



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:08 AM UTC

PDB ID : 8W0Y / pdb_00008w0y
Title : Crystal structure of broadly neutralizing antibody hcab17 in complex with Hepatitis C virus envelope glycoprotein E2 ectodomain
Authors : Flyak, A.I.; Wilcox, X.E.
Deposited on : 2024-02-14
Resolution : 3.31 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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

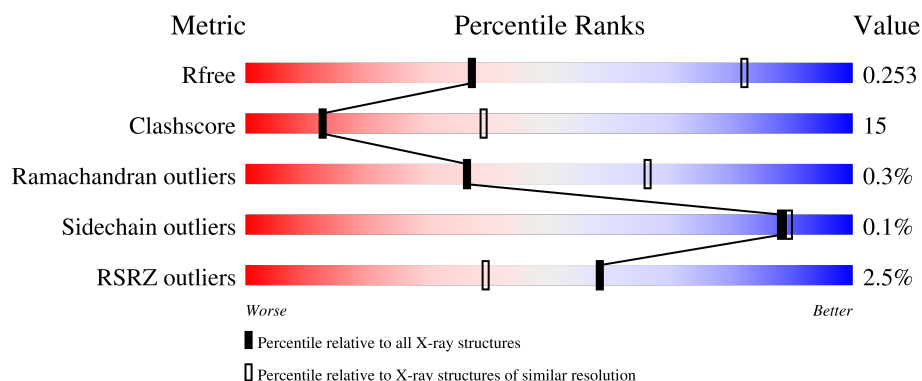
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1153 (3.34-3.30)
Clashscore	190562	1193 (3.34-3.30)
Ramachandran outliers	187476	1172 (3.34-3.30)
Sidechain outliers	187428	1171 (3.34-3.30)
RSRZ outliers	180081	1153 (3.34-3.30)

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	236	68% 28% .
1	H	236	69% 25% 5%
2	B	214	% 67% 32%
2	L	214	% 66% 33%
3	C	262	6% 63% 30% 6%

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Mol	Chain	Length	Quality of chain
3	D	262	 4% 62% 29% 8%
4	E	2	 100%
4	F	2	 100%
4	I	2	 50% 50%
4	K	2	 100%
4	M	2	 50% 50%
4	O	2	 50% 50%
4	P	2	 50% 50%
5	G	5	 40% 60%
6	J	3	 100%
6	N	3	 100%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10803 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called hcab17 Fab Heavy Chain.

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

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

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

- Molecule 3 is a protein called Envelope glycoprotein E2.

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

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



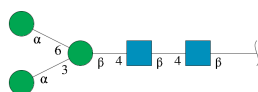
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

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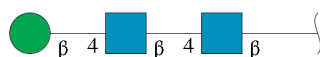
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	O	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



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

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



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

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

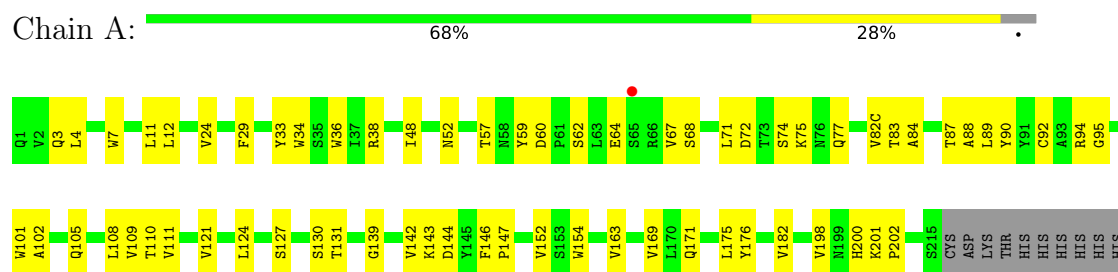
- Molecule 8 is water.

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

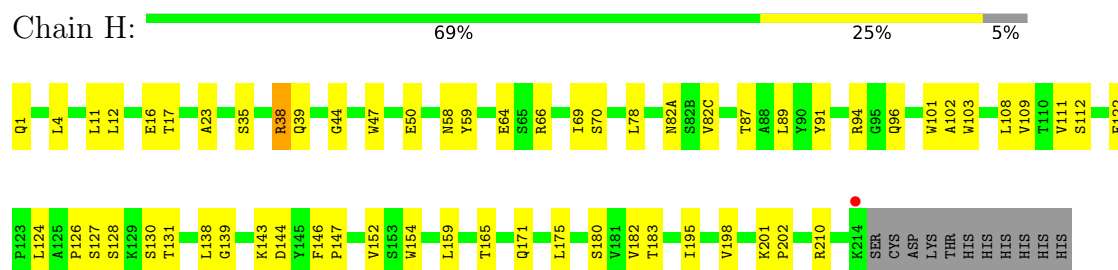
3 Residue-property plots

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

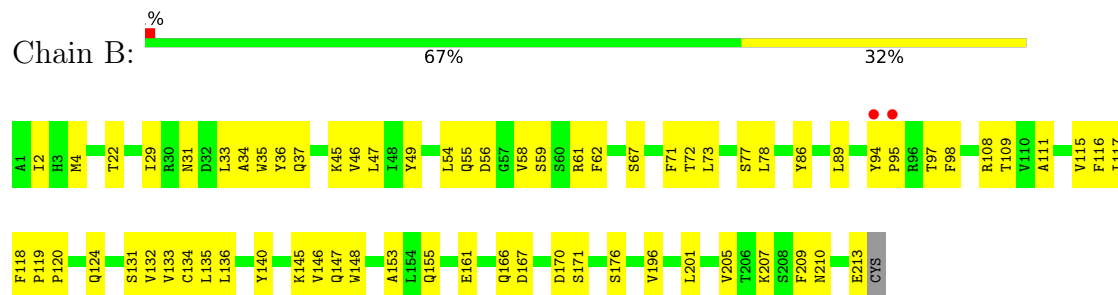
• Molecule 1: hcab17 Fab Heavy Chain



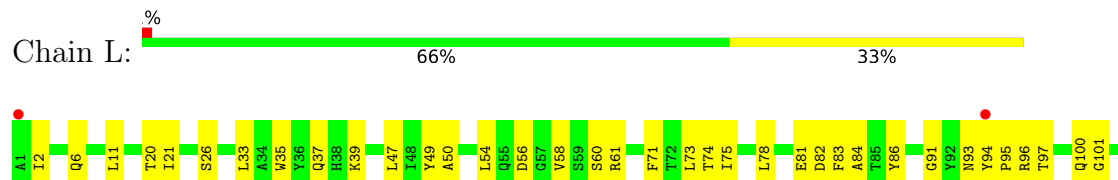
• Molecule 1: hcab17 Fab Heavy Chain



• Molecule 2: hcab17 Fab Light Chain

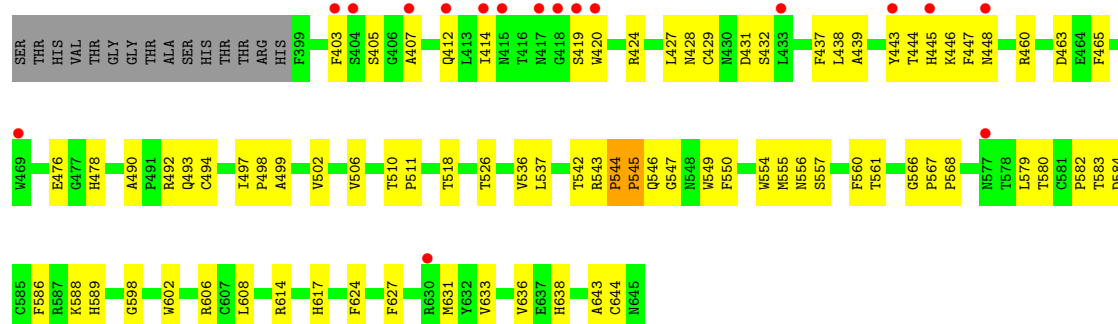


• Molecule 2: hcab17 Fab Light Chain

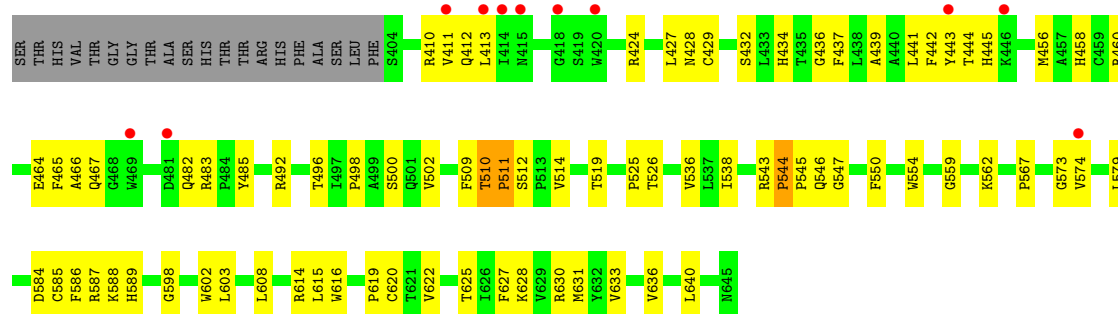




- Molecule 3: Envelope glycoprotein E2



- Molecule 3: Envelope glycoprotein E2



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



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

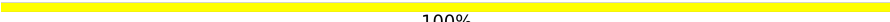


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  50% 50%

MAG1
MAG2

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

Chain K:  100%

MAG1
MAG2

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

Chain M:  50% 50%

MAG1
MAG2

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

Chain O:  50% 50%

MAG1
MAG2

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

Chain P:  50% 50%

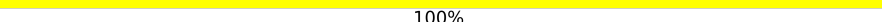
MAG1
MAG2

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

Chain G:  40% 60%

MAG1
MAG2
BMA3
MAN4
MAN5

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

Chain J:  100%

MAG1
MAG2
BMA3

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

Chain N:

