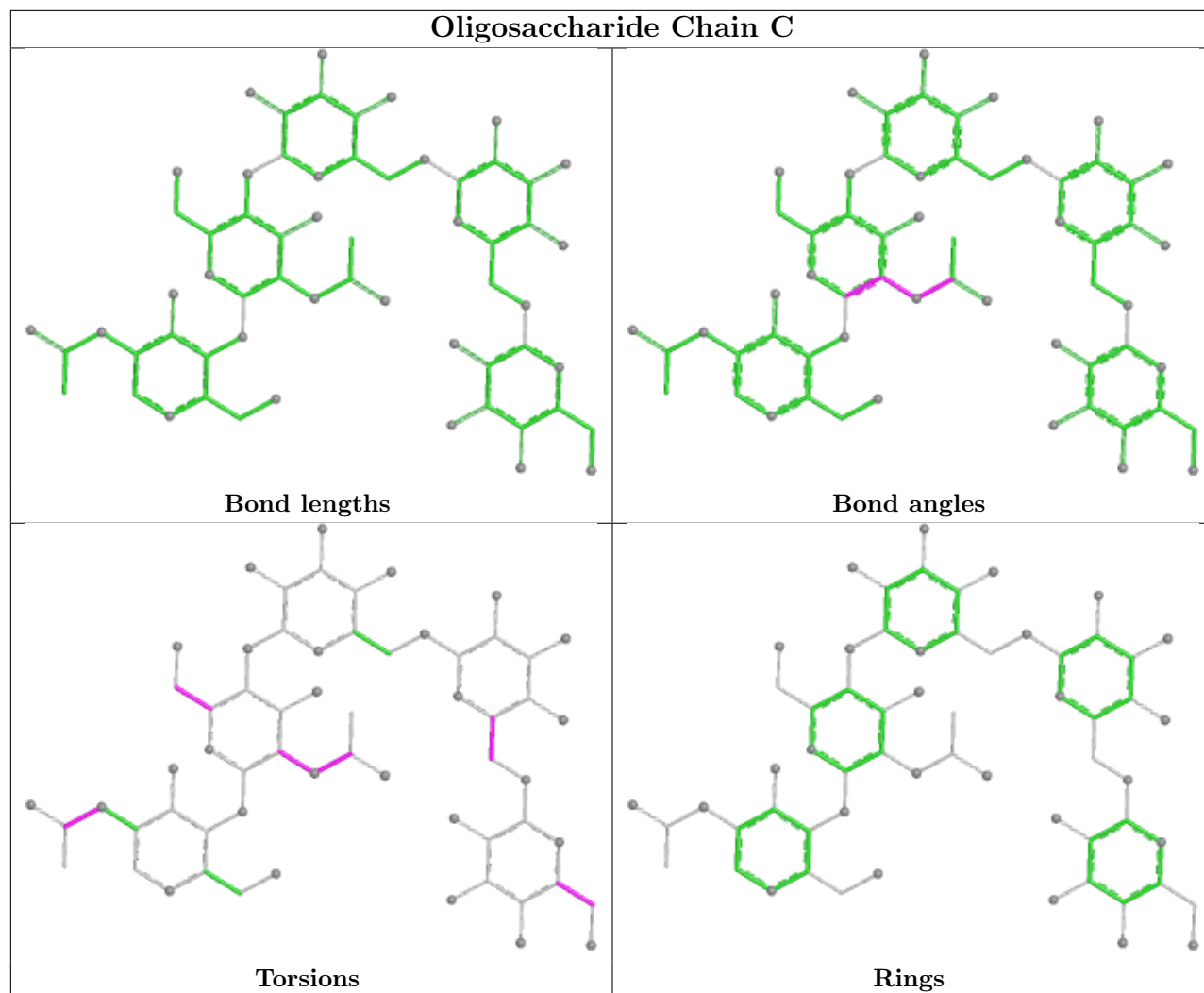
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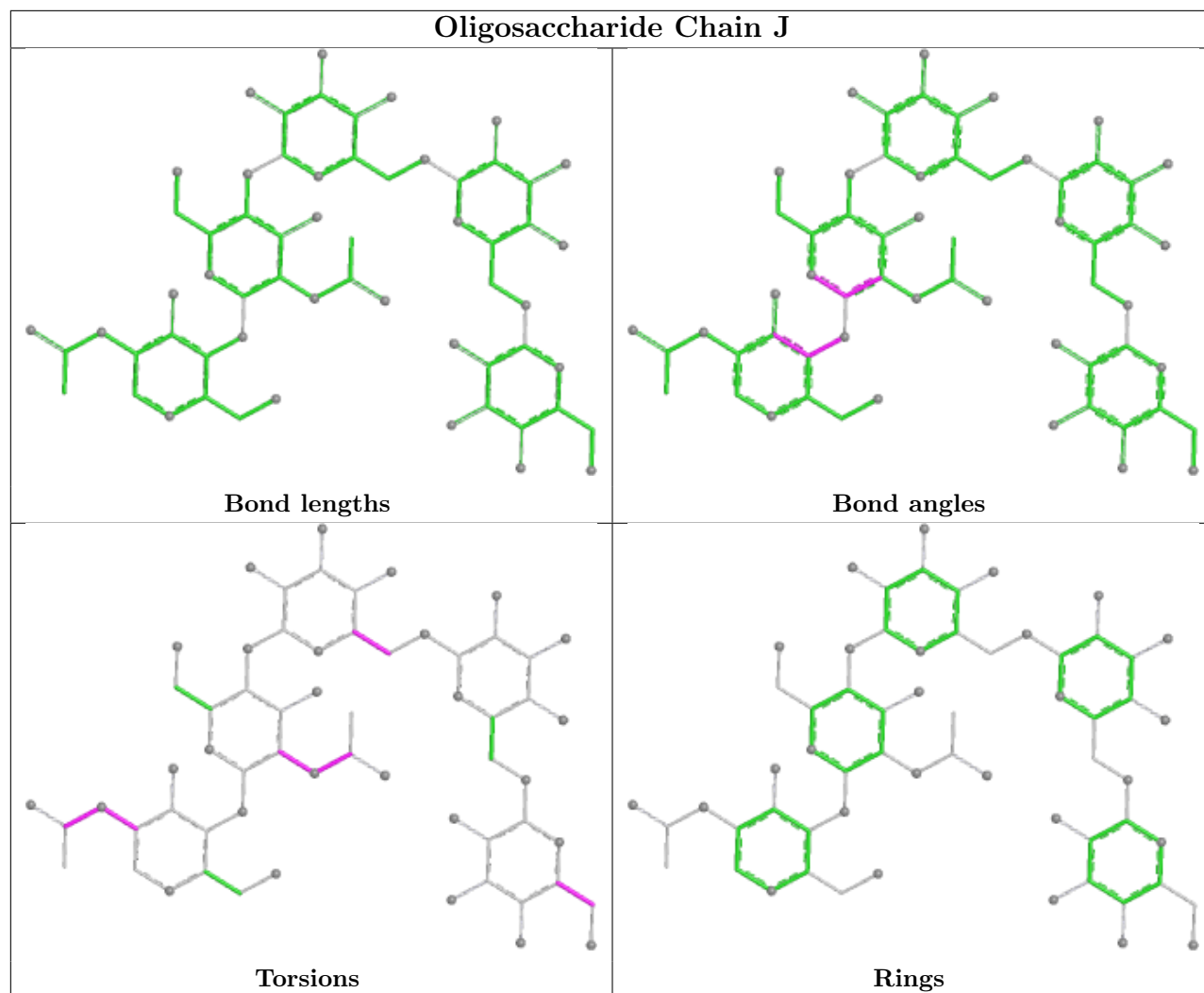
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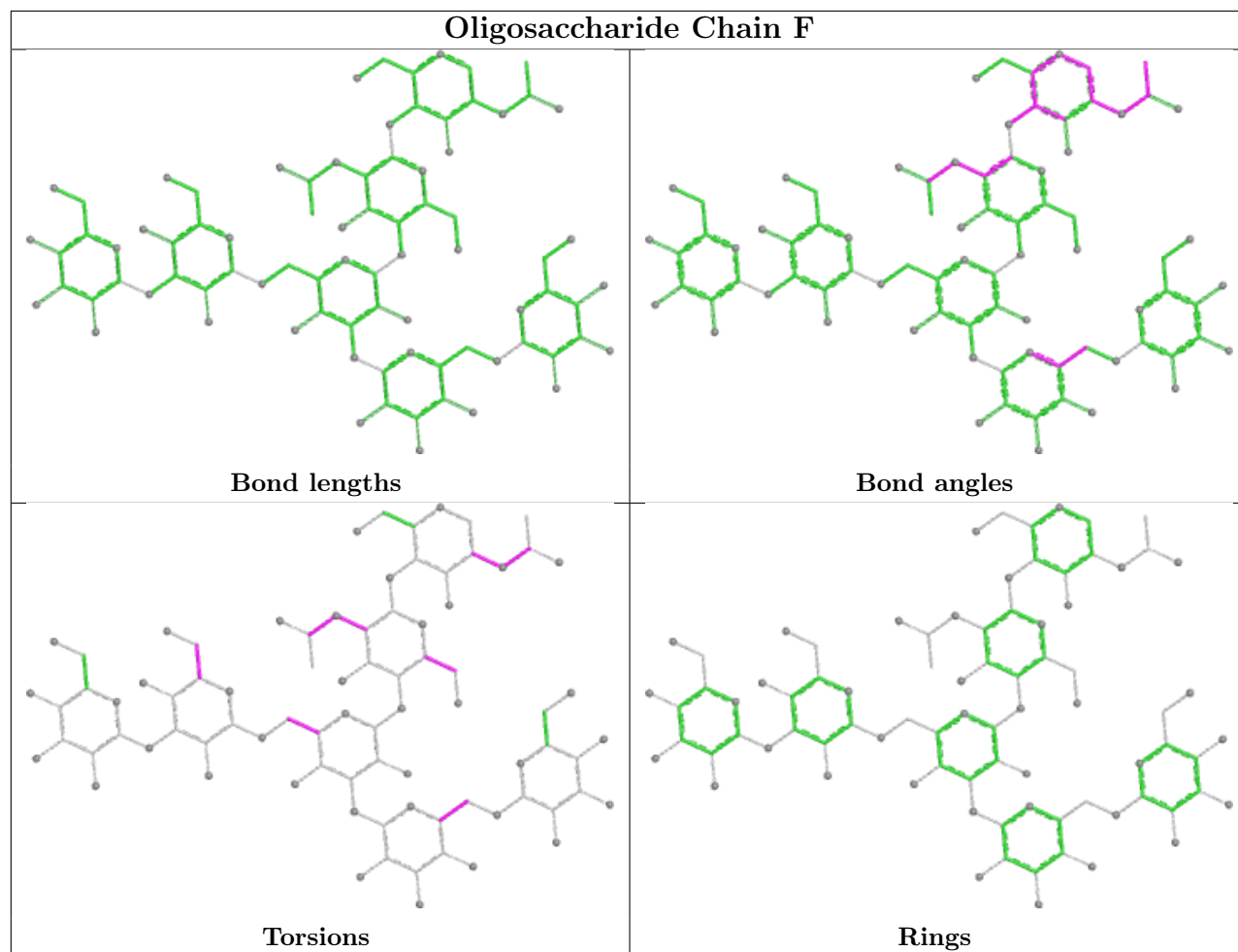
Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	V	6	MAN	1	0
10	U	5	MAN	2	0
9	F	1	NAG	1	0
17	S	1	NAG	14	0
7	A	3	BMA	1	0
12	K	2	NAG	1	0
8	C	2	NAG	1	0
15	N	2	NAG	2	0
11	I	1	NAG	1	0
18	V	2	NAG	1	0
7	O	1	NAG	2	0
18	V	9	MAN	1	0
10	H	3	BMA	2	0
14	M	1	NAG	2	0
14	M	4	MAN	1	0
15	N	3	BMA	2	0
10	U	3	BMA	3	0
12	K	1	NAG	3	0
10	H	2	NAG	1	0
7	A	2	NAG	1	0
11	I	4	MAN	4	0
9	F	6	MAN	1	0
11	I	5	MAN	3	0
11	I	7	MAN	1	0
8	C	3	BMA	1	0
17	S	2	NAG	2	0
10	U	4	MAN	1	0
9	F	3	BMA	1	0
18	V	1	NAG	1	0
17	S	3	BMA	1	0
8	J	2	NAG	1	0

