



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:27 PM UTC

PDB ID : 5CEZ / pdb_00005cez
Title : Crystal Structure of the BG505 SOSIP gp140 HIV-1 Env trimer in Complex with an early putative precursor of the PGT121 family at 3.0 Angstrom
Authors : Wilson, I.A.; Garces, F.
Deposited on : 2015-07-08
Resolution : 3.03 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

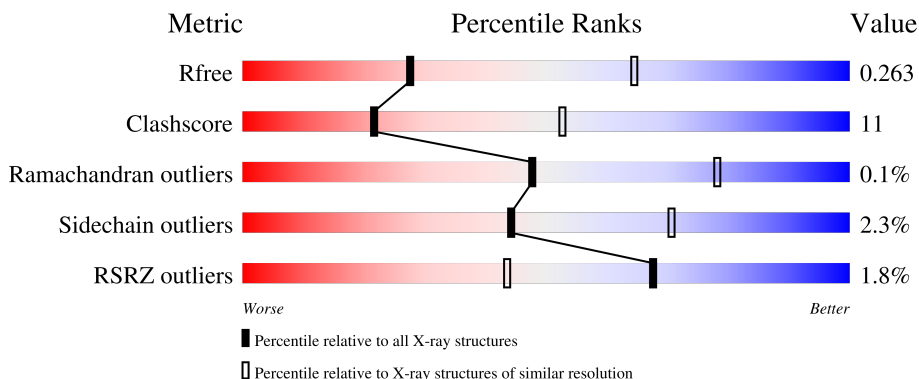
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.03 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	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

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	G	480	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 72%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 21%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: grey;"></div> </div>
2	B	153	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 73%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 22%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div>
3	L	218	<div style="display: flex; align-items: center;"> <div style="width: 1%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 77%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 18%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 4%; height: 10px; background-color: grey;"></div> </div>
4	H	236	<div style="display: flex; align-items: center;"> <div style="width: 1%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 73%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 24%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div>
5	D	240	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 86%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 14%; height: 10px; background-color: yellow; margin-right: 5px;"></div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
6	E	216	
7	A	7	
8	C	2	
8	F	2	
8	I	2	
8	J	2	
8	K	2	
8	M	2	
9	N	5	
10	O	4	
11	P	6	
12	Q	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
12	MAN	Q	6	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 12135 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 gp160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	G	452	3544	2224	625	668	27	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	137	ALA	ASN	engineered mutation	UNP Q2N0S6
G	332	ASN	THR	engineered mutation	UNP Q2N0S6
G	501	CYS	ALA	engineered mutation	UNP Q2N0S6
G	509	ARG	GLU	insertion	UNP Q2N0S6
G	510	ARG	LYS	insertion	UNP Q2N0S6
G	512	ARG	-	insertion	UNP Q2N0S6
G	513	ARG	-	insertion	UNP Q2N0S6

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	147	1171	740	205	220	6	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP Q2N0S6
B	605	CYS	THR	engineered mutation	UNP Q2N0S6

- Molecule 3 is a protein called 3H+109L Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	211	1603	1007	276	315	5	0	0	0

- Molecule 4 is a protein called 3H+109L Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	231	1744	1108	283	347	6	0	0	0

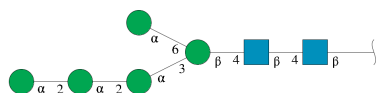
- Molecule 5 is a protein called 35022 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	D	240	1813	1150	303	352	8	0	0	0

- Molecule 6 is a protein called 35022 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	E	213	1615	1012	267	328	8	0	0	0

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-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			
7	A	7	83	46	2	35	0	0	0

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



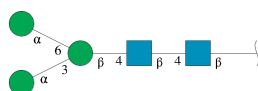
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
8	C	2	28	16	2	10	0	0	0
8	F	2	28	16	2	10	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
8	I	2	Total 28	C 16	N 2	O 10	0	0	0
8	J	2	Total 28	C 16	N 2	O 10	0	0	0
8	K	2	Total 28	C 16	N 2	O 10	0	0	0
8	M	2	Total 28	C 16	N 2	O 10	0	0	0

- Molecule 9 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.



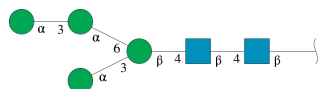
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	N	5	Total 61	C 34	N 2	O 25	0	0	0

- Molecule 10 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.



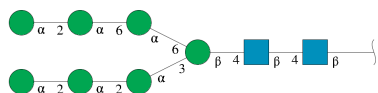
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
10	O	4	Total 50	C 28	N 2	O 20	0	0	0

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-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.



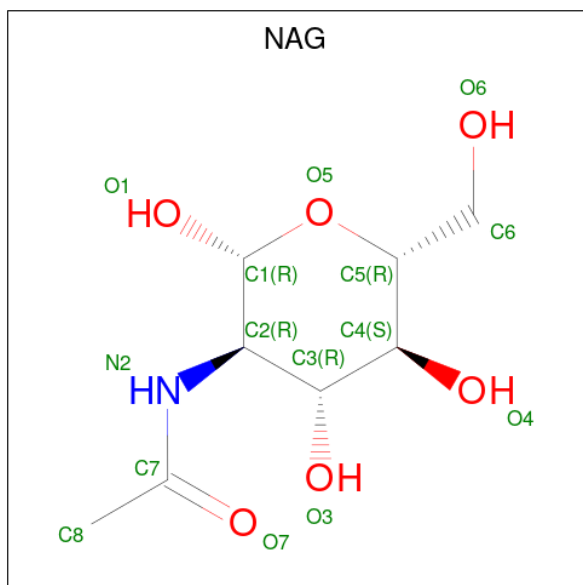
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
11	P	6	72	40	2	30	0	0	0

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-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			
12	Q	9	105	58	2	45	0	0	0

- Molecule 13 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



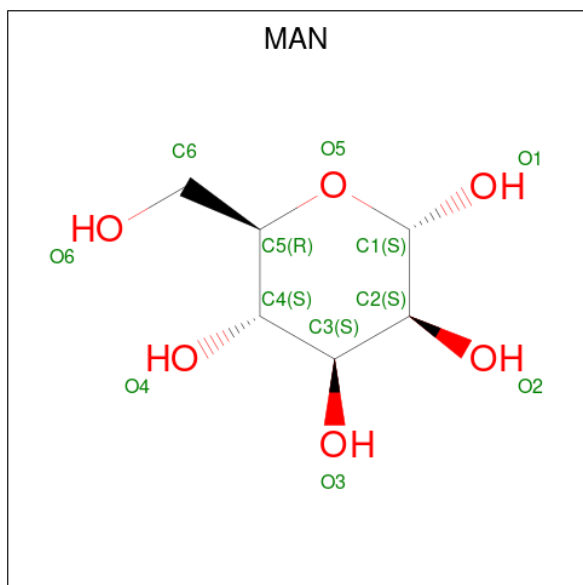
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
13	G	1	14	8	1	5	0	0
13	G	1	14	8	1	5	0	0
13	G	1	14	8	1	5	0	0

Continued on next page...

Continued from previous page...

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

- Molecule 14 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).

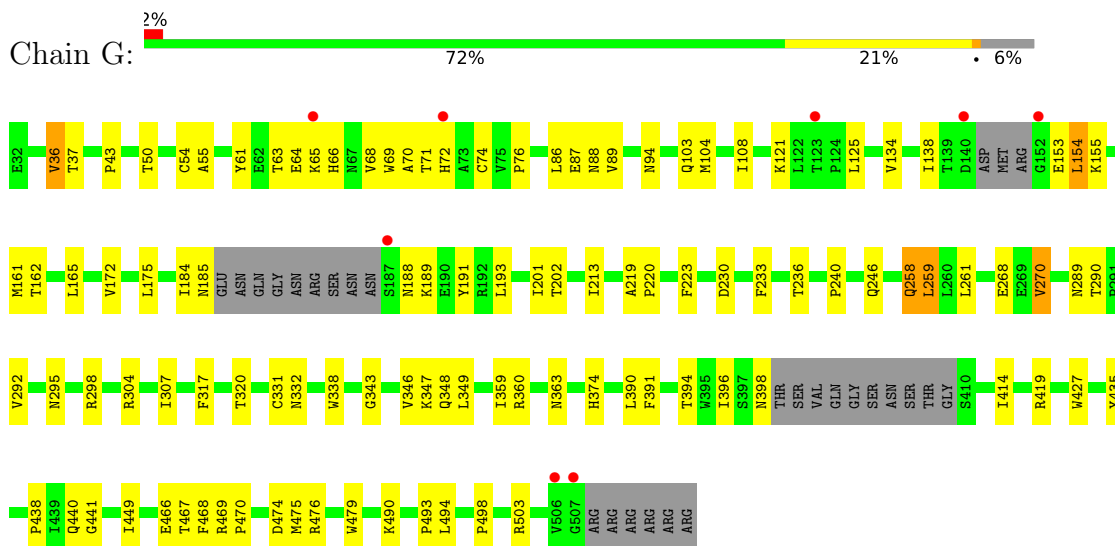


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	H	1	Total	C	O	0	0
			11	6	5		
14	D	1	Total	C	O	0	0
			11	6	5		

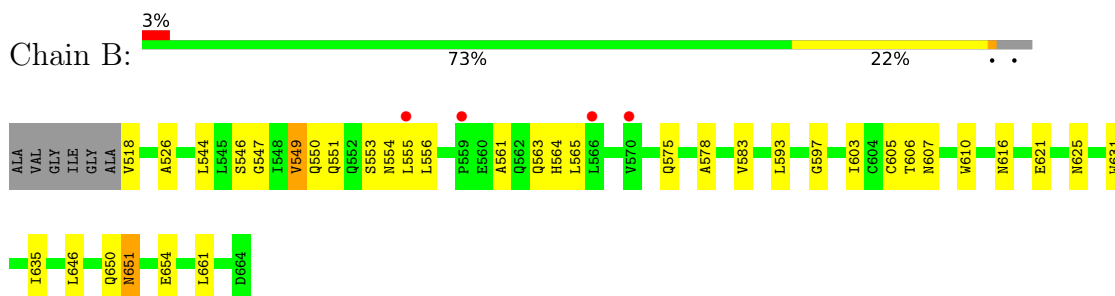
3 Residue-property plots

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.

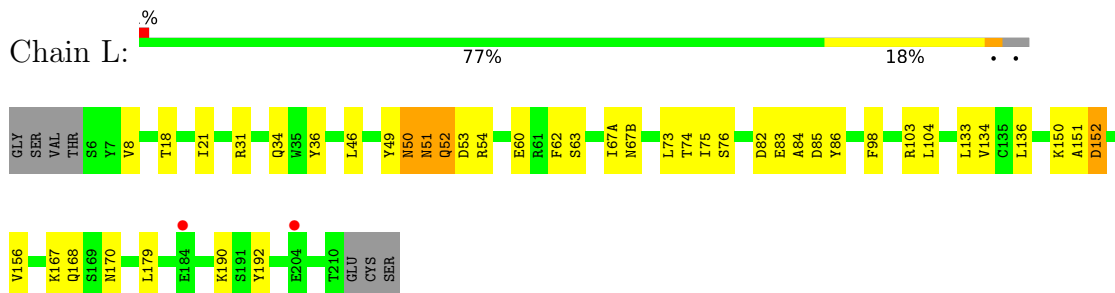
- Molecule 1: Envelope glycoprotein gp160