100%

MAG1
MAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	179.41Å 179.41Å 168.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	77.69 – 3.31 77.69 – 3.31	Depositor EDS
% Data completeness (in resolution range)	99.8 (77.69-3.31) 99.8 (77.69-3.31)	Depositor EDS
R_{merge}	0.48	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.209 , 0.253 0.209 , 0.253	Depositor DCC
R_{free} test set	2252 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	94.1	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 105.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.039 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10803	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% of the height of the origin peak. No significant pseudotranslation is detected.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, NAG, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.33	0/1726	0.59	0/2358
1	H	0.39	0/1720	0.62	0/2350
2	B	0.33	0/1673	0.57	0/2270
2	L	0.36	0/1684	0.62	2/2285 (0.1%)
3	C	0.36	0/1992	0.63	0/2726
3	D	0.35	0/1949	0.59	0/2668
All	All	0.35	0/10744	0.60	2/14657 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	2
3	C	0	2
3	D	0	3
All	All	0	7

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	50	ALA	CA-C-N	5.15	131.37	121.54
2	L	50	ALA	C-N-CA	5.15	131.37	121.54

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

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

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1684	0	1641	54	1
1	H	1678	0	1636	51	0
2	B	1637	0	1591	51	1
2	L	1644	0	1598	56	0
3	C	1924	0	1778	66	0
3	D	1883	0	1740	63	0
4	E	28	0	25	3	0
4	F	28	0	25	0	0
4	I	28	0	25	1	0
4	K	28	0	25	0	0
4	M	28	0	25	0	0
4	O	28	0	25	1	0
4	P	28	0	25	0	0
5	G	61	0	52	0	0
6	J	39	0	34	0	0
6	N	39	0	34	2	0
7	C	14	0	13	1	0
8	A	1	0	0	0	0
8	C	2	0	0	0	0
8	D	1	0	0	0	0
All	All	10803	0	10292	320	1

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

The worst 5 of 320 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:1:NAG:H61	4:E:2:NAG:HN2	1.36	0.90
2:L:94:TYR:CG	2:L:95:PRO:HD3	2.08	0.87
3:D:456:MET:HE1	3:D:485:TYR:HB2	1.61	0.81
1:A:3:GLN:H	6:N:1:NAG:H81	1.43	0.81
1:A:60:ASP:OD2	1:A:62:SER:HB3	1.82	0.80

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

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	224/236 (95%)	217 (97%)	7 (3%)	0	100	100
1	H	223/236 (94%)	212 (95%)	11 (5%)	0	100	100
2	B	211/214 (99%)	197 (93%)	14 (7%)	0	100	100
2	L	212/214 (99%)	197 (93%)	15 (7%)	0	100	100
3	C	245/262 (94%)	203 (83%)	40 (16%)	2 (1%)	16	45
3	D	240/262 (92%)	206 (86%)	32 (13%)	2 (1%)	16	45
All	All	1355/1424 (95%)	1232 (91%)	119 (9%)	4 (0%)	36	66

All (4) Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/200 (95%)	190 (100%)	0	100	100
1	H	189/200 (94%)	189 (100%)	0	100	100
2	B	184/185 (100%)	184 (100%)	0	100	100
2	L	185/185 (100%)	184 (100%)	1 (0%)	81	82
3	C	207/219 (94%)	207 (100%)	0	100	100
3	D	203/219 (93%)	203 (100%)	0	100	100
All	All	1158/1208 (96%)	1157 (100%)	1 (0%)	88	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	176	SER

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

Mol	Chain	Res	Type
2	L	137	ASN
2	L	152	ASN
2	L	189	HIS
3	D	428	ASN
3	D	458	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

25 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	NAG	E	1	3,4	14,14,15	0.39	0	17,19,21	1.48	3 (17%)
4	NAG	E	2	4	14,14,15	0.57	0	17,19,21	1.44	2 (11%)
4	NAG	F	1	3,4	14,14,15	0.59	0	17,19,21	0.77	1 (5%)
4	NAG	F	2	4	14,14,15	0.57	0	17,19,21	0.90	1 (5%)
5	NAG	G	1	3,5	14,14,15	0.39	0	17,19,21	0.87	0
5	NAG	G	2	5	14,14,15	0.41	0	17,19,21	1.10	2 (11%)
5	BMA	G	3	5	11,11,12	1.18	0	15,15,17	0.87	0
5	MAN	G	4	5	11,11,12	1.45	4 (36%)	15,15,17	1.52	1 (6%)
5	MAN	G	5	5	11,11,12	1.35	2 (18%)	15,15,17	1.06	1 (6%)
4	NAG	I	1	3,4	14,14,15	0.33	0	17,19,21	1.01	2 (11%)
4	NAG	I	2	4	14,14,15	0.47	0	17,19,21	0.83	0
6	NAG	J	1	6,3	14,14,15	0.52	0	17,19,21	1.56	4 (23%)
6	NAG	J	2	6	14,14,15	0.83	1 (7%)	17,19,21	1.41	1 (5%)
6	BMA	J	3	6	11,11,12	2.02	3 (27%)	15,15,17	1.17	1 (6%)
4	NAG	K	1	3,4	14,14,15	0.45	0	17,19,21	1.20	2 (11%)
4	NAG	K	2	4	14,14,15	0.67	0	17,19,21	1.01	1 (5%)
4	NAG	M	1	3,4	14,14,15	0.52	0	17,19,21	1.20	2 (11%)
4	NAG	M	2	4	14,14,15	0.55	0	17,19,21	0.86	0
6	NAG	N	1	6,3	14,14,15	0.35	0	17,19,21	0.66	0
6	NAG	N	2	6	14,14,15	0.38	0	17,19,21	0.80	1 (5%)
6	BMA	N	3	6	11,11,12	1.25	1 (9%)	15,15,17	0.72	0
4	NAG	O	1	3,4	14,14,15	0.36	0	17,19,21	1.52	3 (17%)
4	NAG	O	2	4	14,14,15	0.58	0	17,19,21	0.78	0
4	NAG	P	1	3,4	14,14,15	0.63	0	17,19,21	1.95	5 (29%)
4	NAG	P	2	4	14,14,15	0.39	0	17,19,21	0.81	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	1	3,4	-	4/6/23/26	0/1/1/1
4	NAG	E	2	4	-	3/6/23/26	0/1/1/1
4	NAG	F	1	3,4	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
5	NAG	G	1	3,5	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	0/1/1/1
5	MAN	G	5	5	-	0/2/19/22	0/1/1/1
4	NAG	I	1	3,4	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
6	NAG	J	1	6,3	-	3/6/23/26	0/1/1/1
6	NAG	J	2	6	-	3/6/23/26	0/1/1/1
6	BMA	J	3	6	-	1/2/19/22	0/1/1/1
4	NAG	K	1	3,4	-	3/6/23/26	0/1/1/1
4	NAG	K	2	4	-	4/6/23/26	0/1/1/1
4	NAG	M	1	3,4	-	3/6/23/26	0/1/1/1
4	NAG	M	2	4	-	3/6/23/26	0/1/1/1
6	NAG	N	1	6,3	-	4/6/23/26	0/1/1/1
6	NAG	N	2	6	-	1/6/23/26	0/1/1/1
6	BMA	N	3	6	-	1/2/19/22	0/1/1/1
4	NAG	O	1	3,4	-	3/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	NAG	P	1	3,4	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	2/6/23/26	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	3	BMA	C2-C3	3.94	1.58	1.52
6	J	3	BMA	O5-C5	3.73	1.50	1.43
5	G	5	MAN	C1-C2	2.93	1.59	1.52
6	J	3	BMA	O5-C1	2.91	1.48	1.43
5	G	4	MAN	C1-C2	2.51	1.58	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	4	MAN	C1-O5-C5	5.13	119.06	112.19
4	E	2	NAG	C2-N2-C7	4.56	129.02	122.90
6	J	2	NAG	O5-C1-C2	-4.53	104.28	111.29
4	P	1	NAG	O5-C1-C2	-4.43	104.44	111.29
6	J	1	NAG	O4-C4-C5	-4.22	98.94	109.32