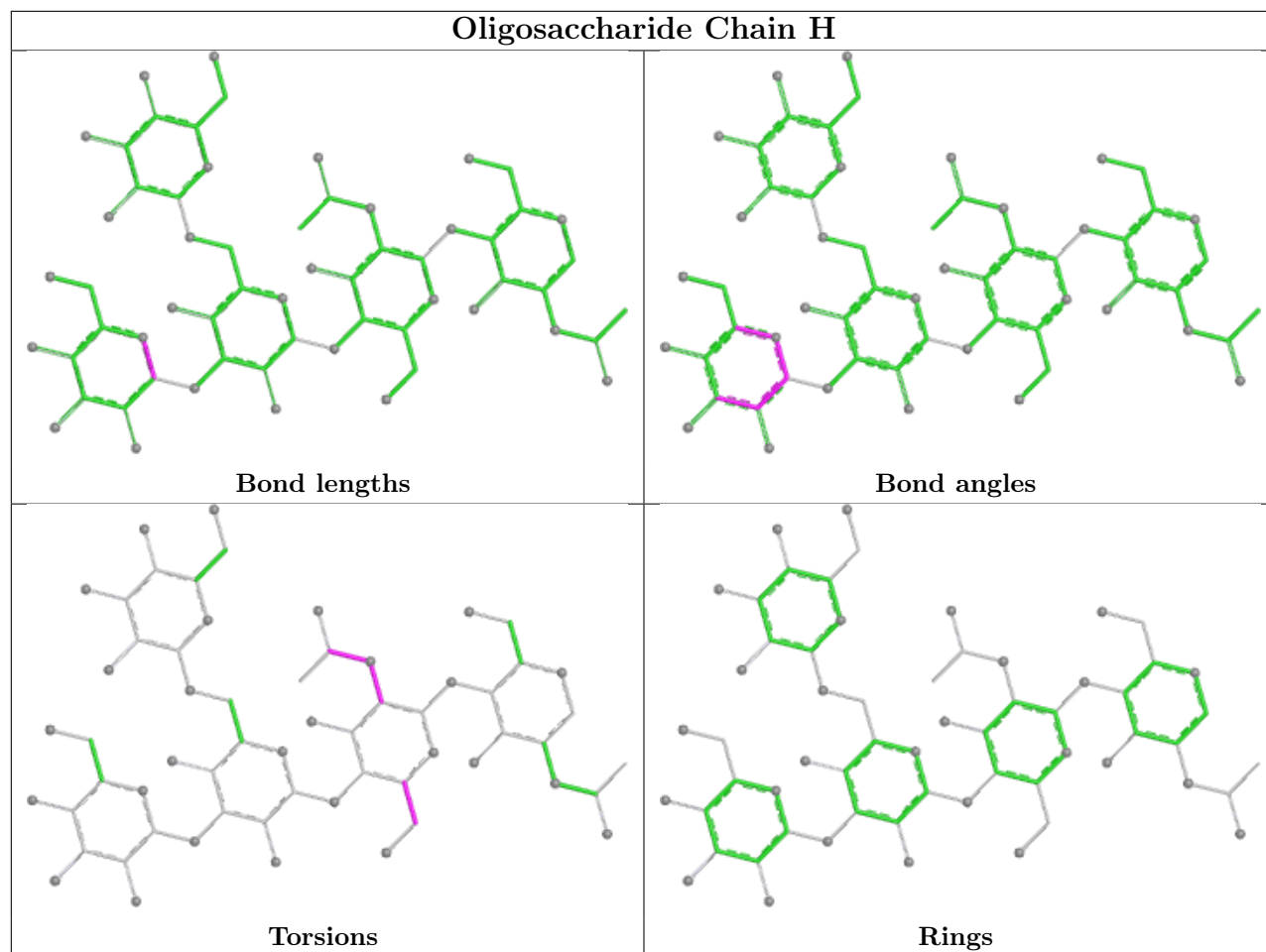
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

