



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:27 AM UTC

PDB ID : 6BF4 / pdb_00006bf4
Title : Crystal Structure of HIV-1 Clade AE Strain CNE55 gp120 Core in Complex with Neutralizing Antibody VRC-PG05 that Targets the Center of the Silent Face on the Outer Domain of gp120
Authors : Zhou, T.; Kwong, P.D.
Deposited on : 2017-10-25
Resolution : 2.38 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

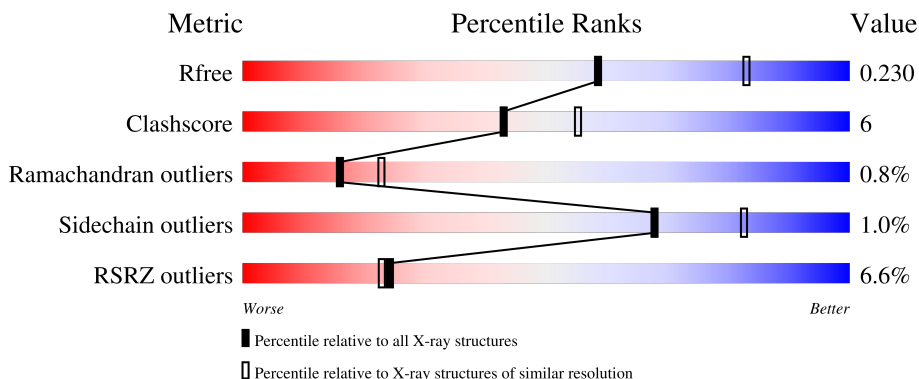
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	344	 10% 79% 18% ..
1	G	344	 5% 83% 13% ..
2	B	229	 9% 74% 24% ..
2	H	229	 3% 82% 14% .
3	C	219	 6% 87% 12%

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Mol	Chain	Length	Quality of chain
3	L	219	<p>4% 86% 13%</p>
4	D	10	<p>20% 80%</p>
5	E	2	<p>100%</p>
6	F	6	<p>33% 67%</p>
7	I	9	<p>11% 89%</p>
7	N	9	<p>22% 78%</p>
8	J	11	<p>18% 82%</p>
9	K	5	<p>60% 40%</p>
10	M	5	<p>40% 60%</p>

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 13124 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 HIV-1 clade AE gp120 core.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	337	Total	C	N	O	S	0	0	0
			2639	1656	460	503	20			
1	G	333	Total	C	N	O	S	0	0	0
			2607	1639	452	496	20			

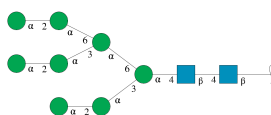
- Molecule 2 is a protein called VRC-PG05 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	225	Total	C	N	O	S	0	0	0
			1702	1077	290	326	9			
2	H	221	Total	C	N	O	S	0	0	0
			1676	1062	285	320	9			

- Molecule 3 is a protein called VRC-PG05 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	219	Total	C	N	O	S	0	0	0
			1714	1077	291	340	6			
3	L	218	Total	C	N	O	S	0	0	0
			1707	1074	290	338	5			

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



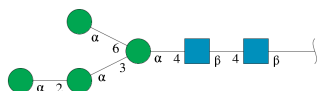
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	D	10	116	64	2	50	0	0	0

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



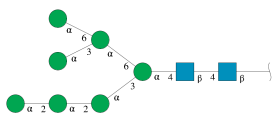
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	E	2	28	16	2	10	0	0	0

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-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			
6	F	6	72	40	2	30	0	0	0

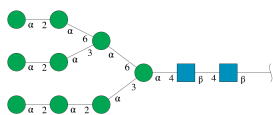
- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
7	I	9	105	58	2	45	0	0	0
7	N	9	105	58	2	45	0	0	0

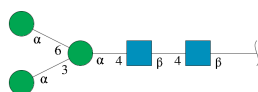
- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

ose-(1-2)-alpha-D-mannopyranose-(1-3)-[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)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



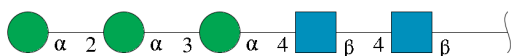
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
8	J	11	127	70	2	55	0	0	0

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



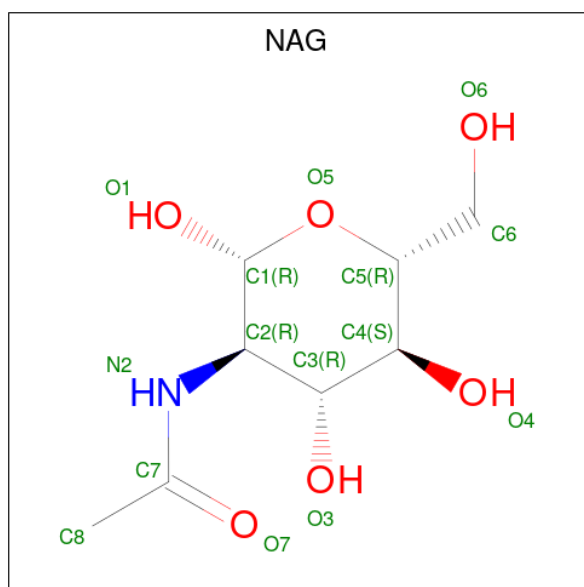
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	K	5	61	34	2	25	0	0	0

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



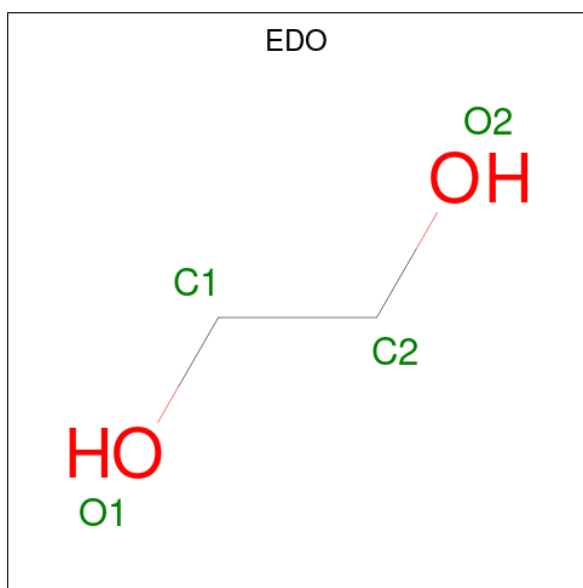
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
10	M	5	61	34	2	25	0	0	0

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



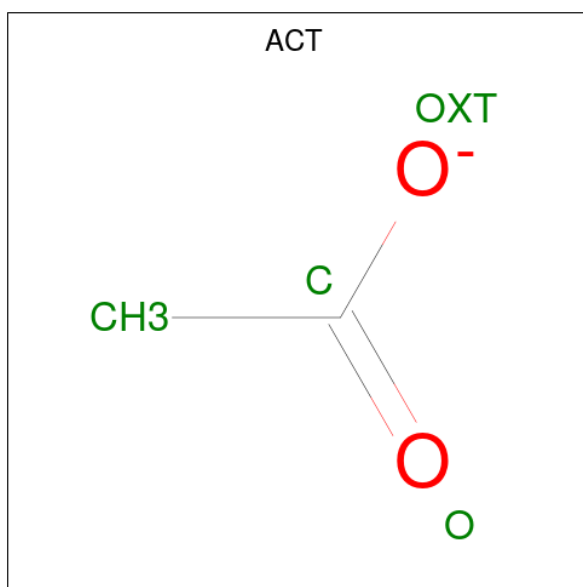
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
11	A	1	Total 14	8	1	5	0	0
11	A	1	Total 14	8	1	5	0	0
11	A	1	Total 14	8	1	5	0	0
11	A	1	Total 14	8	1	5	0	0
11	A	1	Total 14	8	1	5	0	0
11	A	1	Total 14	8	1	5	0	0
11	C	1	Total 14	8	1	5	0	0
11	G	1	Total 14	8	1	5	0	0
11	G	1	Total 14	8	1	5	0	0
11	G	1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

- Molecule 12 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	1	Total C O 4 2 2	0	0
12	B	1	Total C O 4 2 2	0	0
12	B	1	Total C O 4 2 2	0	0
12	G	1	Total C O 4 2 2	0	0
12	H	1	Total C O 4 2 2	0	0
12	L	1	Total C O 4 2 2	0	0
12	L	1	Total C O 4 2 2	0	0

- Molecule 13 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	B	1	Total C O 4 2 2	0	0

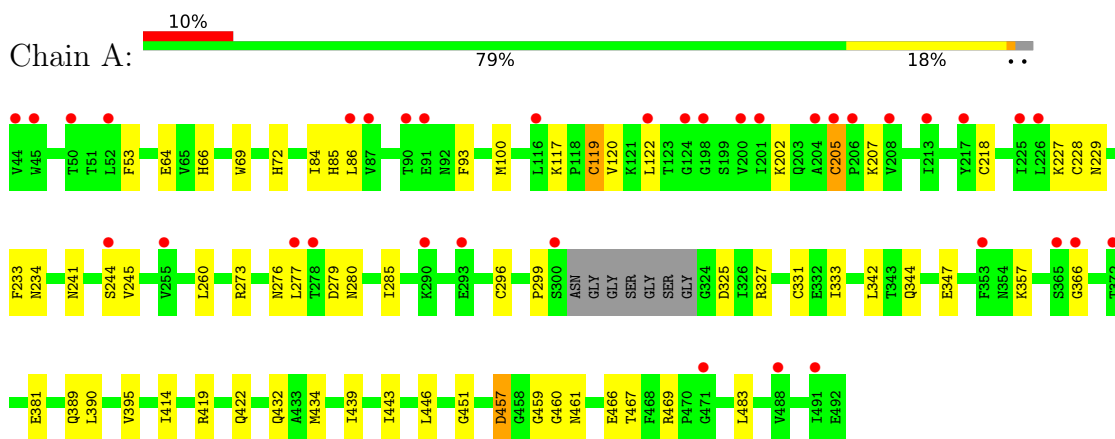
- Molecule 14 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	A	7	Total O 7 7	0	0
14	B	26	Total O 26 26	0	0
14	C	30	Total O 30 30	0	0
14	G	36	Total O 36 36	0	0
14	H	38	Total O 38 38	0	0
14	L	39	Total O 39 39	0	0