- Molecule 2: Envelope glycoprotein gp160



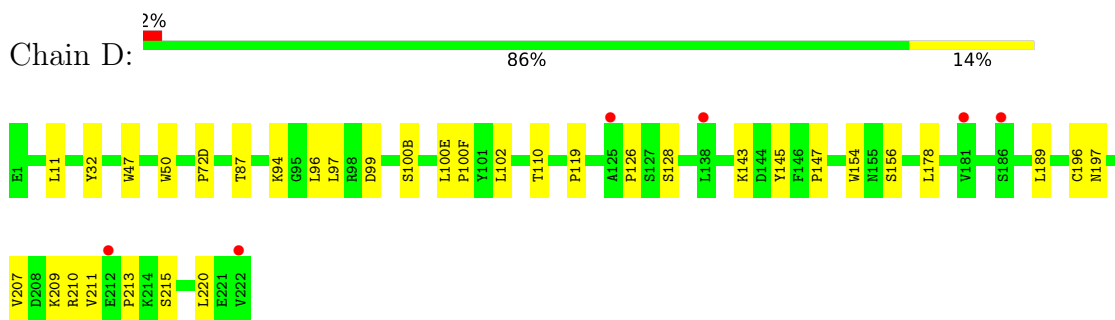
- Molecule 3: 3H+109L Fab Light Chain



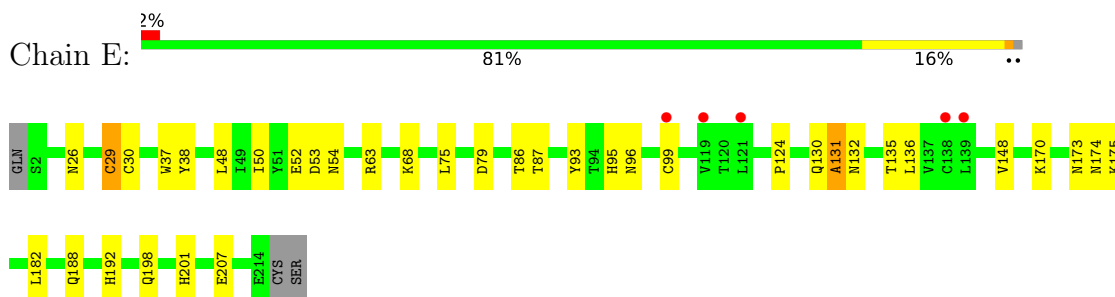
- Molecule 4: 3H+109L Fab Heavy Chain



- Molecule 5: 35022 Fab Heavy Chain



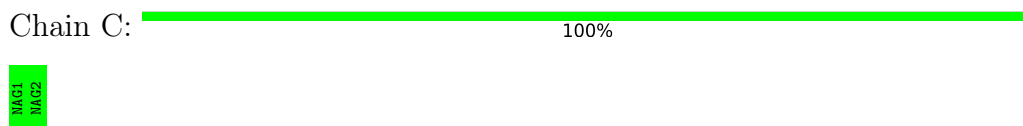
- Molecule 6: 35022 Fab Light Chain



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-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



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



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

Chain F:  100%

MAG1
MAG2

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

Chain I:  50% 50%

MAG1
MAG2

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

Chain J:  50% 50%

MAG1
MAG2

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

Chain K:  100%

MAG1
MAG2

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

Chain M:  100%


MAG1
MAG2

- Molecule 9: 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 N:  40% 60%

MAG1
MAG2
MAG3
MAN4
MAN5

- Molecule 10: 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 O:  75% 25%



- Molecule 11: alpha-D-mannopyranose-(1-3)-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:  17% 33% 50%



- Molecule 12: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-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 Q:  33% 56% 11%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	127.98Å 127.98Å 316.12Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.49 – 3.03 40.49 – 3.03	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.49-3.03) 99.7 (40.49-3.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.233 , 0.266 0.233 , 0.263	Depositor DCC
R_{free} test set	2813 reflections (3.04%)	wwPDB-VP
Wilson B-factor (Å ²)	92.6	Xtrriage
Anisotropy	0.668	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 72.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.046 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12135	wwPDB-VP
Average B, all atoms (Å ²)	123.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% 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	G	0.18	0/3617	0.41	1/4911 (0.0%)
2	B	0.16	0/1192	0.40	0/1618
3	L	0.16	0/1646	0.36	0/2247
4	H	0.13	0/1787	0.35	0/2436
5	D	0.11	0/1860	0.30	0/2533
6	E	0.15	0/1659	0.51	3/2269 (0.1%)
All	All	0.15	0/11761	0.39	4/16014 (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
3	L	0	3
4	H	0	2
6	E	0	1
All	All	0	6

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	30	CYS	N-CA-C	11.21	123.49	111.28
6	E	131	ALA	N-CA-C	7.84	119.83	111.28
1	G	268	GLU	CB-CA-C	-5.96	109.13	117.23
6	E	29	CYS	N-CA-C	5.36	118.42	109.96

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	H	131	GLY	Peptide
4	H	132	GLY	Peptide
3	L	150	LYS	Peptide
3	L	50	ASN	Peptide
3	L	52	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	3544	0	3474	107	0
2	B	1171	0	1158	48	1
3	L	1603	0	1545	39	0
4	H	1744	0	1710	40	0
5	D	1813	0	1784	21	0
6	E	1615	0	1544	24	1
7	A	83	0	70	6	0
8	C	28	0	25	0	0
8	F	28	0	25	0	0
8	I	28	0	25	0	0
8	J	28	0	25	0	0
8	K	28	0	25	0	0
8	M	28	0	25	0	0
9	N	61	0	52	1	0
10	O	50	0	43	0	0
11	P	72	0	59	3	0
12	Q	105	0	85	18	0
13	B	42	0	38	1	0
13	G	42	0	39	0	0
14	D	11	0	10	0	0
14	H	11	0	10	4	0
All	All	12135	0	11771	259	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 11.

The worst 5 of 259 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:259:LEU:HD13	1:G:449:ILE:CD1	1.74	1.16
1:G:259:LEU:CD1	1:G:449:ILE:HD12	1.75	1.14
1:G:65:LYS:HD2	2:B:563:GLN:NE2	1.65	1.11
1:G:259:LEU:HD13	1:G:449:ILE:HD12	1.31	1.06
1:G:71:THR:HG22	1:G:72:HIS:H	1.21	1.03

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)
2:B:518:VAL:CG2	6:E:130:GLN:O[2_5115]	1.27	0.93

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	G	444/480 (92%)	423 (95%)	21 (5%)	0	100	100
2	B	145/153 (95%)	136 (94%)	9 (6%)	0	100	100
3	L	209/218 (96%)	201 (96%)	7 (3%)	1 (0%)	24	57
4	H	227/236 (96%)	222 (98%)	5 (2%)	0	100	100
5	D	238/240 (99%)	236 (99%)	2 (1%)	0	100	100
6	E	211/216 (98%)	206 (98%)	5 (2%)	0	100	100
All	All	1474/1543 (96%)	1424 (97%)	49 (3%)	1 (0%)	48	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	84	ALA

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	G	401/427 (94%)	391 (98%)	10 (2%)	42 69
2	B	127/129 (98%)	121 (95%)	6 (5%)	23 55
3	L	175/181 (97%)	170 (97%)	5 (3%)	37 67
4	H	200/205 (98%)	194 (97%)	6 (3%)	36 66
5	D	203/203 (100%)	202 (100%)	1 (0%)	81 86
6	E	186/189 (98%)	184 (99%)	2 (1%)	65 80
All	All	1292/1334 (97%)	1262 (98%)	30 (2%)	44 70

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	651	ASN
5	D	178	LEU
3	L	51	ASN
6	E	99	CYS
4	H	103	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
5	D	192	GLN
6	E	96	ASN
6	E	201	HIS
6	E	112	GLN
2	B	543	ASN

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](#)

43 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	0.28	0	17,19,21	0.49	0
7	NAG	A	2	7	14,14,15	0.32	0	17,19,21	0.43	0
7	BMA	A	3	7	11,11,12	0.66	0	15,15,17	0.65	0
7	MAN	A	4	7	11,11,12	0.67	0	15,15,17	1.02	2 (13%)
7	MAN	A	5	7	11,11,12	0.53	0	15,15,17	0.65	0
7	MAN	A	6	7	11,11,12	0.62	0	15,15,17	0.55	0
7	MAN	A	7	7	11,11,12	0.65	0	15,15,17	1.05	2 (13%)
8	NAG	C	1	1,8	14,14,15	0.20	0	17,19,21	0.51	0
8	NAG	C	2	8	14,14,15	0.26	0	17,19,21	0.38	0
8	NAG	F	1	1,8	14,14,15	0.29	0	17,19,21	0.49	0
8	NAG	F	2	8	14,14,15	0.18	0	17,19,21	0.41	0
8	NAG	I	1	1,8	14,14,15	0.26	0	17,19,21	0.64	0
8	NAG	I	2	8	14,14,15	1.38	1 (7%)	17,19,21	0.42	0
8	NAG	J	1	1,8	14,14,15	0.17	0	17,19,21	0.44	0
8	NAG	J	2	8	14,14,15	2.82	3 (21%)	17,19,21	0.89	1 (5%)
8	NAG	K	1	1,8	14,14,15	0.23	0	17,19,21	0.39	0
8	NAG	K	2	8	14,14,15	0.20	0	17,19,21	0.44	0
8	NAG	M	1	1,8	14,14,15	0.23	0	17,19,21	0.40	0
8	NAG	M	2	8	14,14,15	0.24	0	17,19,21	0.46	0
9	NAG	N	1	1,9	14,14,15	0.26	0	17,19,21	0.39	0
9	NAG	N	2	9	14,14,15	0.20	0	17,19,21	0.39	0
9	BMA	N	3	9	11,11,12	0.58	0	15,15,17	0.73	0
9	MAN	N	4	9	11,11,12	0.68	0	15,15,17	0.99	2 (13%)
9	MAN	N	5	9	11,11,12	0.67	0	15,15,17	1.04	2 (13%)
10	NAG	O	1	1,10	14,14,15	0.27	0	17,19,21	0.38	0
10	NAG	O	2	10	14,14,15	0.24	0	17,19,21	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	BMA	O	3	10	11,11,12	0.60	0	15,15,17	0.73	0
10	MAN	O	4	10	11,11,12	0.66	0	15,15,17	1.00	2 (13%)
11	NAG	P	1	1,11	14,14,15	0.31	0	17,19,21	0.43	0
11	NAG	P	2	11	14,14,15	0.94	1 (7%)	17,19,21	1.36	2 (11%)
11	BMA	P	3	11	11,11,12	0.67	0	15,15,17	0.71	0
11	MAN	P	4	11	11,11,12	0.81	1 (9%)	15,15,17	1.20	2 (13%)
11	MAN	P	5	11	11,11,12	0.68	0	15,15,17	0.96	2 (13%)
11	MAN	P	6	11	11,11,12	0.63	0	15,15,17	1.12	2 (13%)
12	NAG	Q	1	1,12	14,14,15	0.35	0	17,19,21	0.88	1 (5%)
12	NAG	Q	2	12	14,14,15	0.38	0	17,19,21	0.91	0
12	BMA	Q	3	12	11,11,12	1.47	3 (27%)	15,15,17	4.08	4 (26%)
12	MAN	Q	4	12	11,11,12	0.22	0	15,15,17	0.66	0
12	MAN	Q	5	12	11,11,12	0.28	0	15,15,17	0.63	0
12	MAN	Q	6	12	11,11,12	0.34	0	15,15,17	0.58	0
12	MAN	Q	7	12	11,11,12	0.23	0	15,15,17	0.73	0
12	MAN	Q	8	12	11,11,12	0.28	0	15,15,17	0.67	0
12	MAN	Q	9	12	11,11,12	0.24	0	15,15,17	0.56	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
7	NAG	A	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	2	7	-	2/6/23/26	0/1/1/1
7	BMA	A	3	7	-	0/2/19/22	0/1/1/1
7	MAN	A	4	7	-	2/2/19/22	0/1/1/1
7	MAN	A	5	7	-	1/2/19/22	0/1/1/1
7	MAN	A	6	7	-	0/2/19/22	0/1/1/1
7	MAN	A	7	7	-	0/2/19/22	0/1/1/1
8	NAG	C	1	1,8	-	4/6/23/26	0/1/1/1
8	NAG	C	2	8	-	0/6/23/26	0/1/1/1
8	NAG	F	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	F	2	8	-	2/6/23/26	0/1/1/1
8	NAG	I	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	I	2	8	-	0/6/23/26	0/1/1/1
8	NAG	J	1	1,8	-	2/6/23/26	0/1/1/1
8	NAG	J	2	8	-	1/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	K	1	1,8	-	1/6/23/26	0/1/1/1
8	NAG	K	2	8	-	2/6/23/26	0/1/1/1
8	NAG	M	1	1,8	-	1/6/23/26	0/1/1/1
8	NAG	M	2	8	-	2/6/23/26	0/1/1/1
9	NAG	N	1	1,9	-	2/6/23/26	0/1/1/1
9	NAG	N	2	9	-	2/6/23/26	0/1/1/1
9	BMA	N	3	9	-	2/2/19/22	0/1/1/1
9	MAN	N	4	9	-	1/2/19/22	0/1/1/1
9	MAN	N	5	9	-	0/2/19/22	0/1/1/1
10	NAG	O	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	O	2	10	-	2/6/23/26	0/1/1/1
10	BMA	O	3	10	-	2/2/19/22	0/1/1/1
10	MAN	O	4	10	-	1/2/19/22	0/1/1/1
11	NAG	P	1	1,11	-	2/6/23/26	0/1/1/1
11	NAG	P	2	11	-	6/6/23/26	0/1/1/1
11	BMA	P	3	11	-	2/2/19/22	0/1/1/1
11	MAN	P	4	11	-	0/2/19/22	0/1/1/1
11	MAN	P	5	11	-	0/2/19/22	0/1/1/1
11	MAN	P	6	11	-	0/2/19/22	0/1/1/1
12	NAG	Q	1	1,12	-	4/6/23/26	0/1/1/1
12	NAG	Q	2	12	-	1/6/23/26	0/1/1/1
12	BMA	Q	3	12	-	0/2/19/22	0/1/1/1
12	MAN	Q	4	12	-	2/2/19/22	0/1/1/1
12	MAN	Q	5	12	-	2/2/19/22	0/1/1/1
12	MAN	Q	6	12	-	2/2/19/22	0/1/1/1
12	MAN	Q	7	12	-	0/2/19/22	0/1/1/1
12	MAN	Q	8	12	-	2/2/19/22	0/1/1/1
12	MAN	Q	9	12	-	2/2/19/22	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	J	2	NAG	C1-C2	8.90	1.64	1.52
8	J	2	NAG	C2-N2	-5.20	1.37	1.46
8	I	2	NAG	C8-C7	-5.07	1.40	1.50
11	P	2	NAG	O6-C6	3.09	1.55	1.42
12	Q	3	BMA	O5-C1	2.54	1.48	1.43