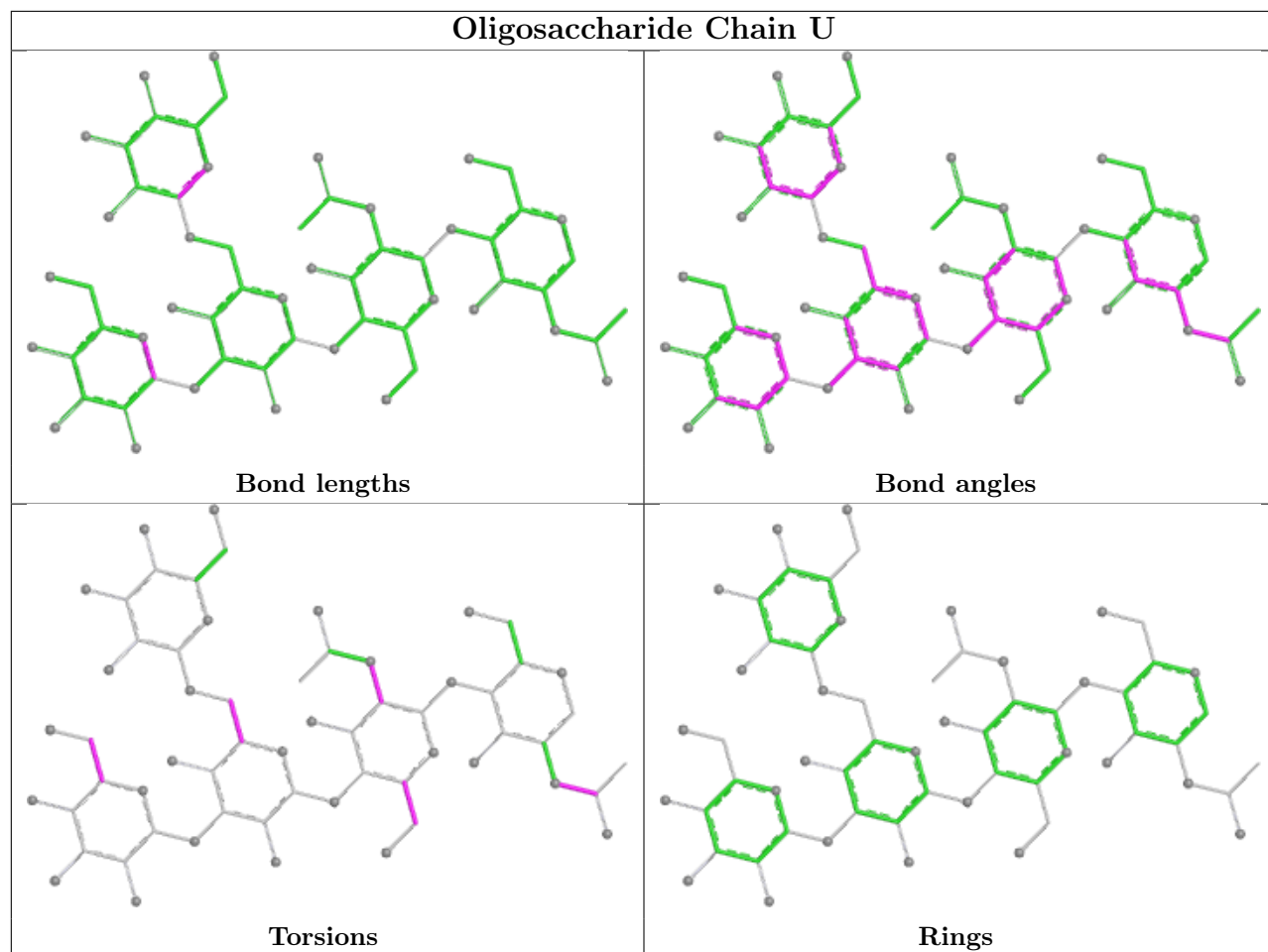


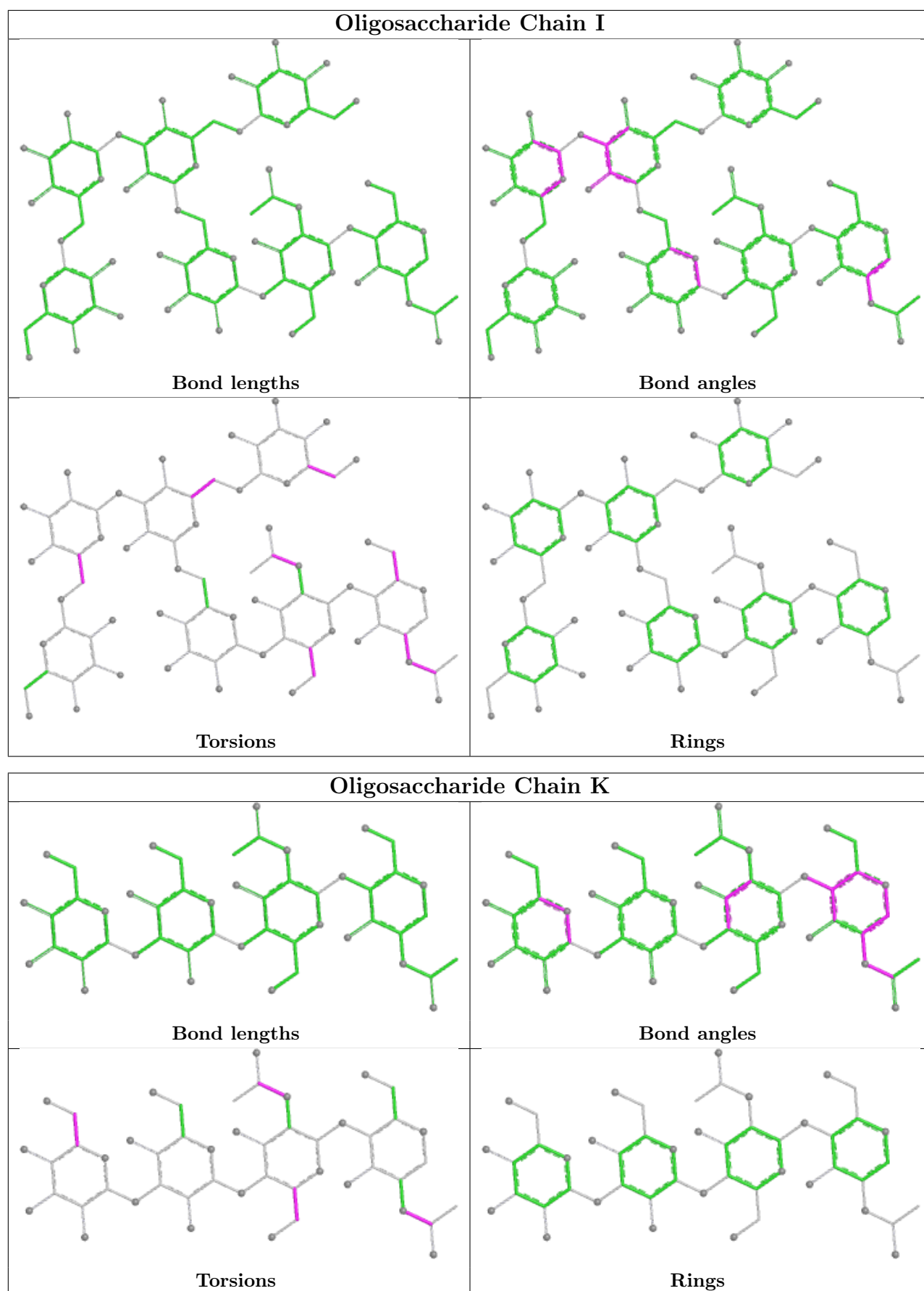


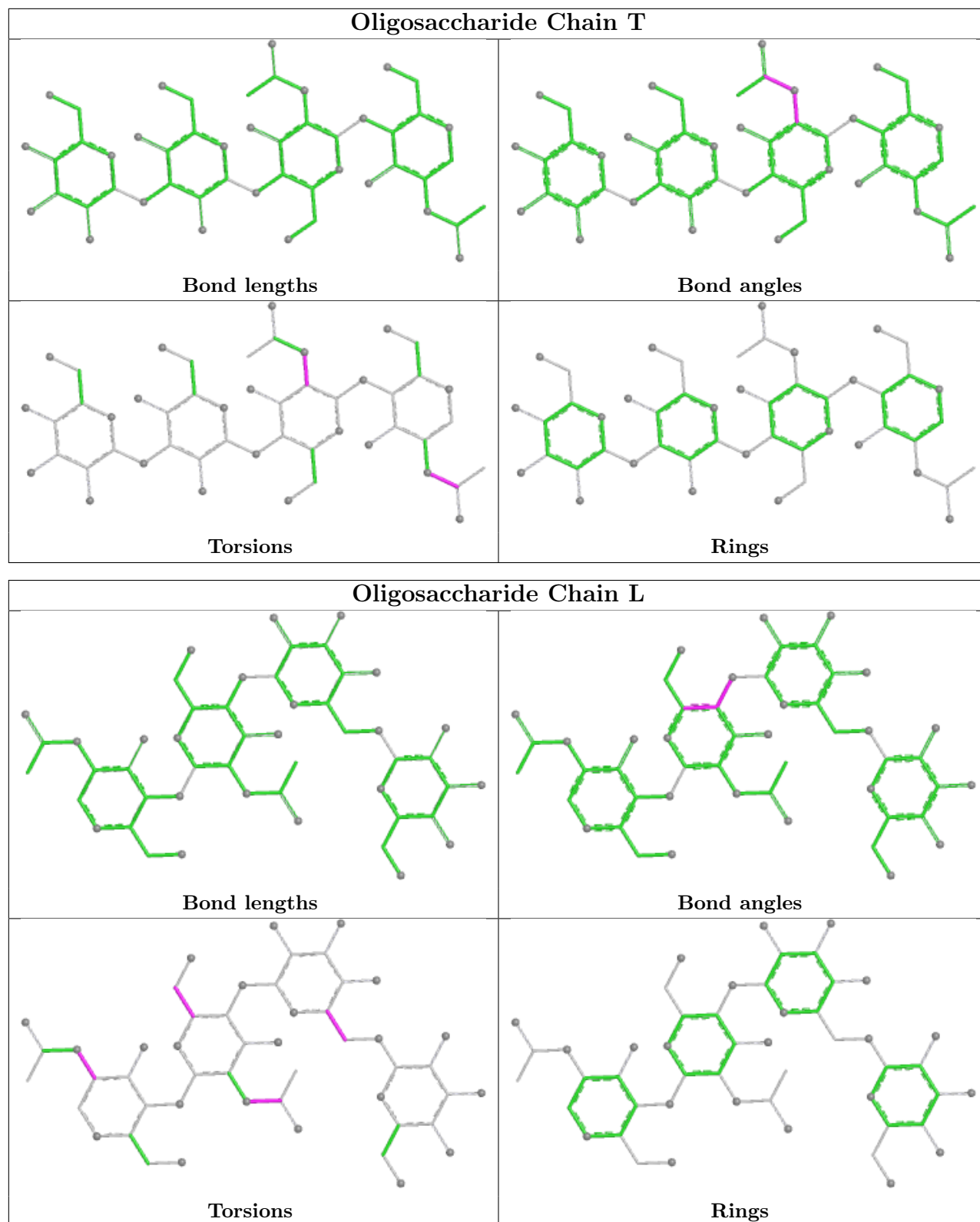


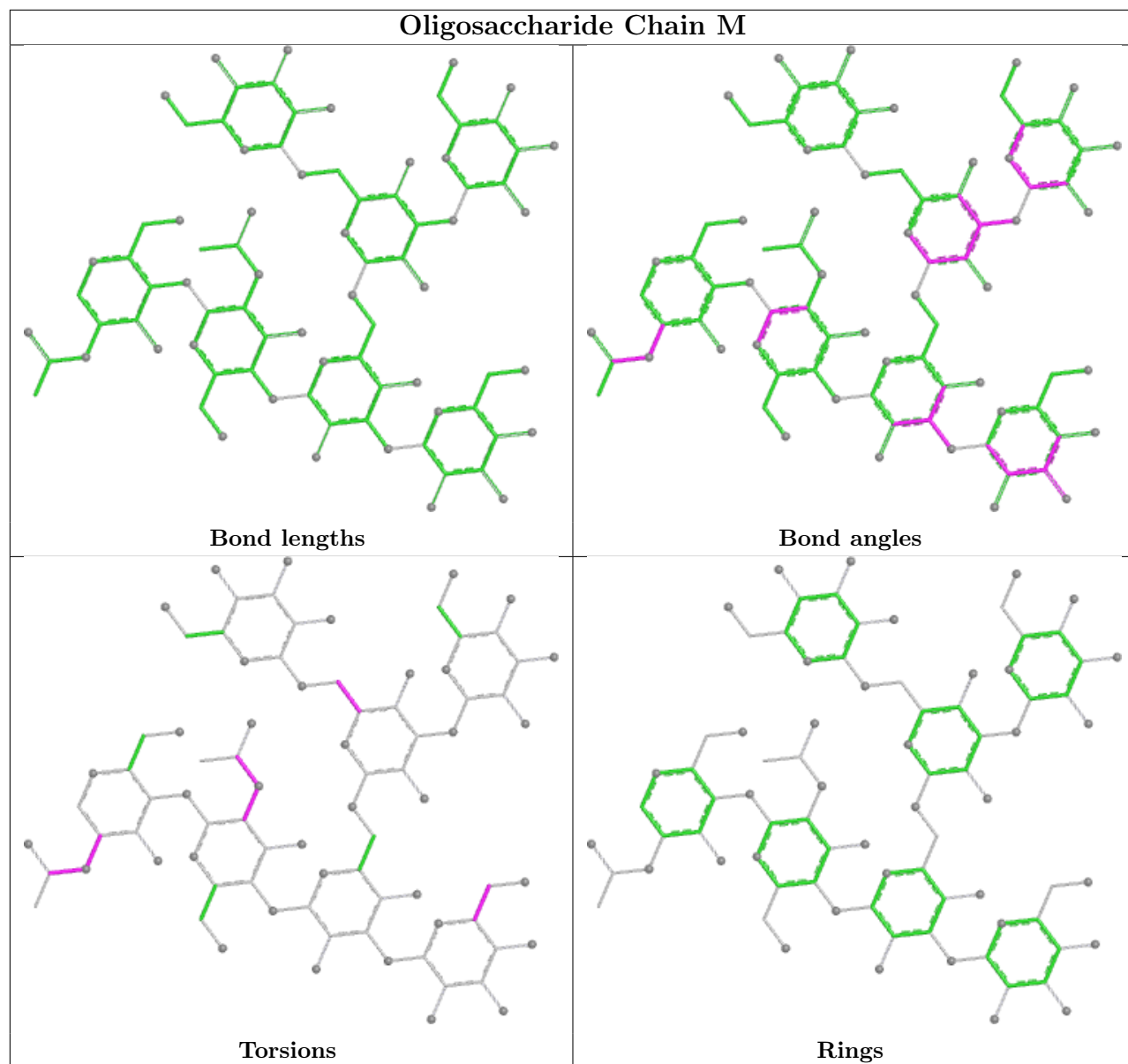


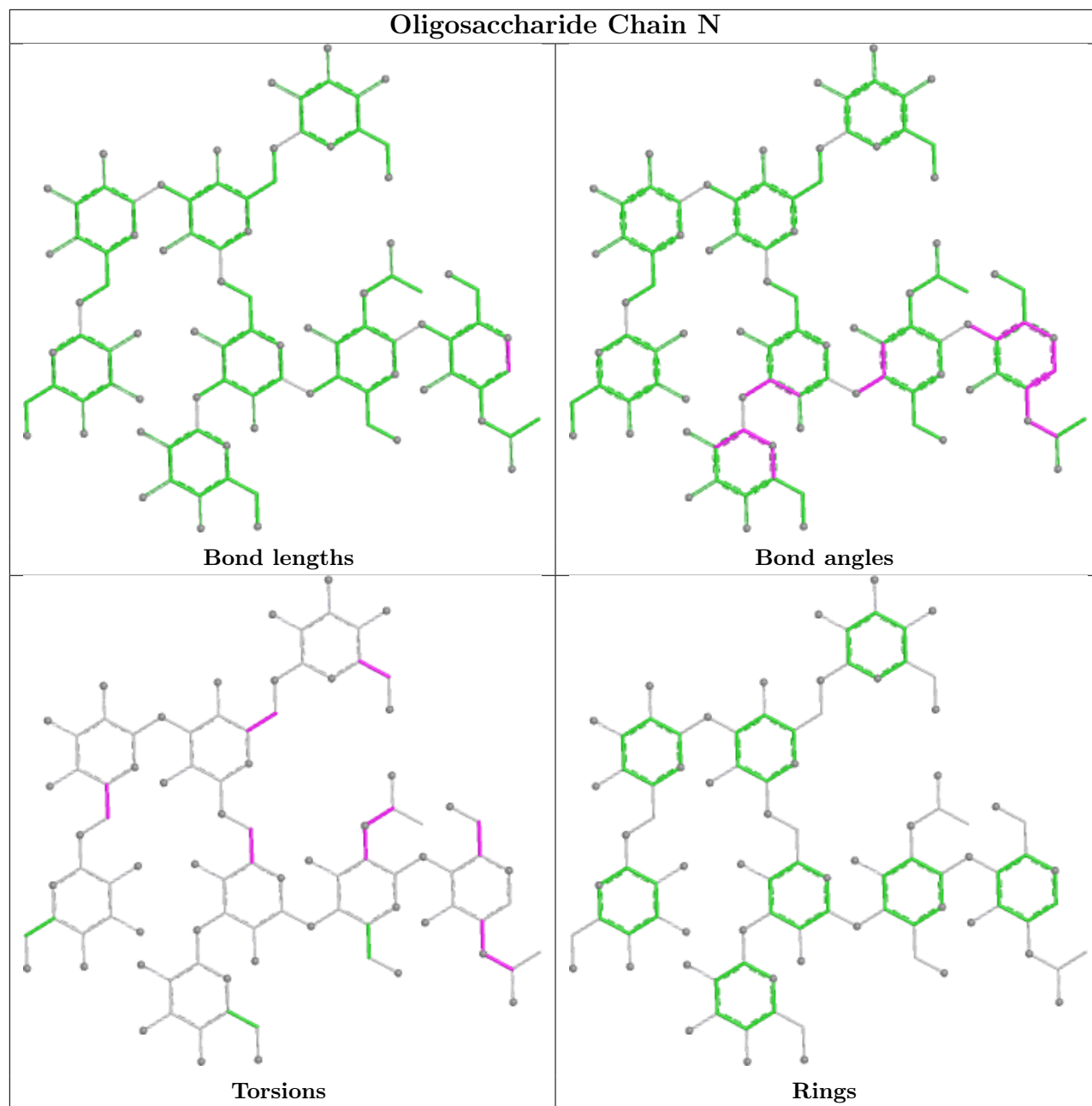


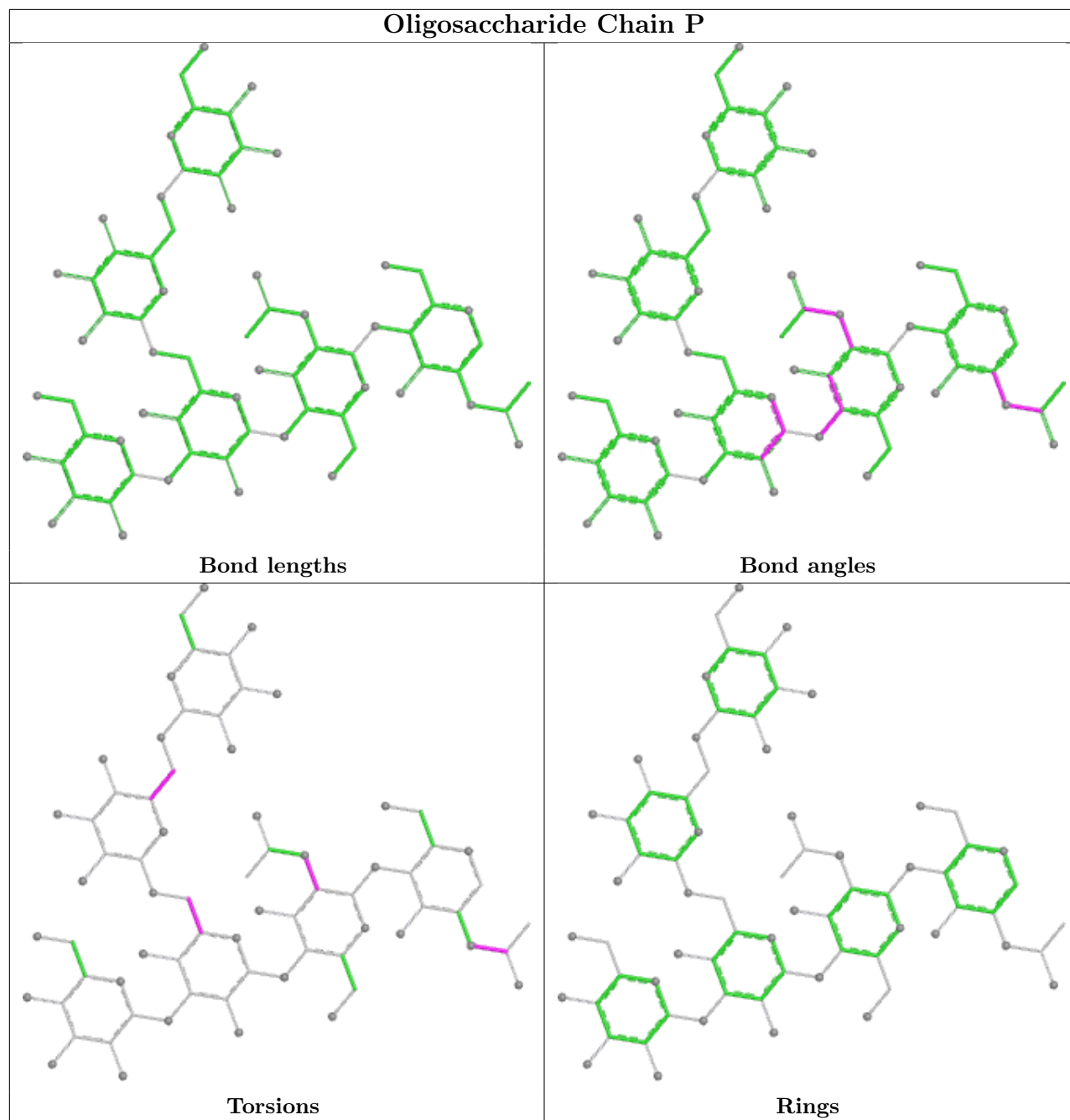


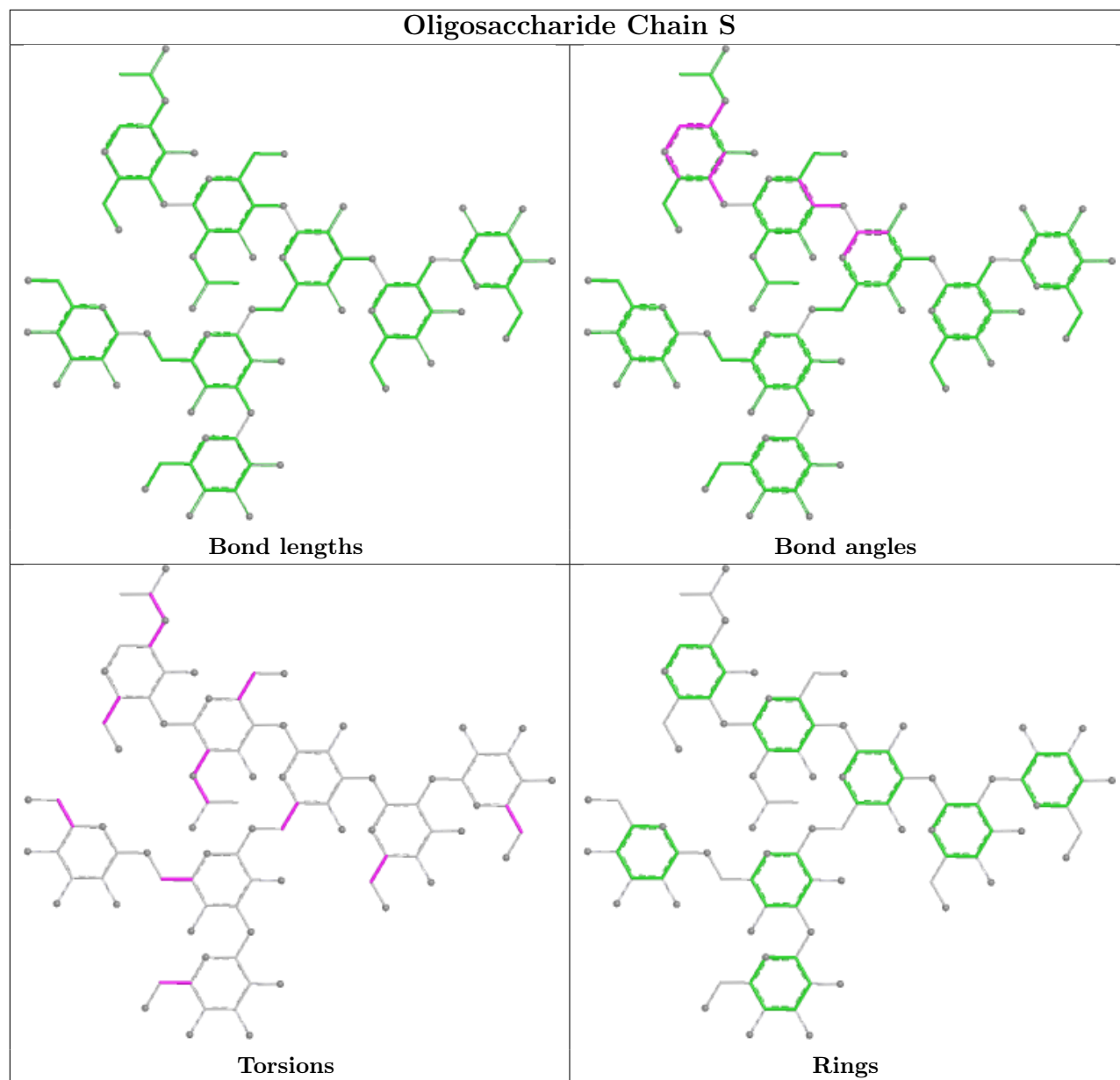


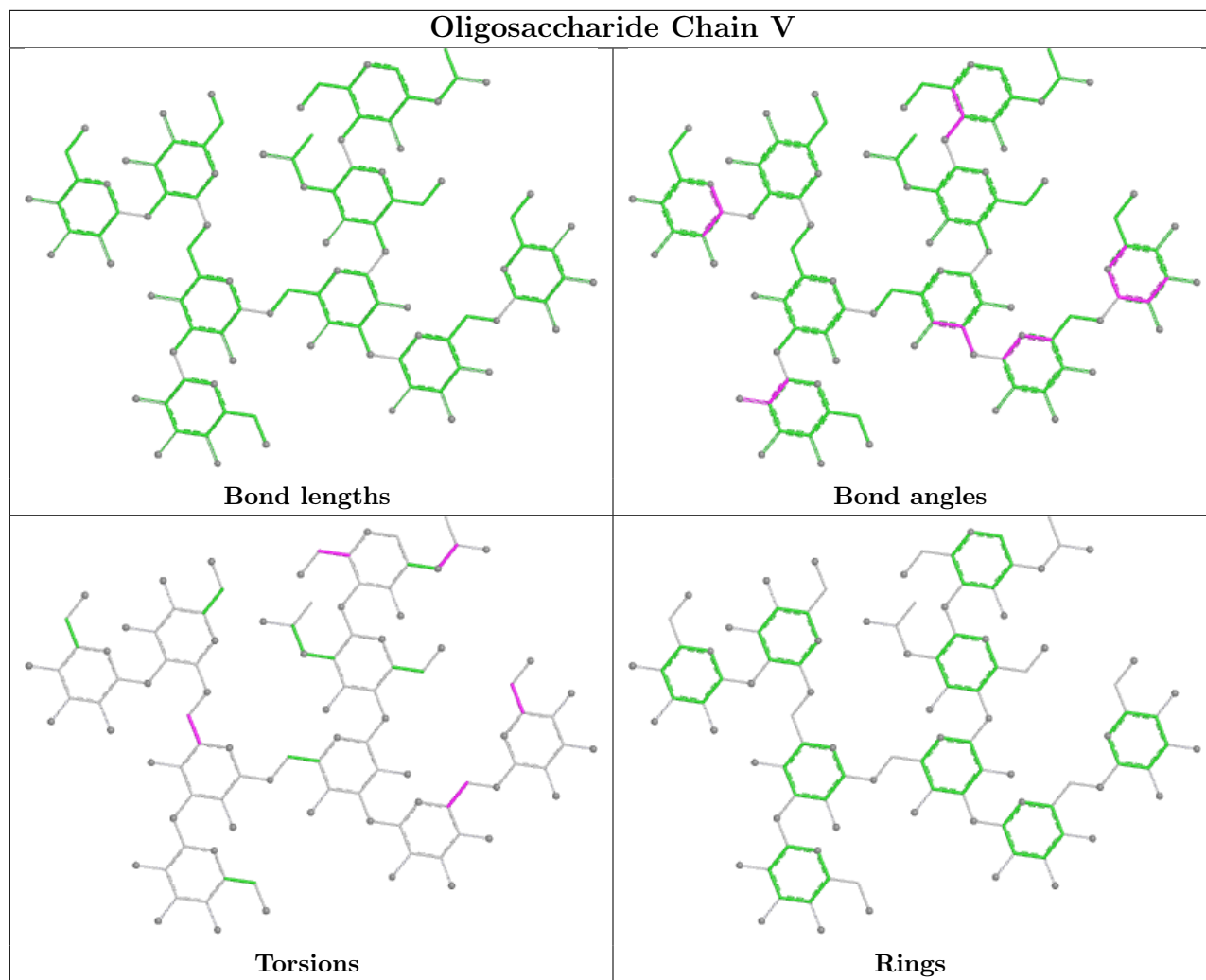












5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
19	NAG	G	603	4	14,14,15	0.32	0	17,19,21	0.83	0
19	NAG	G	601	4	14,14,15	0.30	0	17,19,21	0.74	0
19	NAG	B	701	1	14,14,15	0.29	0	17,19,21	0.61	0
19	NAG	G	602	4	14,14,15	0.36	0	17,19,21	0.89	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
19	NAG	G	603	4	-	3/6/23/26	0/1/1/1
19	NAG	G	601	4	-	4/6/23/26	0/1/1/1
19	NAG	B	701	1	-	2/6/23/26	0/1/1/1
19	NAG	G	602	4	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	B	701	NAG	C8-C7-N2-C2
19	B	701	NAG	O7-C7-N2-C2
19	G	602	NAG	C1-C2-N2-C7
19	G	603	NAG	C3-C2-N2-C7
19	G	603	NAG	C8-C7-N2-C2

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, 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	B	139/153 (90%)	0.54	5 (3%) 46 35	110, 185, 251, 286	0
2	D	235/243 (96%)	0.19	3 (1%) 75 58	155, 240, 318, 372	0
3	E	210/216 (97%)	0.38	8 (3%) 44 34	150, 223, 312, 352	0
4	G	451/479 (94%)	0.33	16 (3%) 47 35	129, 186, 258, 335	0
5	Q	228/241 (94%)	0.20	3 (1%) 75 58	170, 227, 285, 309	0
6	R	211/215 (98%)	0.42	6 (2%) 55 41	184, 257, 311, 324	0
All	All	1474/1547 (95%)	0.33	41 (2%) 55 41	110, 214, 303, 372	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	G	507	GLY	8.1
4	G	379	GLY	4.1
4	G	151	ARG	3.6
1	B	564	HIS	3.6
4	G	326	ILE	3.4

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(\AA^2)	Q<0.9
7	NAG	A	1	14/15	-	-	219,264,305,315	0
7	NAG	A	2	14/15	-	-	277,311,319,323	0
7	BMA	A	3	11/12	-	-	291,319,332,336	0
13	MAN	L	4	11/12	-0.35	0.15	303,335,344,344	0