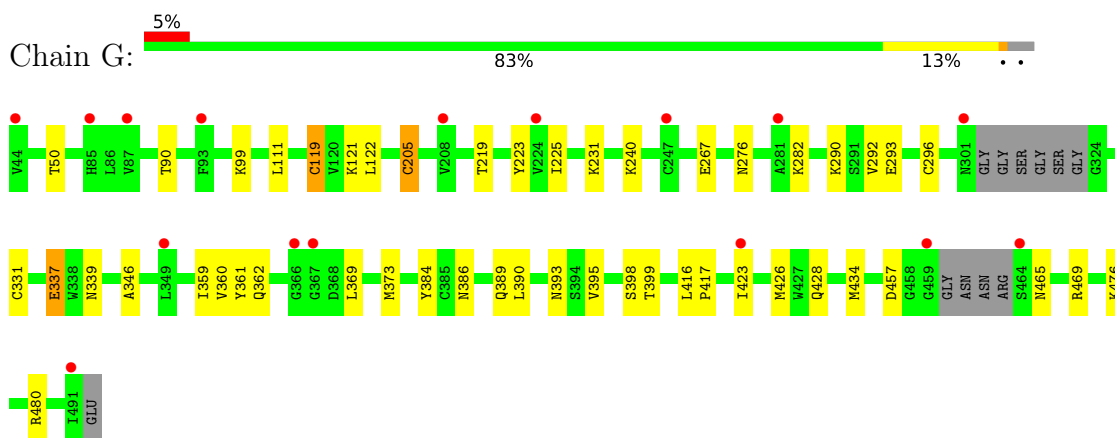
3 Residue-property plots [i](#)

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

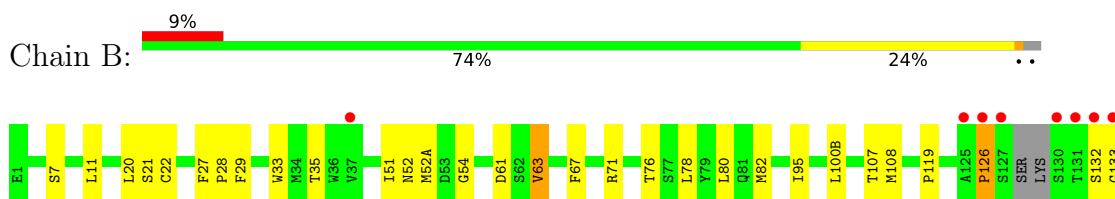
- Molecule 1: HIV-1 clade AE gp120 core

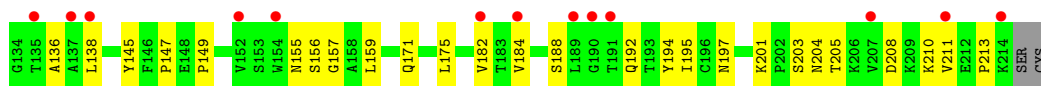


- Molecule 1: HIV-1 clade AE gp120 core

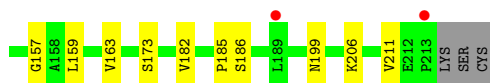
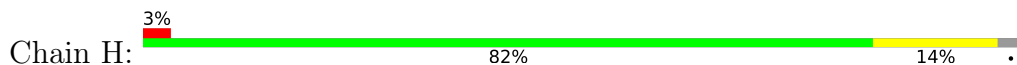


- Molecule 2: VRC-PG05 Fab heavy chain

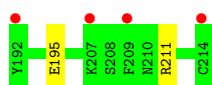
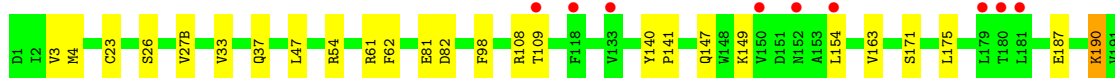
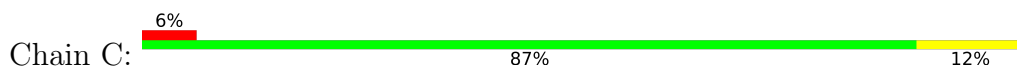




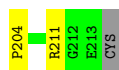
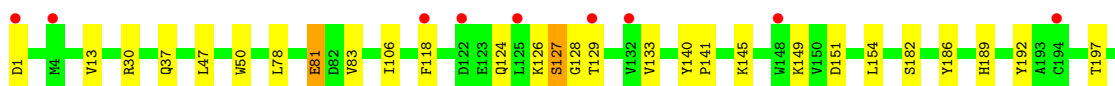
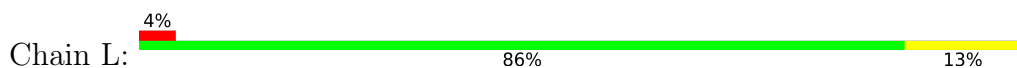
- Molecule 2: VRC-PG05 Fab heavy chain



- Molecule 3: VRC-PG05 Fab light chain



- Molecule 3: VRC-PG05 Fab light chain



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



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2

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

Chain F:  33% 67%MAG1
MAG2
MAN3
MAN4
MAN5
MAN6

- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  11% 89%MAG1
MAG2
MAN3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9

- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  22% 78%MAG1
MAG2
MAN3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9

- Molecule 8: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  18% 82%MAG1
MAG2
MAN3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10
MAN11

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

Chain K:  60% 40%MAG1
MAG2
MAN3
MAN5

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

Chain M:



MAN1
MAN2
MAN3
MAN4
MAN5

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	231.44Å 89.25Å 123.41Å 90.00° 119.15° 90.00°	Depositor
Resolution (Å)	39.85 – 2.38 39.85 – 2.38	Depositor EDS
% Data completeness (in resolution range)	88.5 (39.85-2.38) 88.5 (39.85-2.38)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.192 , 0.228 0.194 , 0.230	Depositor DCC
R_{free} test set	3888 reflections (4.42%)	wwPDB-VP
Wilson B-factor (Å ²)	49.6	Xtrriage
Anisotropy	0.758	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 61.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13124	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: MAN, EDO, NAG, ACT

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	0.11	0/2696	0.31	0/3661
1	G	0.12	0/2663	0.31	0/3616
2	B	0.14	0/1743	0.35	0/2370
2	H	0.15	0/1717	0.38	0/2336
3	C	0.12	0/1755	0.33	0/2383
3	L	0.13	0/1748	0.34	0/2375
All	All	0.13	0/12322	0.33	0/16741

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2639	0	2569	42	0
1	G	2607	0	2540	31	0
2	B	1702	0	1677	32	0
2	H	1676	0	1649	17	0
3	C	1714	0	1647	19	0
3	L	1707	0	1642	18	0
4	D	116	0	97	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	28	0	25	3	0
6	F	72	0	61	1	0
7	I	105	0	88	1	0
7	N	105	0	88	0	0
8	J	127	0	106	0	0
9	K	61	0	52	0	0
10	M	61	0	52	0	0
11	A	84	0	78	3	0
11	C	14	0	13	0	0
11	G	84	0	78	1	0
11	L	14	0	13	0	0
12	A	4	0	6	0	0
12	B	8	0	12	3	0
12	G	4	0	6	2	0
12	H	4	0	6	0	0
12	L	8	0	12	0	0
13	B	4	0	3	0	0
14	A	7	0	0	0	0
14	B	26	0	0	0	0
14	C	30	0	0	0	0
14	G	36	0	0	0	0
14	H	38	0	0	0	0
14	L	39	0	0	1	0
All	All	13124	0	12520	157	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 6.

The worst 5 of 157 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)
3:L:189:HIS:O	3:L:211:ARG:NH1	2.05	0.90
2:H:9:GLY:HA2	2:H:18:LEU:HD21	1.55	0.86
1:A:357:LYS:NZ	1:A:461:ASN:O	2.07	0.86
1:G:50:THR:O	1:G:99:LYS:NZ	2.10	0.84
1:G:389:GLN:HB3	11:G:527:NAG:H61	1.62	0.82

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	333/344 (97%)	303 (91%)	25 (8%)	5 (2%)	8 10
1	G	327/344 (95%)	312 (95%)	14 (4%)	1 (0%)	36 48
2	B	221/229 (96%)	200 (90%)	17 (8%)	4 (2%)	6 8
2	H	217/229 (95%)	203 (94%)	12 (6%)	2 (1%)	14 20
3	C	217/219 (99%)	207 (95%)	10 (5%)	0	100 100
3	L	216/219 (99%)	207 (96%)	8 (4%)	1 (0%)	24 34
All	All	1531/1584 (97%)	1432 (94%)	86 (6%)	13 (1%)	16 23

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	204	ASN
3	L	127	SER
1	A	460	GLY
2	B	126	PRO
1	A	85	HIS

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	299/302 (99%)	295 (99%)	4 (1%)	61 78
1	G	296/302 (98%)	292 (99%)	4 (1%)	59 77
2	B	189/193 (98%)	188 (100%)	1 (0%)	81 90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	186/193 (96%)	183 (98%)	3 (2%)	55	74
3	C	193/193 (100%)	192 (100%)	1 (0%)	81	90
3	L	192/193 (100%)	191 (100%)	1 (0%)	81	90
All	All	1355/1376 (98%)	1341 (99%)	14 (1%)	68	82

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

Mol	Chain	Res	Type
1	G	119	CYS
1	G	205	CYS
3	L	81	GLU
2	H	63	VAL
2	H	173	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	42	GLN
3	L	138	ASN
1	A	389	GLN
1	A	444	ASN
3	C	210	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](#)

