



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 05:53 AM UTC

PDB ID : 6IEQ / pdb_00006ieq
Title : Crystal Structure of HIV-1 Env ConM SOSIP.v7 in Complex with bNAb PGT124 and 35O22
Authors : Han, B.W.; Wilson, I.A.
Deposited on : 2018-09-16
Resolution : 3.90 Å(reported)

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

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

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

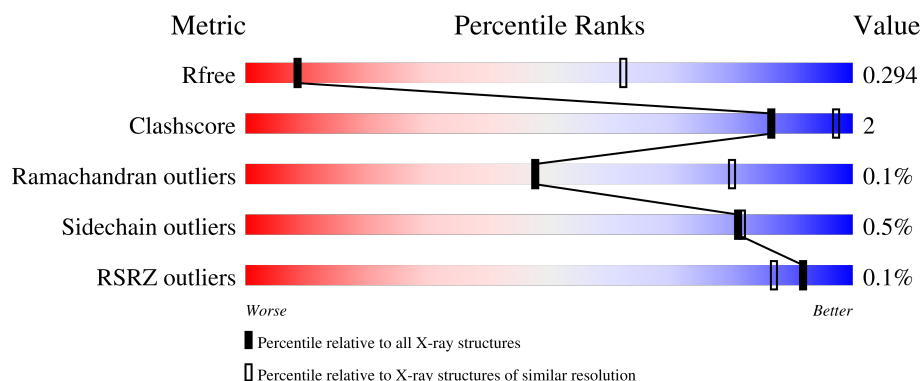
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

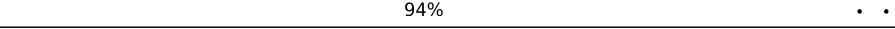
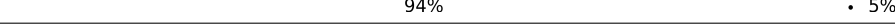
The reported resolution of this entry is 3.90 Å.

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



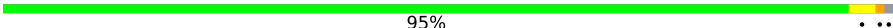
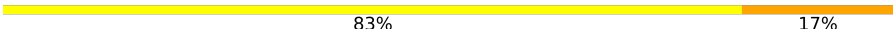
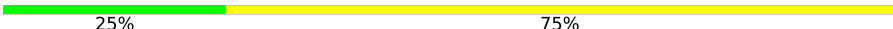
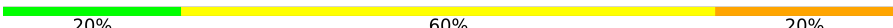
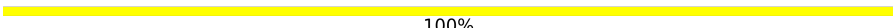
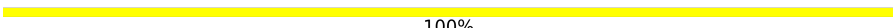
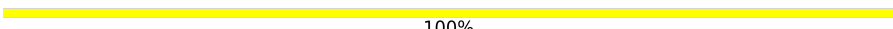
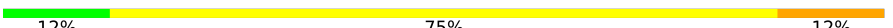
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1270 (4.10-3.70)
Clashscore	190562	1034 (4.08-3.72)
Ramachandran outliers	187476	1251 (4.10-3.70)
Sidechain outliers	187428	1243 (4.10-3.70)
RSRZ outliers	180081	1269 (4.10-3.70)

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	497	 82% 6% 12%
2	B	153	 80% 5% 14%
3	L	214	 93% 5% .
4	H	236	 94% . .
5	D	240	 94% . 5%

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Mol	Chain	Length	Quality of chain
6	E	216	 95% ..
7	A	6	 83% 17%
8	C	4	 25% 75%
9	F	2	 50% 50%
9	M	2	 50% 50%
9	O	2	 50% 50%
10	I	5	 20% 60% 20%
10	K	5	 100%
10	N	5	 100%
11	J	2	 100%
12	P	8	 12% 75% 12%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 11846 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
1	G	439	Total	C	N	O	S	0	0	0
			3483	2188	612	657	26			

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	131	Total	C	N	O	S	0	0	0
			1043	656	176	204	7			

- Molecule 3 is a protein called PGT124 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	210	Total	C	N	O	S	0	0	0
			1595	1005	270	315	5			

- Molecule 4 is a protein called PGT124 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	231	Total	C	N	O	S	0	0	0
			1754	1111	293	345	5			

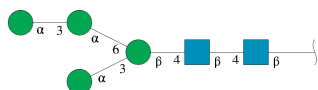
- Molecule 5 is a protein called 35O22 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	229	Total	C	N	O	S	0	0	0
			1731	1100	290	334	7			

- Molecule 6 is a protein called 35O22 Fab Light Chain.

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

- Molecule 7 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
7	A	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 8 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.



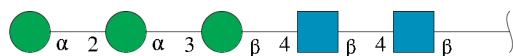
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	C	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 9 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
9	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
9	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
9	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



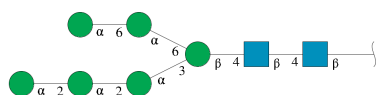
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	I	5	Total	C	N	O	0	0	0
			61	34	2	25			
10	K	5	Total	C	N	O	0	0	0
			61	34	2	25			
10	N	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose.



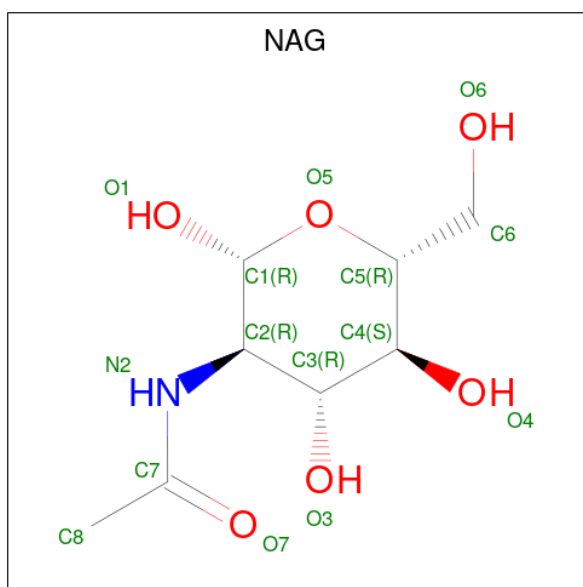
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
11	J	2	Total	C	O	0	0	0
			22	12	10			

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)-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.



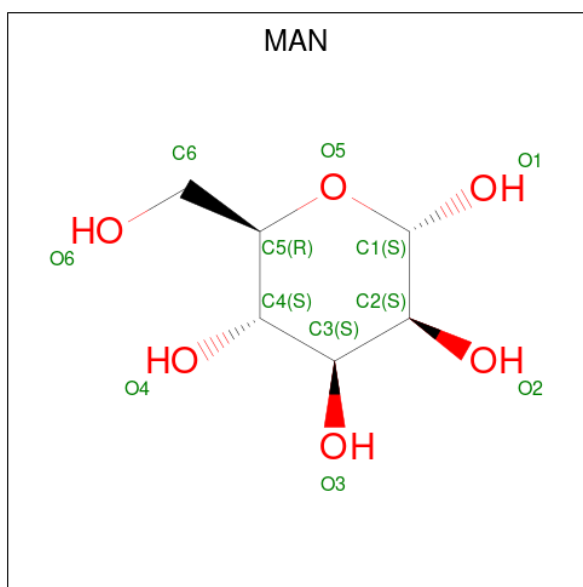
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	P	8	Total	C	N	O	0	0	0
			94	52	2	40			

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



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

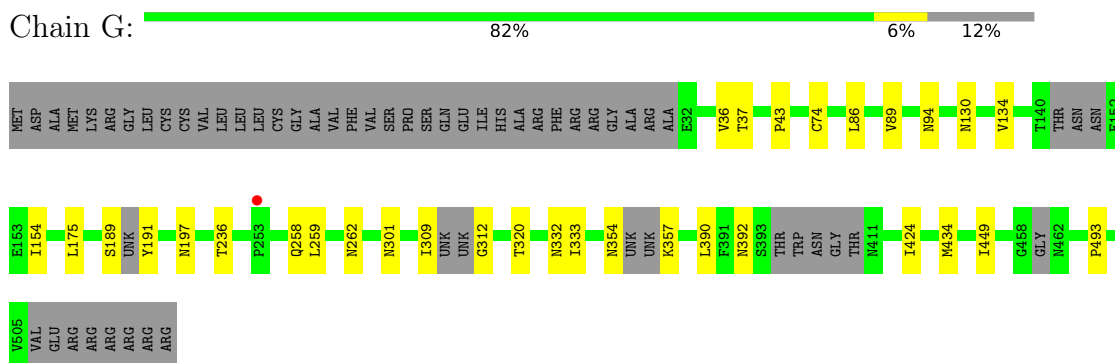


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	L	1	Total	C	O	0	0
			11	6	5		
14	H	1	Total	C	O	0	0
			11	6	5		

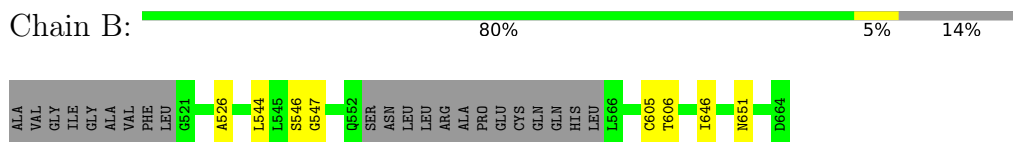
3 Residue-property plots [i](#)

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.

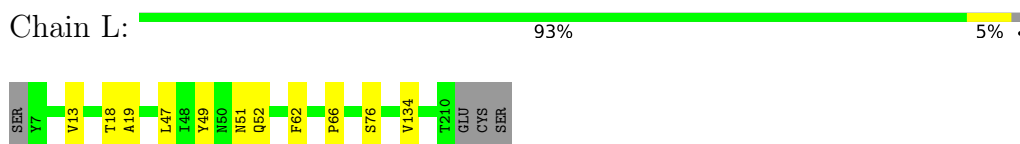
- Molecule 1: Envelope glycoprotein gp160



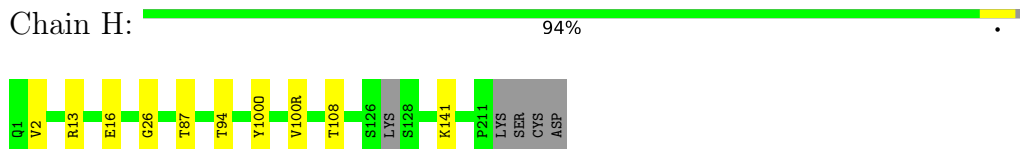
- Molecule 2: Envelope glycoprotein gp160