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	Q	3	BMA	O3-C3-C2	-11.79	85.99	110.05
12	Q	3	BMA	O3-C3-C4	9.29	132.27	110.38
11	P	2	NAG	C2-N2-C7	4.68	129.17	122.90
12	Q	3	BMA	C1-O5-C5	2.95	116.14	112.19
11	P	4	MAN	C1-O5-C5	2.90	116.07	112.19

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

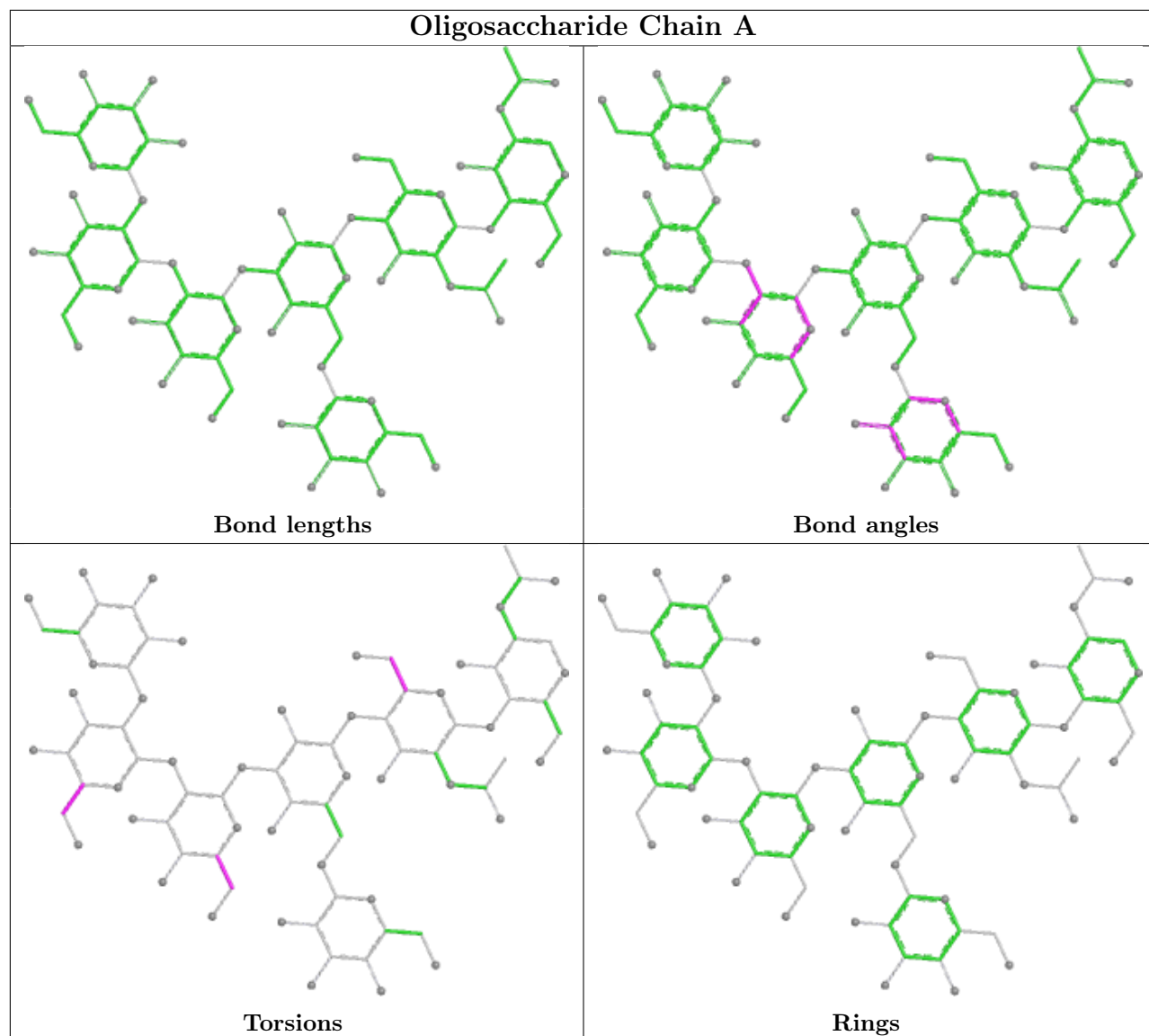
Mol	Chain	Res	Type	Atoms
12	Q	1	NAG	C8-C7-N2-C2
12	Q	1	NAG	O7-C7-N2-C2
9	N	3	BMA	C4-C5-C6-O6
10	O	3	BMA	C4-C5-C6-O6
12	Q	4	MAN	O5-C5-C6-O6

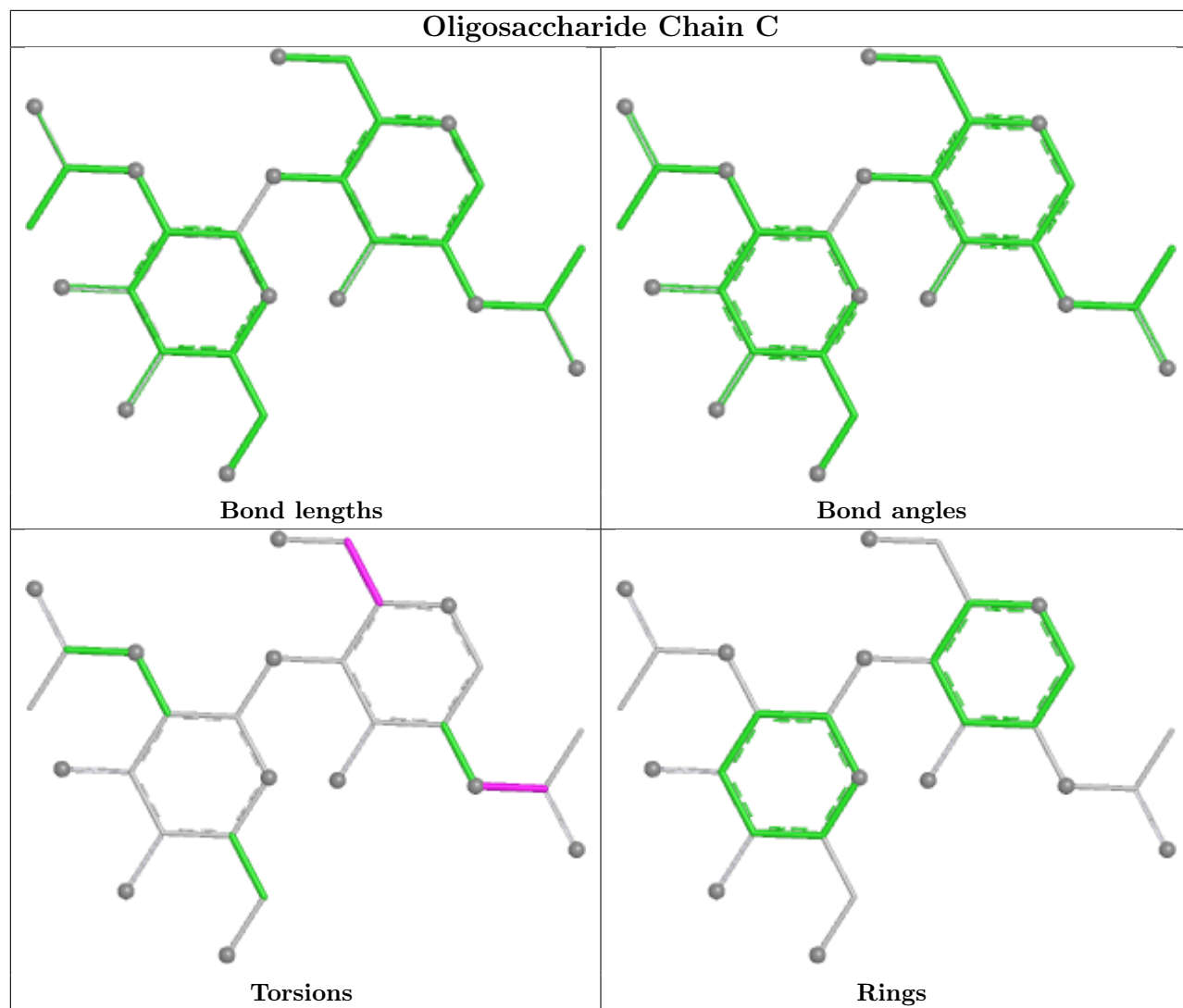
There are no ring outliers.