57 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	D	1	4,1	14,14,15	0.34	0	17,19,21	0.54	0
4	MAN	D	10	4	11,11,12	0.67	0	15,15,17	1.35	2 (13%)
4	NAG	D	2	4	14,14,15	0.30	0	17,19,21	0.50	0
4	MAN	D	3	4	11,11,12	0.74	0	15,15,17	0.95	1 (6%)
4	MAN	D	4	4	11,11,12	0.53	0	15,15,17	1.17	2 (13%)
4	MAN	D	5	4	11,11,12	0.72	0	15,15,17	1.41	2 (13%)
4	MAN	D	6	4	11,11,12	0.68	0	15,15,17	0.96	2 (13%)
4	MAN	D	7	4	11,11,12	0.72	0	15,15,17	1.24	2 (13%)
4	MAN	D	8	4	11,11,12	0.66	0	15,15,17	1.05	2 (13%)
4	MAN	D	9	4	11,11,12	0.67	0	15,15,17	1.10	1 (6%)
5	NAG	E	1	5,1	14,14,15	0.23	0	17,19,21	0.63	0
5	NAG	E	2	5	14,14,15	0.26	0	17,19,21	0.53	0
6	NAG	F	1	1,6	14,14,15	0.25	0	17,19,21	0.49	0
6	NAG	F	2	6	14,14,15	0.28	0	17,19,21	0.56	0
6	MAN	F	3	6	11,11,12	0.77	0	15,15,17	0.92	0
6	MAN	F	4	6	11,11,12	0.66	0	15,15,17	1.09	1 (6%)
6	MAN	F	5	6	11,11,12	0.72	0	15,15,17	1.06	1 (6%)
6	MAN	F	6	6	11,11,12	0.72	0	15,15,17	0.99	2 (13%)
7	NAG	I	1	1,7	14,14,15	0.17	0	17,19,21	0.64	0
7	NAG	I	2	7	14,14,15	0.29	0	17,19,21	0.50	0
7	MAN	I	3	7	11,11,12	0.75	0	15,15,17	0.97	2 (13%)
7	MAN	I	4	7	11,11,12	1.05	1 (9%)	15,15,17	0.99	0
7	MAN	I	5	7	11,11,12	0.72	0	15,15,17	1.22	2 (13%)
7	MAN	I	6	7	11,11,12	0.74	0	15,15,17	0.94	2 (13%)
7	MAN	I	7	7	11,11,12	0.68	0	15,15,17	1.29	2 (13%)
7	MAN	I	8	7	11,11,12	0.66	0	15,15,17	1.09	2 (13%)
7	MAN	I	9	7	11,11,12	0.63	0	15,15,17	1.03	2 (13%)
8	NAG	J	1	8,1	14,14,15	0.26	0	17,19,21	0.51	0
8	MAN	J	10	8	11,11,12	0.82	0	15,15,17	0.96	1 (6%)
8	MAN	J	11	8	11,11,12	0.66	0	15,15,17	0.99	2 (13%)
8	NAG	J	2	8	14,14,15	0.39	0	17,19,21	0.57	0
8	MAN	J	3	8	11,11,12	0.83	1 (9%)	15,15,17	1.25	1 (6%)
8	MAN	J	4	8	11,11,12	0.66	0	15,15,17	1.04	2 (13%)
8	MAN	J	5	8	11,11,12	0.75	0	15,15,17	1.30	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	MAN	J	6	8	11,11,12	0.71	0	15,15,17	1.21	1 (6%)
8	MAN	J	7	8	11,11,12	0.61	0	15,15,17	1.13	2 (13%)
8	MAN	J	8	8	11,11,12	0.71	0	15,15,17	1.26	2 (13%)
8	MAN	J	9	8	11,11,12	0.78	0	15,15,17	1.09	2 (13%)
9	NAG	K	1	9,1	14,14,15	0.21	0	17,19,21	0.42	0
9	NAG	K	2	9	14,14,15	0.23	0	17,19,21	0.63	0
9	MAN	K	3	9	11,11,12	1.07	0	15,15,17	0.73	0
9	MAN	K	4	9	11,11,12	1.26	2 (18%)	15,15,17	1.47	2 (13%)
9	MAN	K	5	9	11,11,12	0.98	1 (9%)	15,15,17	1.22	2 (13%)
10	NAG	M	1	1,10	14,14,15	0.36	0	17,19,21	0.50	0
10	NAG	M	2	10	14,14,15	0.26	0	17,19,21	0.59	0
10	MAN	M	3	10	11,11,12	0.94	0	15,15,17	0.87	1 (6%)
10	MAN	M	4	10	11,11,12	0.69	0	15,15,17	1.09	1 (6%)
10	MAN	M	5	10	11,11,12	0.77	0	15,15,17	1.10	1 (6%)
7	NAG	N	1	1,7	14,14,15	0.42	0	17,19,21	0.60	0
7	NAG	N	2	7	14,14,15	0.31	0	17,19,21	0.52	0
7	MAN	N	3	7	11,11,12	0.79	0	15,15,17	1.11	2 (13%)
7	MAN	N	4	7	11,11,12	0.96	1 (9%)	15,15,17	0.89	0
7	MAN	N	5	7	11,11,12	0.84	0	15,15,17	1.18	2 (13%)
7	MAN	N	6	7	11,11,12	0.78	0	15,15,17	0.96	2 (13%)
7	MAN	N	7	7	11,11,12	0.87	1 (9%)	15,15,17	0.98	1 (6%)
7	MAN	N	8	7	11,11,12	0.74	0	15,15,17	0.89	1 (6%)
7	MAN	N	9	7	11,11,12	0.67	0	15,15,17	0.98	1 (6%)

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	D	1	4,1	-	0/6/23/26	0/1/1/1
4	MAN	D	10	4	-	0/2/19/22	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	MAN	D	3	4	-	2/2/19/22	1/1/1/1
4	MAN	D	4	4	-	0/2/19/22	0/1/1/1
4	MAN	D	5	4	-	1/2/19/22	0/1/1/1
4	MAN	D	6	4	-	2/2/19/22	0/1/1/1
4	MAN	D	7	4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MAN	D	8	4	-	1/2/19/22	0/1/1/1
4	MAN	D	9	4	-	1/2/19/22	0/1/1/1
5	NAG	E	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1
6	NAG	F	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	F	2	6	-	2/6/23/26	0/1/1/1
6	MAN	F	3	6	-	2/2/19/22	0/1/1/1
6	MAN	F	4	6	-	2/2/19/22	0/1/1/1
6	MAN	F	5	6	-	0/2/19/22	0/1/1/1
6	MAN	F	6	6	-	1/2/19/22	0/1/1/1
7	NAG	I	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	I	2	7	-	0/6/23/26	0/1/1/1
7	MAN	I	3	7	-	2/2/19/22	1/1/1/1
7	MAN	I	4	7	-	0/2/19/22	0/1/1/1
7	MAN	I	5	7	-	1/2/19/22	0/1/1/1
7	MAN	I	6	7	-	1/2/19/22	0/1/1/1
7	MAN	I	7	7	-	0/2/19/22	0/1/1/1
7	MAN	I	8	7	-	0/2/19/22	0/1/1/1
7	MAN	I	9	7	-	0/2/19/22	0/1/1/1
8	NAG	J	1	8,1	-	0/6/23/26	0/1/1/1
8	MAN	J	10	8	-	0/2/19/22	0/1/1/1
8	MAN	J	11	8	-	1/2/19/22	0/1/1/1
8	NAG	J	2	8	-	2/6/23/26	0/1/1/1
8	MAN	J	3	8	-	2/2/19/22	1/1/1/1
8	MAN	J	4	8	-	0/2/19/22	0/1/1/1
8	MAN	J	5	8	-	2/2/19/22	0/1/1/1
8	MAN	J	6	8	-	0/2/19/22	0/1/1/1
8	MAN	J	7	8	-	0/2/19/22	0/1/1/1
8	MAN	J	8	8	-	0/2/19/22	0/1/1/1
8	MAN	J	9	8	-	0/2/19/22	0/1/1/1
9	NAG	K	1	9,1	-	2/6/23/26	0/1/1/1
9	NAG	K	2	9	-	0/6/23/26	0/1/1/1
9	MAN	K	3	9	-	2/2/19/22	0/1/1/1
9	MAN	K	4	9	-	1/2/19/22	0/1/1/1
9	MAN	K	5	9	-	0/2/19/22	1/1/1/1
10	NAG	M	1	1,10	-	2/6/23/26	0/1/1/1
10	NAG	M	2	10	-	2/6/23/26	0/1/1/1
10	MAN	M	3	10	-	2/2/19/22	1/1/1/1

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

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	K	4	MAN	C4-C5	2.72	1.58	1.53
9	K	5	MAN	C1-C2	2.49	1.58	1.52
9	K	4	MAN	O5-C5	2.49	1.48	1.43
8	J	3	MAN	O5-C5	2.24	1.47	1.43
7	N	7	MAN	O5-C1	-2.22	1.40	1.43

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	5	MAN	C1-O5-C5	4.45	118.15	112.19
4	D	10	MAN	C1-O5-C5	4.30	117.95	112.19
9	K	4	MAN	C1-O5-C5	3.94	117.47	112.19
8	J	6	MAN	C1-O5-C5	3.77	117.23	112.19
8	J	3	MAN	C1-O5-C5	3.63	117.05	112.19

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	6	MAN	O5-C5-C6-O6
9	K	1	NAG	O5-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6
6	F	3	MAN	C4-C5-C6-O6
7	N	3	MAN	C4-C5-C6-O6