12	BMA	K	3	11/12	-0.11	0.13	312,330,344,345	0
8	MAN	J	4	11/12	-0.11	0.12	319,331,349,350	0
8	NAG	C	1	14/15	-	-	215,260,300,306	0
8	NAG	C	2	14/15	-	-	271,316,342,357	0
8	BMA	C	3	11/12	-	-	309,353,369,378	0
8	MAN	C	4	11/12	-	-	373,383,391,392	0
8	MAN	C	5	11/12	-	-	316,356,370,377	0
17	MAN	S	5	11/12	-0.02	0.14	292,310,320,323	0
8	MAN	J	5	11/12	0.00	0.11	317,345,353,355	0
15	MAN	N	4	11/12	0.10	0.10	328,344,348,353	0
17	MAN	S	4	11/12	0.20	0.17	278,315,328,329	0
16	MAN	P	4	11/12	0.30	0.10	337,353,368,374	0
9	NAG	F	1	14/15	-	-	209,229,240,259	0
9	NAG	F	2	14/15	-	-	209,246,269,283	0
9	BMA	F	3	11/12	-	-	209,233,269,291	0
9	MAN	F	4	11/12	-	-	249,256,277,284	0
9	MAN	F	5	11/12	-	-	271,284,296,300	0
9	MAN	F	6	11/12	-	-	209,209,225,242	0
9	MAN	F	7	11/12	-	-	227,243,271,292	0
17	MAN	S	7	11/12	0.34	0.10	329,343,352,353	0
17	MAN	S	6	11/12	0.35	0.09	298,333,339,350	0
16	MAN	P	5	11/12	0.35	0.13	339,350,367,372	0
10	MAN	H	4	11/12	0.36	0.09	307,327,350,352	0
10	BMA	U	3	11/12	0.37	0.12	339,346,356,373	0
12	MAN	K	4	11/12	0.39	0.11	302,342,349,351	0
12	MAN	T	4	11/12	0.41	0.25	223,238,277,286	0
17	MAN	S	8	11/12	0.41	0.13	288,308,326,326	0
15	BMA	N	3	11/12	0.43	0.10	315,321,339,347	0
16	MAN	P	6	11/12	0.44	0.08	331,360,370,372	0
10	BMA	H	3	11/12	0.46	0.13	298,322,334,344	0
8	BMA	J	3	11/12	0.48	0.10	329,340,357,360	0
14	MAN	M	4	11/12	0.49	0.10	286,308,331,339	0
13	BMA	L	3	11/12	0.50	0.12	289,314,339,347	0
10	NAG	H	2	14/15	0.54	0.11	267,303,321,325	0
11	NAG	I	2	14/15	0.55	0.20	249,297,327,348	0
13	NAG	L	2	14/15	0.56	0.13	268,301,316,317	0
10	MAN	U	5	11/12	0.57	0.10	296,344,357,364	0
10	MAN	H	5	11/12	0.58	0.11	272,312,330,333	0
17	BMA	S	3	11/12	0.62	0.08	303,320,323,323	0

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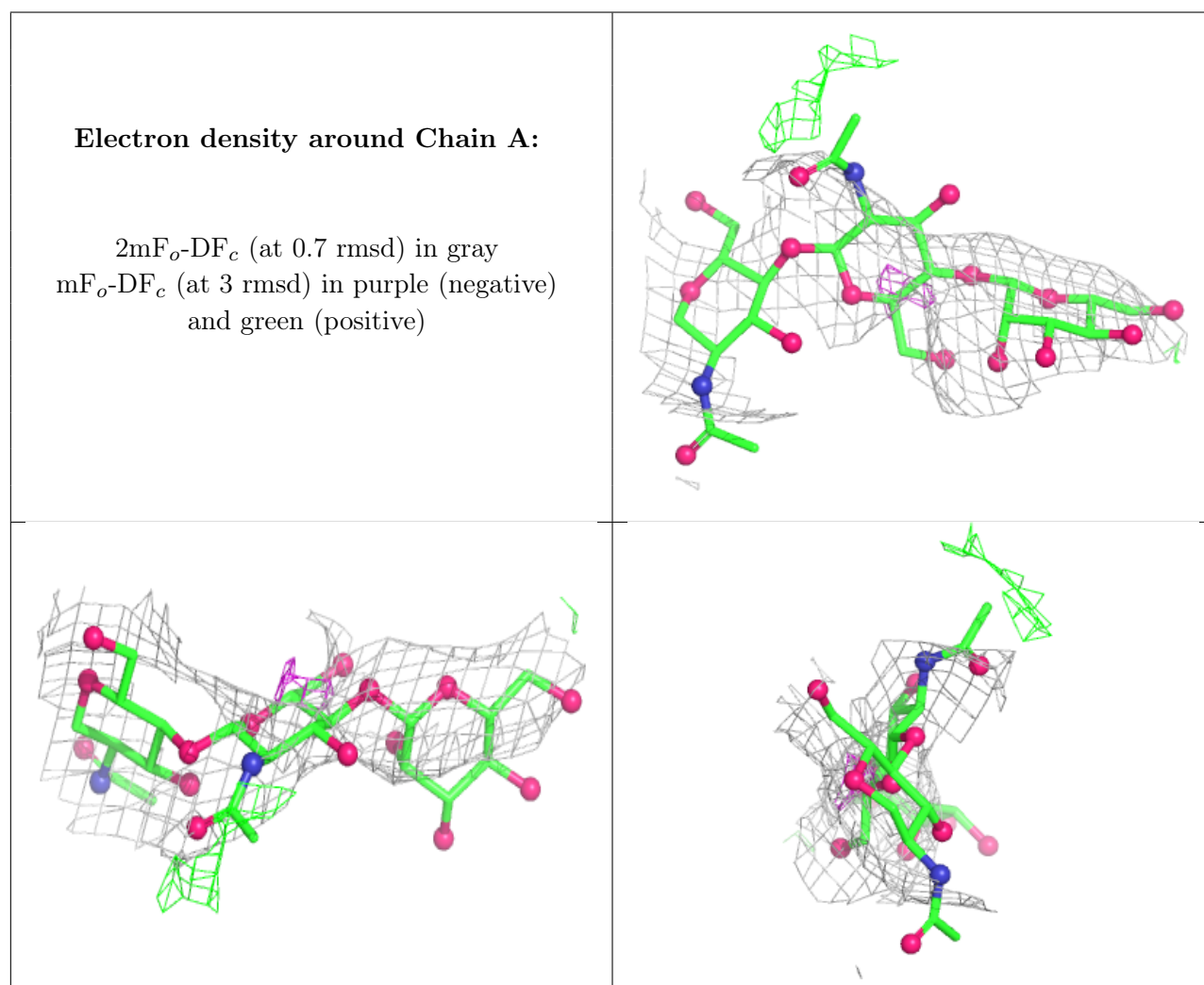
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