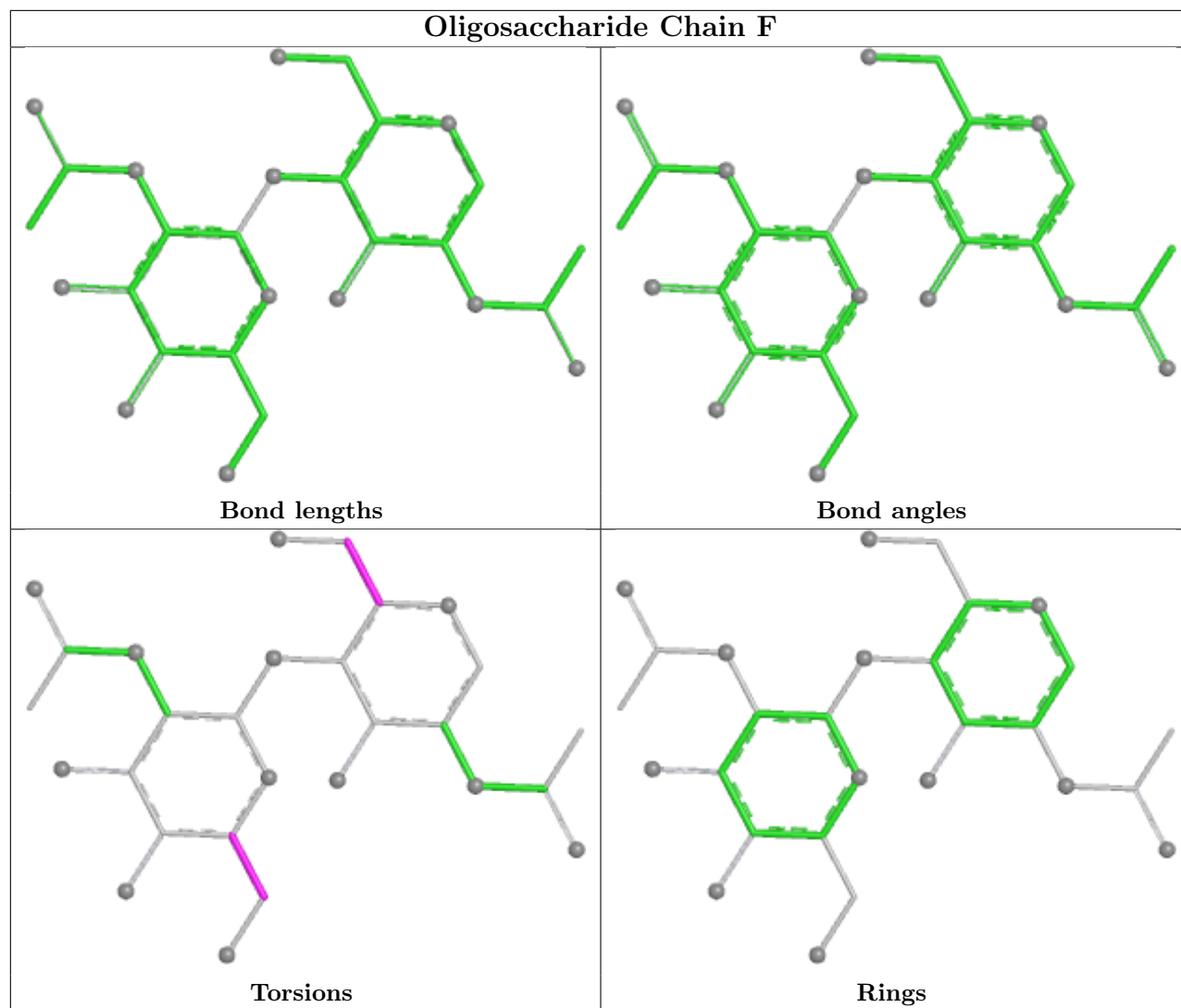
14 monomers are involved in 28 short contacts:

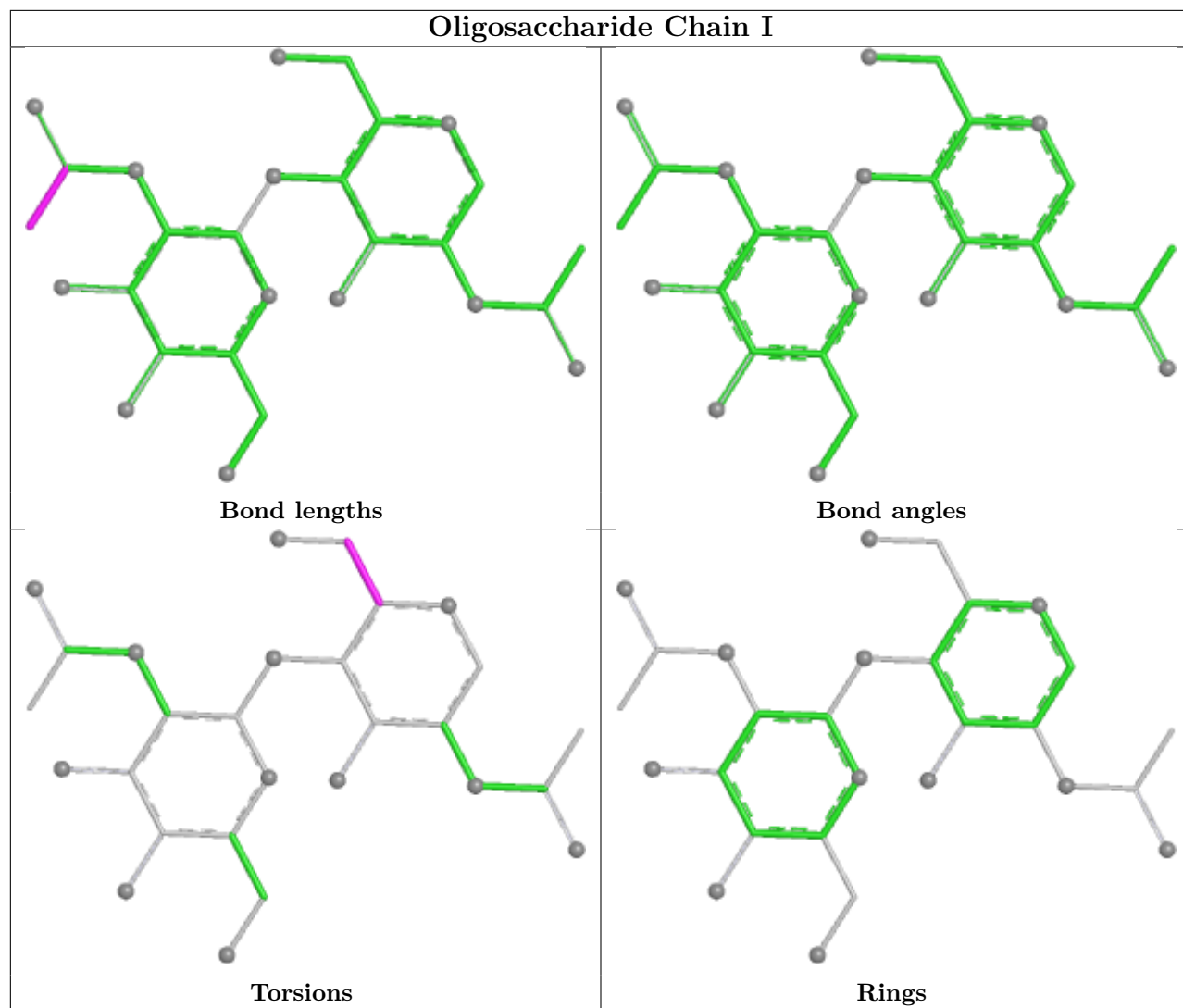
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	P	2	NAG	1	0
7	A	1	NAG	1	0
11	P	4	MAN	1	0
12	Q	2	NAG	2	0
7	A	4	MAN	1	0
12	Q	7	MAN	4	0
9	N	1	NAG	1	0
11	P	6	MAN	1	0
7	A	6	MAN	4	0
7	A	2	NAG	1	0
11	P	3	BMA	1	0
12	Q	5	MAN	2	0
12	Q	1	NAG	5	0
12	Q	6	MAN	6	0

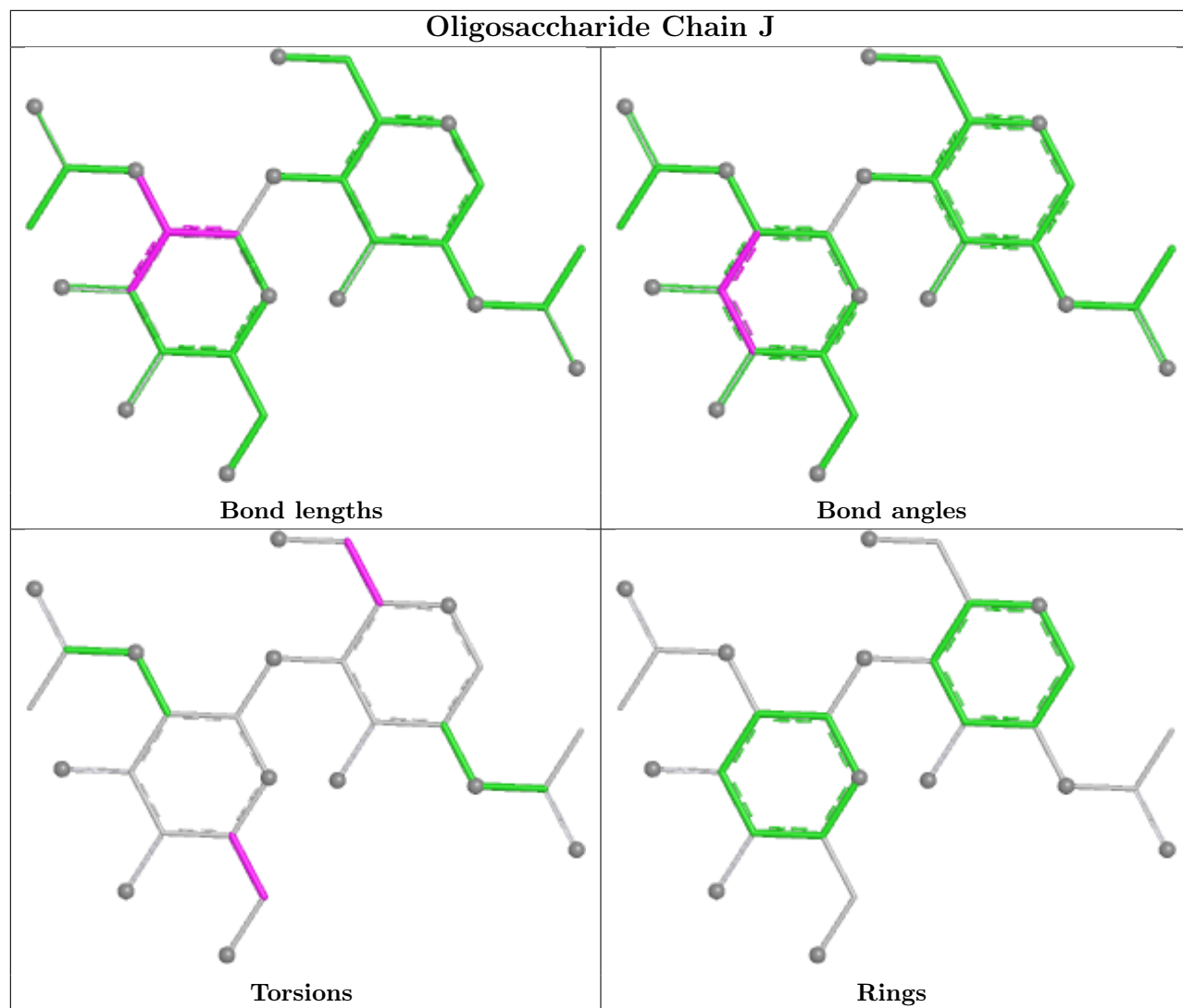
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