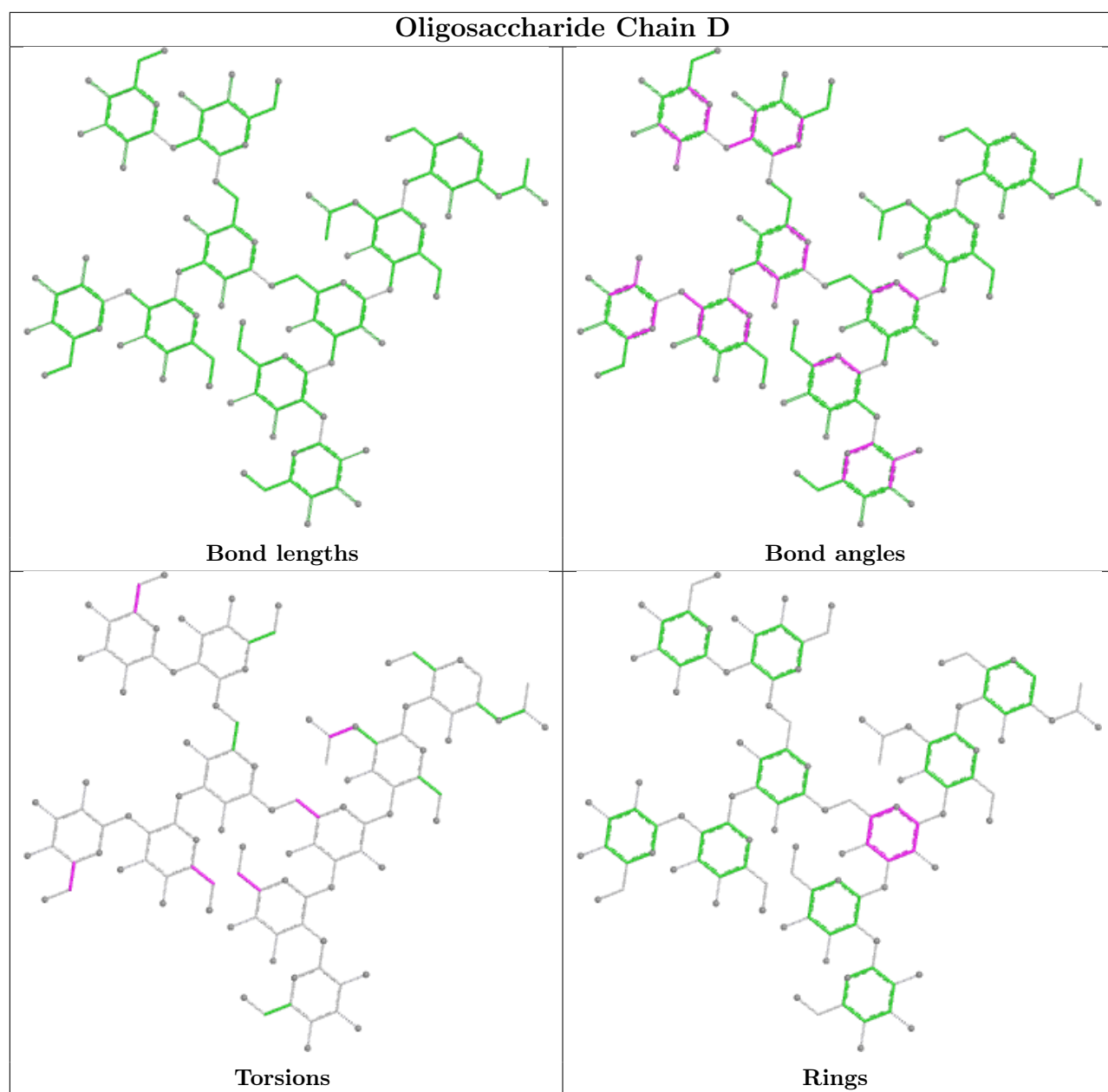
All (5) ring outliers are listed below:

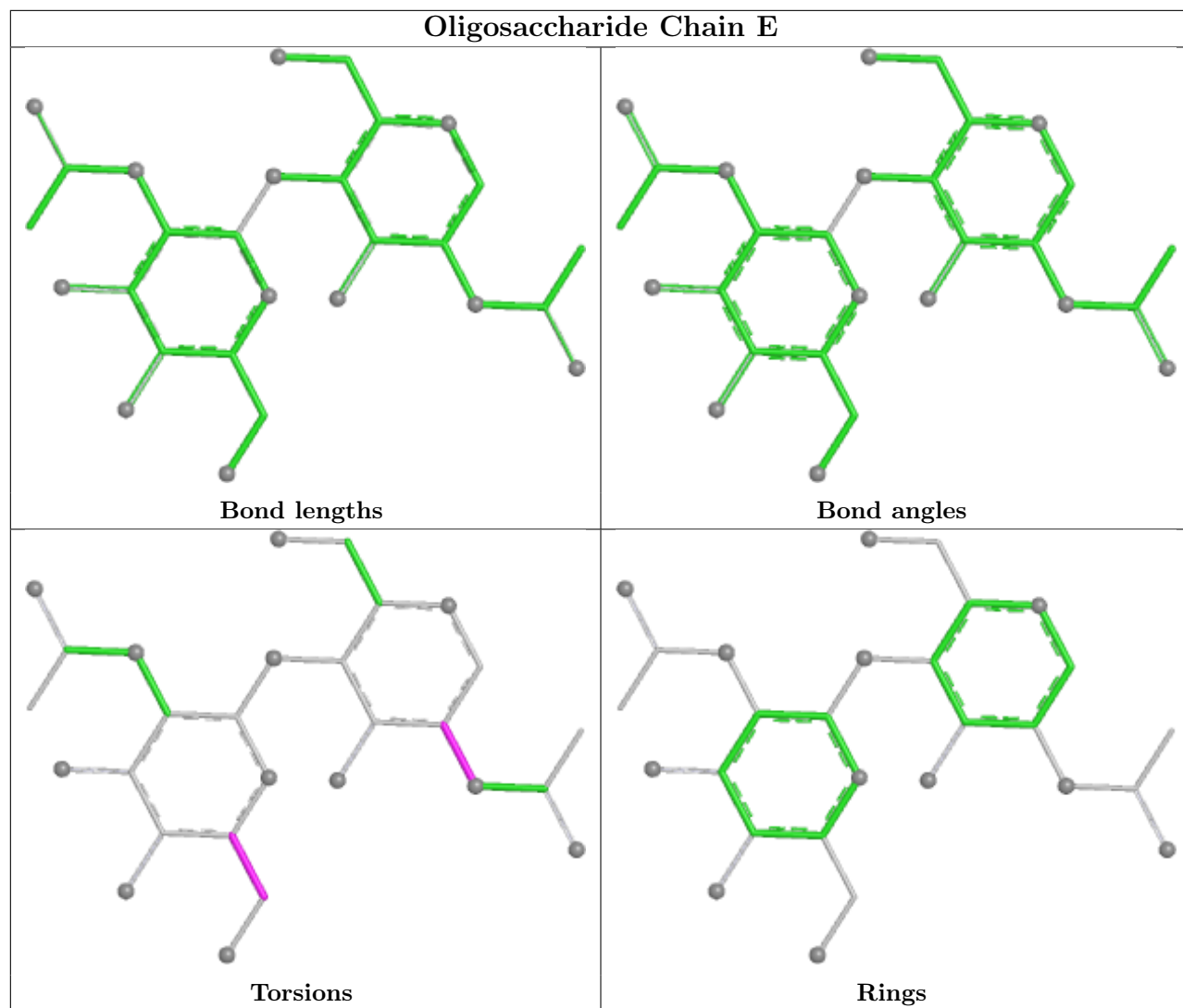
Mol	Chain	Res	Type	Atoms
9	K	5	MAN	C1-C2-C3-C4-C5-O5
7	I	3	MAN	C1-C2-C3-C4-C5-O5
10	M	3	MAN	C1-C2-C3-C4-C5-O5
8	J	3	MAN	C1-C2-C3-C4-C5-O5
4	D	3	MAN	C1-C2-C3-C4-C5-O5

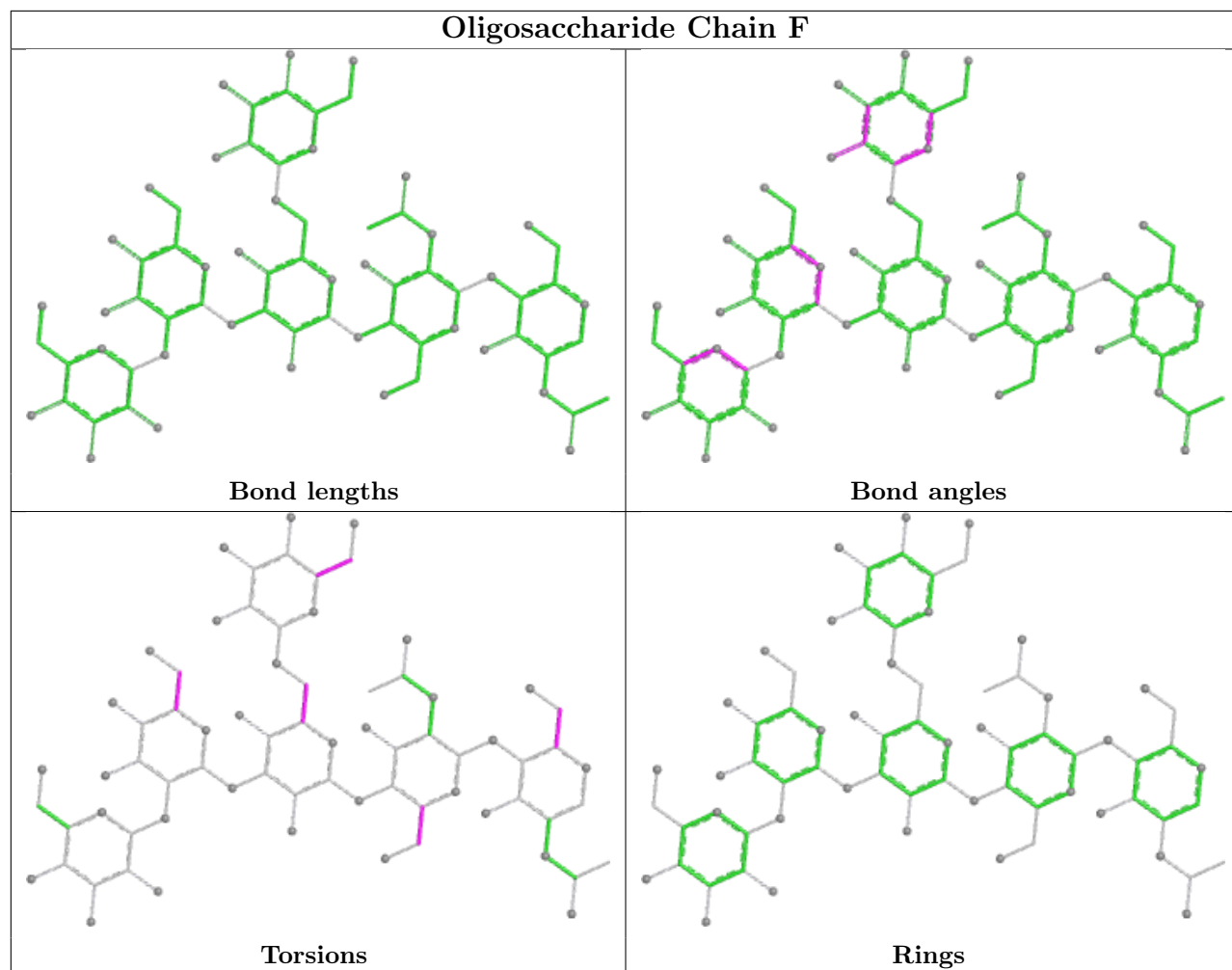
4 monomers are involved in 5 short contacts:

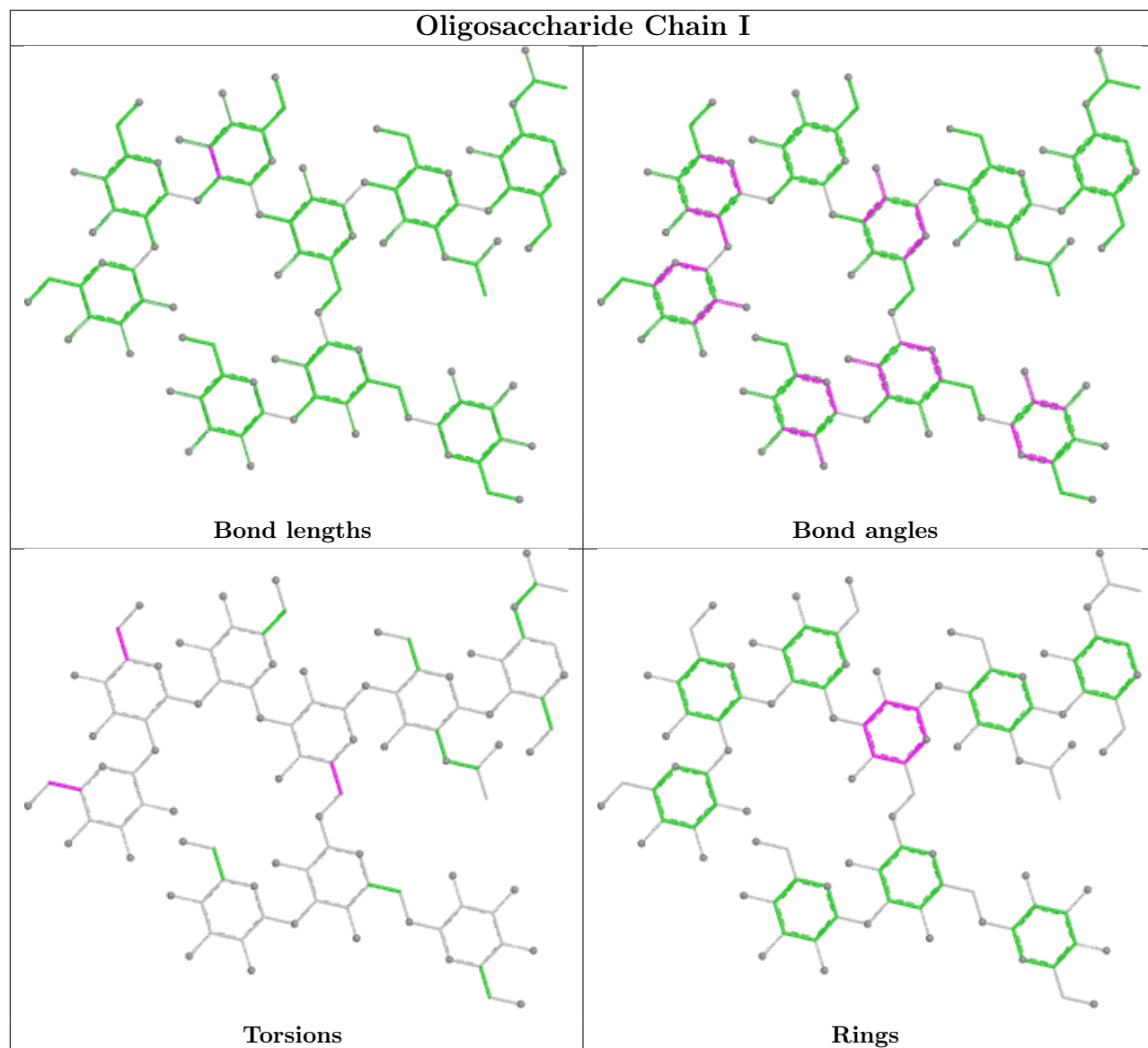
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	2	NAG	3	0
6	F	1	NAG	1	0
5	E	1	NAG	1	0
7	I	1	NAG	1	0

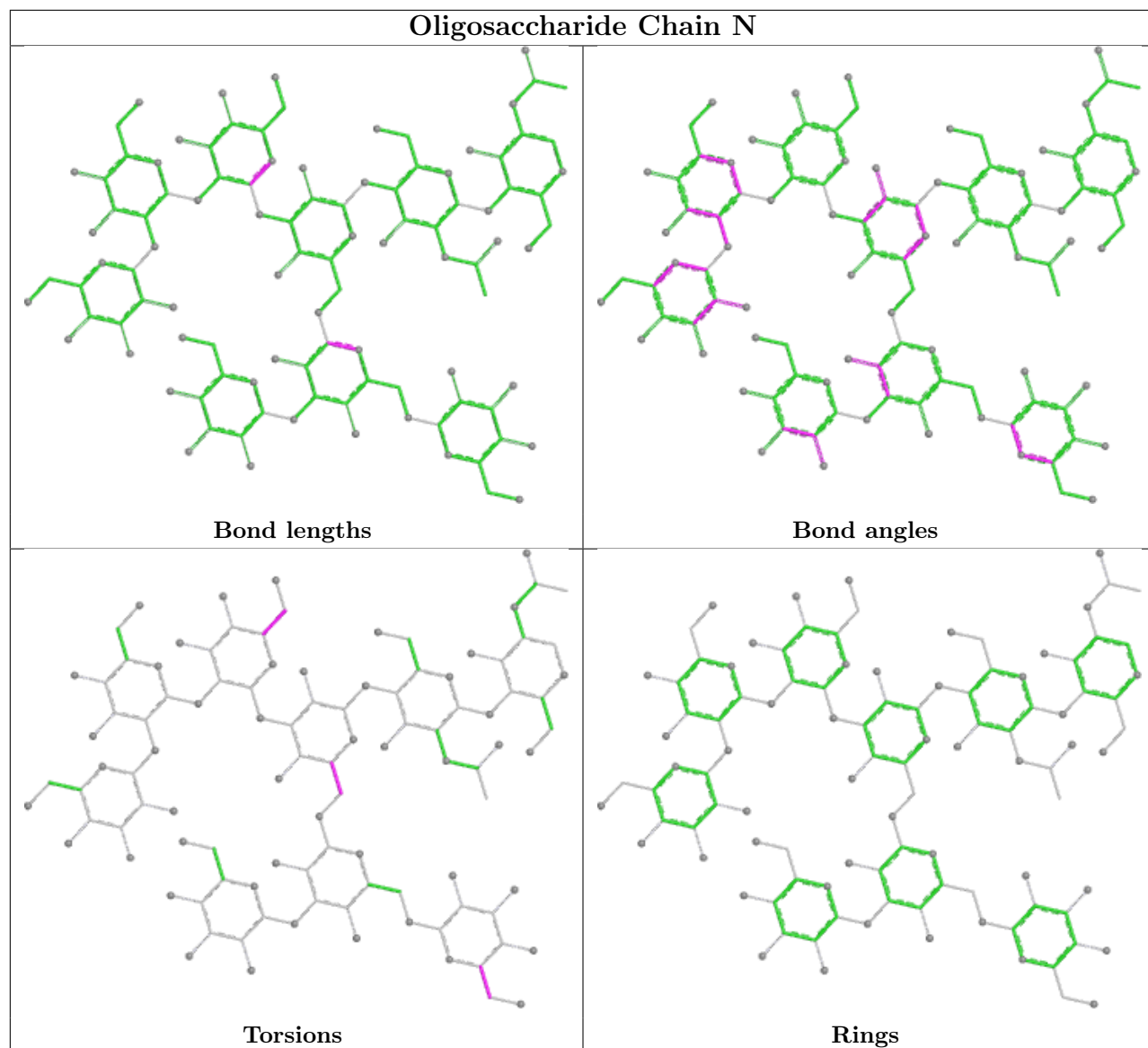
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