14	BMA	M	3	11/12	0.62	0.11	265,271,281,282	0
11	MAN	I	7	11/12	0.63	0.12	327,347,364,367	0
8	NAG	J	2	14/15	0.63	0.10	254,281,315,338	0
10	MAN	U	4	11/12	0.64	0.13	291,317,337,338	0
18	MAN	V	7	11/12	0.69	0.18	275,283,294,298	0
16	NAG	P	2	14/15	0.70	0.10	273,300,329,350	0
18	MAN	V	9	11/12	0.70	0.21	213,219,246,253	0
11	MAN	I	5	11/12	0.72	0.15	396,405,410,413	0
8	NAG	J	1	14/15	0.73	0.13	209,241,271,280	0
17	NAG	S	2	14/15	0.77	0.12	263,297,316,319	0
16	BMA	P	3	11/12	0.79	0.07	347,361,374,376	0
15	NAG	N	1	14/15	0.80	0.20	226,256,267,270	0
15	NAG	N	2	14/15	0.80	0.16	265,284,302,318	0
14	MAN	M	5	11/12	-	-	298,313,330,333	0
14	MAN	M	6	11/12	-	-	295,321,330,333	0
14	MAN	M	7	11/12	-	-	213,291,312,322	0
10	NAG	H	1	14/15	0.80	0.10	231,262,279,288	0
12	NAG	K	2	14/15	0.82	0.11	249,281,312,318	0
14	NAG	M	2	14/15	0.83	0.14	211,225,242,251	0
12	NAG	K	1	14/15	0.83	0.15	210,230,261,261	0
15	MAN	N	5	11/12	-	-	327,338,356,364	0
15	MAN	N	6	11/12	-	-	327,338,353,353	0
15	MAN	N	7	11/12	-	-	311,319,334,337	0
15	MAN	N	8	11/12	-	-	277,322,345,346	0
17	NAG	S	1	14/15	0.83	0.14	214,237,276,295	0
11	NAG	I	1	14/15	0.84	0.16	209,225,246,251	0
10	NAG	U	2	14/15	0.84	0.13	252,282,319,327	0
12	BMA	T	3	11/12	0.85	0.13	250,283,301,306	0
16	NAG	P	1	14/15	0.87	0.11	216,241,264,279	0
14	NAG	M	1	14/15	0.88	0.09	211,211,226,257	0
12	NAG	T	1	14/15	0.88	0.09	241,279,310,320	0
11	BMA	I	3	11/12	0.88	0.12	326,350,366,369	0
13	NAG	L	1	14/15	0.89	0.12	212,254,276,290	0
7	BMA	O	3	11/12	0.90	0.10	281,313,324,327	0
18	MAN	V	6	11/12	0.91	0.13	213,228,240,241	0
10	NAG	U	1	14/15	0.91	0.10	215,240,255,265	0
18	MAN	V	8	11/12	0.91	0.13	213,219,260,269	0
18	MAN	V	5	11/12	0.91	0.09	220,227,239,250	0
7	NAG	O	1	14/15	0.92	0.18	211,223,264,274	0
11	MAN	I	6	11/12	0.92	0.12	374,388,396,400	0
12	NAG	T	2	14/15	0.92	0.08	291,311,327,328	0
11	MAN	I	4	11/12	0.92	0.07	372,382,403,404	0