- Molecule 3: PGT124 Fab Light Chain

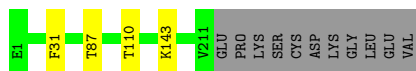


- Molecule 4: PGT124 Fab Heavy Chain



- Molecule 5: 35O22 Fab Heavy Chain





- Molecule 6: 35O22 Fab Light Chain

Chain E: 95%



- Molecule 7: 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 A: 83%



- Molecule 8: 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 C: 25%



- Molecule 9: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 50%



- Molecule 9: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M: 50%

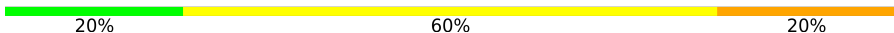


- Molecule 9: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O: 50%

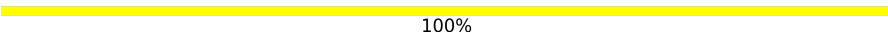


- Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  20% 60% 20%

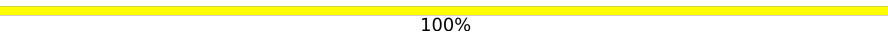

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%

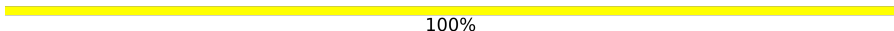

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%

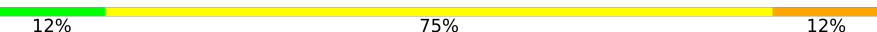

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 11: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose

Chain J:  100%


MAN1
MAN2

- Molecule 12: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-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 P:  12% 75% 12%


MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8

4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	127.59Å 127.59Å 315.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.01 – 3.90 50.01 – 3.90	Depositor EDS
% Data completeness (in resolution range)	88.9 (50.01-3.90) 88.9 (50.01-3.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.32 (at 3.88Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.247 , 0.296 0.249 , 0.294	Depositor DCC
R_{free} test set	1193 reflections (4.51%)	wwPDB-VP
Wilson B-factor (Å ²)	132.8	Xtriage
Anisotropy	0.716	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 189.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.105 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11846	wwPDB-VP
Average B, all atoms (Å ²)	256.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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: BMA, MAN, NAG

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	0.52	0/3550	0.73	0/4815
2	B	0.54	0/1060	0.81	0/1436
3	L	0.52	0/1638	0.71	0/2238
4	H	0.54	0/1797	0.70	0/2453
5	D	0.52	0/1777	0.64	0/2422
6	E	0.55	0/1659	0.70	2/2269 (0.1%)
All	All	0.53	0/11481	0.71	2/15633 (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
6	E	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
6	E	30	CYS	N-CA-C	6.72	121.56	113.23
6	E	131	ALA	N-CA-C	6.46	117.99	111.07

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	E	29	CYS	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	G	3483	0	3432	24	0
2	B	1043	0	1013	6	0
3	L	1595	0	1541	8	0
4	H	1754	0	1719	5	0
5	D	1731	0	1702	4	0
6	E	1615	0	1544	4	0
7	A	72	0	61	1	0
8	C	50	0	43	0	0
9	F	28	0	25	0	0
9	M	28	0	25	2	0
9	O	28	0	25	1	0
10	I	61	0	52	1	0
10	K	61	0	52	0	0
10	N	61	0	52	0	0
11	J	22	0	19	0	0
12	P	94	0	79	4	0
13	B	28	0	26	0	0
13	G	70	0	65	1	0
14	H	11	0	9	5	0
14	L	11	0	10	5	0
All	All	11846	0	11494	48	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 48 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)
14:L:301:MAN:O2	14:H:309:MAN:C1	2.11	0.98
14:L:301:MAN:C2	14:H:309:MAN:C1	2.52	0.85
14:L:301:MAN:HO2	14:H:309:MAN:C1	1.97	0.73
1:G:189:SER:O	1:G:191:TYR:N	2.26	0.69
1:G:262:ASN:HD21	10:I:1:NAG:C1	2.14	0.60

There are no symmetry-related clashes.

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	G	425/497 (86%)	406 (96%)	18 (4%)	1 (0%)	43	74
2	B	127/153 (83%)	120 (94%)	7 (6%)	0	100	100
3	L	208/214 (97%)	201 (97%)	6 (3%)	1 (0%)	24	59
4	H	227/236 (96%)	221 (97%)	6 (3%)	0	100	100
5	D	227/240 (95%)	220 (97%)	7 (3%)	0	100	100
6	E	211/216 (98%)	205 (97%)	6 (3%)	0	100	100
All	All	1425/1556 (92%)	1373 (96%)	50 (4%)	2 (0%)	48	80

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	258	GLN
3	L	51	ASN

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	397/440 (90%)	396 (100%)	1 (0%)	86	85
2	B	114/131 (87%)	113 (99%)	1 (1%)	70	75
3	L	176/180 (98%)	175 (99%)	1 (1%)	78	80
4	H	199/204 (98%)	198 (100%)	1 (0%)	81	82
5	D	193/203 (95%)	193 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	E	186/189 (98%)	184 (99%)	2 (1%)	65	74
All	All	1265/1347 (94%)	1259 (100%)	6 (0%)	81	82

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	141	LYS
6	E	29	CYS
6	E	99	CYS
2	B	651	ASN
1	G	74	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	168	GLN
5	D	30	ASN
4	H	81	GLN
5	D	58	ASN
1	G	386	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](#)

41 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	7,1	14,14,15	0.50	0	17,19,21	1.42	3 (17%)
7	NAG	A	2	7	14,14,15	0.58	0	17,19,21	2.25	4 (23%)
7	BMA	A	3	7	11,11,12	0.50	0	15,15,17	1.20	2 (13%)
7	MAN	A	4	7	11,11,12	0.64	0	15,15,17	2.27	3 (20%)
7	MAN	A	5	7	11,11,12	0.65	0	15,15,17	1.74	2 (13%)
7	MAN	A	6	7	11,11,12	0.26	0	15,15,17	0.80	1 (6%)
8	NAG	C	1	8,1	14,14,15	0.62	0	17,19,21	2.33	5 (29%)
8	NAG	C	2	8	14,14,15	0.62	0	17,19,21	2.31	6 (35%)
8	BMA	C	3	8	11,11,12	0.50	0	15,15,17	0.57	0
8	MAN	C	4	8	11,11,12	0.43	0	15,15,17	1.04	2 (13%)
9	NAG	F	1	9,1	14,14,15	0.67	0	17,19,21	1.43	3 (17%)
9	NAG	F	2	9	14,14,15	0.36	0	17,19,21	0.86	0
10	NAG	I	1	10	14,14,15	0.51	0	17,19,21	1.39	3 (17%)
10	NAG	I	2	10	14,14,15	0.35	0	17,19,21	0.82	0
10	BMA	I	3	10	11,11,12	0.58	0	15,15,17	1.51	2 (13%)
10	MAN	I	4	10	11,11,12	0.55	0	15,15,17	1.58	3 (20%)
10	MAN	I	5	10	11,11,12	0.41	0	15,15,17	1.30	1 (6%)
11	MAN	J	1	11	11,11,12	0.49	0	15,15,17	1.42	3 (20%)
11	MAN	J	2	11	11,11,12	0.45	0	15,15,17	1.00	1 (6%)
10	NAG	K	1	10	14,14,15	0.49	0	17,19,21	1.57	3 (17%)
10	NAG	K	2	10	14,14,15	0.72	0	17,19,21	1.37	1 (5%)
10	BMA	K	3	10	11,11,12	0.70	0	15,15,17	1.63	4 (26%)
10	MAN	K	4	10	11,11,12	0.32	0	15,15,17	0.87	1 (6%)
10	MAN	K	5	10	11,11,12	0.37	0	15,15,17	1.52	2 (13%)
9	NAG	M	1	9	14,14,15	0.42	0	17,19,21	1.11	1 (5%)
9	NAG	M	2	9	14,14,15	0.51	0	17,19,21	1.12	2 (11%)
10	NAG	N	1	10	14,14,15	0.44	0	17,19,21	1.47	4 (23%)
10	NAG	N	2	10	14,14,15	0.58	0	17,19,21	0.94	2 (11%)
10	BMA	N	3	10	11,11,12	0.55	0	15,15,17	1.08	1 (6%)
10	MAN	N	4	10	11,11,12	0.33	0	15,15,17	0.92	1 (6%)
10	MAN	N	5	10	11,11,12	0.45	0	15,15,17	1.81	2 (13%)
9	NAG	O	1	9	14,14,15	0.45	0	17,19,21	0.88	1 (5%)
9	NAG	O	2	9	14,14,15	0.48	0	17,19,21	1.45	2 (11%)
12	NAG	P	1	12	14,14,15	0.55	0	17,19,21	2.13	6 (35%)
12	NAG	P	2	12	14,14,15	0.34	0	17,19,21	1.23	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	BMA	P	3	12	11,11,12	0.42	0	15,15,17	1.01	2 (13%)
12	MAN	P	4	12	11,11,12	0.32	0	15,15,17	1.56	3 (20%)
12	MAN	P	5	12	11,11,12	0.48	0	15,15,17	0.74	0
12	MAN	P	6	12	11,11,12	0.56	0	15,15,17	1.61	4 (26%)
12	MAN	P	7	12	11,11,12	0.35	0	15,15,17	0.69	0
12	MAN	P	8	12	11,11,12	0.51	0	15,15,17	1.15	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	7,1	-	0/6/23/26	0/1/1/1
7	NAG	A	2	7	-	4/6/23/26	0/1/1/1
7	BMA	A	3	7	-	2/2/19/22	0/1/1/1
7	MAN	A	4	7	-	2/2/19/22	0/1/1/1
7	MAN	A	5	7	-	2/2/19/22	0/1/1/1
7	MAN	A	6	7	-	1/2/19/22	0/1/1/1
8	NAG	C	1	8,1	-	3/6/23/26	0/1/1/1
8	NAG	C	2	8	-	2/6/23/26	0/1/1/1
8	BMA	C	3	8	-	0/2/19/22	0/1/1/1
8	MAN	C	4	8	-	1/2/19/22	0/1/1/1
9	NAG	F	1	9,1	-	3/6/23/26	0/1/1/1
9	NAG	F	2	9	-	2/6/23/26	0/1/1/1
10	NAG	I	1	10	-	1/6/23/26	0/1/1/1
10	NAG	I	2	10	-	0/6/23/26	0/1/1/1
10	BMA	I	3	10	-	0/2/19/22	0/1/1/1
10	MAN	I	4	10	-	2/2/19/22	0/1/1/1
10	MAN	I	5	10	-	2/2/19/22	0/1/1/1
11	MAN	J	1	11	-	2/2/19/22	1/1/1/1
11	MAN	J	2	11	-	2/2/19/22	0/1/1/1
10	NAG	K	1	10	-	0/6/23/26	0/1/1/1
10	NAG	K	2	10	-	0/6/23/26	0/1/1/1
10	BMA	K	3	10	-	1/2/19/22	0/1/1/1
10	MAN	K	4	10	-	1/2/19/22	0/1/1/1
10	MAN	K	5	10	-	1/2/19/22	0/1/1/1
9	NAG	M	1	9	-	1/6/23/26	0/1/1/1
9	NAG	M	2	9	-	2/6/23/26	0/1/1/1

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

There are no bond length outliers.