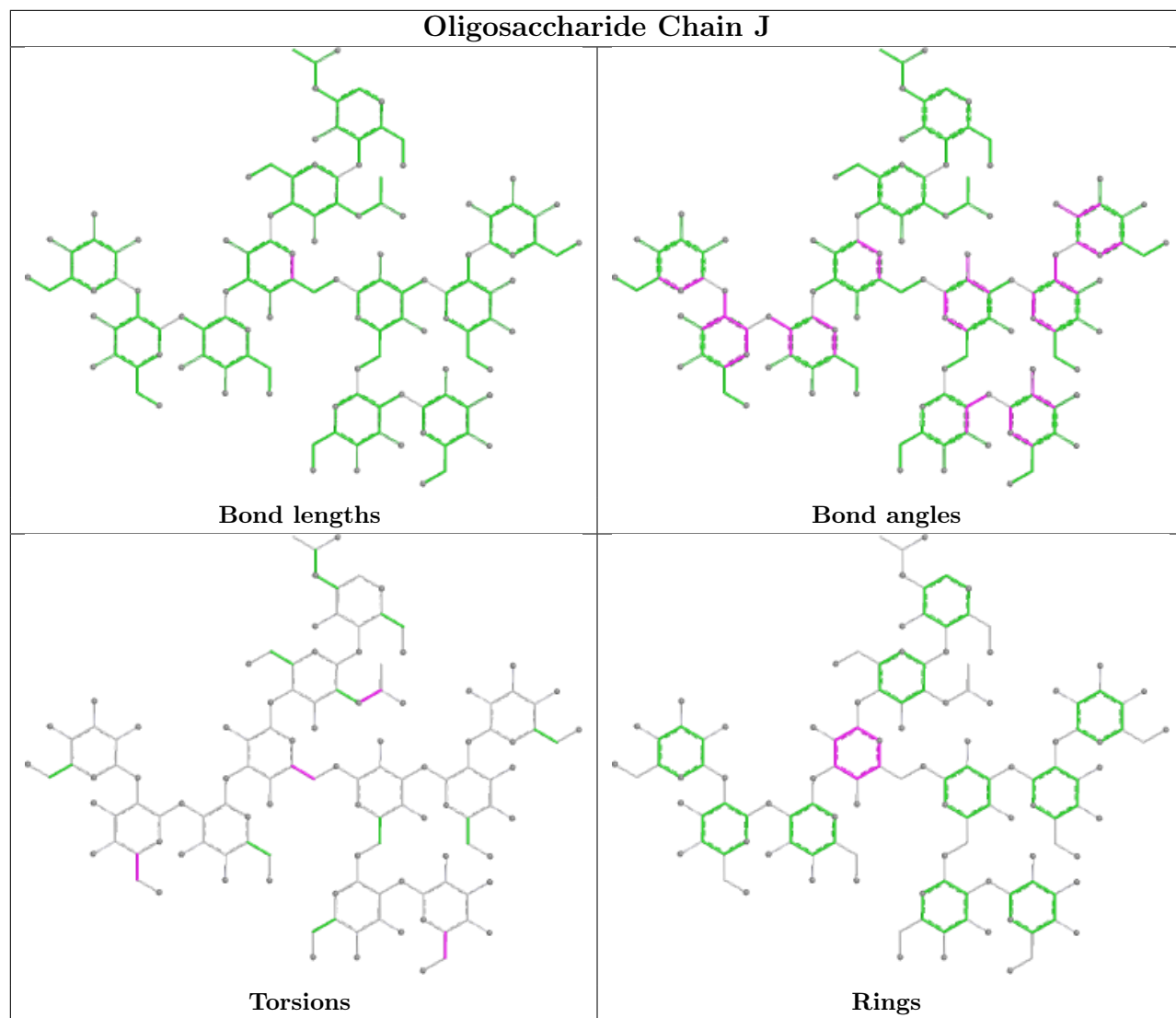


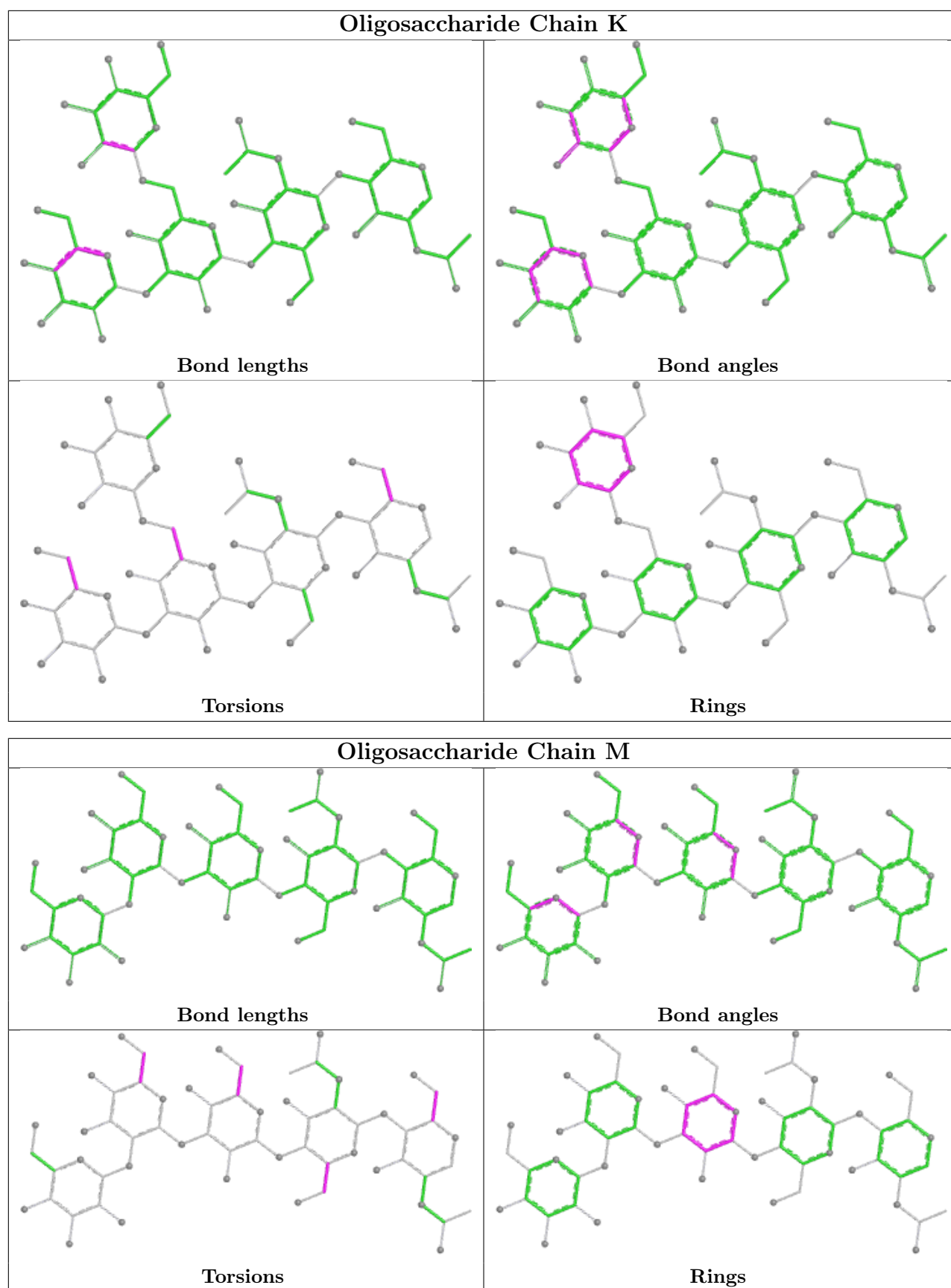












5.6 Ligand geometry

22 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
12	EDO	H	301	-	3,3,3	0.44	0	2,2,2	0.47	0
12	EDO	B	302	-	3,3,3	0.42	0	2,2,2	0.37	0
12	EDO	B	301	-	3,3,3	0.44	0	2,2,2	0.33	0
11	NAG	A	522	1	14,14,15	0.24	0	17,19,21	0.46	0
11	NAG	A	512	1	14,14,15	0.21	0	17,19,21	0.57	0
11	NAG	G	514	1	14,14,15	0.45	0	17,19,21	0.67	1 (5%)
11	NAG	L	301	3	14,14,15	0.29	0	17,19,21	0.43	0
11	NAG	G	527	1	14,14,15	0.39	0	17,19,21	0.37	0
12	EDO	G	537	-	3,3,3	0.42	0	2,2,2	0.33	0
11	NAG	G	525	1	14,14,15	0.53	0	17,19,21	0.47	0
11	NAG	A	501	1	14,14,15	0.24	0	17,19,21	0.42	0
11	NAG	A	524	1	14,14,15	0.31	0	17,19,21	0.61	1 (5%)
11	NAG	C	301	3	14,14,15	0.22	0	17,19,21	0.43	0
12	EDO	A	534	-	3,3,3	0.44	0	2,2,2	0.36	0
12	EDO	L	303	-	3,3,3	0.45	0	2,2,2	0.35	0
11	NAG	A	521	1	14,14,15	0.16	0	17,19,21	0.41	0
11	NAG	G	502	1	14,14,15	0.26	0	17,19,21	0.39	0
12	EDO	L	302	-	3,3,3	0.46	0	2,2,2	0.33	0
11	NAG	A	523	1	14,14,15	0.35	0	17,19,21	0.36	0
13	ACT	B	303	-	3,3,3	0.82	0	3,3,3	1.33	0
11	NAG	G	501	1	14,14,15	0.18	0	17,19,21	0.35	0
11	NAG	G	526	1	14,14,15	0.23	0	17,19,21	0.48	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
12	EDO	H	301	-	-	1/1/1/1	-
12	EDO	B	302	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	EDO	B	301	-	-	0/1/1/1	-
11	NAG	A	522	1	-	0/6/23/26	0/1/1/1
11	NAG	A	512	1	-	3/6/23/26	0/1/1/1
11	NAG	G	514	1	-	2/6/23/26	0/1/1/1
11	NAG	L	301	3	-	0/6/23/26	0/1/1/1
11	NAG	G	527	1	-	2/6/23/26	0/1/1/1
12	EDO	G	537	-	-	0/1/1/1	-
11	NAG	G	525	1	-	1/6/23/26	0/1/1/1
11	NAG	A	501	1	-	2/6/23/26	0/1/1/1
11	NAG	A	524	1	-	2/6/23/26	0/1/1/1
11	NAG	C	301	3	-	0/6/23/26	0/1/1/1
12	EDO	A	534	-	-	0/1/1/1	-
12	EDO	L	303	-	-	0/1/1/1	-
11	NAG	A	521	1	-	0/6/23/26	0/1/1/1
11	NAG	G	502	1	-	2/6/23/26	0/1/1/1
12	EDO	L	302	-	-	0/1/1/1	-
11	NAG	A	523	1	-	1/6/23/26	0/1/1/1
11	NAG	G	501	1	-	2/6/23/26	0/1/1/1
11	NAG	G	526	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	G	514	NAG	C1-O5-C5	2.06	114.95	112.19
11	A	524	NAG	C1-O5-C5	2.05	114.93	112.19

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	501	NAG	C4-C5-C6-O6
11	A	501	NAG	O5-C5-C6-O6
11	G	502	NAG	O5-C5-C6-O6
11	A	524	NAG	O5-C5-C6-O6
11	A	524	NAG	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	B	302	EDO	2	0
12	B	301	EDO	1	0
11	G	527	NAG	1	0
12	G	537	EDO	2	0
11	A	501	NAG	2	0
11	A	523	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	337/344 (97%)	1.02	36 (10%) 11 10	66, 116, 187, 209	0
1	G	333/344 (96%)	0.65	16 (4%) 35 35	48, 93, 136, 171	0
2	B	225/229 (98%)	0.57	21 (9%) 14 13	48, 79, 148, 183	0
2	H	221/229 (96%)	0.23	7 (3%) 50 50	30, 63, 136, 171	0
3	C	219/219 (100%)	0.42	13 (5%) 28 27	37, 67, 140, 198	0
3	L	218/219 (99%)	0.26	9 (4%) 41 41	34, 63, 144, 181	0
All	All	1553/1584 (98%)	0.57	102 (6%) 24 23	30, 87, 158, 209	0

The worst 5 of 102 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	44	VAL	4.2
1	G	491	ILE	4.1
1	A	87	VAL	3.5
1	G	367	GLY	3.5
2	B	132	SER	3.5

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.