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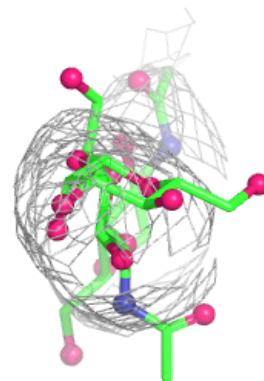
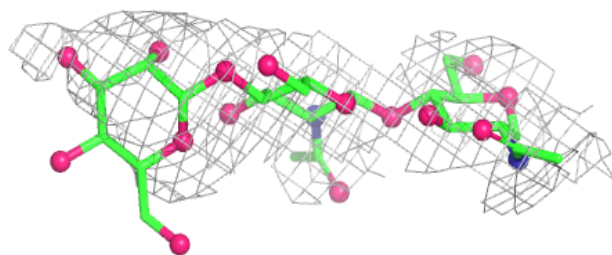
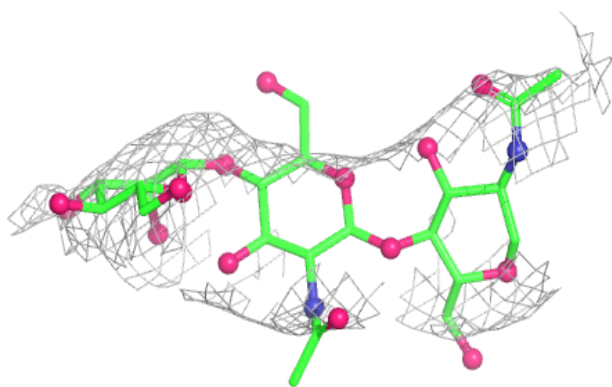
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
18	MAN	V	4	11/12	0.93	0.10	230,247,262,275	0
7	NAG	O	2	14/15	0.93	0.12	269,288,312,319	0
18	NAG	V	1	14/15	0.95	0.10	213,214,228,234	0
18	BMA	V	3	11/12	0.95	0.06	213,213,228,249	0
18	NAG	V	2	14/15	0.96	0.17	213,224,238,248	0

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.

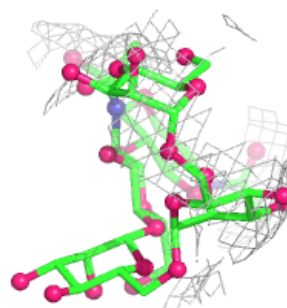
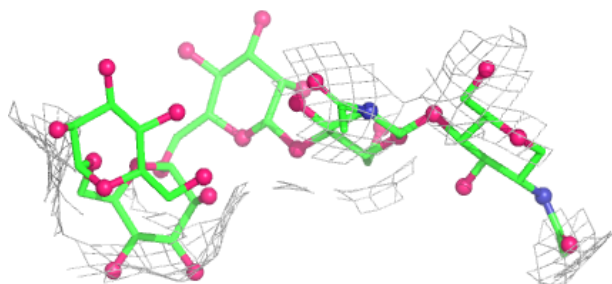
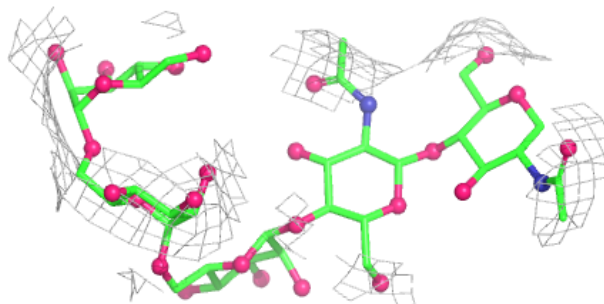


Electron density around Chain O:

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

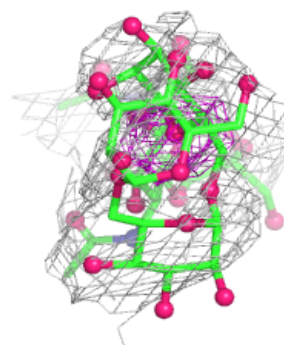
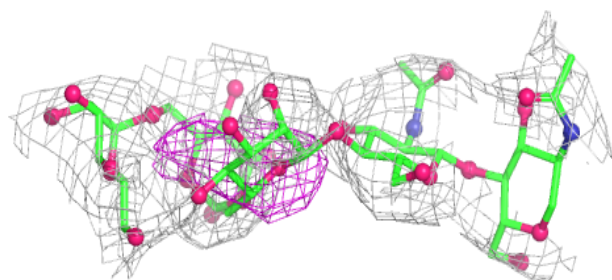
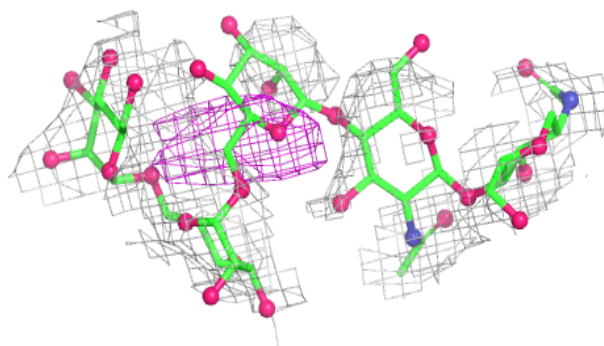
**Electron density around Chain C:**

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

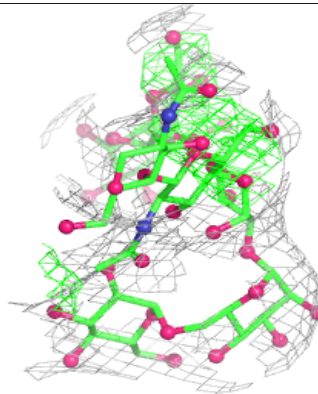
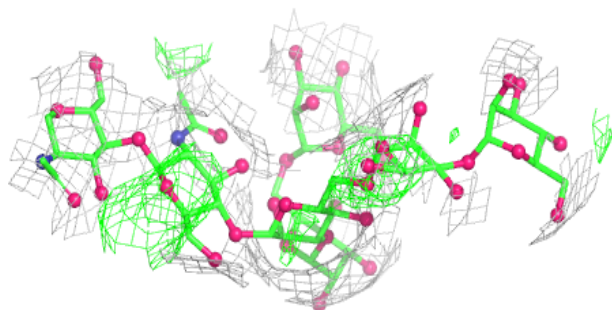
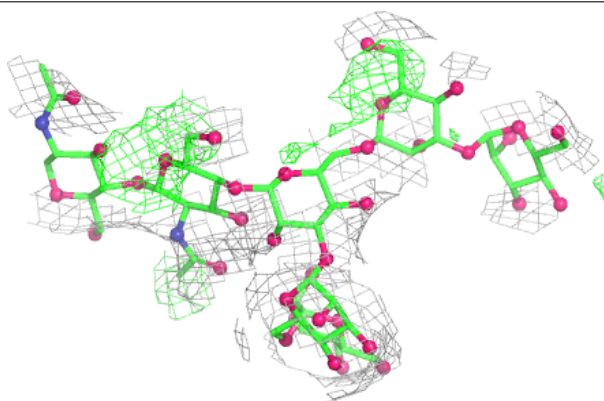


Electron density around Chain J:

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

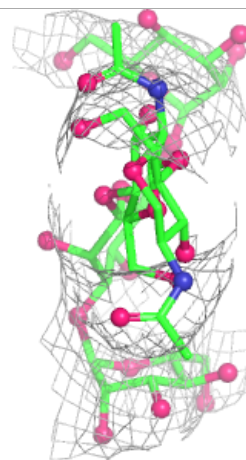
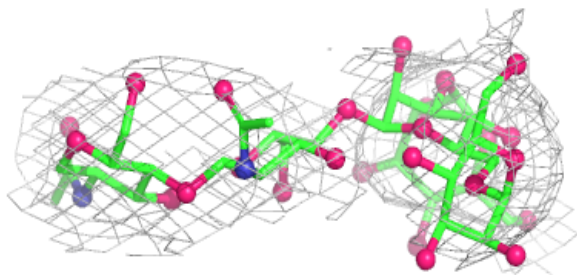
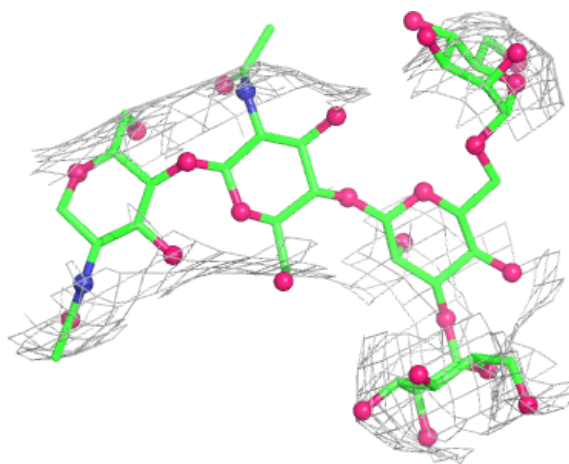
**Electron density around Chain F:**