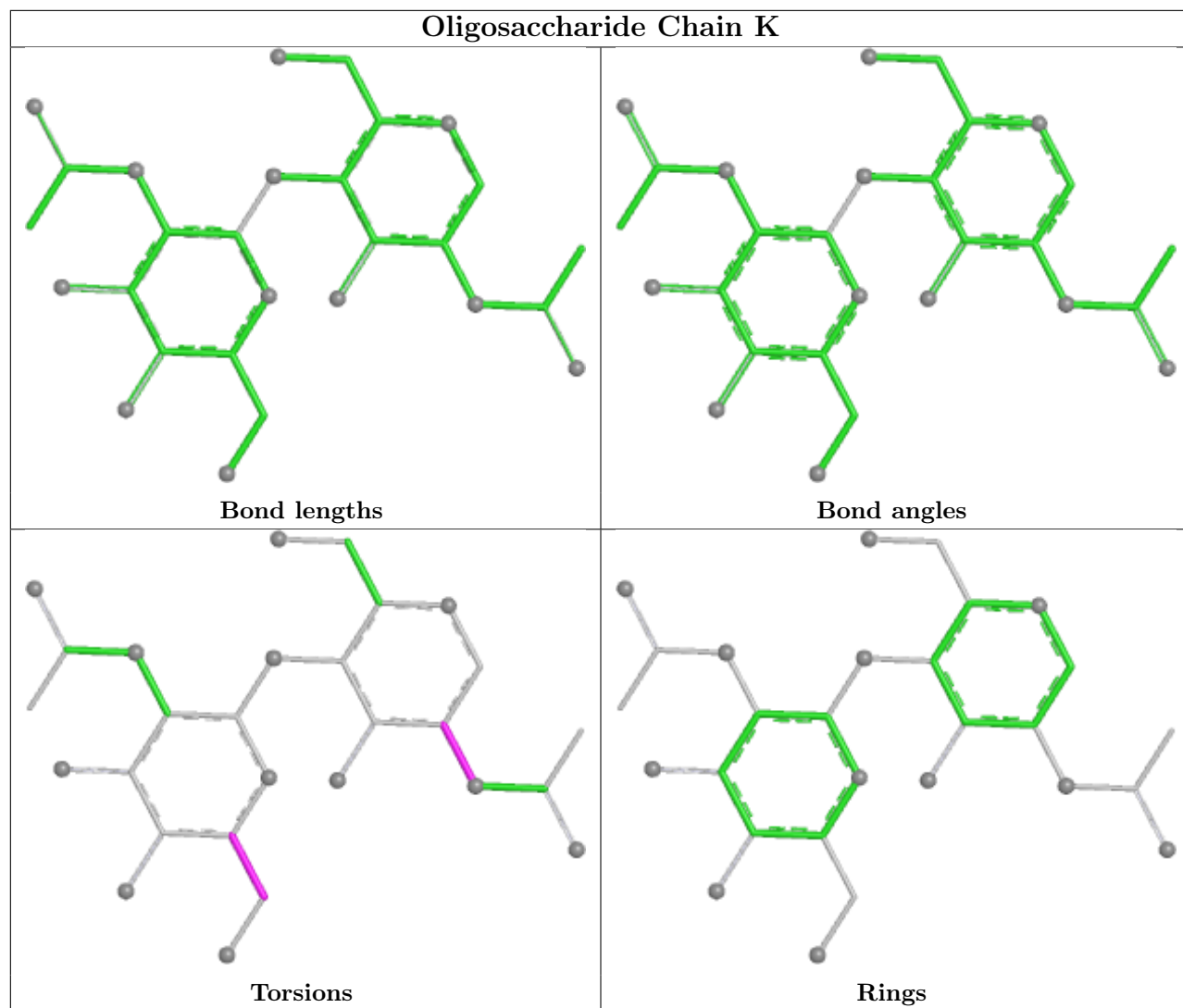


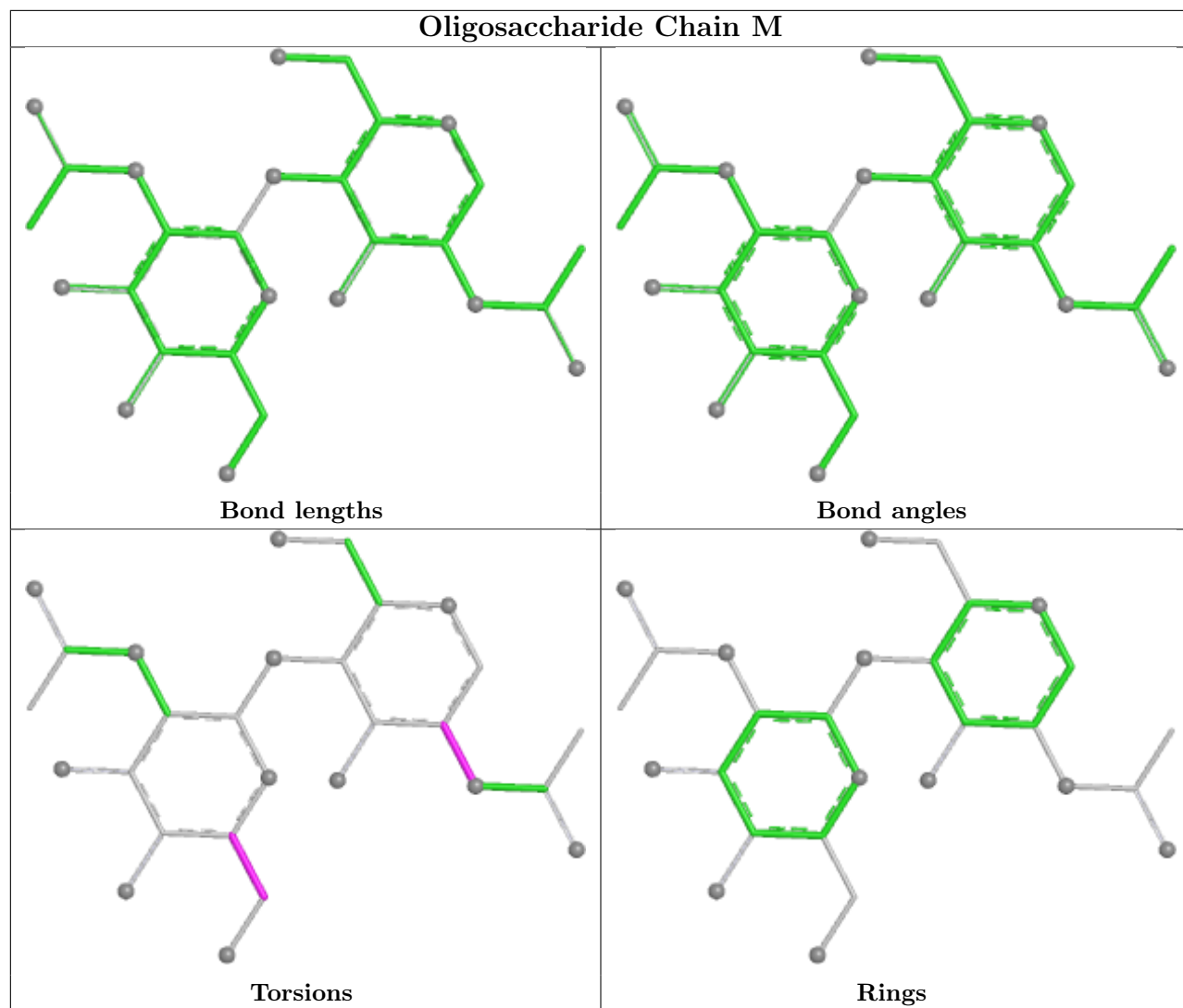


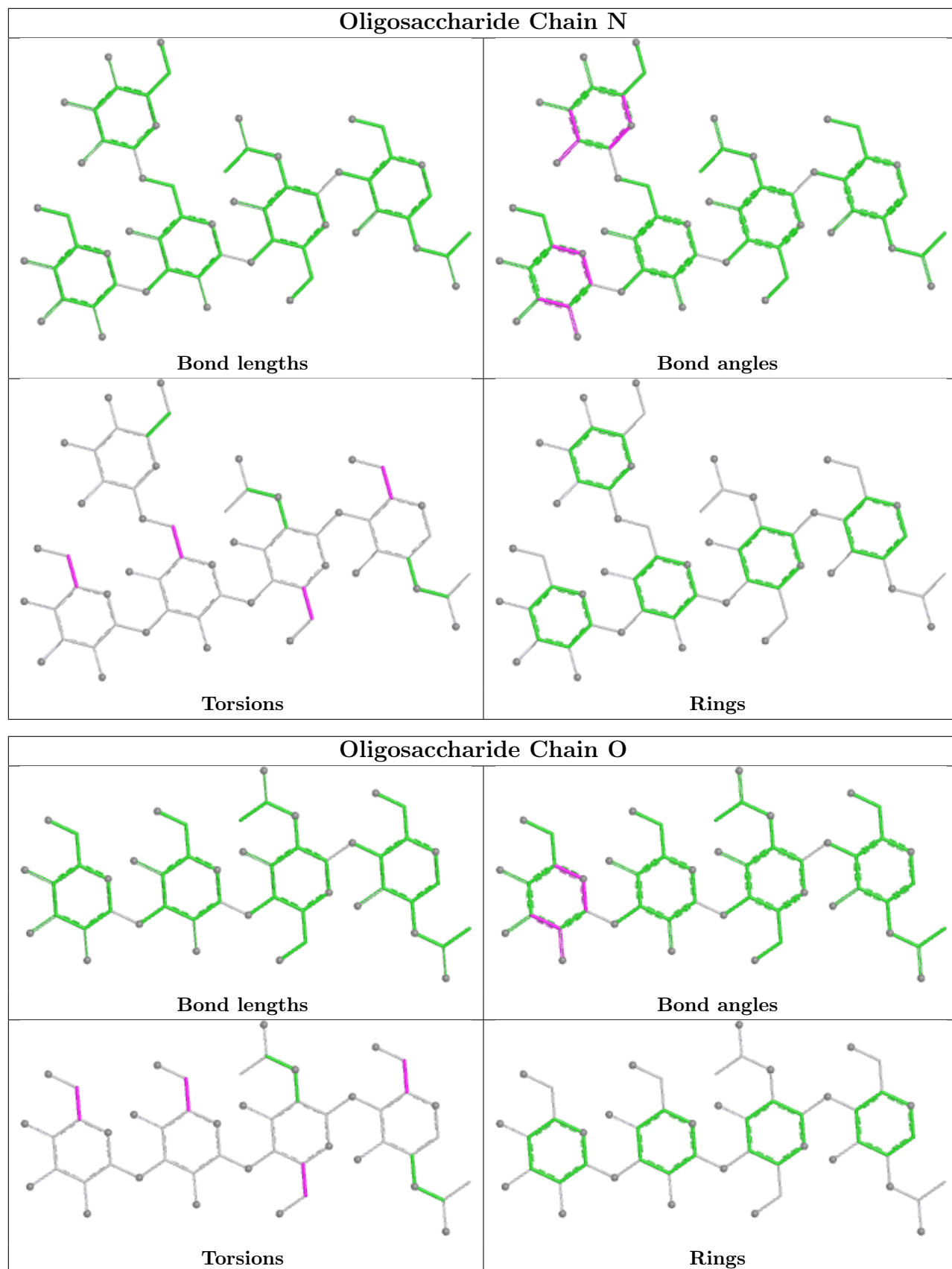


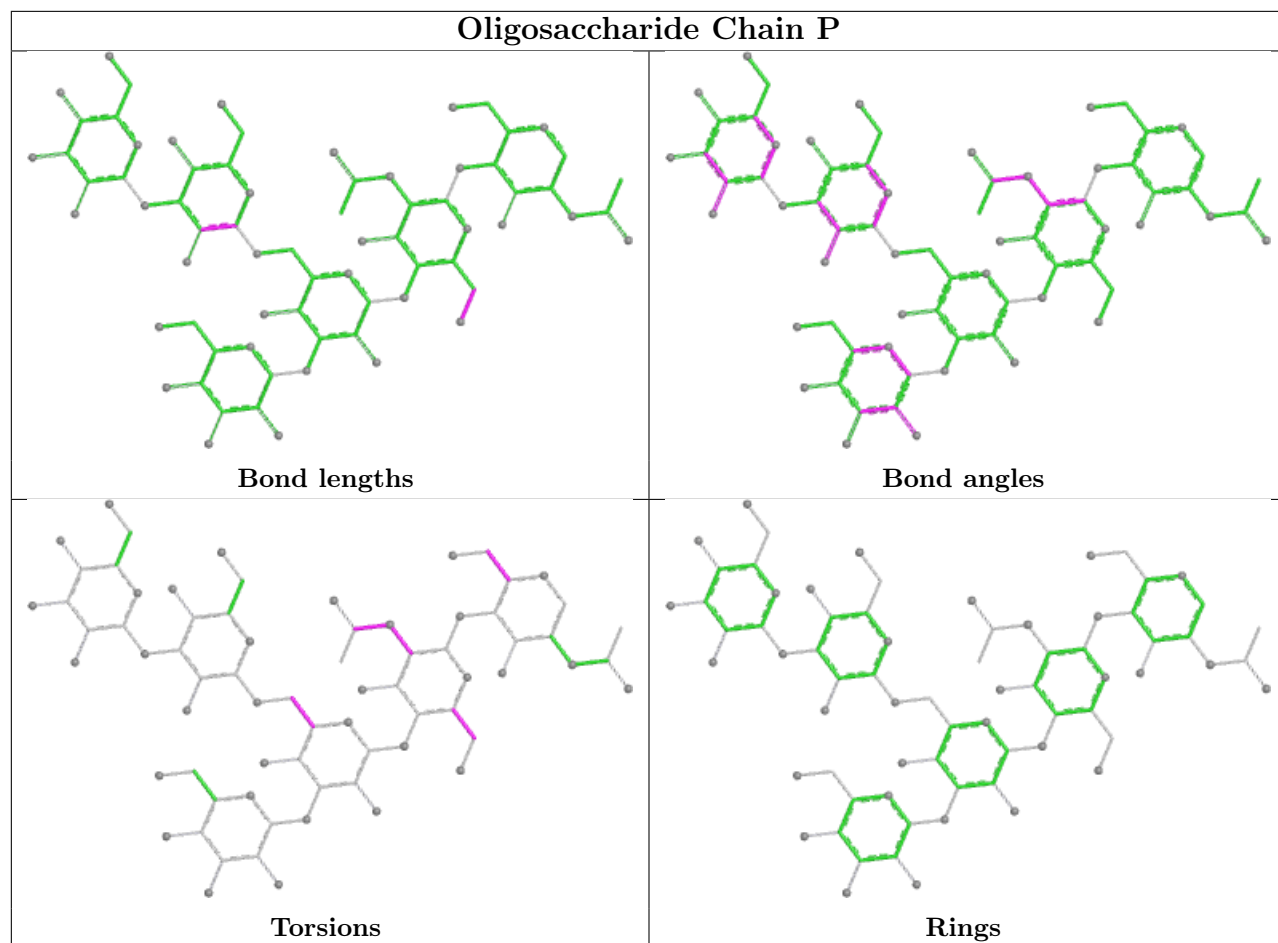


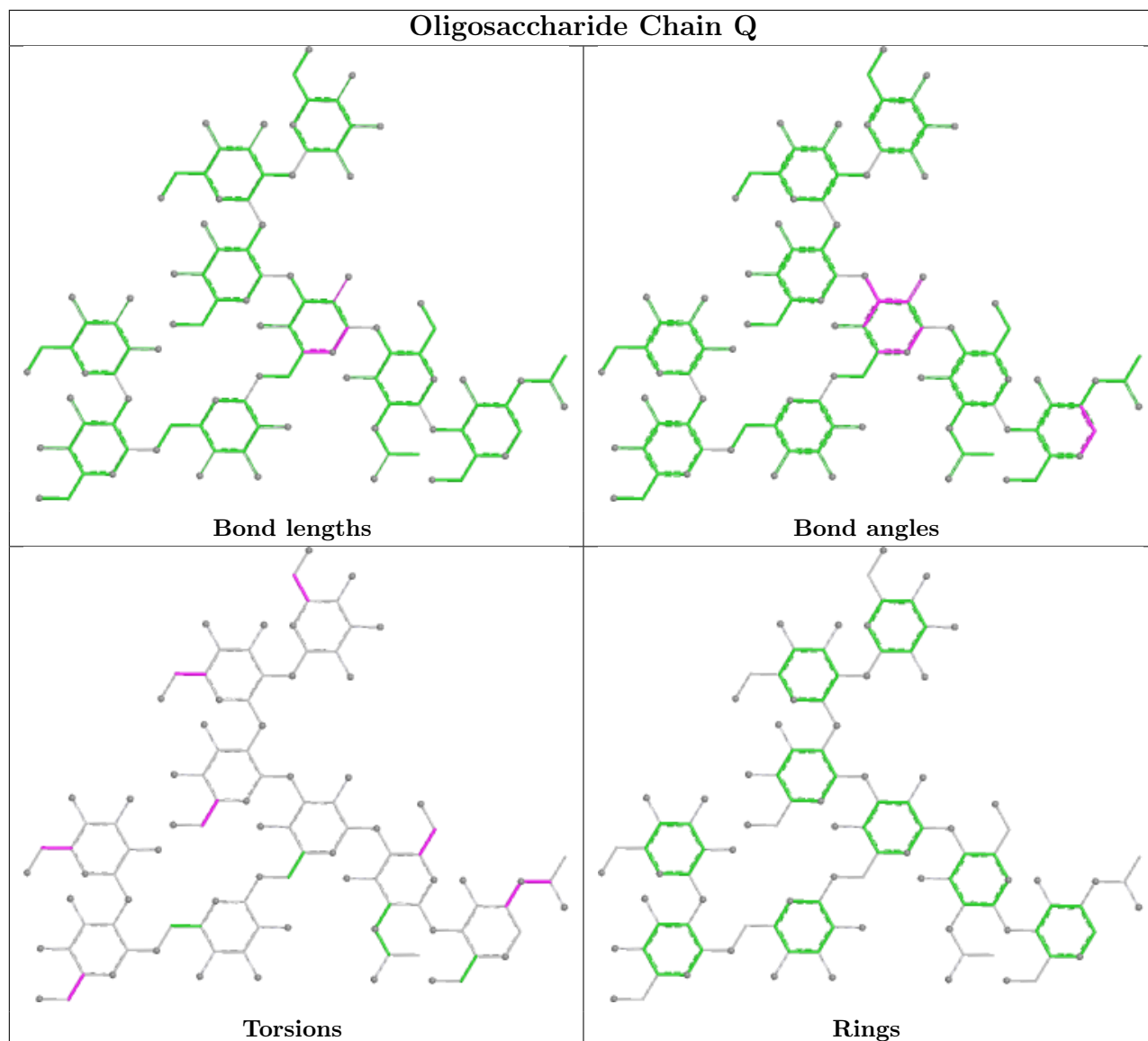












5.6 Ligand geometry [i](#)

8 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
13	NAG	G	601	1	14,14,15	0.17	0	17,19,21	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	NAG	B	701	2	14,14,15	2.72	3 (21%)	17,19,21	1.37	1 (5%)
13	NAG	B	703	2	14,14,15	0.20	0	17,19,21	0.43	0
14	MAN	D	301	-	11,11,12	0.63	0	15,15,17	1.04	2 (13%)
13	NAG	G	602	1	14,14,15	0.18	0	17,19,21	0.43	0
13	NAG	G	603	1	14,14,15	0.21	0	17,19,21	0.38	0
14	MAN	H	301	-	11,11,12	0.25	0	15,15,17	0.58	0
13	NAG	B	702	2	14,14,15	2.04	2 (14%)	17,19,21	1.46	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
13	NAG	G	601	1	-	2/6/23/26	0/1/1/1
13	NAG	B	701	2	-	0/6/23/26	0/1/1/1
13	NAG	B	703	2	-	2/6/23/26	0/1/1/1
14	MAN	D	301	-	-	0/2/19/22	0/1/1/1
13	NAG	G	602	1	-	2/6/23/26	0/1/1/1
13	NAG	G	603	1	-	1/6/23/26	0/1/1/1
14	MAN	H	301	-	-	0/2/19/22	0/1/1/1
13	NAG	B	702	2	-	2/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	B	701	NAG	O6-C6	-8.15	1.08	1.42
13	B	702	NAG	O5-C1	5.78	1.53	1.43
13	B	701	NAG	C1-C2	5.25	1.59	1.52