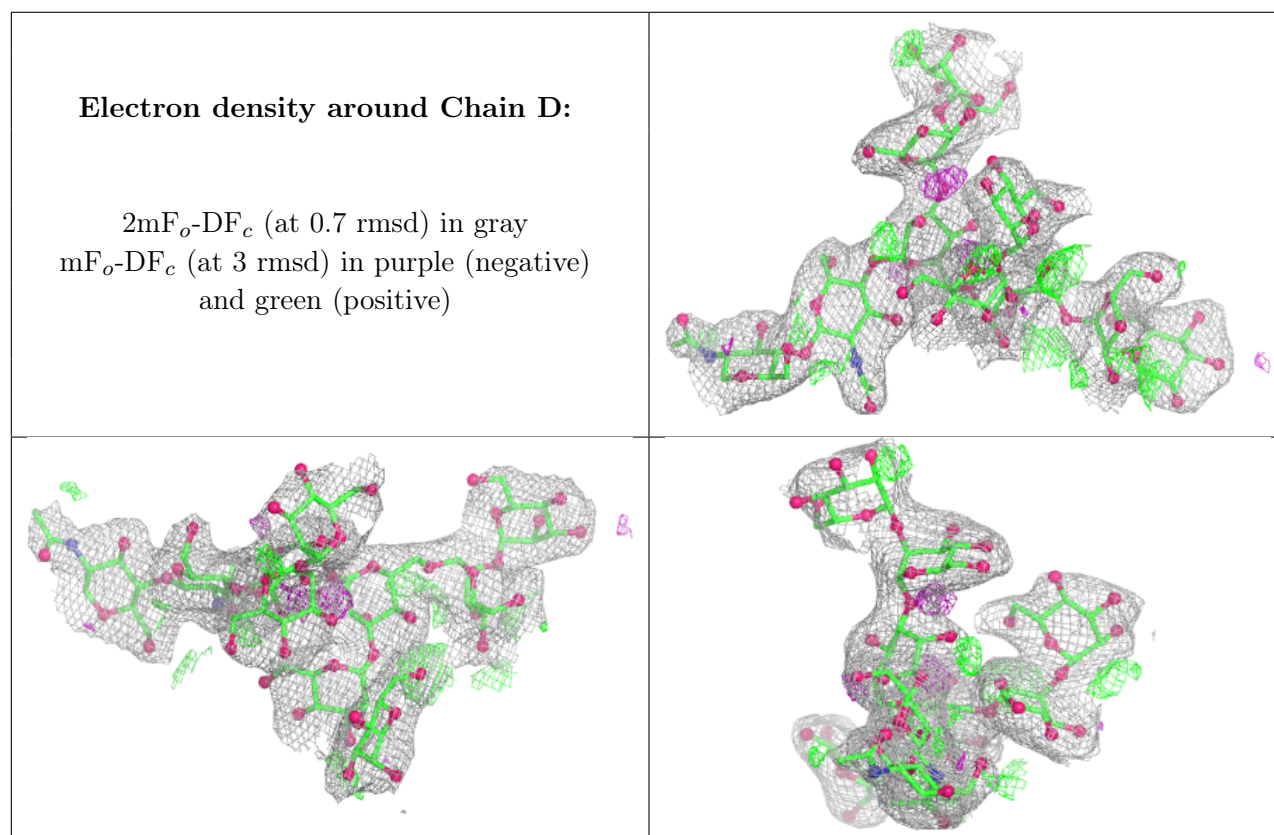
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	D	1	14/15	-	-	44,59,83,89	0
4	NAG	D	2	14/15	-	-	64,68,76,82	0
4	MAN	D	3	11/12	-	-	56,65,75,81	0
4	MAN	D	4	11/12	-	-	56,59,66,68	0
4	MAN	D	5	11/12	-	-	61,64,84,85	0
4	MAN	D	6	11/12	-	-	86,91,96,99	0
4	MAN	D	7	11/12	-	-	65,69,75,78	0
4	MAN	D	8	11/12	-	-	66,71,85,92	0
4	MAN	D	9	11/12	-	-	76,83,91,105	0
4	MAN	D	10	11/12	-	-	119,124,129,130	0
5	NAG	E	1	14/15	-	-	99,120,127,135	0
5	NAG	E	2	14/15	-	-	142,146,149,151	0
6	NAG	F	1	14/15	-	-	61,75,94,95	0
6	NAG	F	2	14/15	-	-	92,97,102,104	0
6	MAN	F	3	11/12	-	-	81,96,106,116	0
6	MAN	F	4	11/12	-	-	66,74,86,97	0
6	MAN	F	5	11/12	-	-	109,119,128,131	0
6	MAN	F	6	11/12	-	-	111,120,129,134	0
7	MAN	I	5	11/12	0.54	0.18	77,92,101,102	0
7	MAN	I	6	11/12	0.64	0.12	74,83,91,94	0
8	MAN	J	4	11/12	0.65	0.12	68,75,86,93	0
10	MAN	M	5	11/12	0.71	0.17	88,101,109,112	0
7	MAN	N	8	11/12	0.74	0.11	84,88,96,98	0
8	MAN	J	8	11/12	0.75	0.13	44,48,53,54	0
7	MAN	I	7	11/12	-	-	66,86,93,101	0
7	MAN	I	8	11/12	-	-	100,111,116,119	0
7	MAN	I	9	11/12	-	-	82,91,95,96	0
10	MAN	M	3	11/12	0.76	0.10	77,83,86,87	0
10	NAG	M	2	14/15	0.79	0.10	76,89,97,98	0
9	MAN	K	5	11/12	0.80	0.13	132,136,138,139	0
7	MAN	I	3	11/12	0.80	0.10	66,78,85,87	0
7	NAG	I	2	14/15	0.83	0.10	57,72,83,89	0
7	MAN	N	9	11/12	0.83	0.13	72,79,84,86	0
10	NAG	M	1	14/15	0.84	0.13	70,83,92,93	0
8	MAN	J	5	11/12	0.88	0.13	82,89,105,119	0
8	NAG	J	1	14/15	0.88	0.10	37,45,50,51	0
8	MAN	J	9	11/12	0.88	0.10	47,52,64,64	0
7	MAN	N	4	11/12	0.88	0.11	71,73,85,89	0
7	NAG	I	1	14/15	0.89	0.10	42,64,73,78	0
8	MAN	J	3	11/12	0.90	0.10	35,42,56,59	0
7	MAN	N	5	11/12	0.90	0.12	59,72,78,81	0
8	NAG	J	2	14/15	0.91	0.09	29,51,58,64	0
8	MAN	J	7	11/12	0.91	0.08	36,38,43,46	0

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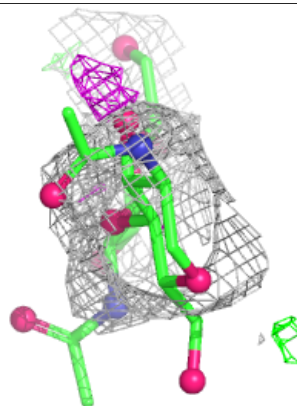
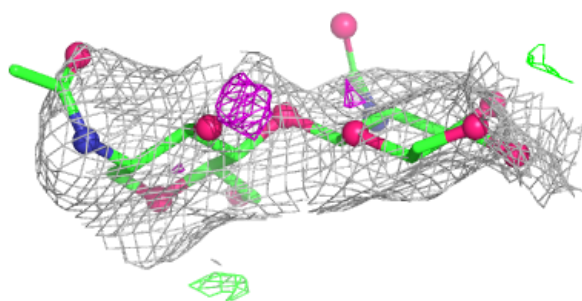
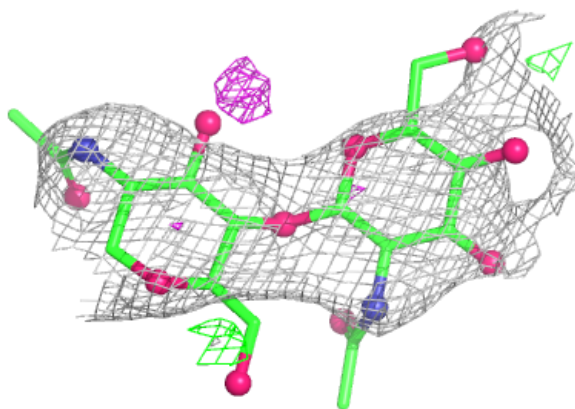
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	MAN	N	6	11/12	0.91	0.14	54,87,91,95	0
7	NAG	N	1	14/15	0.91	0.10	41,50,56,57	0
8	MAN	J	10	11/12	-	-	33,40,45,47	0
8	MAN	J	11	11/12	-	-	48,51,63,71	0
9	MAN	K	3	11/12	0.91	0.11	128,134,140,145	0
9	MAN	K	4	11/12	0.92	0.12	136,142,145,149	0
10	MAN	M	4	11/12	0.92	0.09	50,71,78,91	0
8	MAN	J	6	11/12	0.92	0.12	108,125,126,127	0
7	NAG	N	2	14/15	0.93	0.08	44,49,53,59	0
7	MAN	N	7	11/12	0.94	0.07	54,57,72,75	0
7	MAN	I	4	11/12	0.94	0.09	97,107,112,113	0
9	NAG	K	1	14/15	0.94	0.08	67,83,100,100	0
9	NAG	K	2	14/15	0.94	0.08	65,98,109,118	0
7	MAN	N	3	11/12	0.97	0.07	50,59,64,66	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.