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



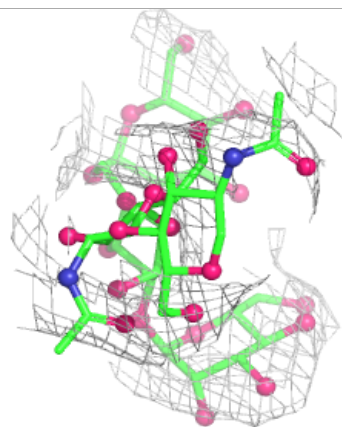
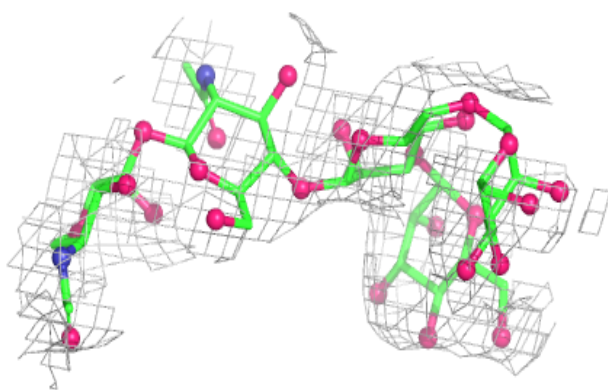
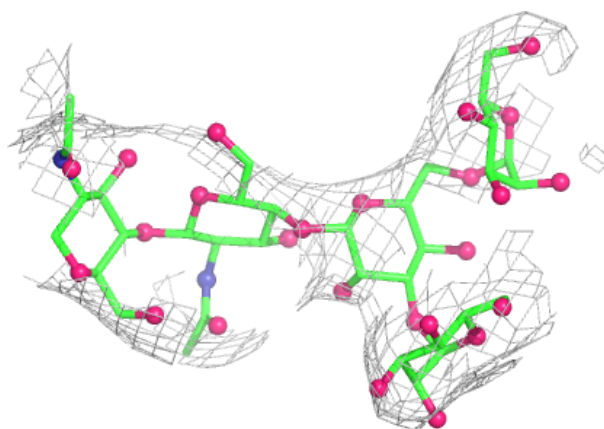
Electron density around Chain H:

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



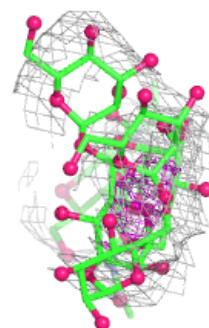
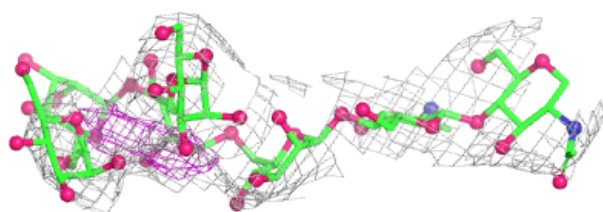
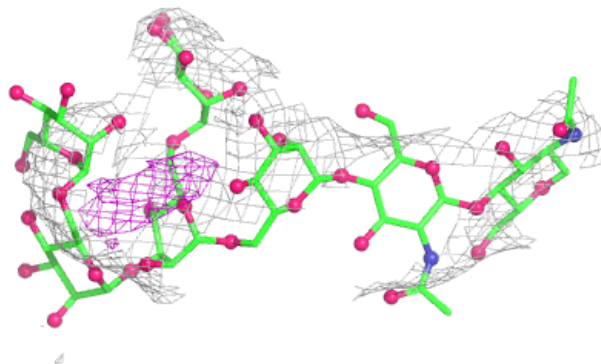
Electron density around Chain U:

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

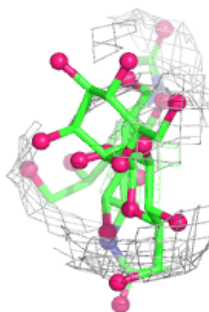
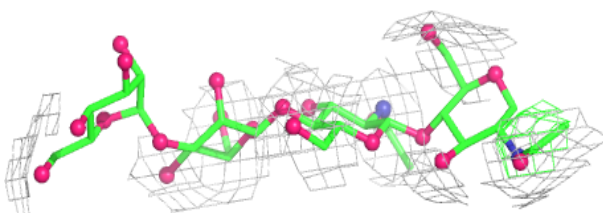
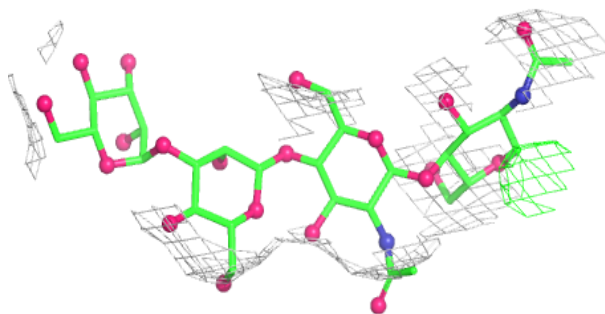


Electron density around Chain I:

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

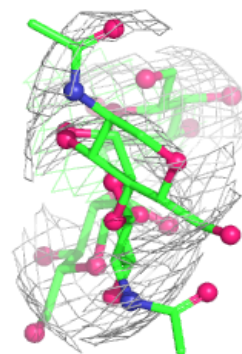
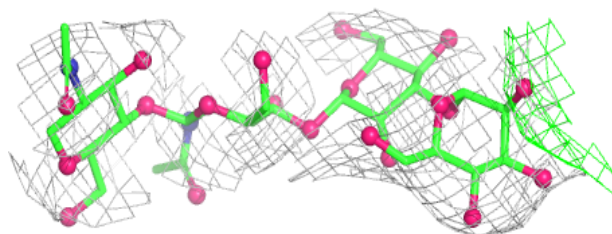
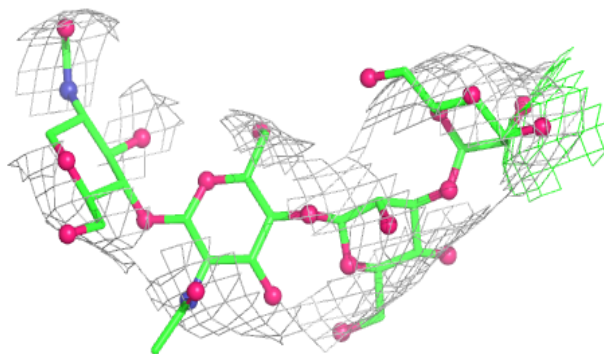
**Electron density around Chain K:**

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

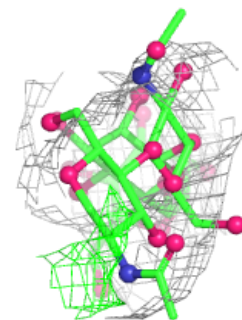
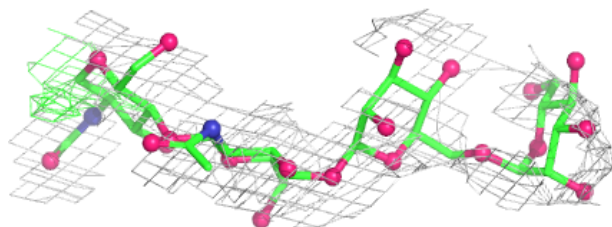
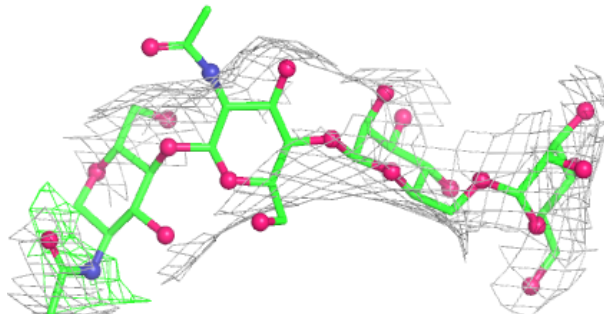


Electron density around Chain T:

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

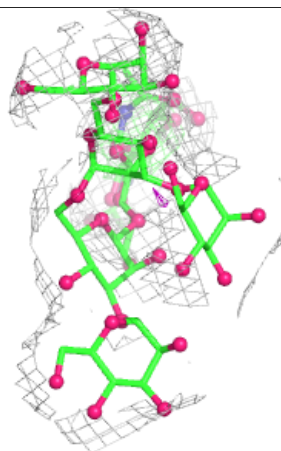
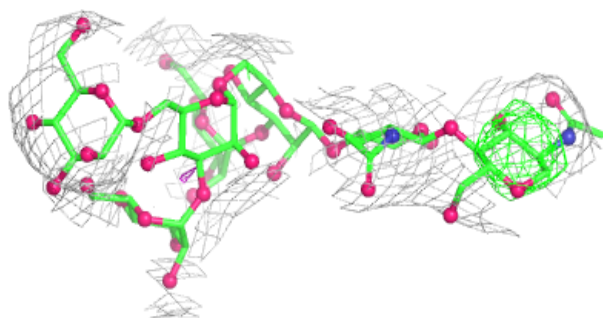
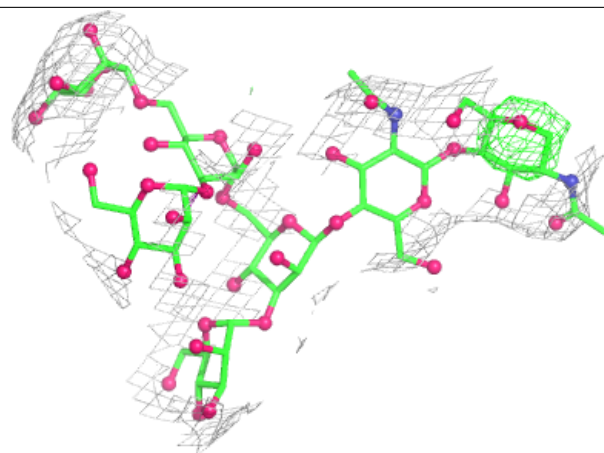
**Electron density around Chain L:**