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	1	NAG	C1-O5-C5	7.53	122.28	112.19
7	A	4	MAN	C1-O5-C5	7.00	121.57	112.19
7	A	2	NAG	C2-N2-C7	6.21	131.22	122.90
10	N	5	MAN	C1-O5-C5	6.08	120.33	112.19
8	C	2	NAG	C1-O5-C5	5.67	119.78	112.19

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	3	BMA	C4-C5-C6-O6
11	J	2	MAN	O5-C5-C6-O6
12	P	8	MAN	O5-C5-C6-O6
10	N	2	NAG	O5-C5-C6-O6
9	O	1	NAG	C4-C5-C6-O6

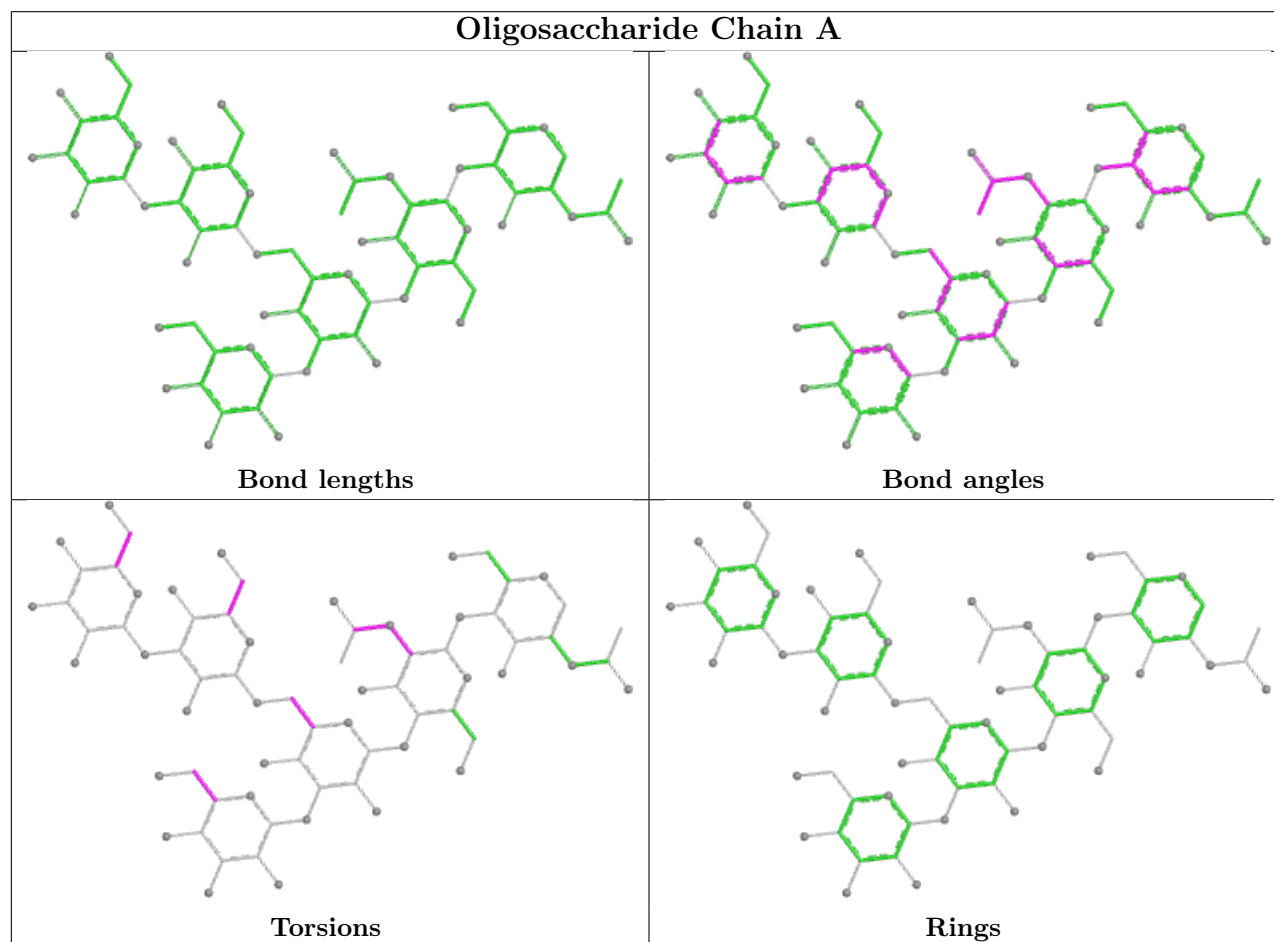
All (1) ring outliers are listed below:

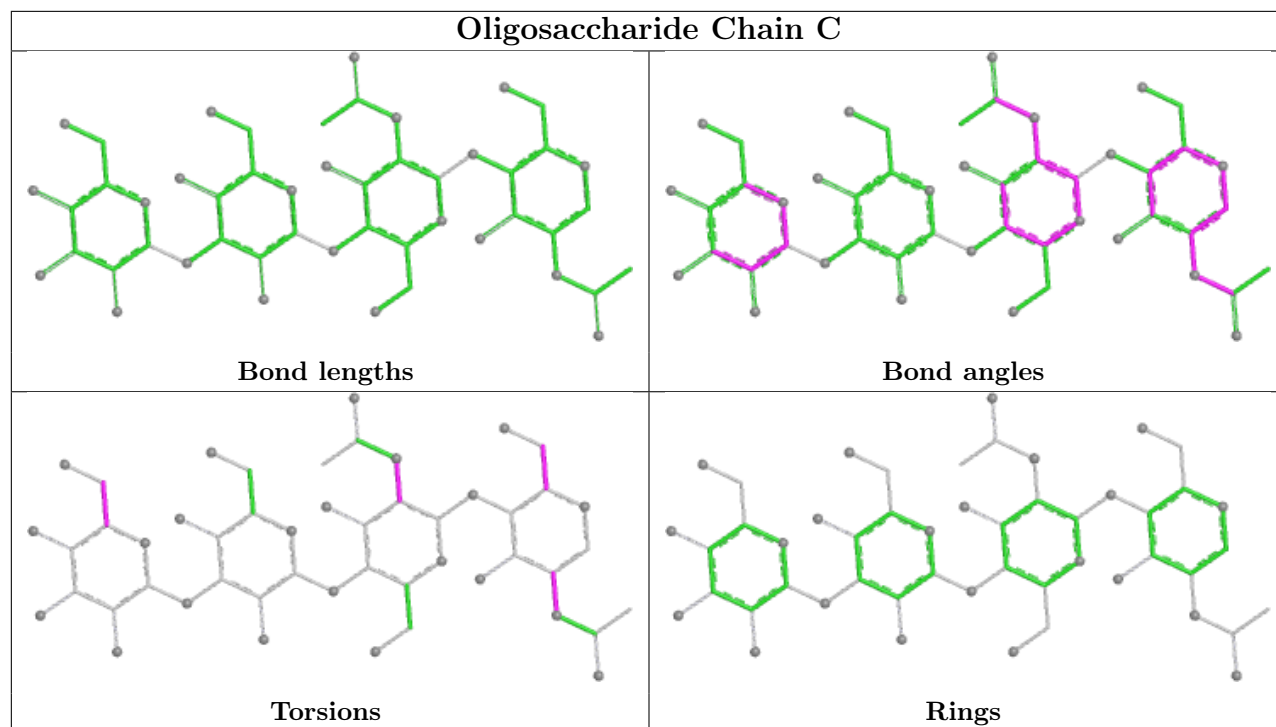
Mol	Chain	Res	Type	Atoms
11	J	1	MAN	C1-C2-C3-C4-C5-O5

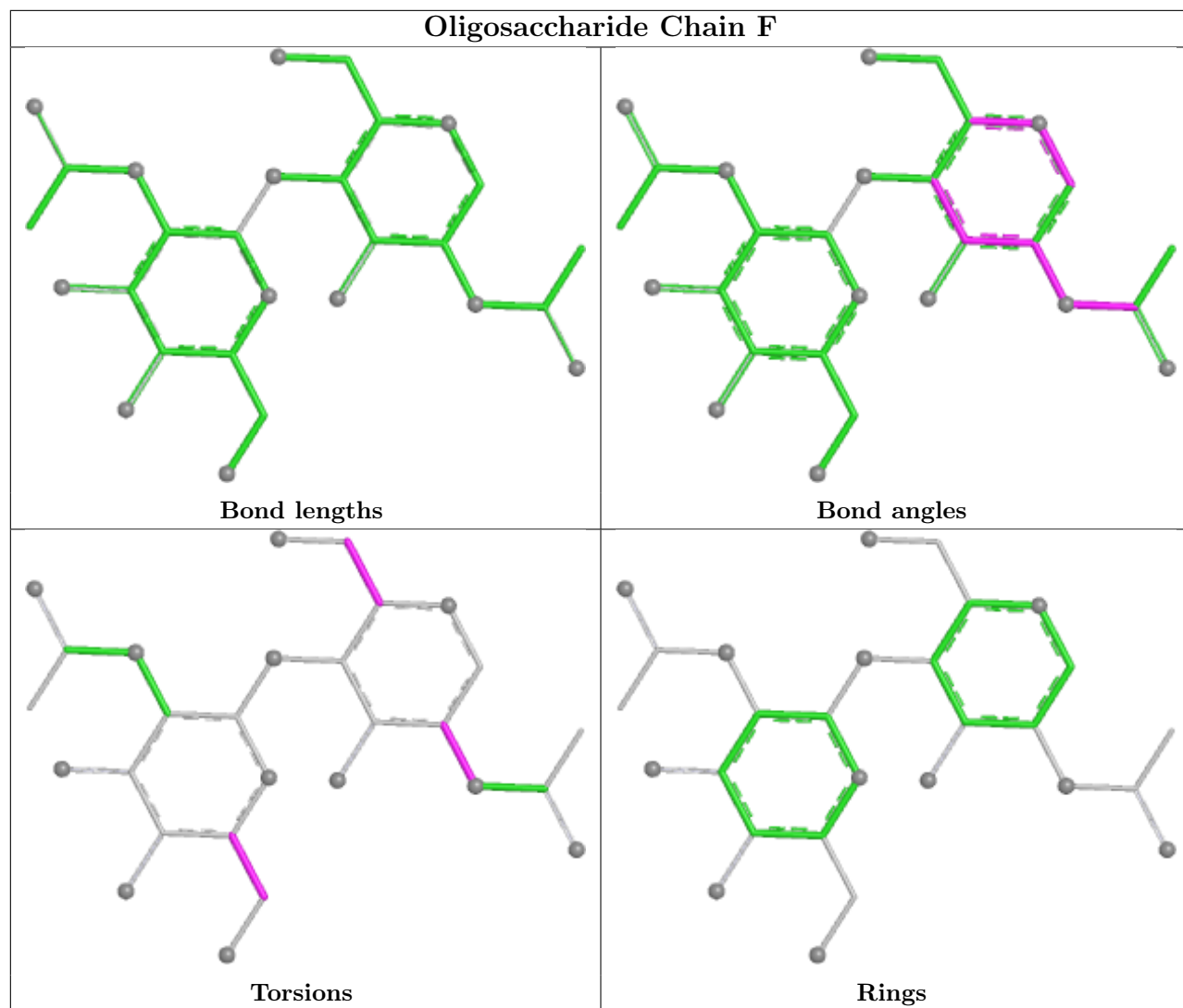
6 monomers are involved in 9 short contacts:

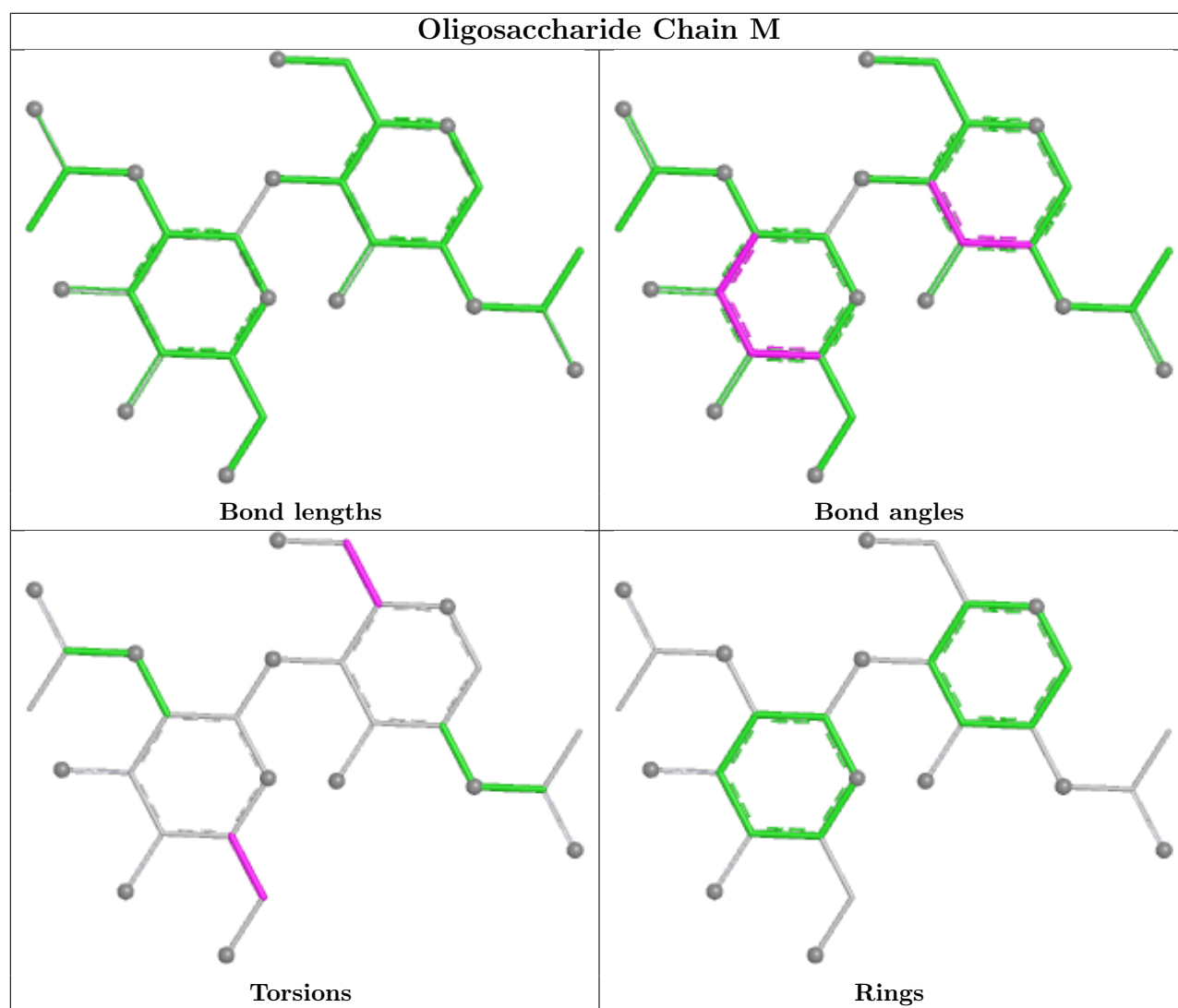
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	P	5	MAN	3	0
12	P	1	NAG	1	0
10	I	1	NAG	1	0
7	A	1	NAG	1	0
9	O	1	NAG	1	0
9	M	1	NAG	2	0

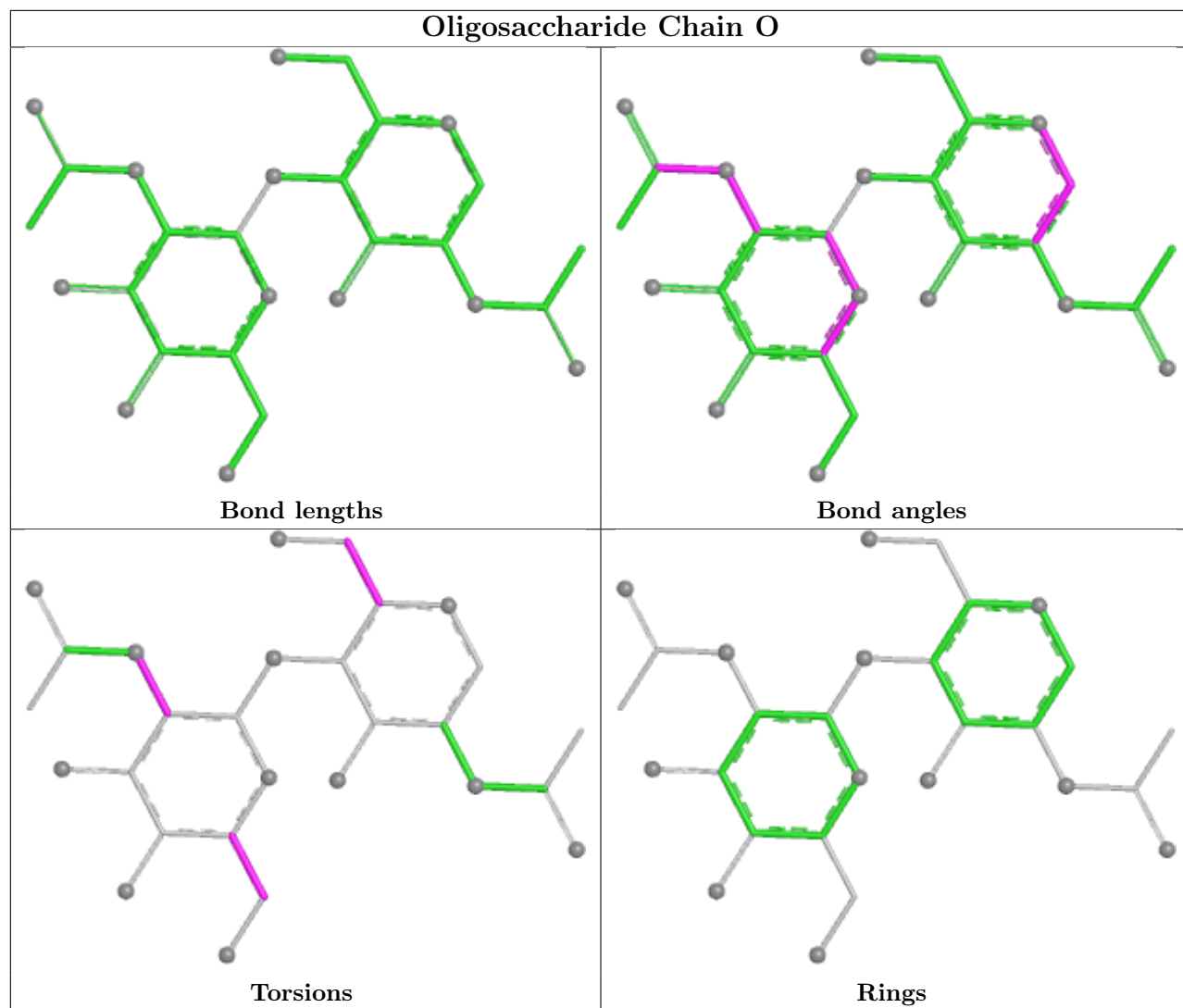
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