13	B	702	NAG	C1-C2	-4.95	1.45	1.52
13	B	701	NAG	O5-C1	3.09	1.48	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	702	NAG	C1-O5-C5	5.53	119.60	112.19
13	B	701	NAG	O5-C1-C2	-5.02	103.52	111.29
14	D	301	MAN	C1-O5-C5	2.56	115.62	112.19
14	D	301	MAN	O2-C2-C3	-2.25	105.50	110.15

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	G	601	NAG	C4-C5-C6-O6
13	G	602	NAG	C4-C5-C6-O6
13	B	702	NAG	C4-C5-C6-O6
13	B	703	NAG	C4-C5-C6-O6
13	B	702	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	H	301	MAN	4	0
13	B	702	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	G	452/480 (94%)	-0.05	8 (1%) 67 43	58, 95, 164, 244	0
2	B	147/153 (96%)	0.12	4 (2%) 56 32	61, 95, 200, 230	0
3	L	211/218 (96%)	-0.09	2 (0%) 81 60	77, 113, 140, 169	0
4	H	231/236 (97%)	-0.14	2 (0%) 81 60	81, 118, 171, 189	0
5	D	240/240 (100%)	0.14	6 (2%) 58 34	71, 143, 294, 323	0
6	E	213/216 (98%)	0.09	5 (2%) 61 37	74, 145, 223, 240	0
All	All	1494/1543 (96%)	-0.00	27 (1%) 67 43	58, 111, 217, 323	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	152	GLY	4.6
1	G	187	SER	3.6
3	L	204	GLU	3.2
6	E	138	CYS	3.2
4	H	138	CYS	3.1

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

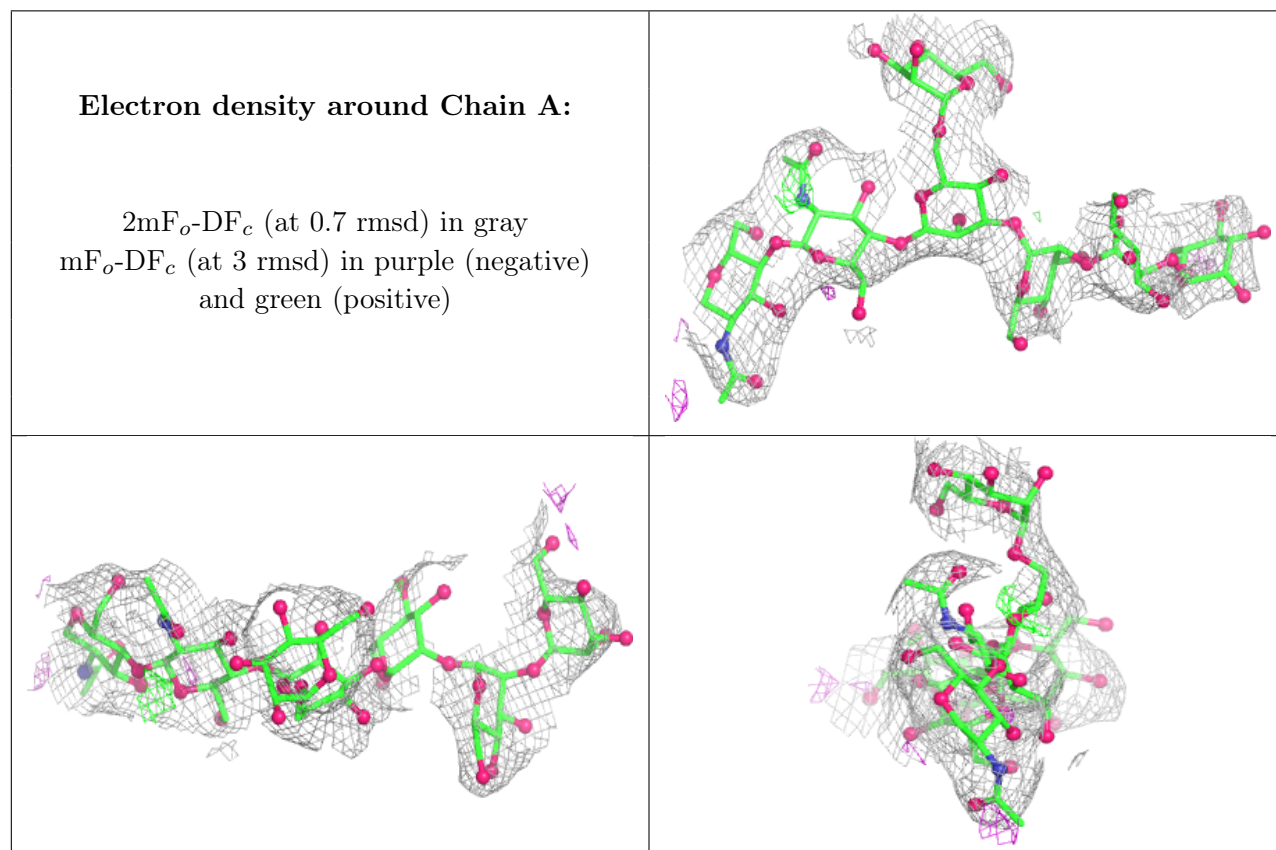
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