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

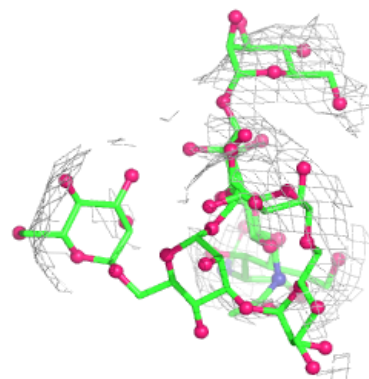
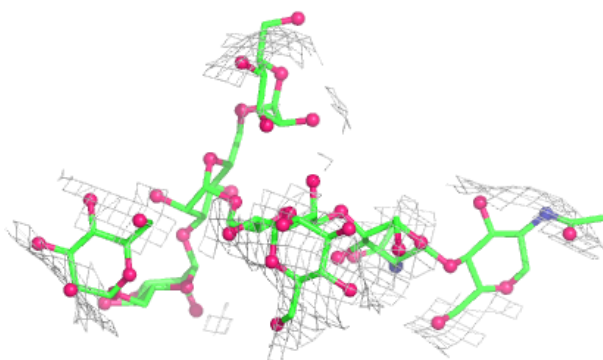
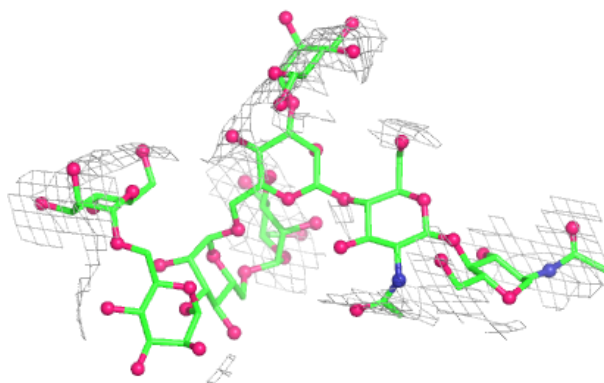


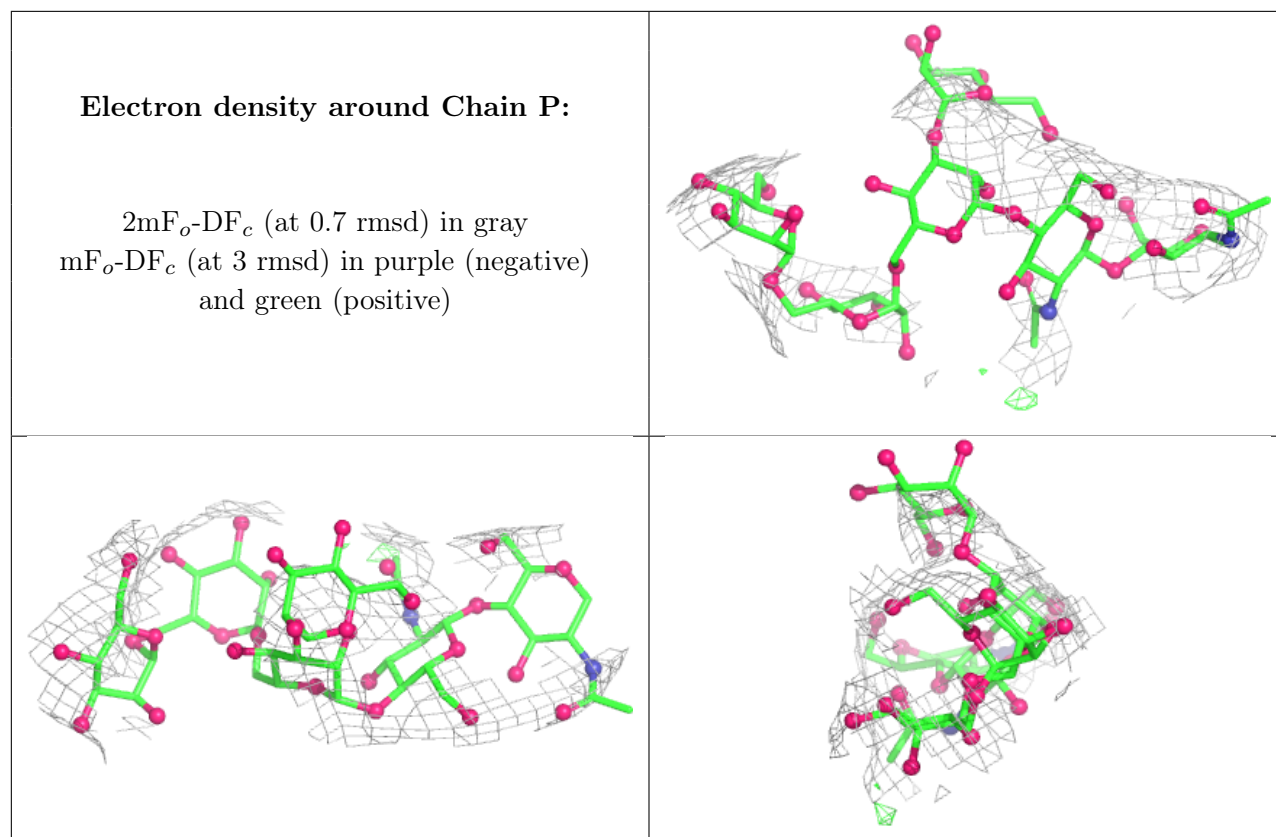
Electron density around Chain M:

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

**Electron density around Chain N:**

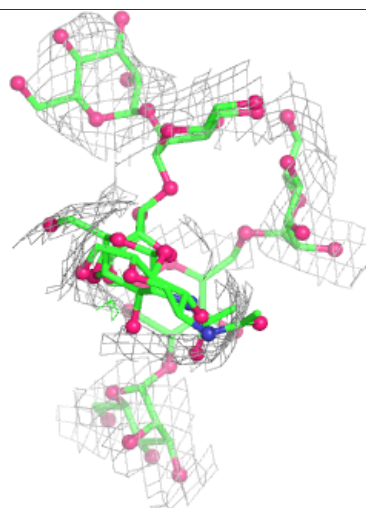
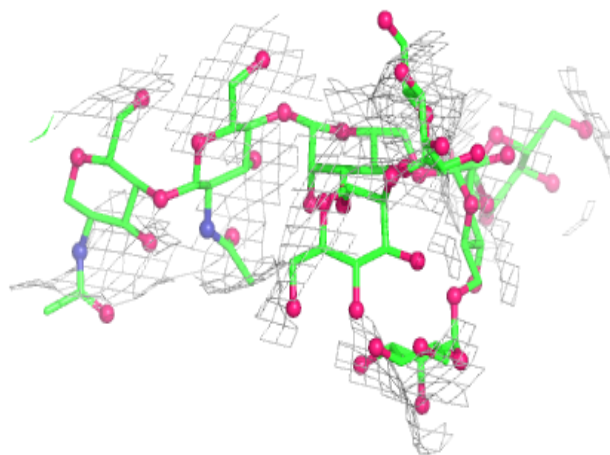
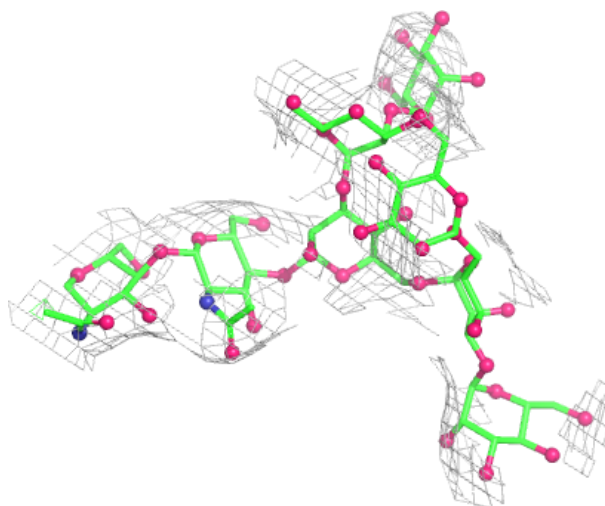
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

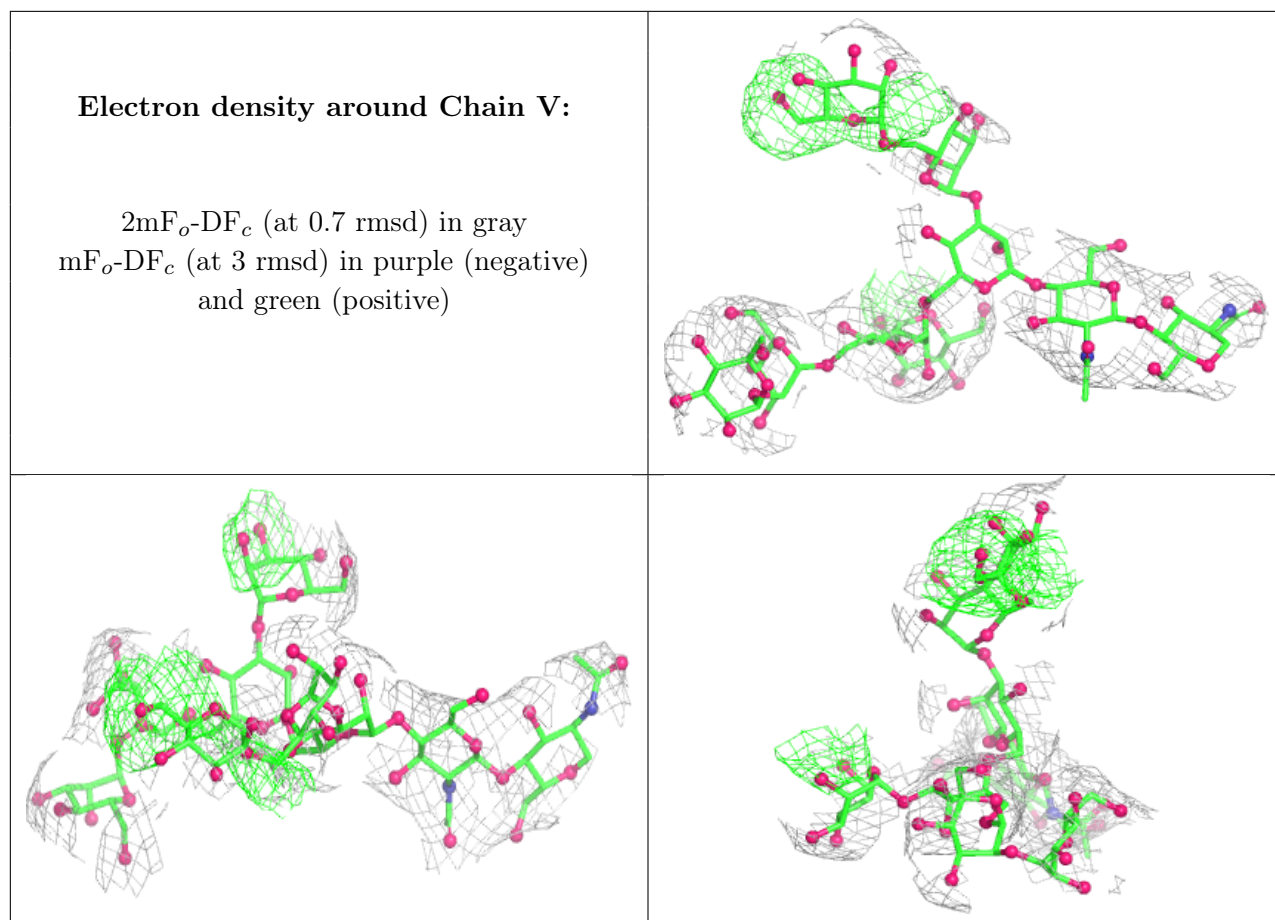




Electron density around Chain S:

$2mF_o-DF_c$ (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
19	NAG	B	701	14/15	0.43	0.16	243,269,290,304	0
19	NAG	G	603	14/15	0.57	0.13	287,309,323,326	0
19	NAG	G	602	14/15	0.63	0.14	213,276,292,301	0
19	NAG	G	601	14/15	0.65	0.11	248,277,292,297	0

6.5 Other polymers [i](#)

There are no such residues in this entry.