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

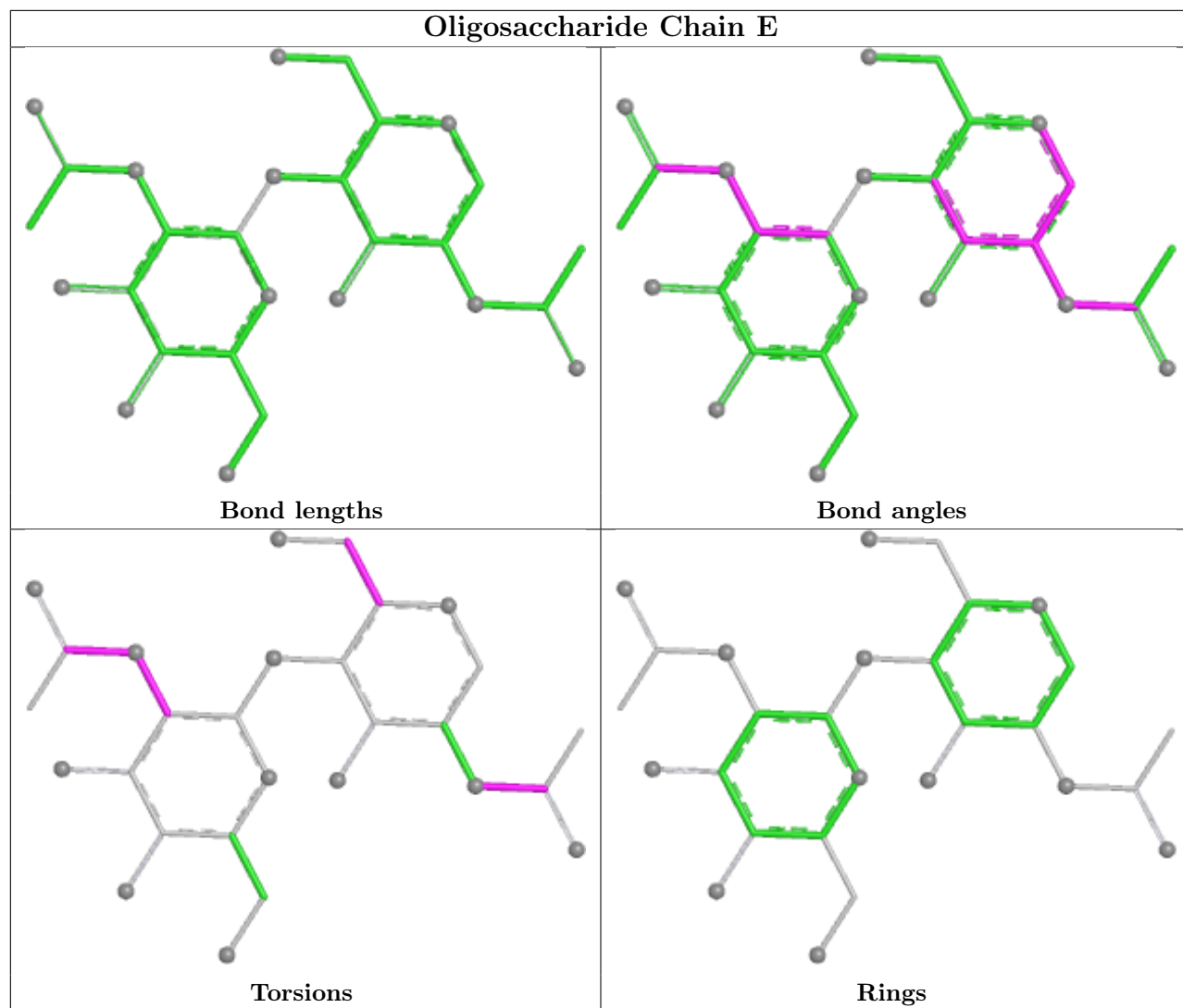
Mol	Chain	Res	Type	Atoms
4	E	2	NAG	C3-C2-N2-C7
4	E	2	NAG	C8-C7-N2-C2
4	E	2	NAG	O7-C7-N2-C2
4	F	1	NAG	O7-C7-N2-C2
4	F	2	NAG	C8-C7-N2-C2

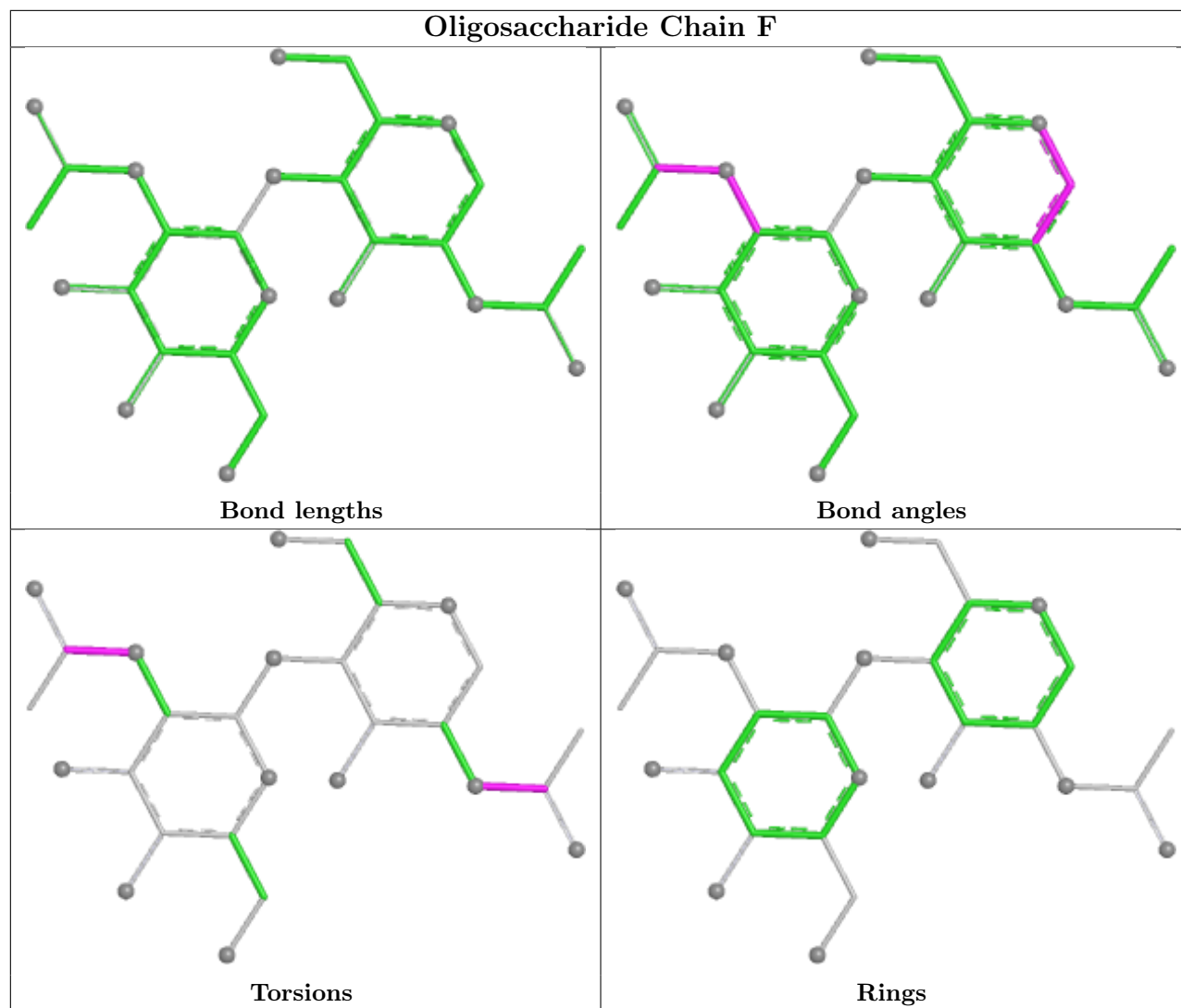
There are no ring outliers.

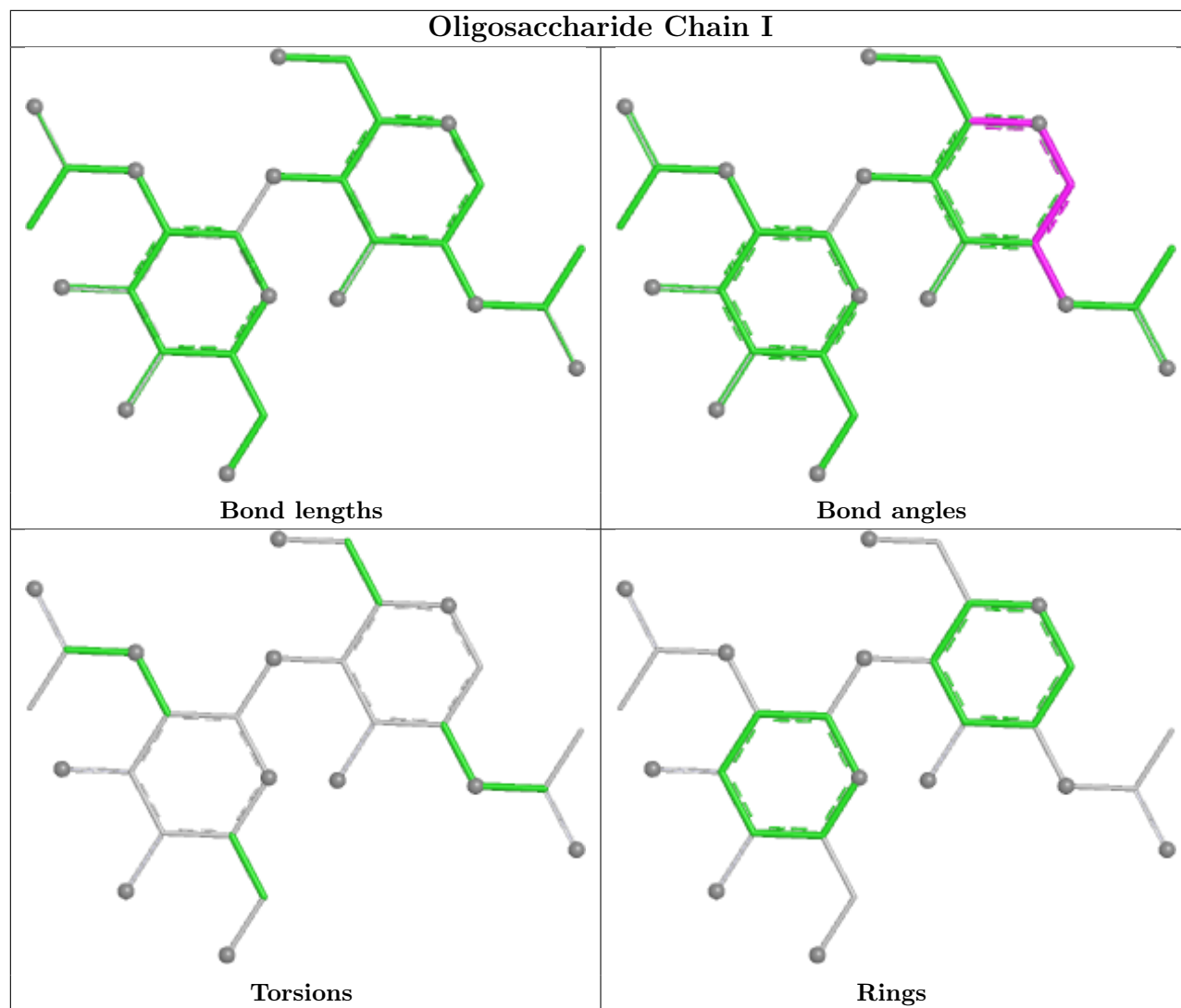
6 monomers are involved in 7 short contacts:

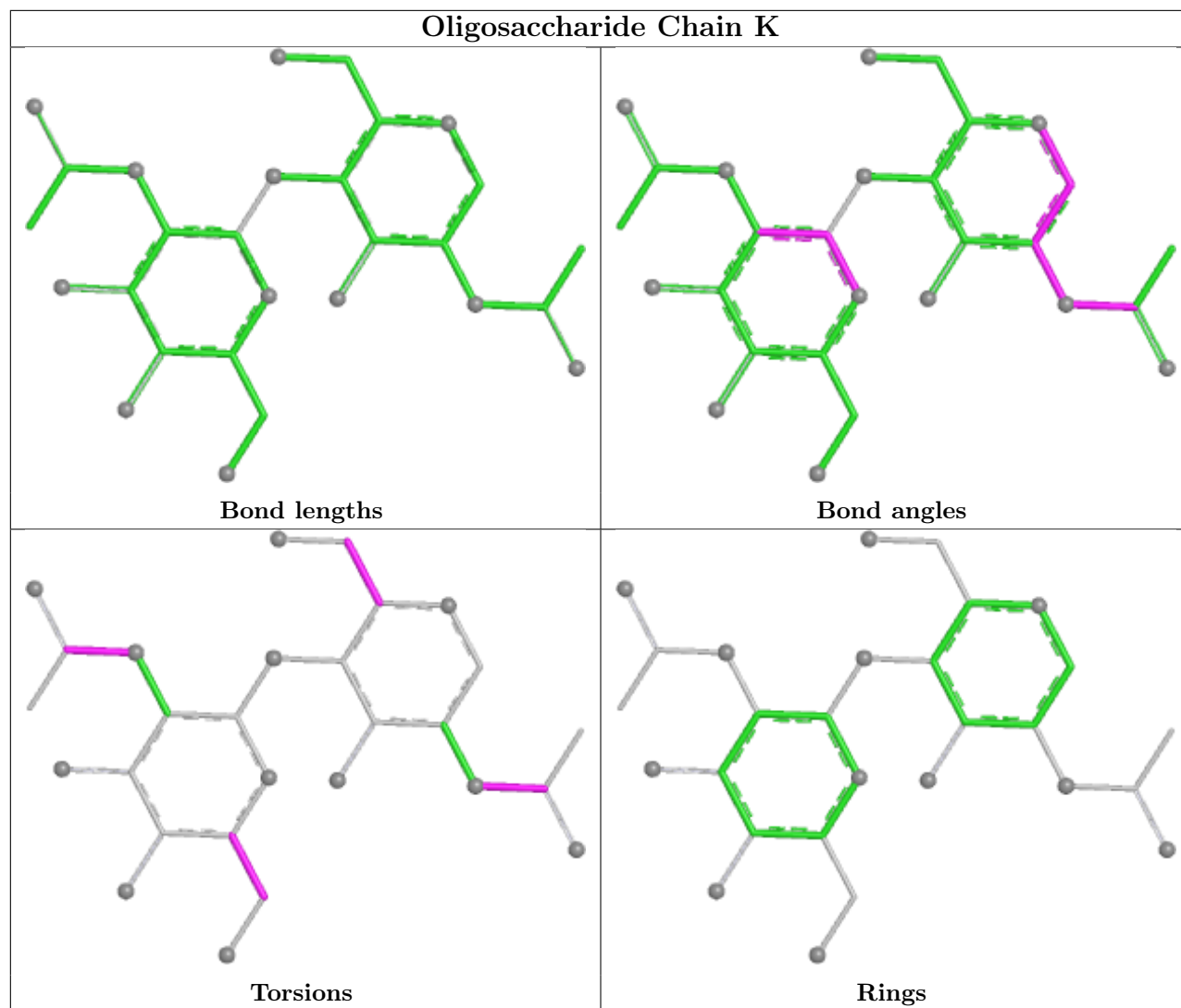
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	1	NAG	1	0
4	E	2	NAG	2	0
4	I	2	NAG	1	0
6	N	1	NAG	2	0
4	O	1	NAG	1	0
4	E	1	NAG	3	0

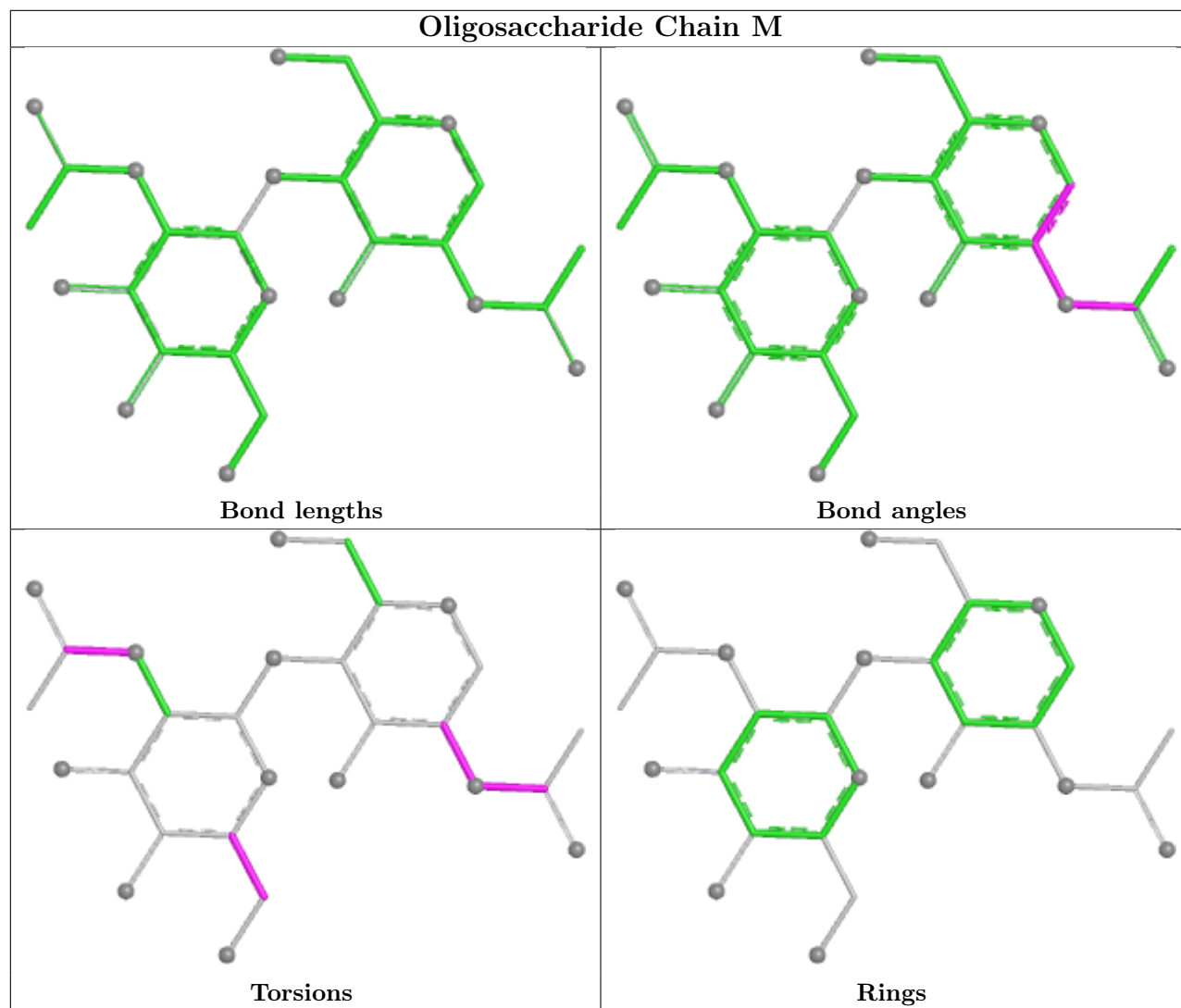
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