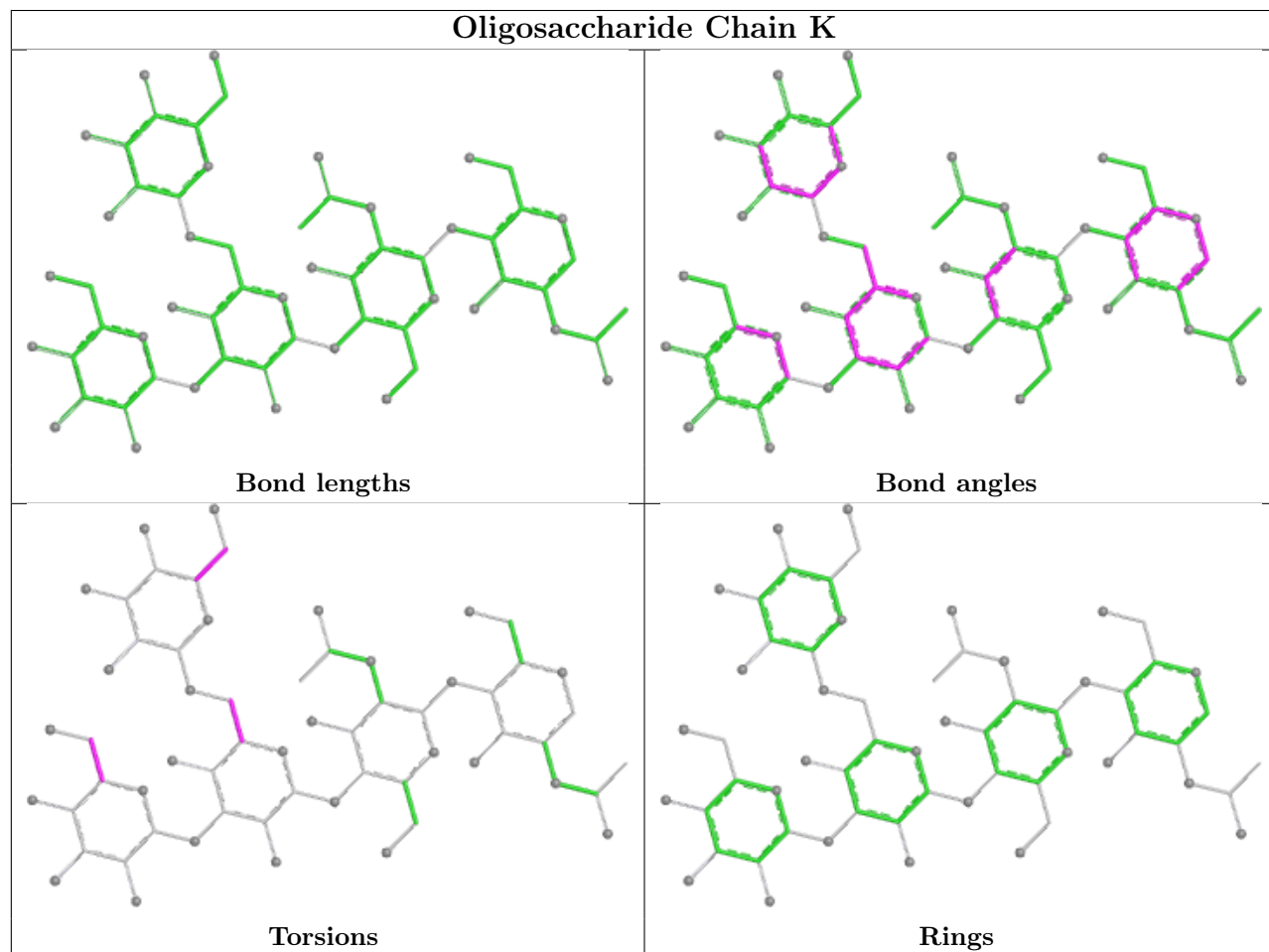
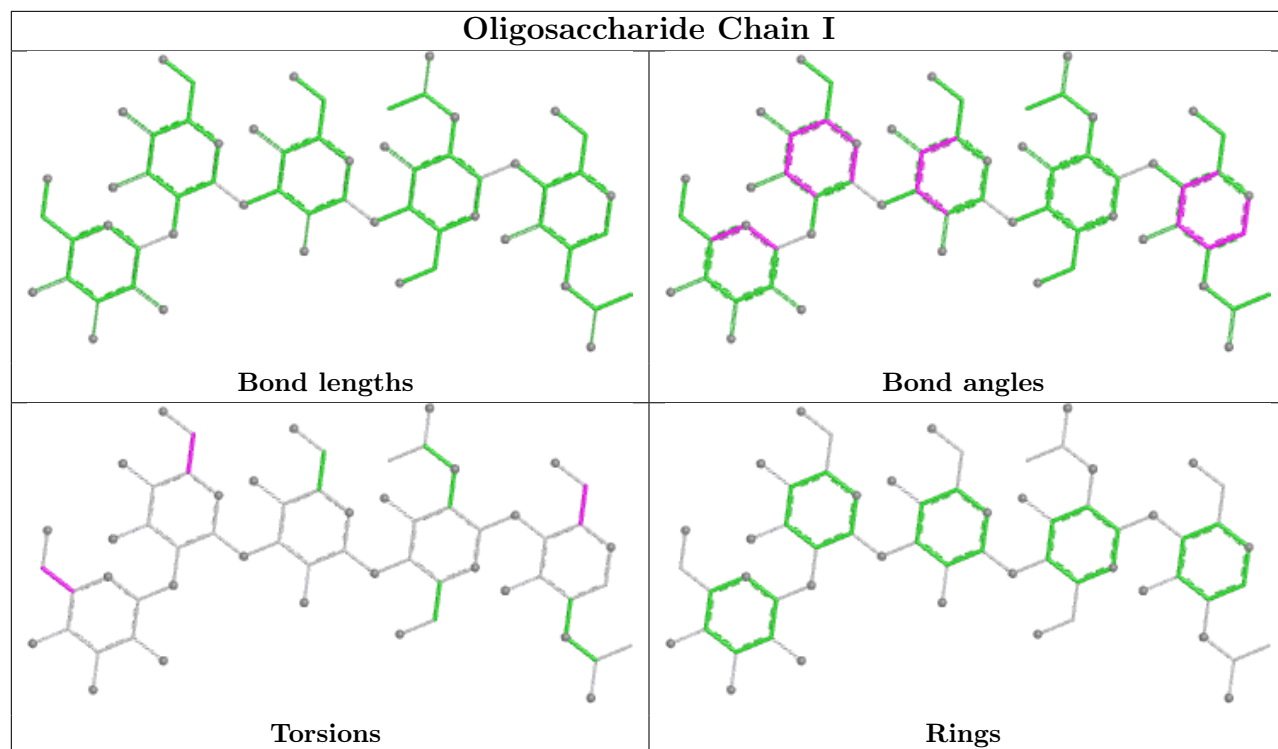


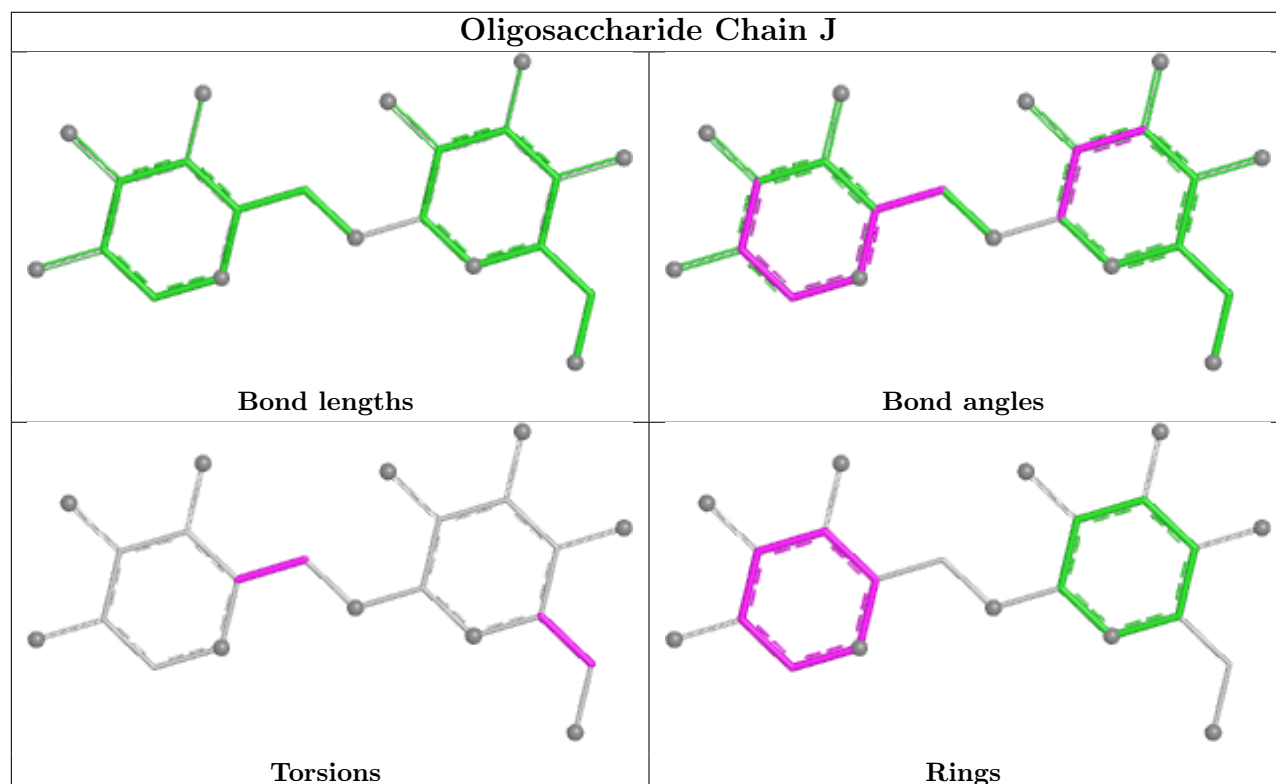
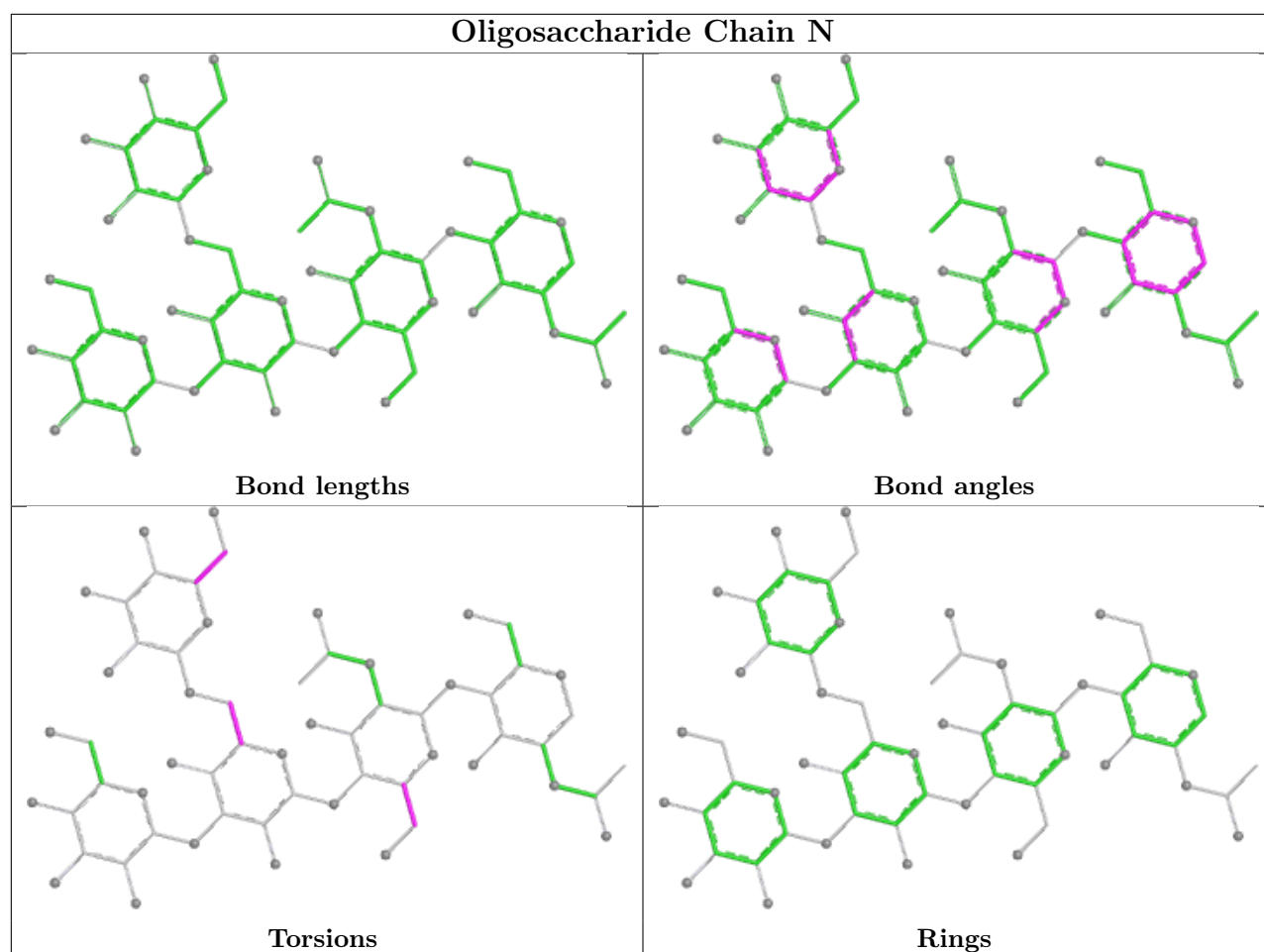