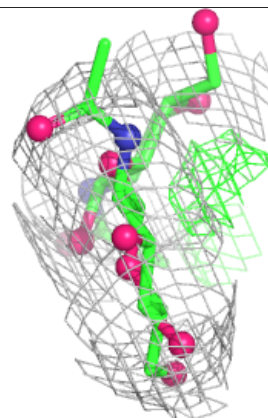
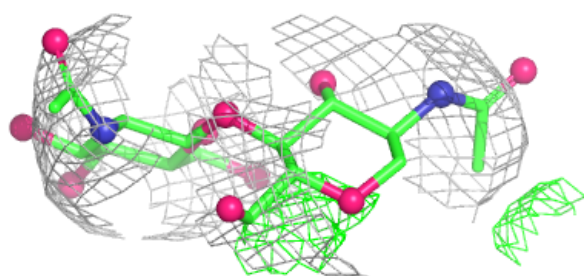
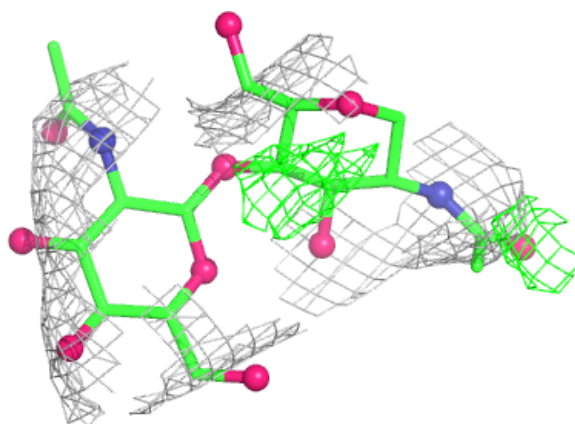
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	NAG	A	1	14/15	-	-	77,92,110,113	0
7	NAG	A	2	14/15	-	-	108,133,150,163	0
7	BMA	A	3	11/12	-	-	176,187,196,202	0
7	MAN	A	4	11/12	-	-	173,199,206,215	0
7	MAN	A	5	11/12	-	-	171,199,222,235	0
7	MAN	A	6	11/12	-	-	223,233,240,249	0
7	MAN	A	7	11/12	-	-	173,200,215,218	0
8	NAG	C	1	14/15	-	-	118,152,170,174	0
8	NAG	C	2	14/15	-	-	163,176,183,206	0
8	NAG	F	1	14/15	-	-	83,104,137,143	0
8	NAG	F	2	14/15	-	-	137,156,165,178	0
9	MAN	N	4	11/12	0.30	0.09	195,215,230,234	0
9	MAN	N	5	11/12	0.36	0.09	251,264,271,276	0
8	NAG	J	2	14/15	0.43	0.11	143,184,189,202	0
10	BMA	O	3	11/12	0.47	0.09	188,209,222,228	0
8	NAG	M	2	14/15	0.48	0.11	157,175,191,195	0
8	NAG	K	2	14/15	0.56	0.12	134,170,177,179	0
10	MAN	O	4	11/12	0.62	0.09	191,222,229,231	0
9	BMA	N	3	11/12	0.73	0.07	229,237,248,259	0
11	MAN	P	5	11/12	0.73	0.12	125,148,163,164	0
12	MAN	Q	8	11/12	0.77	0.09	108,123,130,135	0
9	NAG	N	2	14/15	0.79	0.10	154,200,221,233	0
8	NAG	M	1	14/15	0.79	0.13	136,156,163,166	0
8	NAG	I	2	14/15	0.80	0.08	129,176,187,190	0
10	NAG	O	2	14/15	0.82	0.08	135,146,175,197	0
9	NAG	N	1	14/15	0.85	0.13	108,145,179,182	0
8	NAG	K	1	14/15	0.85	0.14	120,145,166,169	0
8	NAG	J	1	14/15	0.86	0.10	132,143,176,177	0
11	BMA	P	3	11/12	0.87	0.13	78,87,127,130	0
12	MAN	Q	6	11/12	0.89	0.08	89,107,112,113	0
12	NAG	Q	1	14/15	0.89	0.11	92,106,116,116	0
11	MAN	P	4	11/12	0.90	0.09	119,129,145,159	0
12	MAN	Q	7	11/12	0.91	0.08	119,124,135,140	0
12	MAN	Q	5	11/12	0.91	0.09	88,98,116,118	0
12	MAN	Q	9	11/12	0.91	0.10	136,147,157,161	0
12	MAN	Q	4	11/12	0.92	0.08	73,78,107,108	0
12	NAG	Q	2	14/15	0.92	0.08	79,100,119,122	0
8	NAG	I	1	14/15	0.93	0.08	92,142,163,169	0
12	BMA	Q	3	11/12	0.93	0.09	93,96,121,125	0
11	NAG	P	2	14/15	0.94	0.09	60,84,92,97	0
11	NAG	P	1	14/15	0.94	0.12	65,79,91,93	0
11	MAN	P	6	11/12	0.94	0.07	74,92,101,105	0
10	NAG	O	1	14/15	0.96	0.08	86,118,135,138	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.

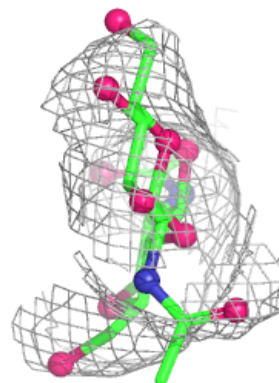
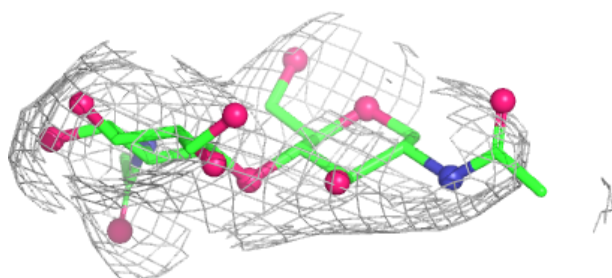
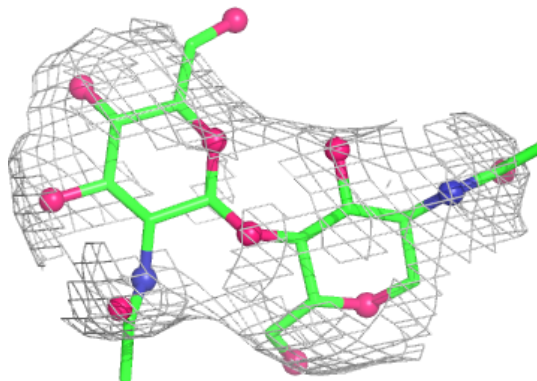


Electron density around Chain C:

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

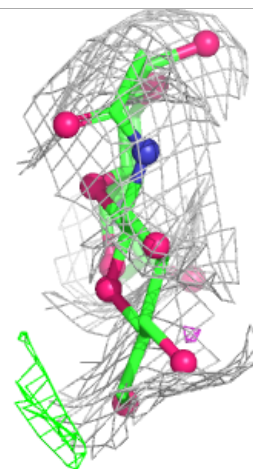
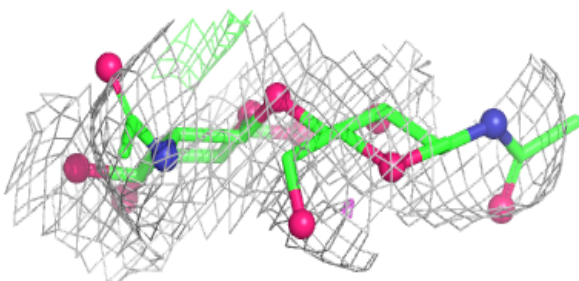
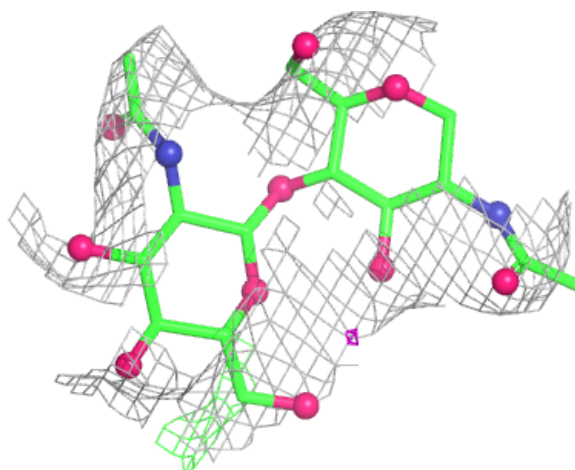
**Electron density around Chain F:**

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



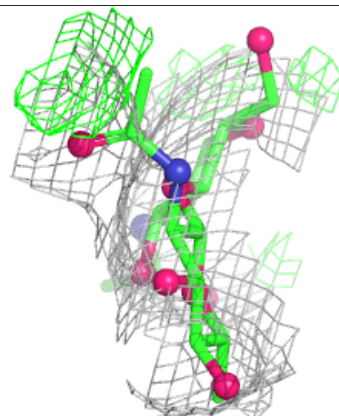
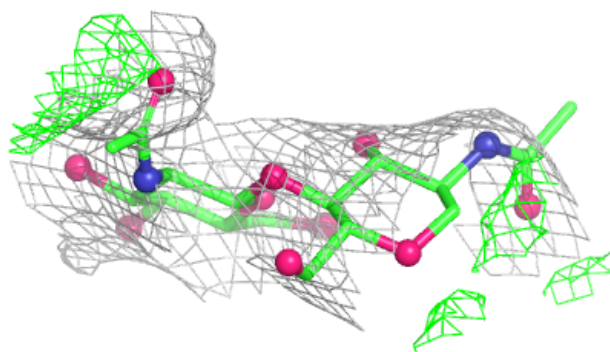
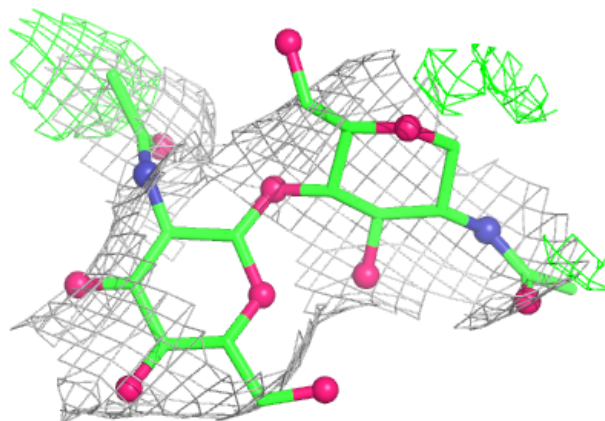
Electron density around Chain I:

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



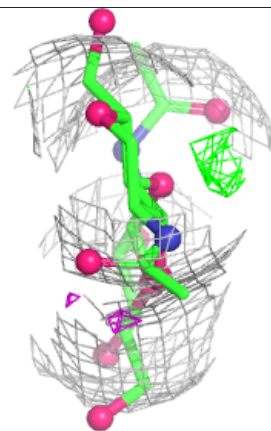
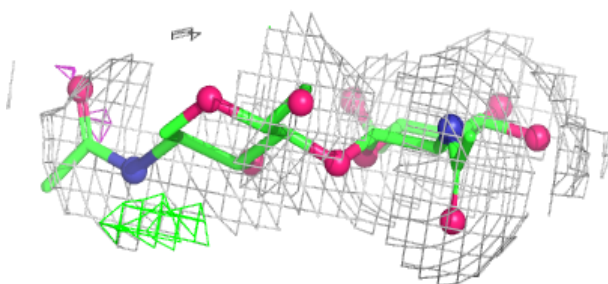
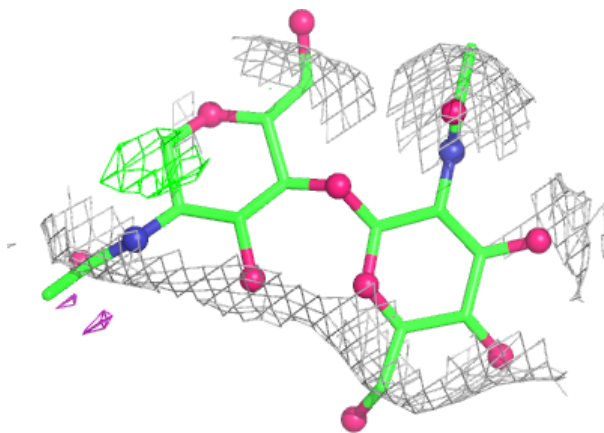
Electron density around Chain J:

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



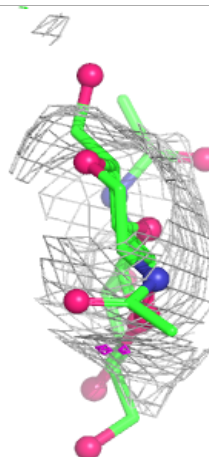
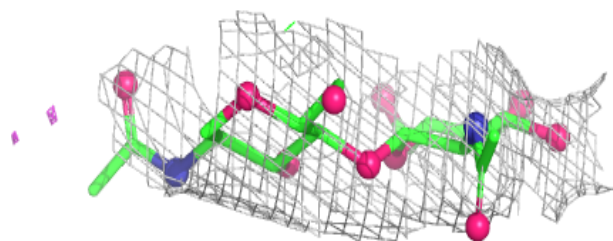
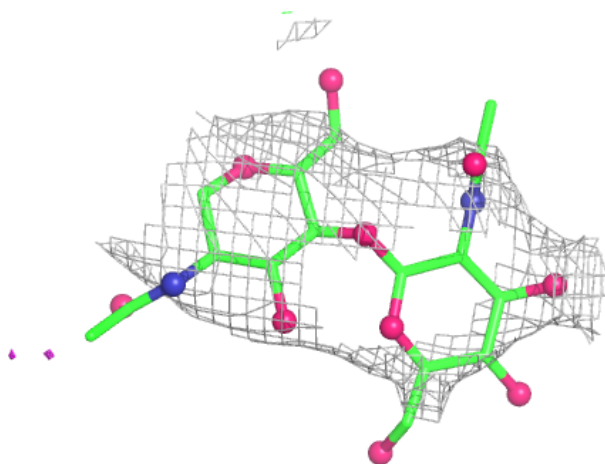
Electron density around Chain K:

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



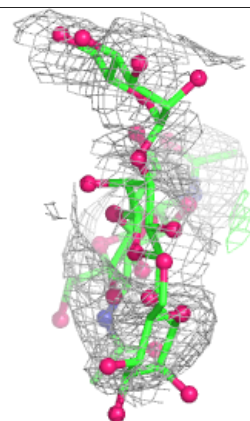
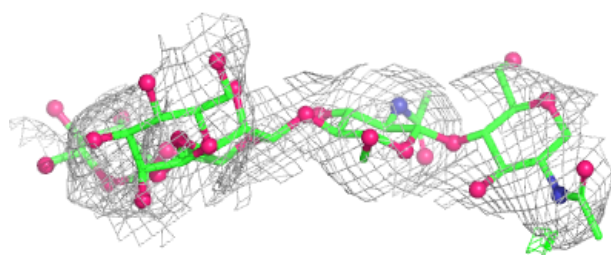
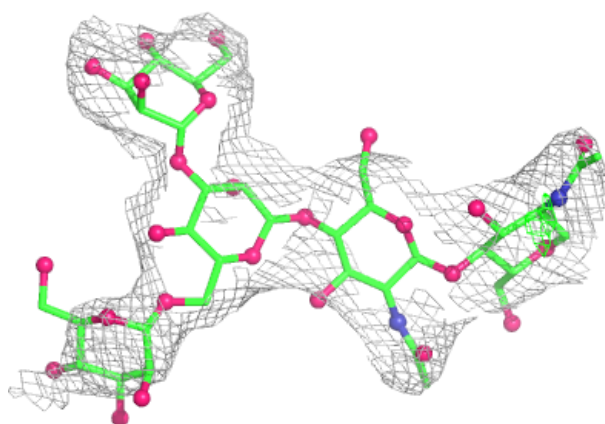
Electron density around Chain M:

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

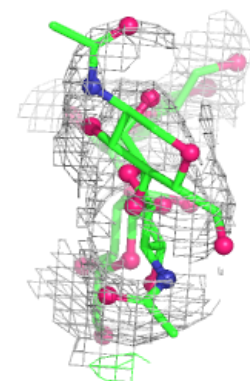
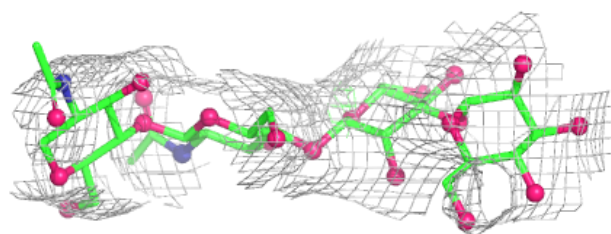
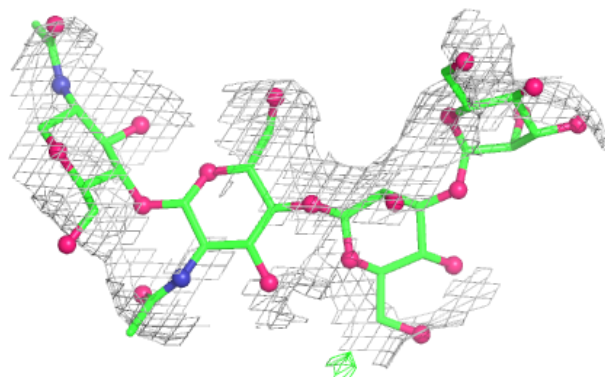


Electron density around Chain N:

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

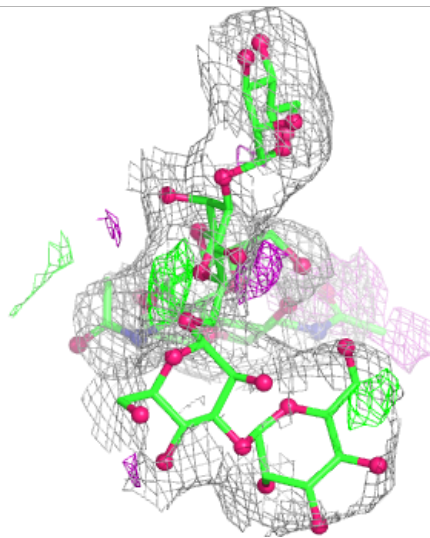
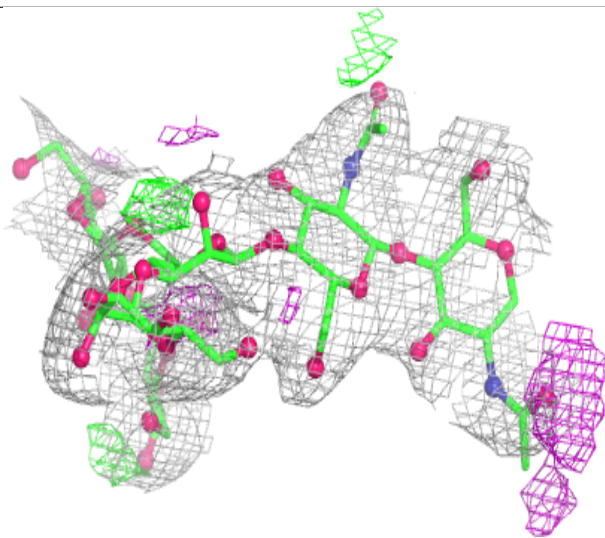
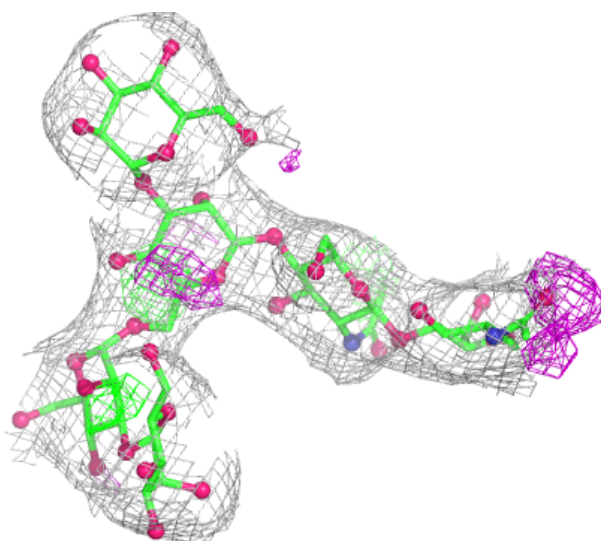
**Electron density around Chain O:**

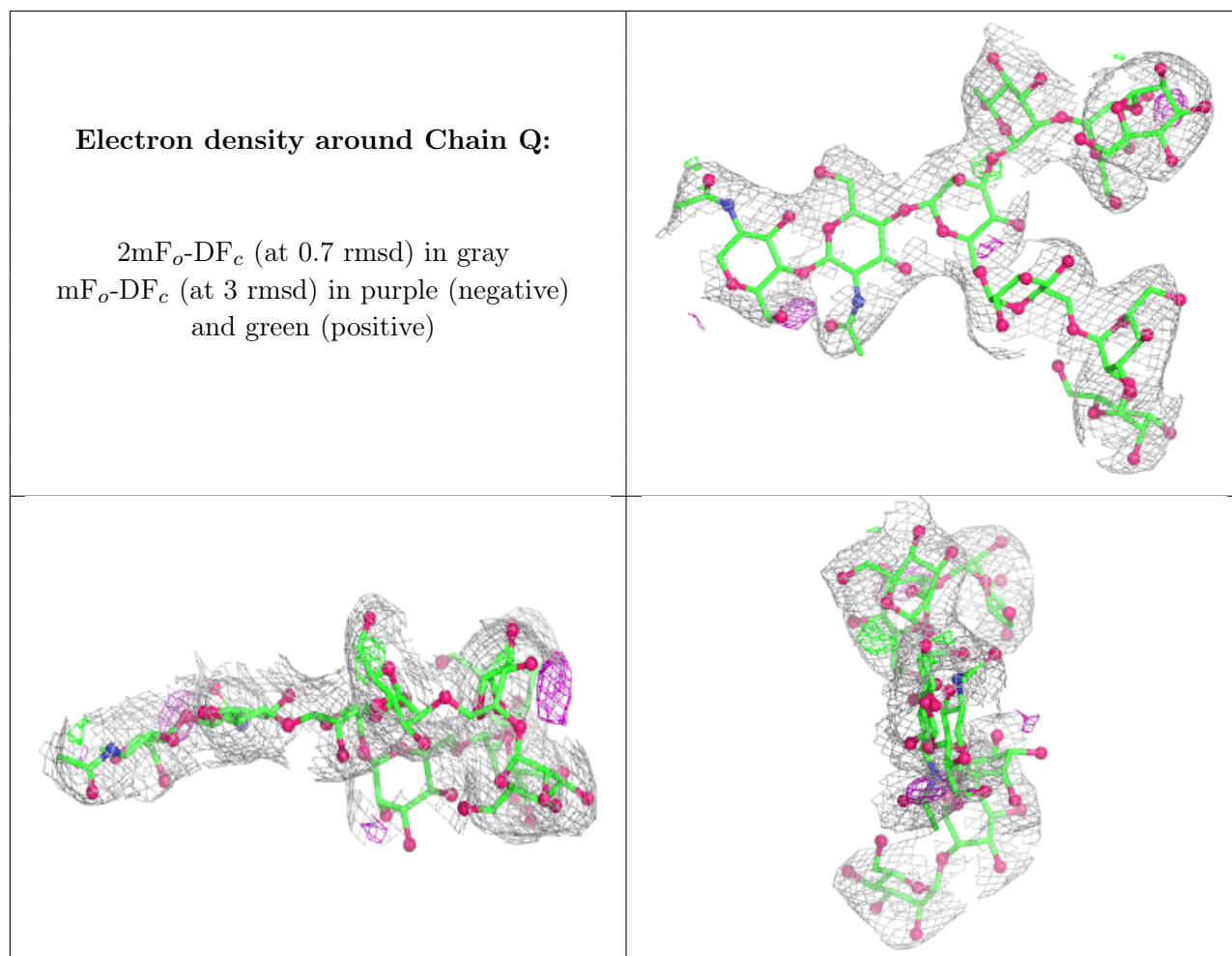
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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
13	NAG	B	702	14/15	0.56	0.13	116,143,159,164	0
14	MAN	H	301	11/12	0.71	0.09	134,138,155,160	0
13	NAG	B	701	14/15	0.74	0.09	129,150,172,172	0
13	NAG	B	703	14/15	0.78	0.10	150,170,188,199	0
14	MAN	D	301	11/12	0.78	0.10	118,135,149,151	0
13	NAG	G	601	14/15	0.80	0.08	104,132,154,161	0
13	NAG	G	603	14/15	0.83	0.11	101,141,154,157	0
13	NAG	G	602	14/15	0.85	0.09	128,151,164,173	0

6.5 Other polymers [i](#)

There are no such residues in this entry.