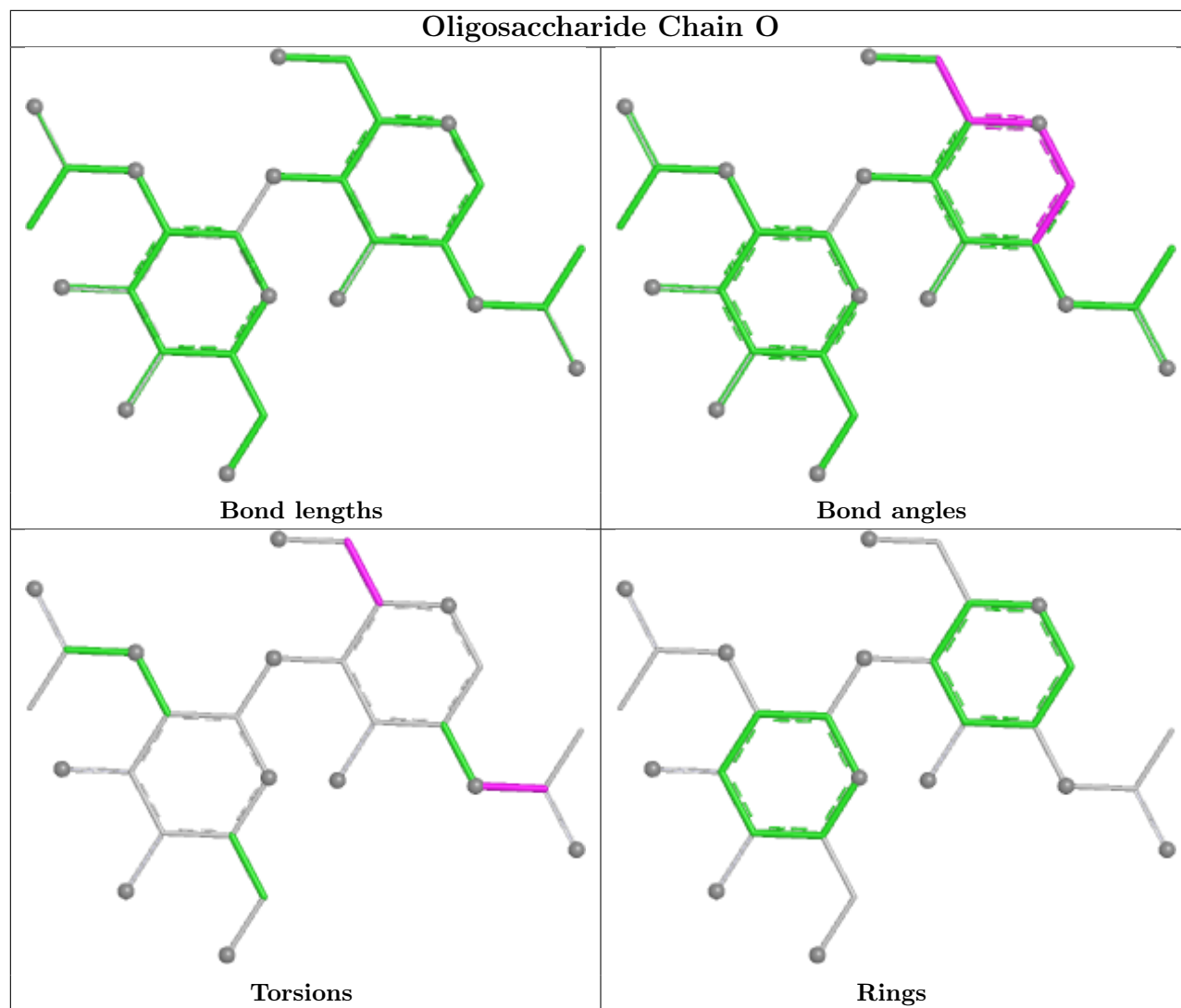


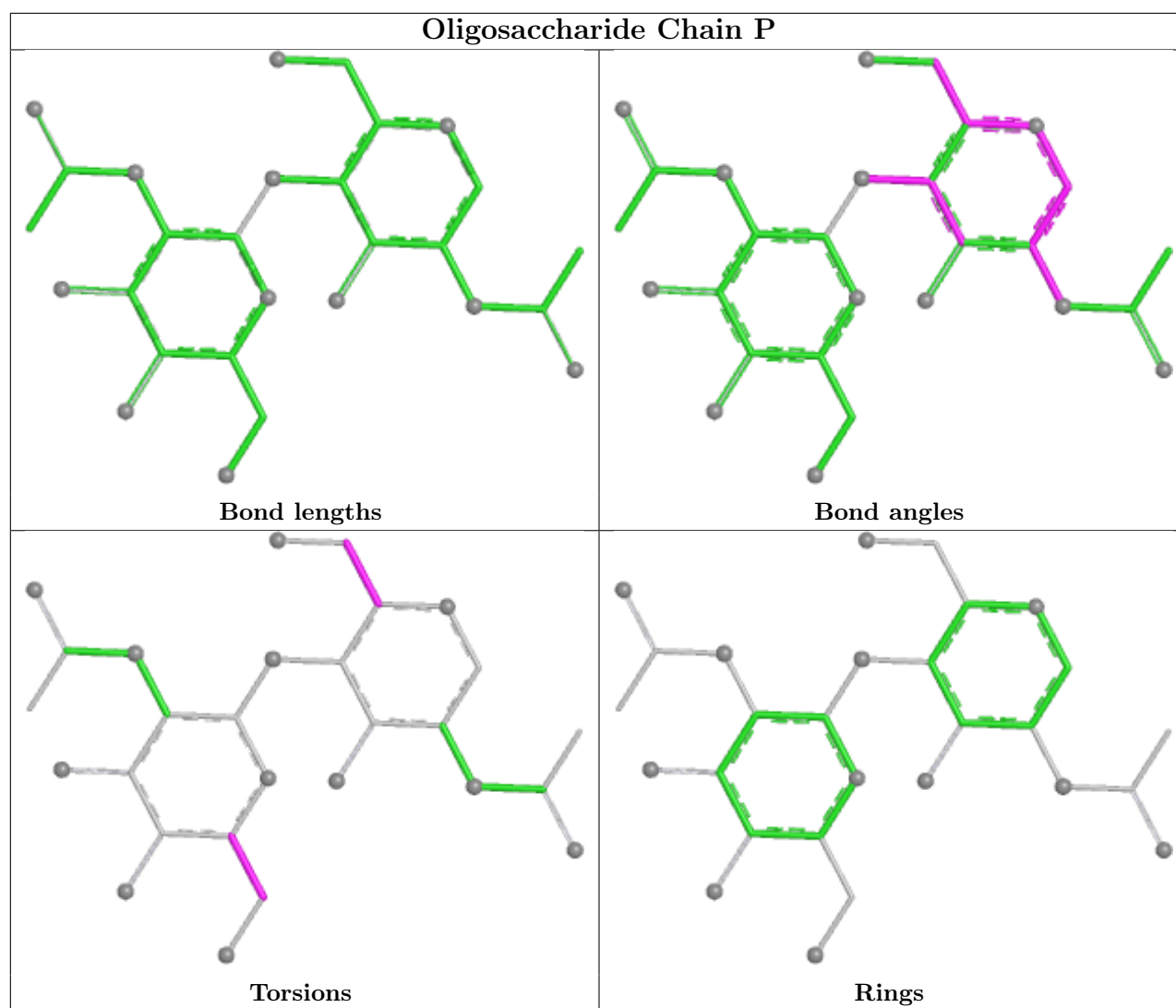


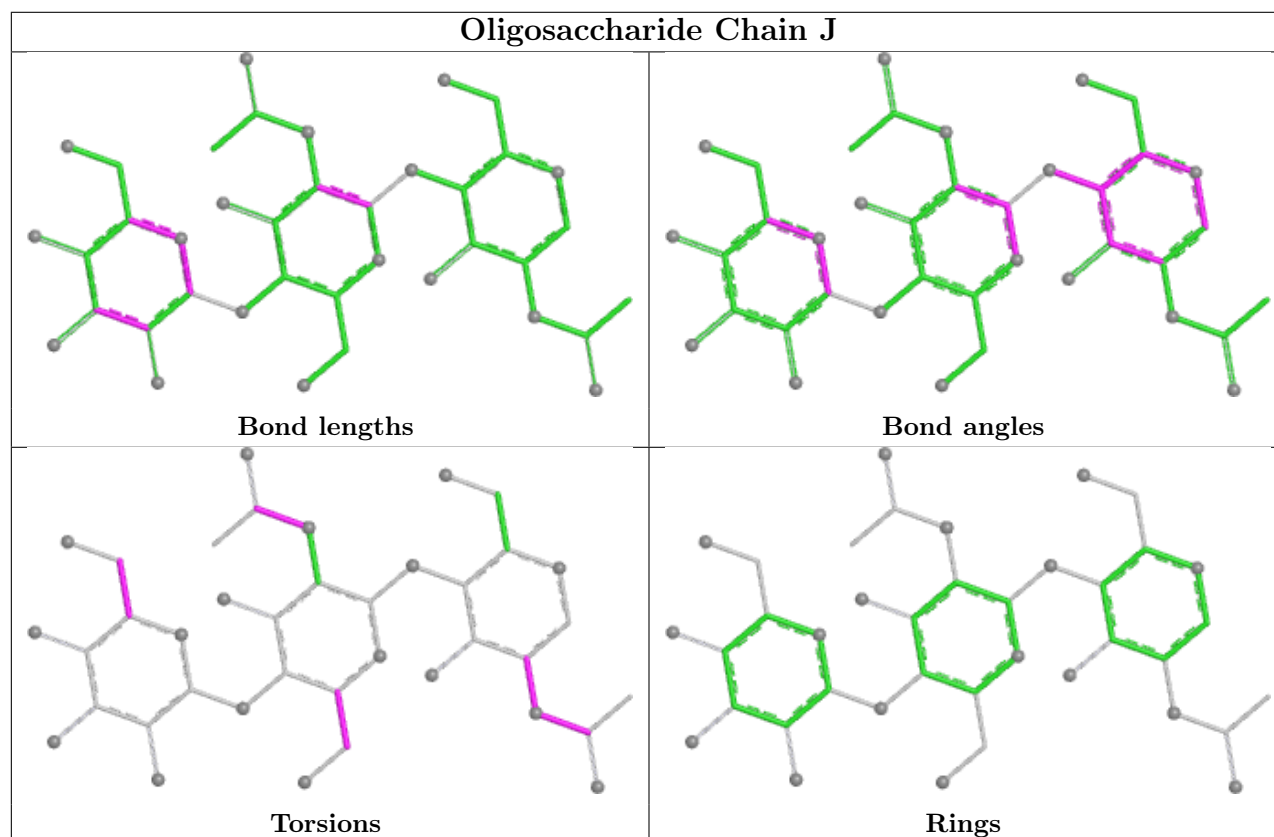
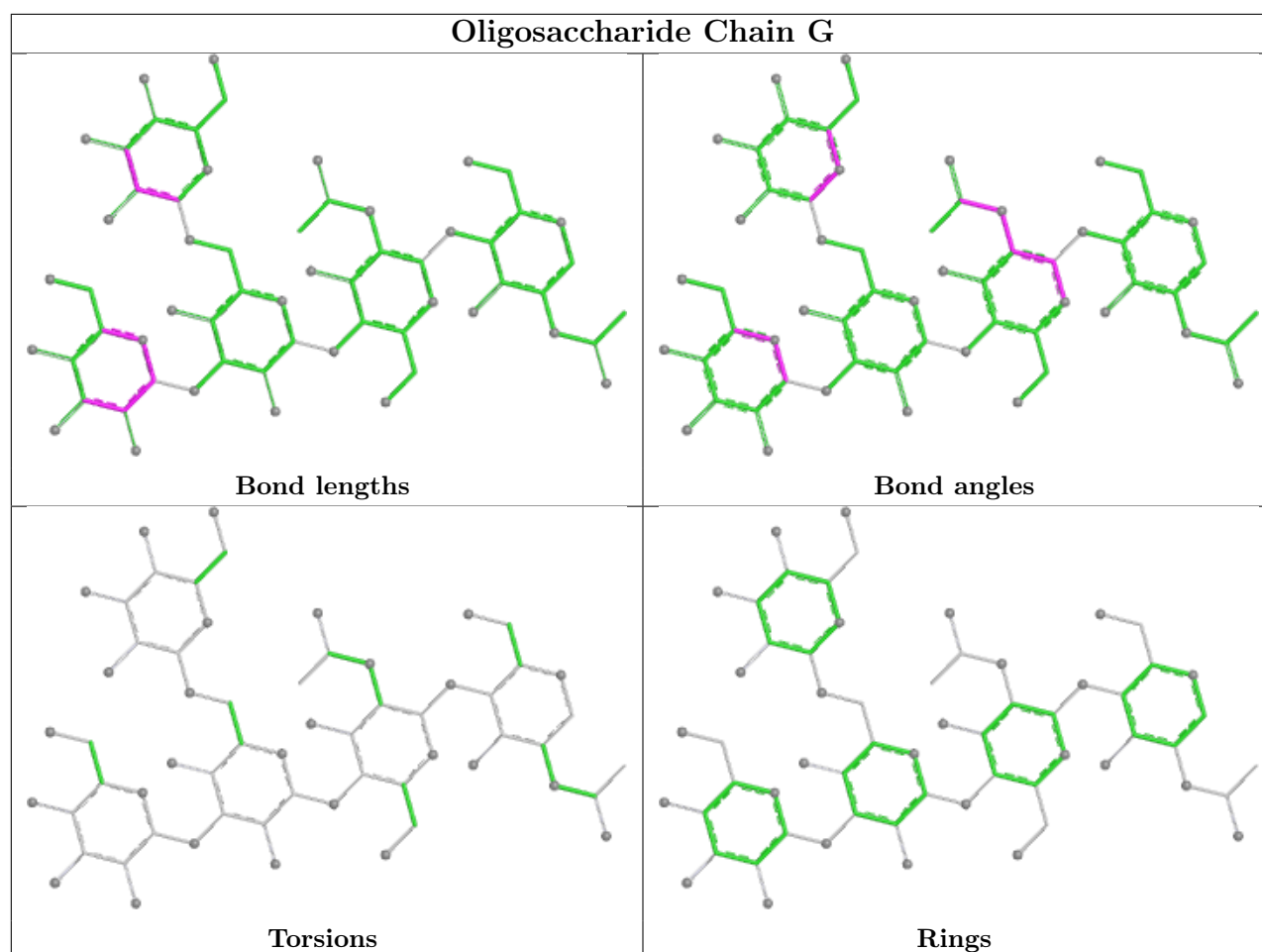


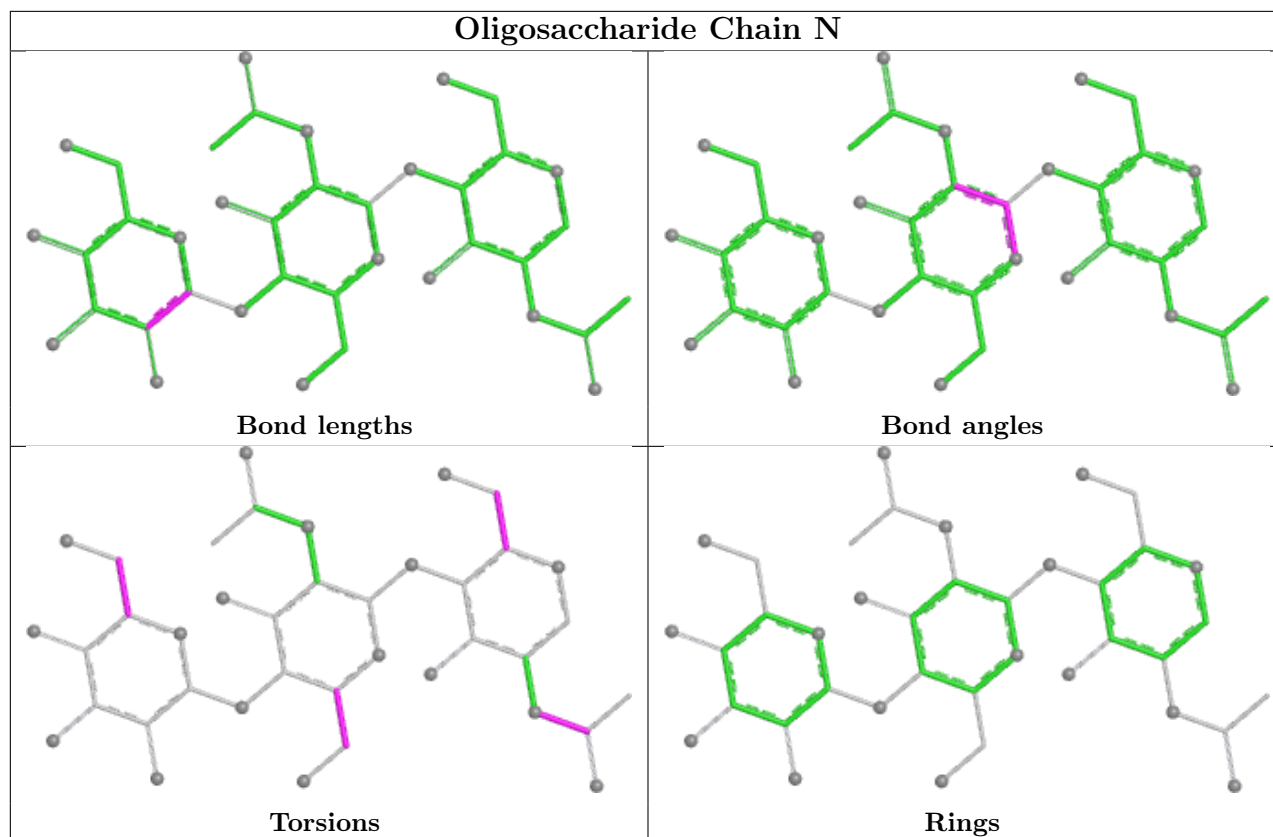












5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
7	NAG	C	701	3	14,14,15	0.56	0	17,19,21	0.79	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	C	701	3	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
7	C	701	NAG	O5-C5-C6	2.05	111.66	107.66

There are no chirality outliers.