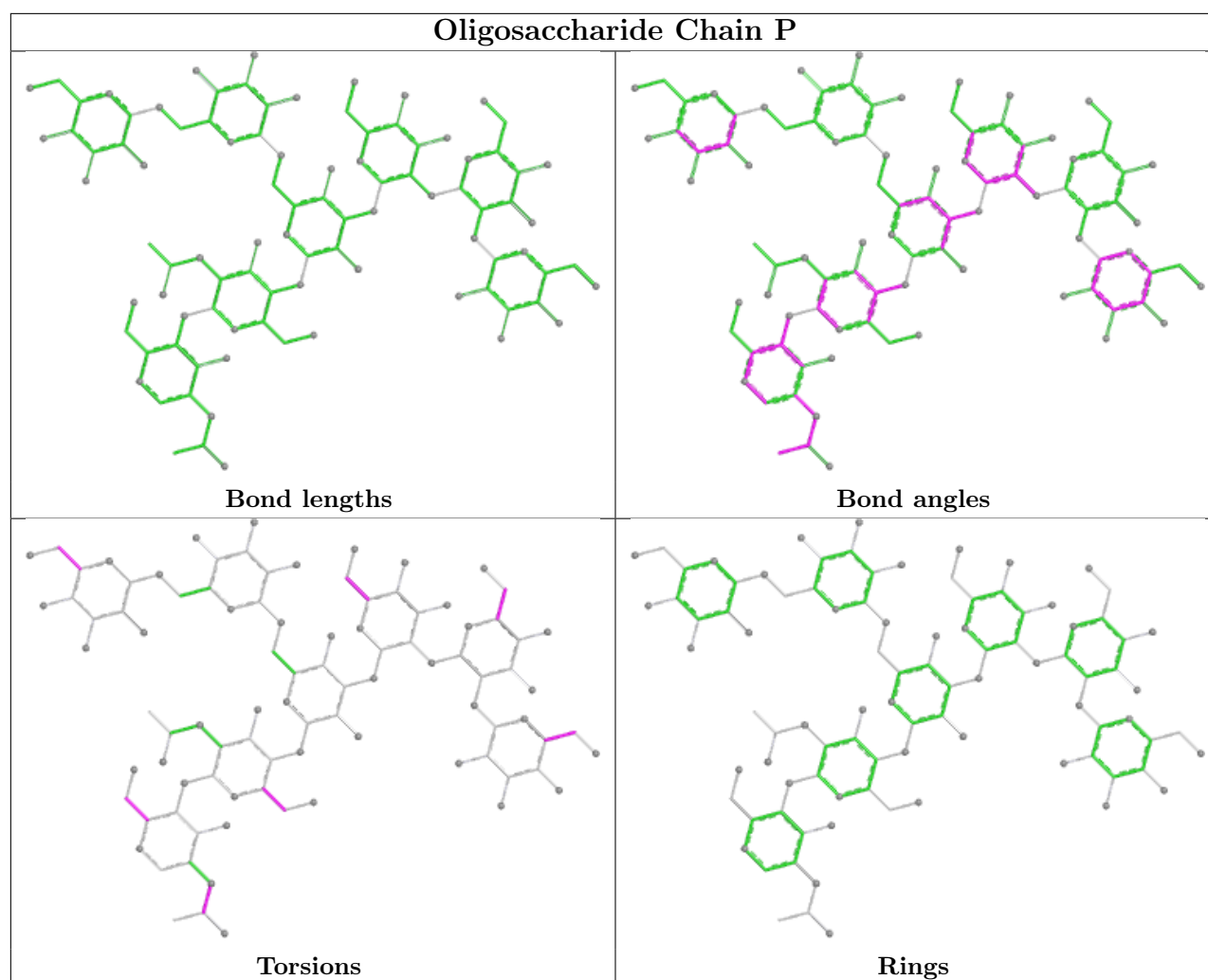












5.6 Ligand geometry [i](#)

9 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	607	1	14,14,15	0.29	0	17,19,21	1.11	1 (5%)
13	NAG	B	702	2	14,14,15	0.43	0	17,19,21	0.97	1 (5%)
14	MAN	H	309	-	11,11,12	0.71	0	15,15,17	2.65	6 (40%)
13	NAG	G	638	-	14,14,15	0.47	0	17,19,21	1.76	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	NAG	G	623	1	14,14,15	0.28	0	17,19,21	2.06	1 (5%)
13	NAG	G	609	-	14,14,15	0.59	0	17,19,21	1.52	2 (11%)
14	MAN	L	301	-	11,11,12	0.26	0	15,15,17	0.52	0
13	NAG	B	701	2	14,14,15	0.33	0	17,19,21	1.26	3 (17%)
13	NAG	G	608	1	14,14,15	0.34	0	17,19,21	0.68	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
13	NAG	G	607	1	-	2/6/23/26	0/1/1/1
13	NAG	B	702	2	-	1/6/23/26	0/1/1/1
14	MAN	H	309	-	-	1/2/19/22	0/1/1/1
13	NAG	G	638	-	-	4/6/23/26	0/1/1/1
13	NAG	G	623	1	-	0/6/23/26	0/1/1/1
13	NAG	G	609	-	-	3/6/23/26	0/1/1/1
14	MAN	L	301	-	-	0/2/19/22	0/1/1/1
13	NAG	B	701	2	-	0/6/23/26	0/1/1/1
13	NAG	G	608	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	G	623	NAG	C1-O5-C5	7.43	122.15	112.19
14	H	309	MAN	C1-O5-C5	6.28	120.61	112.19
14	H	309	MAN	C3-C4-C5	4.77	118.89	110.23
13	G	638	NAG	C2-N2-C7	4.01	128.27	122.90
13	G	638	NAG	C8-C7-N2	3.84	122.48	116.12

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	G	609	NAG	O5-C5-C6-O6
13	G	638	NAG	O5-C5-C6-O6
14	H	309	MAN	O5-C5-C6-O6
13	G	638	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
13	G	638	NAG	O7-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	H	309	MAN	5	0
13	G	609	NAG	1	0
14	L	301	MAN	5	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	439/497 (88%)	-0.68	1 (0%) 91 81	141, 227, 301, 363	0
2	B	131/153 (85%)	-0.68	0 100 100	149, 207, 302, 318	0
3	L	210/214 (98%)	-0.76	0 100 100	204, 251, 289, 313	0
4	H	231/236 (97%)	-0.78	0 100 100	194, 267, 332, 358	0
5	D	229/240 (95%)	-0.91	0 100 100	189, 275, 369, 419	0
6	E	213/216 (98%)	-0.94	0 100 100	209, 282, 373, 405	0
All	All	1453/1556 (93%)	-0.78	1 (0%) 92 87	141, 250, 346, 419	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	253	PRO	2.3

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	A	1	14/15	-	-	170,187,196,197	0
7	NAG	A	2	14/15	-	-	193,203,211,212	0
7	BMA	A	3	11/12	-	-	192,212,234,238	0

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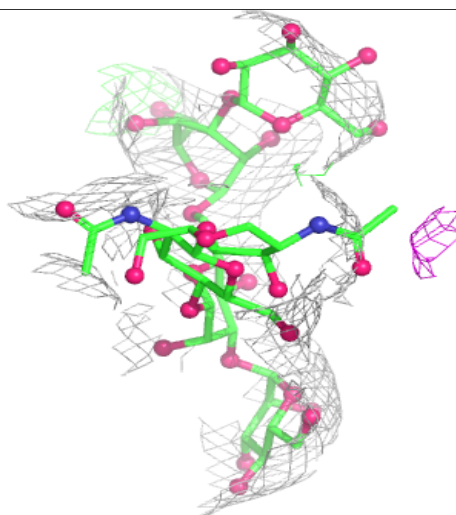
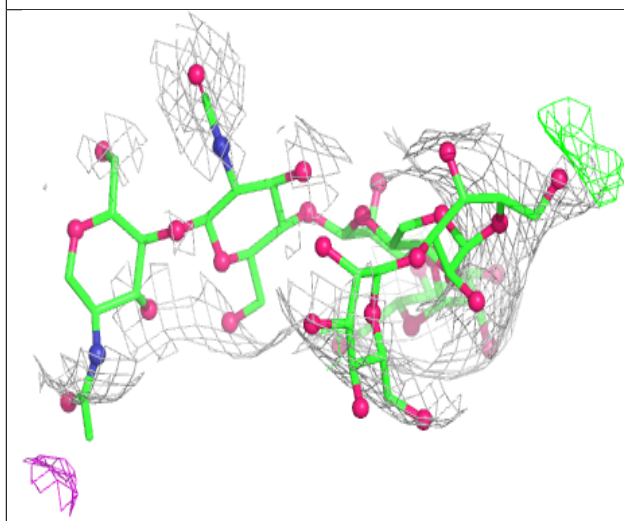
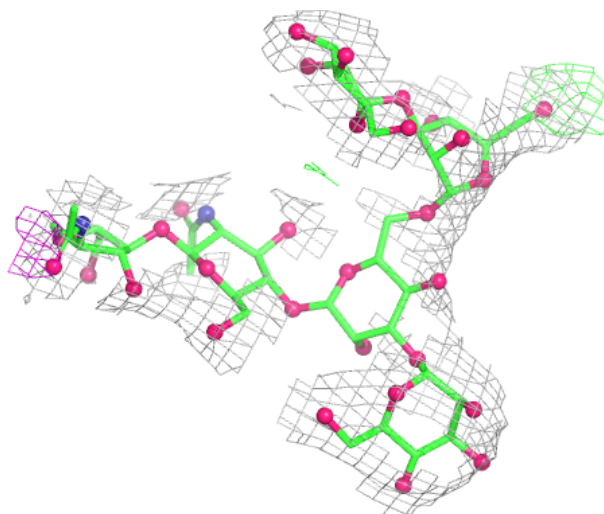
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	MAN	A	4	11/12	-	-	251,273,279,289	0
7	MAN	A	5	11/12	-	-	258,292,302,319	0
7	MAN	A	6	11/12	-	-	223,225,234,237	0
8	NAG	C	1	14/15	-	-	242,274,293,299	0
8	NAG	C	2	14/15	-	-	292,309,328,347	0
8	BMA	C	3	11/12	-	-	342,370,383,396	0
8	MAN	C	4	11/12	-	-	287,316,336,348	0
9	NAG	F	1	14/15	-	-	216,239,282,283	0
9	NAG	F	2	14/15	-	-	264,279,298,300	0
12	MAN	P	8	11/12	0.47	0.10	218,247,254,264	0
10	NAG	N	2	14/15	0.49	0.06	277,305,312,322	0
10	MAN	N	5	11/12	0.60	0.04	304,312,322,328	0
10	NAG	I	2	14/15	0.64	0.09	246,261,274,291	0
9	NAG	O	1	14/15	0.65	0.06	289,295,310,314	0
9	NAG	O	2	14/15	0.65	0.07	265,292,305,307	0
10	BMA	I	3	11/12	-	-	297,306,317,325	0
10	MAN	I	4	11/12	-	-	287,303,311,320	0
10	MAN	I	5	11/12	-	-	300,309,314,315	0
10	NAG	K	1	14/15	-	-	225,244,263,273	0
10	NAG	K	2	14/15	-	-	294,312,331,347	0
10	BMA	K	3	11/12	-	-	342,352,360,363	0
10	MAN	K	4	11/12	-	-	314,335,343,351	0
10	MAN	K	5	11/12	-	-	334,339,344,347	0
9	NAG	M	2	14/15	0.74	0.05	270,286,300,307	0
10	MAN	N	4	11/12	0.74	0.04	297,314,317,319	0
10	NAG	I	1	14/15	0.78	0.10	159,212,239,243	0
10	BMA	N	3	11/12	0.80	0.04	299,307,324,329	0
12	MAN	P	6	11/12	0.85	0.06	227,229,235,240	0
11	MAN	J	1	11/12	-	-	292,311,325,332	0
11	MAN	J	2	11/12	-	-	308,319,330,331	0
9	NAG	M	1	14/15	0.90	0.06	231,252,266,278	0
10	NAG	N	1	14/15	0.94	0.06	218,242,251,270	0
12	MAN	P	7	11/12	0.94	0.05	246,254,259,267	0
12	MAN	P	4	11/12	0.94	0.05	188,197,207,214	0
12	NAG	P	1	14/15	0.95	0.06	199,221,236,240	0
12	NAG	P	2	14/15	0.95	0.06	188,207,219,222	0
12	BMA	P	3	11/12	0.96	0.04	207,215,231,235	0
12	MAN	P	5	11/12	0.98	0.02	207,219,228,232	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.