All (4) torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	701	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	226/236 (95%)	-0.23	1 (0%) 88 79	71, 92, 121, 170	0
1	H	225/236 (95%)	-0.23	1 (0%) 88 79	59, 85, 134, 198	0
2	B	213/214 (99%)	-0.22	2 (0%) 81 66	68, 95, 140, 191	0
2	L	213/214 (99%)	-0.17	2 (0%) 81 66	49, 95, 146, 174	1 (0%)
3	C	247/262 (94%)	0.14	17 (6%) 23 16	69, 95, 168, 228	0
3	D	242/262 (92%)	0.12	11 (4%) 38 25	71, 100, 172, 205	0
All	All	1366/1424 (95%)	-0.09	34 (2%) 58 39	49, 94, 152, 228	1 (0%)

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	574	VAL	4.2
3	C	403	PHE	3.9
3	D	420	TRP	3.3
3	D	469	TRP	3.3
3	C	407	ALA	3.2

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

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

6.3 Carbohydrates [i](#)

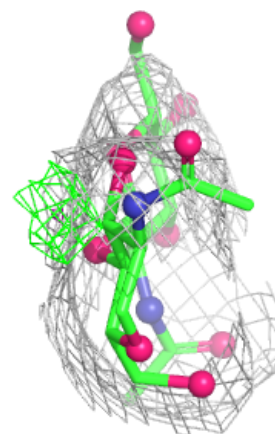
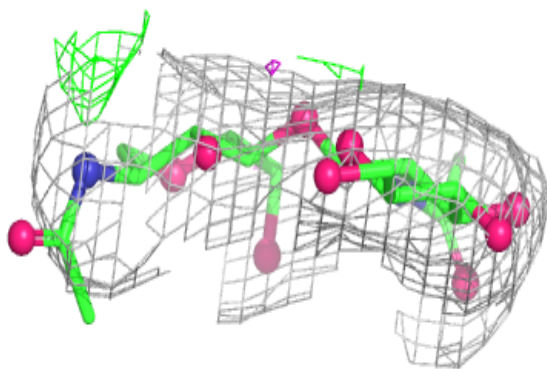
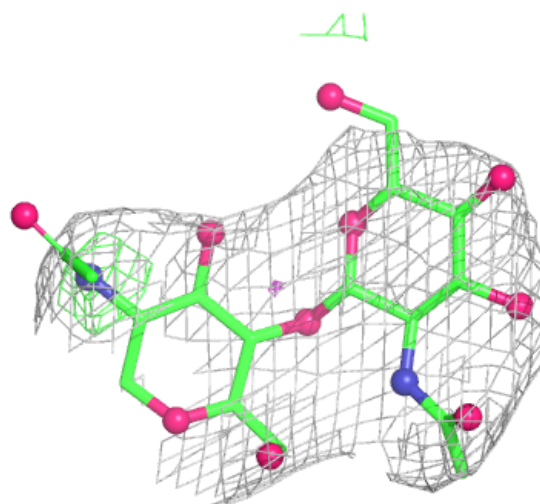
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	E	1	14/15	-	-	116,125,136,142	0
4	NAG	E	2	14/15	-	-	129,140,142,144	0
4	NAG	F	1	14/15	-	-	116,125,137,144	0
4	NAG	F	2	14/15	-	-	146,150,156,156	0
6	BMA	N	3	11/12	0.43	0.14	146,148,153,154	0
4	NAG	M	2	14/15	0.61	0.11	149,158,162,164	0
5	NAG	G	2	14/15	0.71	0.12	109,122,144,158	0
4	NAG	K	2	14/15	0.72	0.12	152,167,173,176	0
4	NAG	M	1	14/15	0.75	0.11	124,132,138,145	0
4	NAG	O	2	14/15	0.79	0.11	116,122,132,135	0
6	NAG	J	2	14/15	0.80	0.10	140,152,157,158	0
5	NAG	G	1	14/15	0.80	0.14	72,89,102,114	0
4	NAG	I	2	14/15	0.82	0.10	119,126,137,140	0
6	NAG	N	2	14/15	0.83	0.10	109,121,134,140	0
4	NAG	P	2	14/15	0.86	0.10	134,139,150,153	0
4	NAG	O	1	14/15	0.86	0.09	105,108,112,116	0
5	BMA	G	3	11/12	-	-	166,169,175,185	0
5	MAN	G	4	11/12	-	-	165,169,174,174	0
5	MAN	G	5	11/12	-	-	148,158,163,165	0
4	NAG	K	1	14/15	0.87	0.11	111,135,153,160	0
4	NAG	P	1	14/15	0.91	0.11	105,126,132,139	0
6	BMA	J	3	11/12	-	-	142,158,164,164	0
6	NAG	N	1	14/15	0.91	0.09	81,96,107,115	0
6	NAG	J	1	14/15	0.92	0.09	131,137,148,152	0
4	NAG	I	1	14/15	0.93	0.10	105,112,120,121	0

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

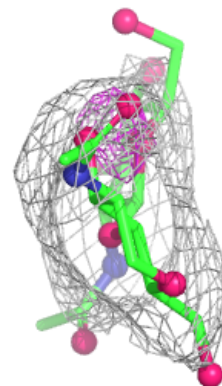
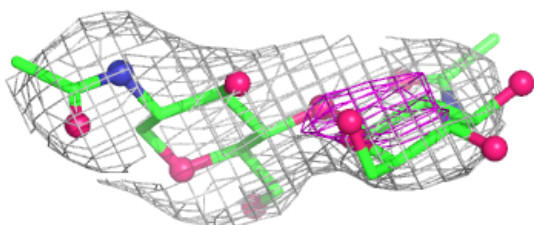
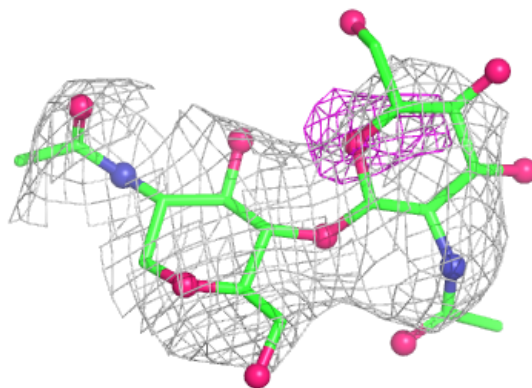
Electron density around Chain E:

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

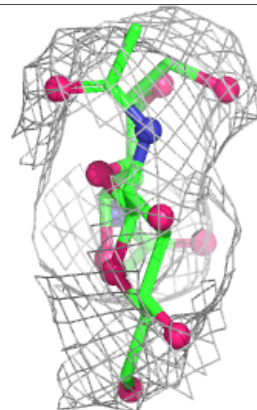
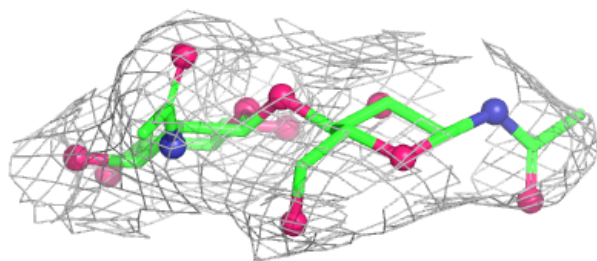
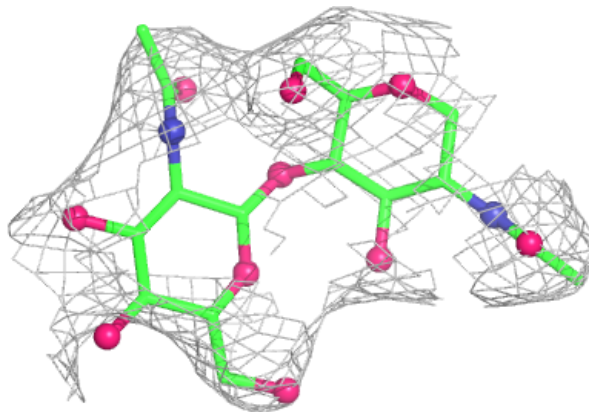


Electron density around Chain F:

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

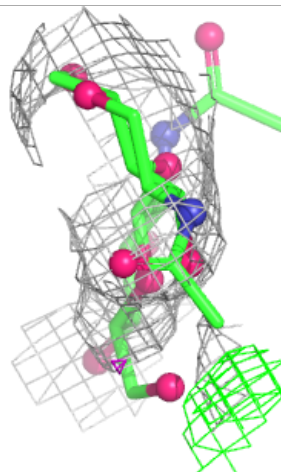
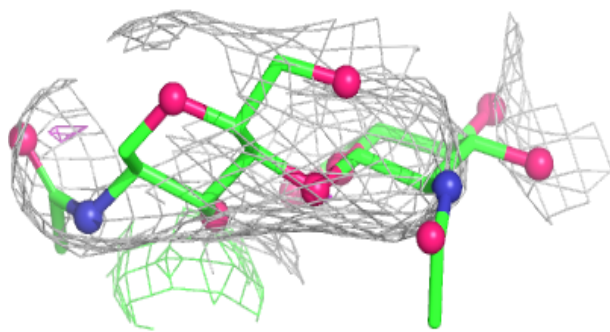
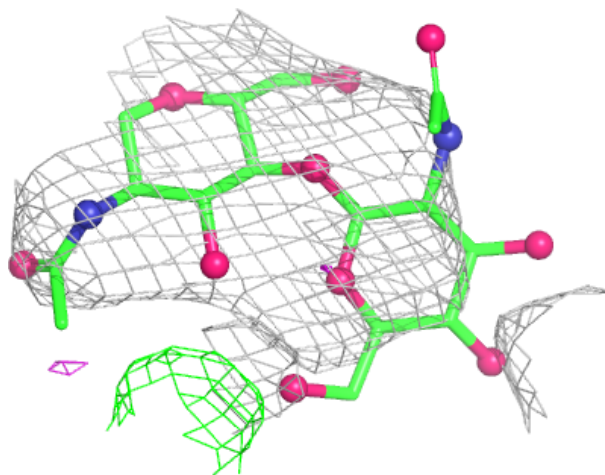
**Electron density around Chain I:**

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



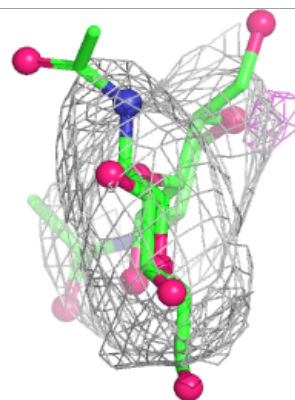
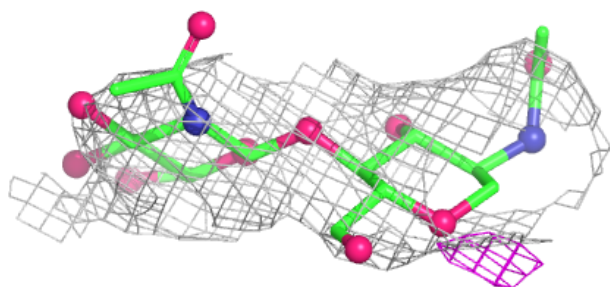
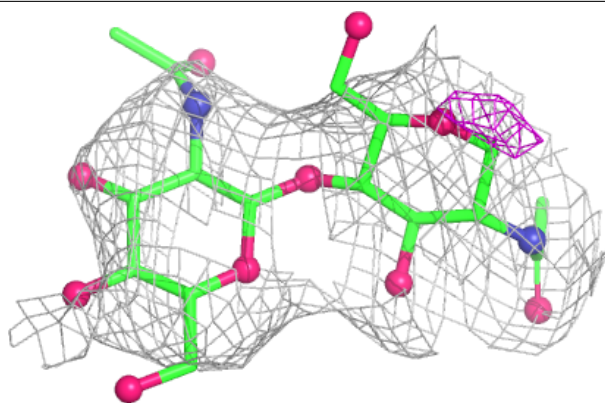
Electron density around Chain K:

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

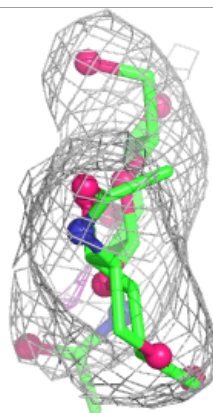
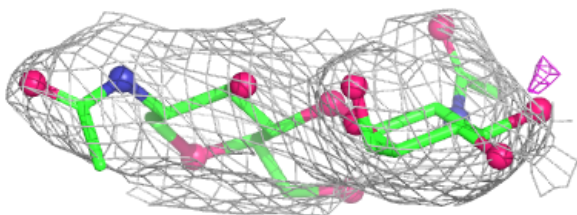
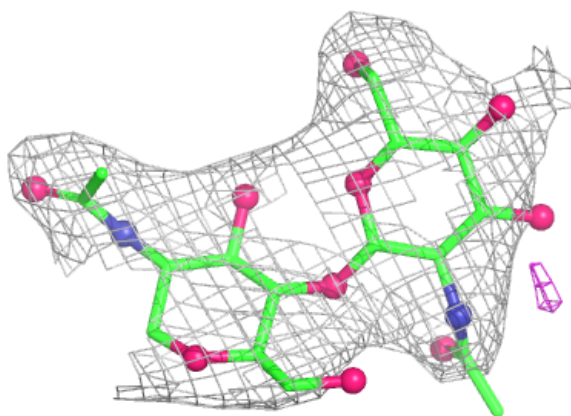


Electron density around Chain M:

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

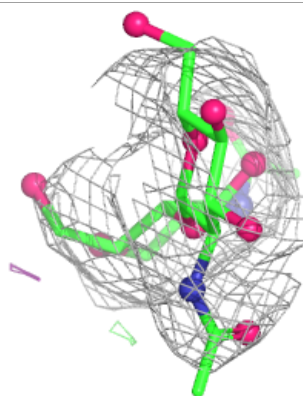
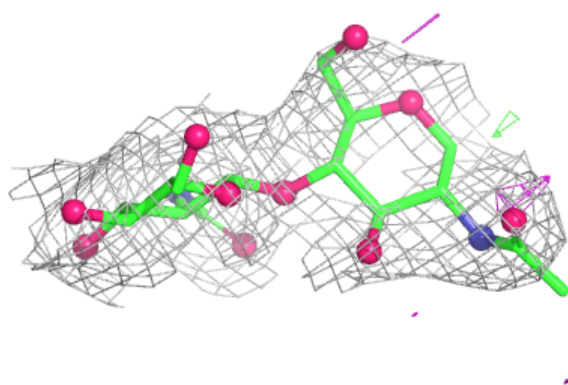
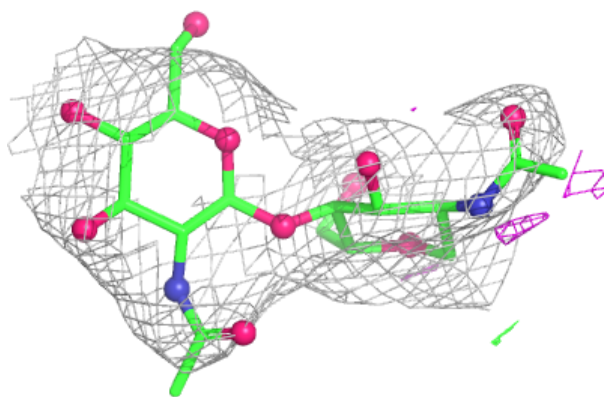
**Electron density around Chain O:**

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

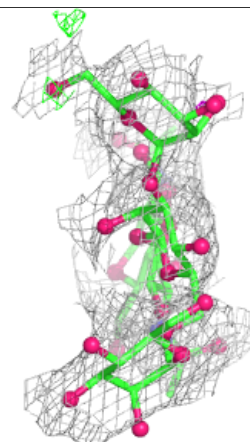
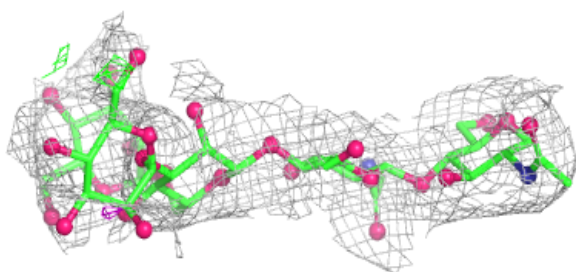
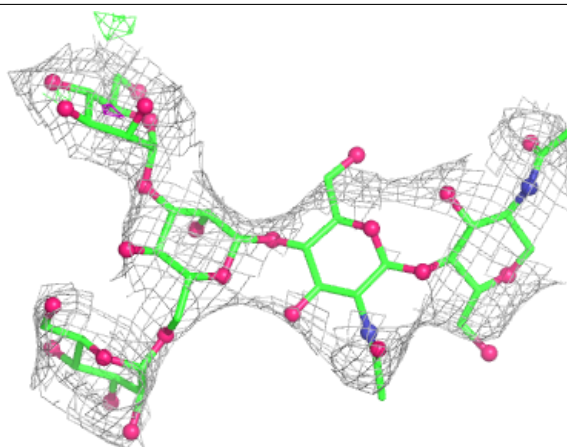


Electron density around Chain P:

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

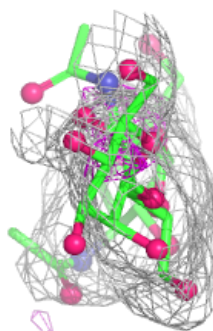
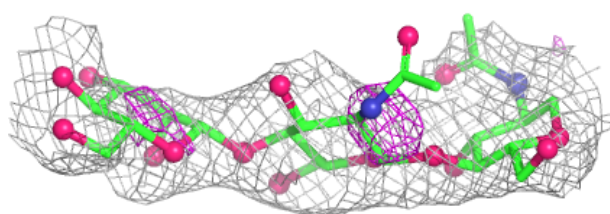
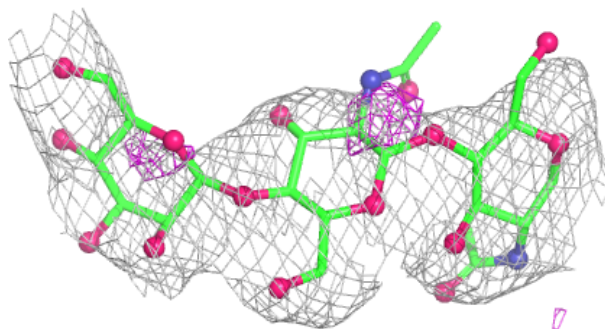
**Electron density around Chain G:**

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

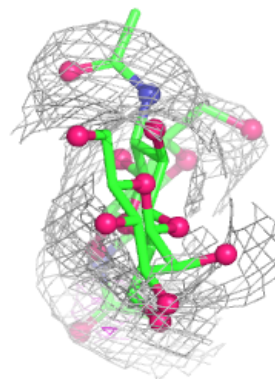
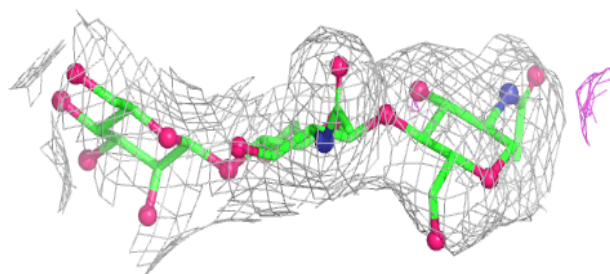
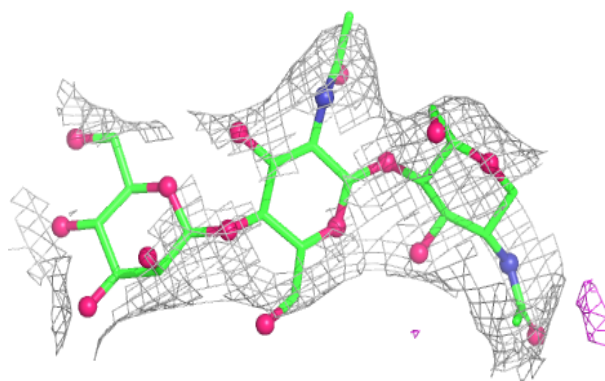


Electron density around Chain J:

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

**Electron density around Chain N:**

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



6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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($\text{\AA}^2$)	Q<0.9
7	NAG	C	701	14/15	0.72	0.19	147,155,162,163	0

6.5 Other polymers [i](#)

There are no such residues in this entry.