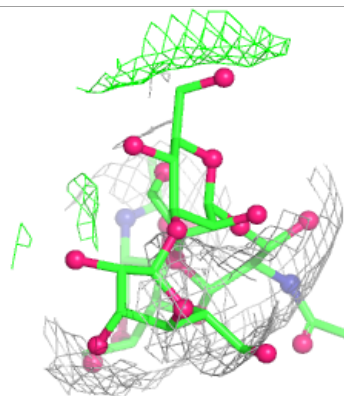
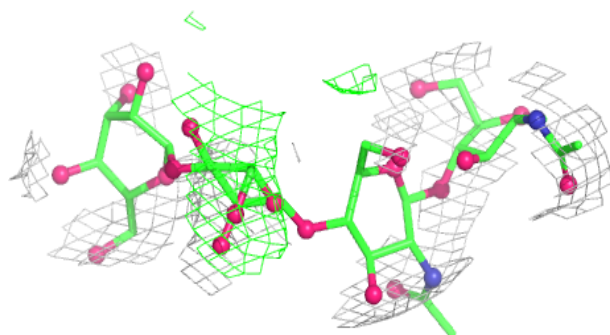
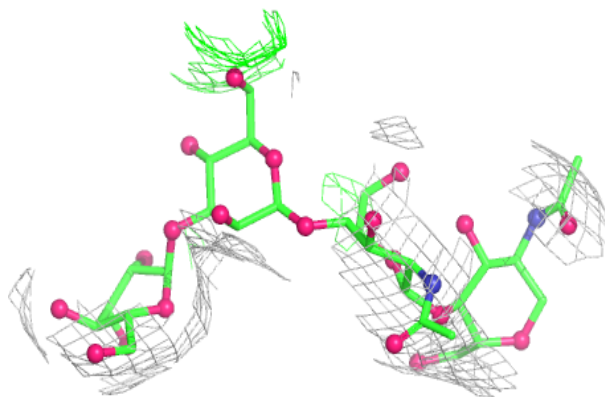
Electron density around Chain A:

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



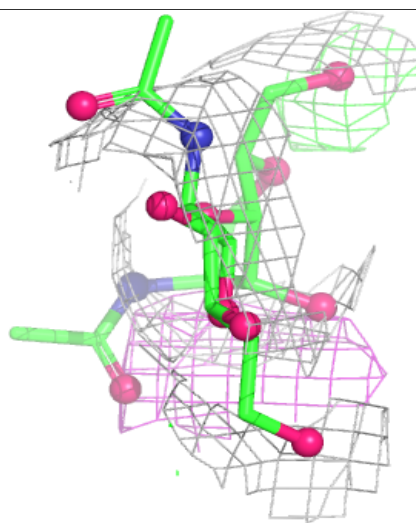
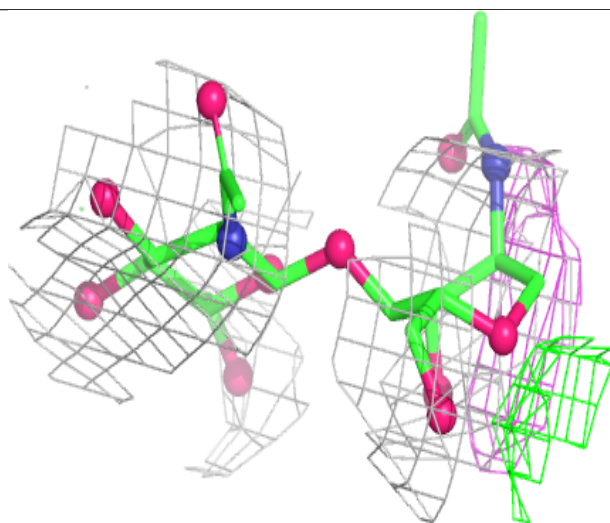
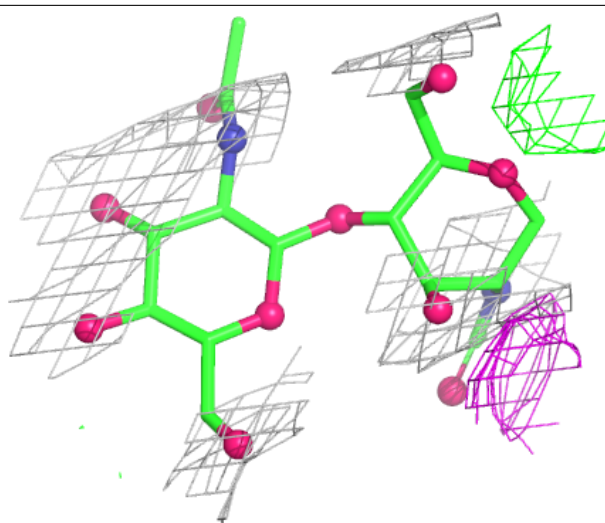
Electron density around Chain C:

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



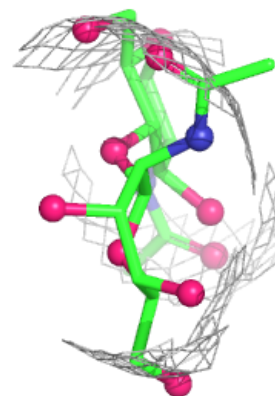
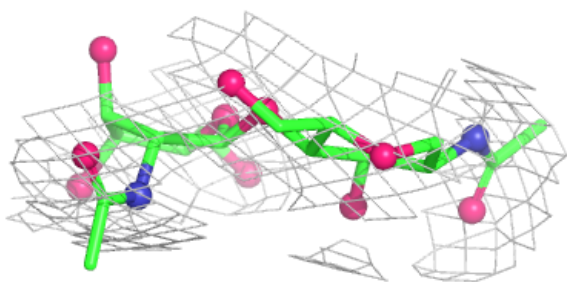
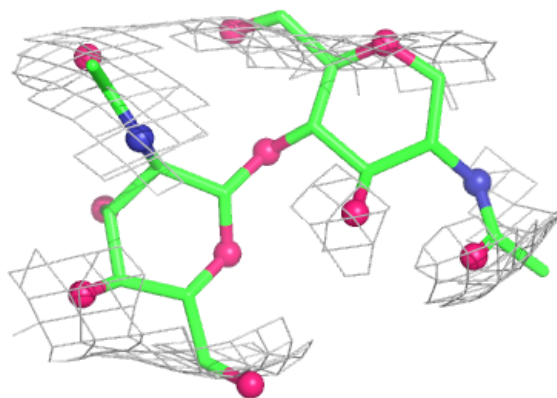
Electron density around Chain F:

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



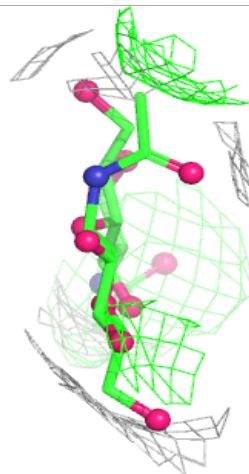
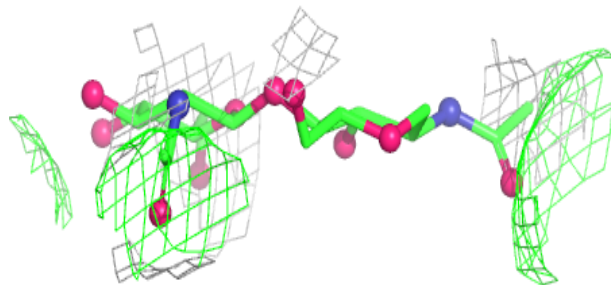
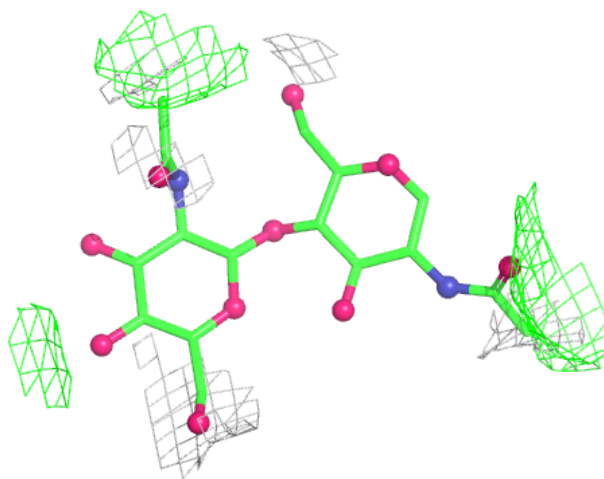
Electron density around Chain M:

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



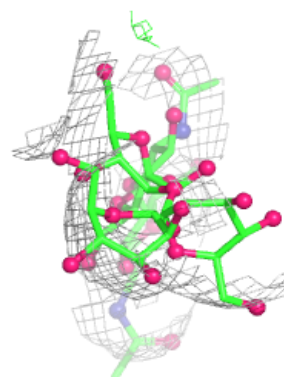
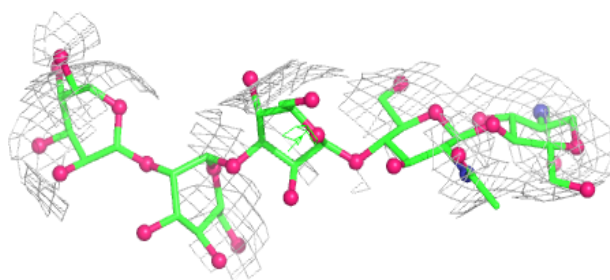
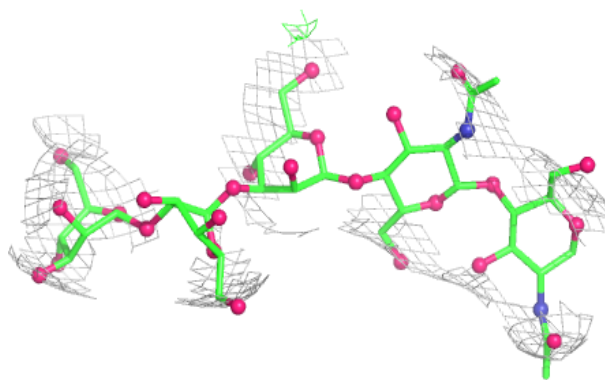
Electron density around Chain O:

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

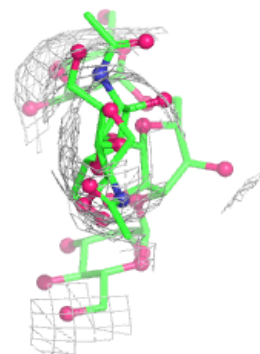
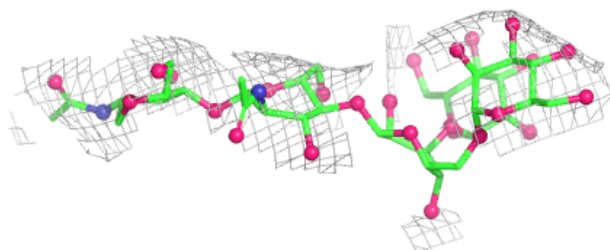
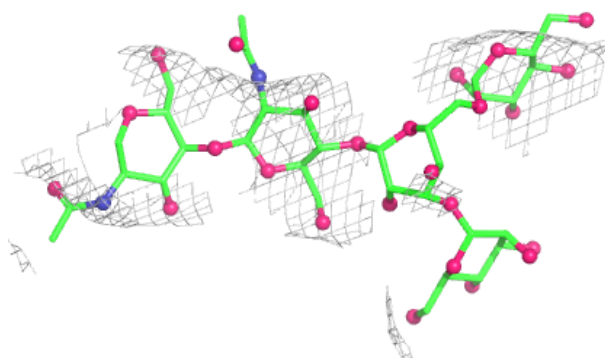


Electron density around Chain I:

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

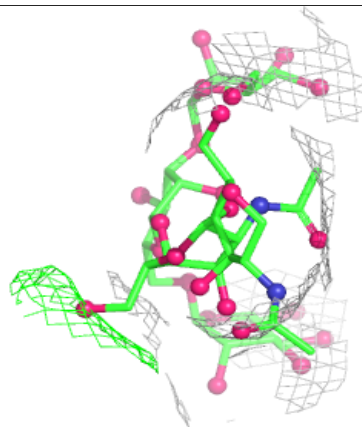
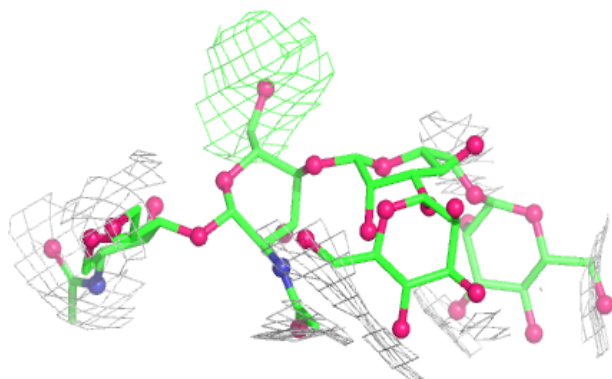
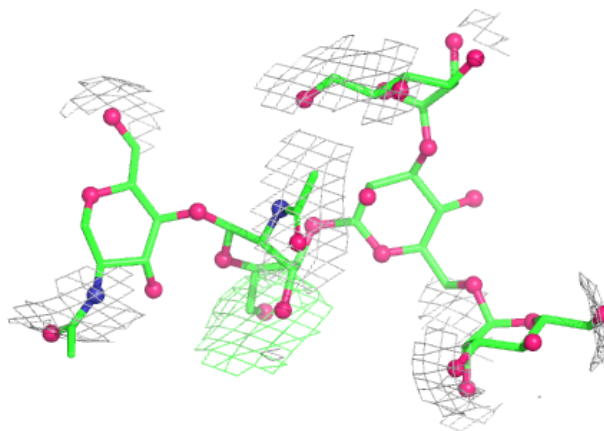
**Electron density around Chain K:**

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



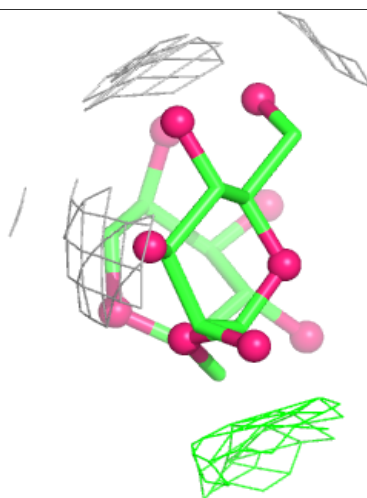
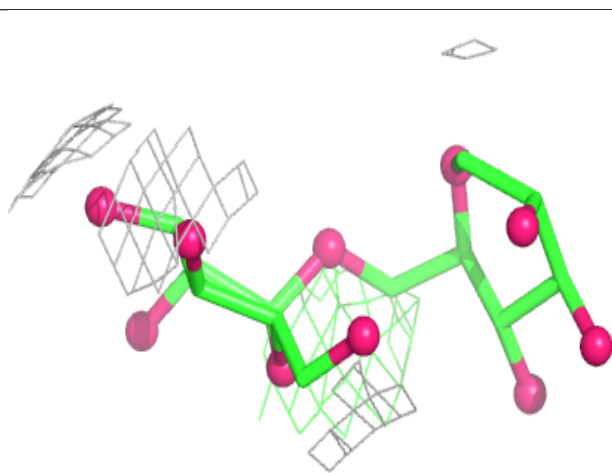
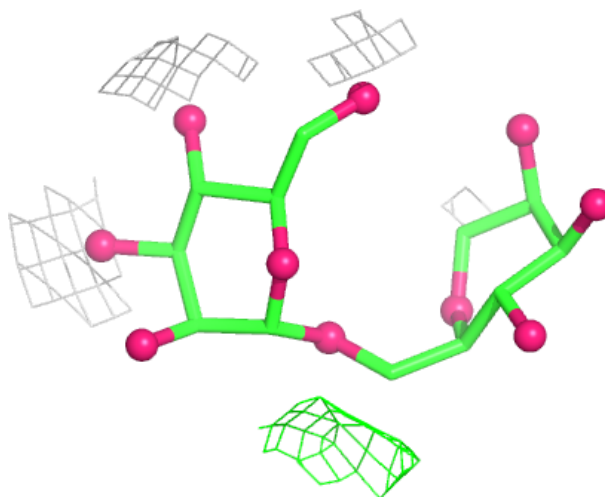
Electron density around Chain N:

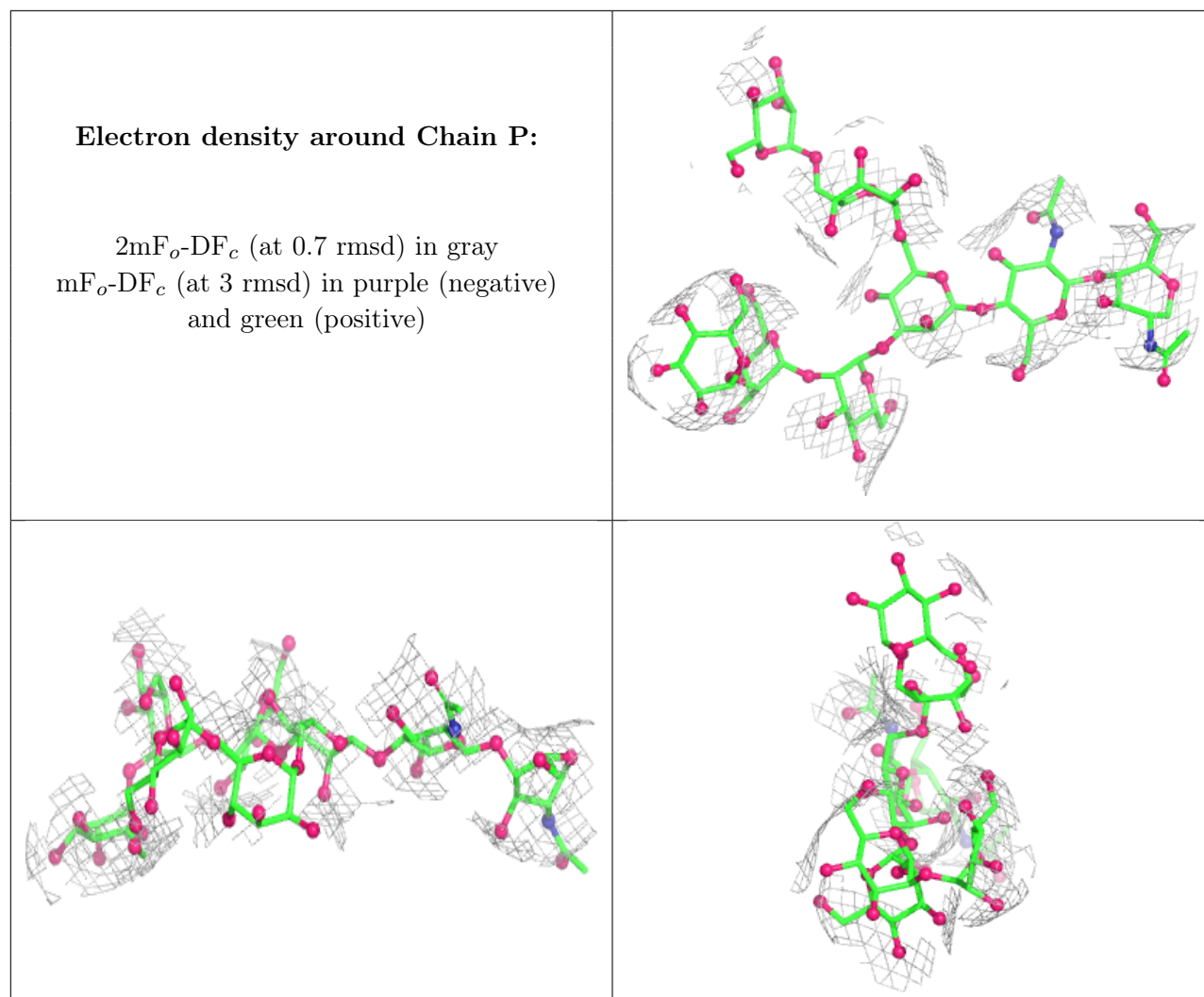
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain J:

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





6.4 Ligands ⓘ

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
13	NAG	G	623	14/15	0.49	0.06	263,292,303,308	0
13	NAG	B	702	14/15	0.68	0.08	289,323,338,343	0
13	NAG	G	607	14/15	0.69	0.07	253,262,281,306	0
13	NAG	G	608	14/15	0.72	0.05	245,264,284,288	0
14	MAN	L	301	11/12	0.79	0.06	283,290,296,300	0
14	MAN	H	309	11/12	0.79	0.06	248,257,279,287	0
13	NAG	B	701	14/15	0.83	0.05	269,284,294,301	0
13	NAG	G	638	14/15	0.83	0.06	209,222,231,235	0
13	NAG	G	609	14/15	0.90	0.05	218,245,253,254	0

6.5 Other polymers [i](#)

There are no such residues in this entry.