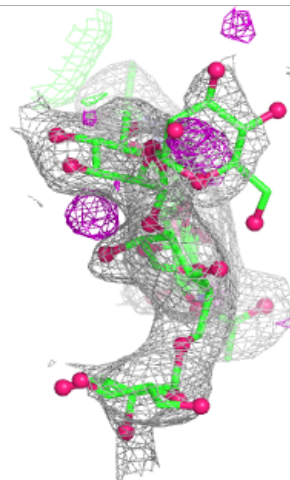
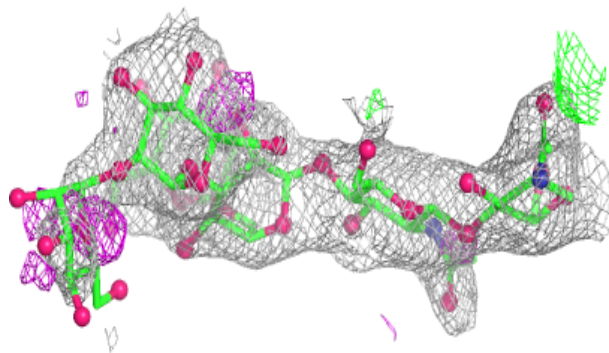
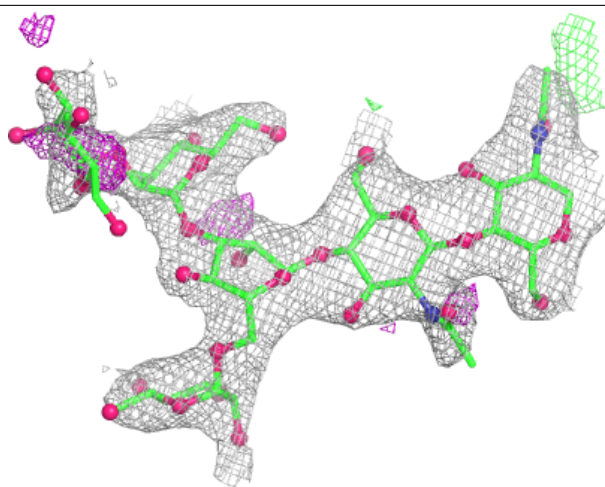
Electron density around Chain E:

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



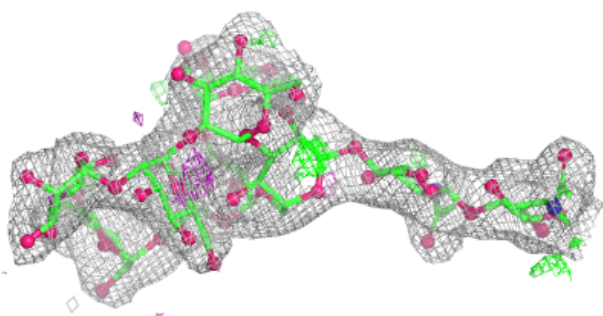
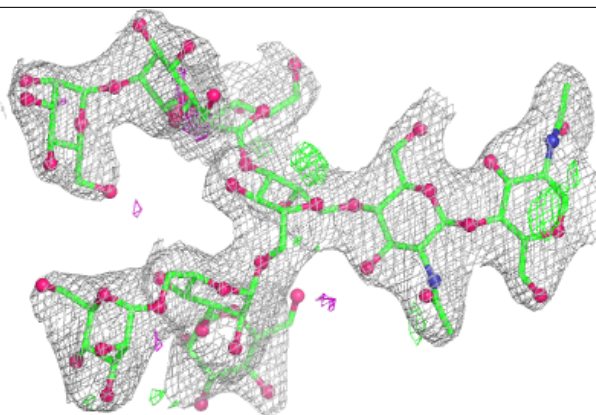
Electron density around Chain F:

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

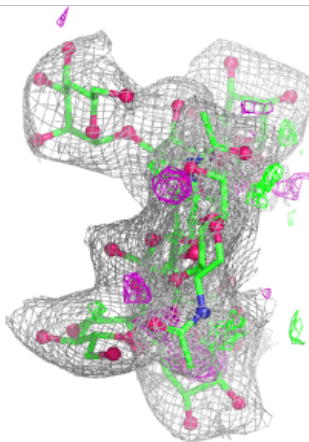
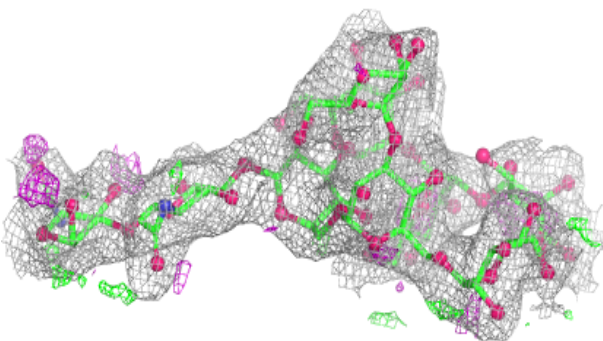
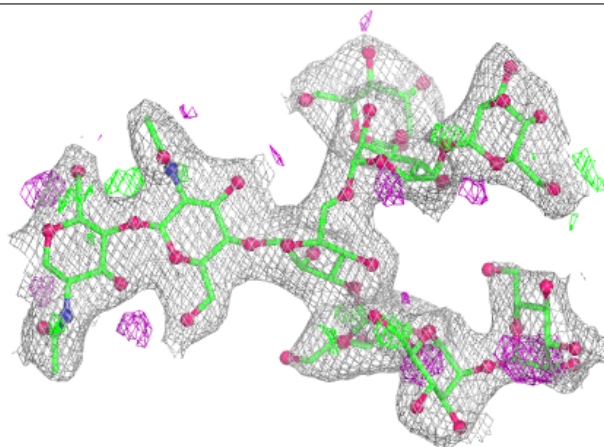


Electron density around Chain I:

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

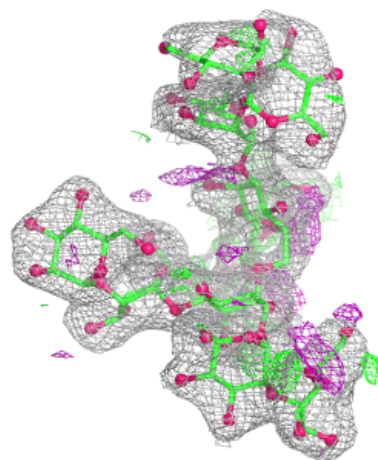
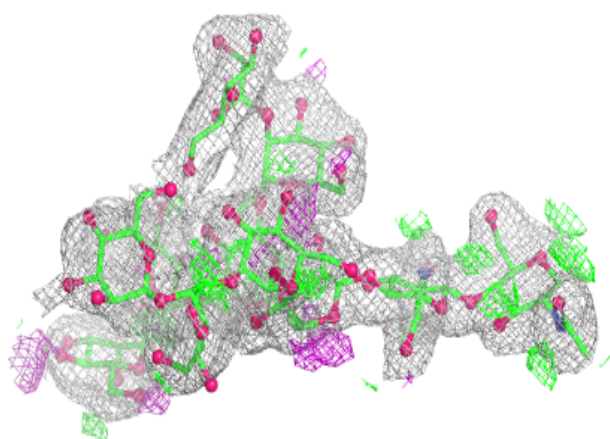
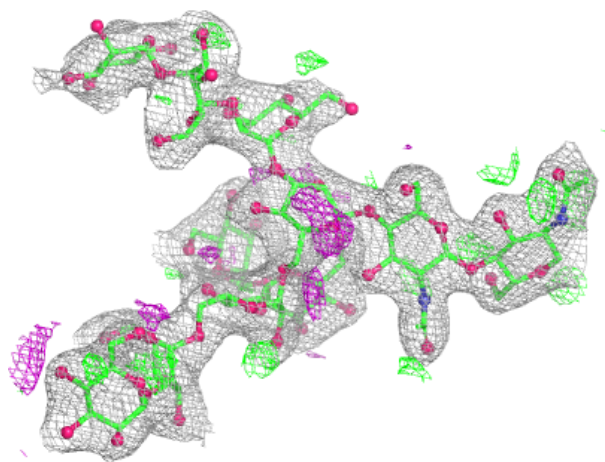
**Electron density around Chain N:**

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



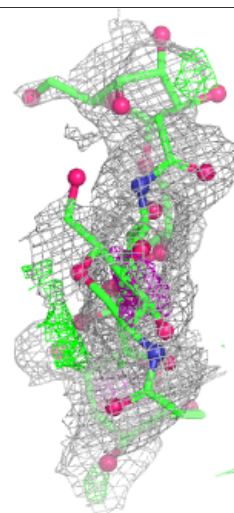
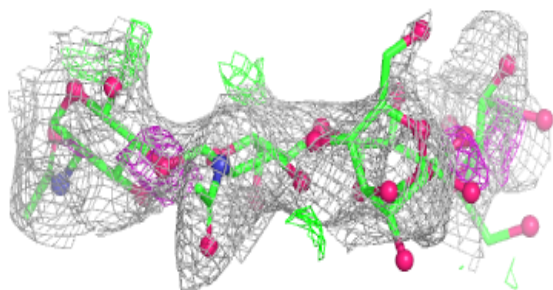
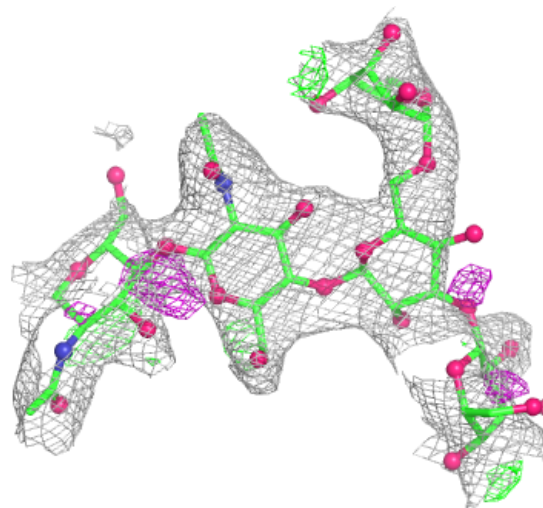
Electron density around Chain J:

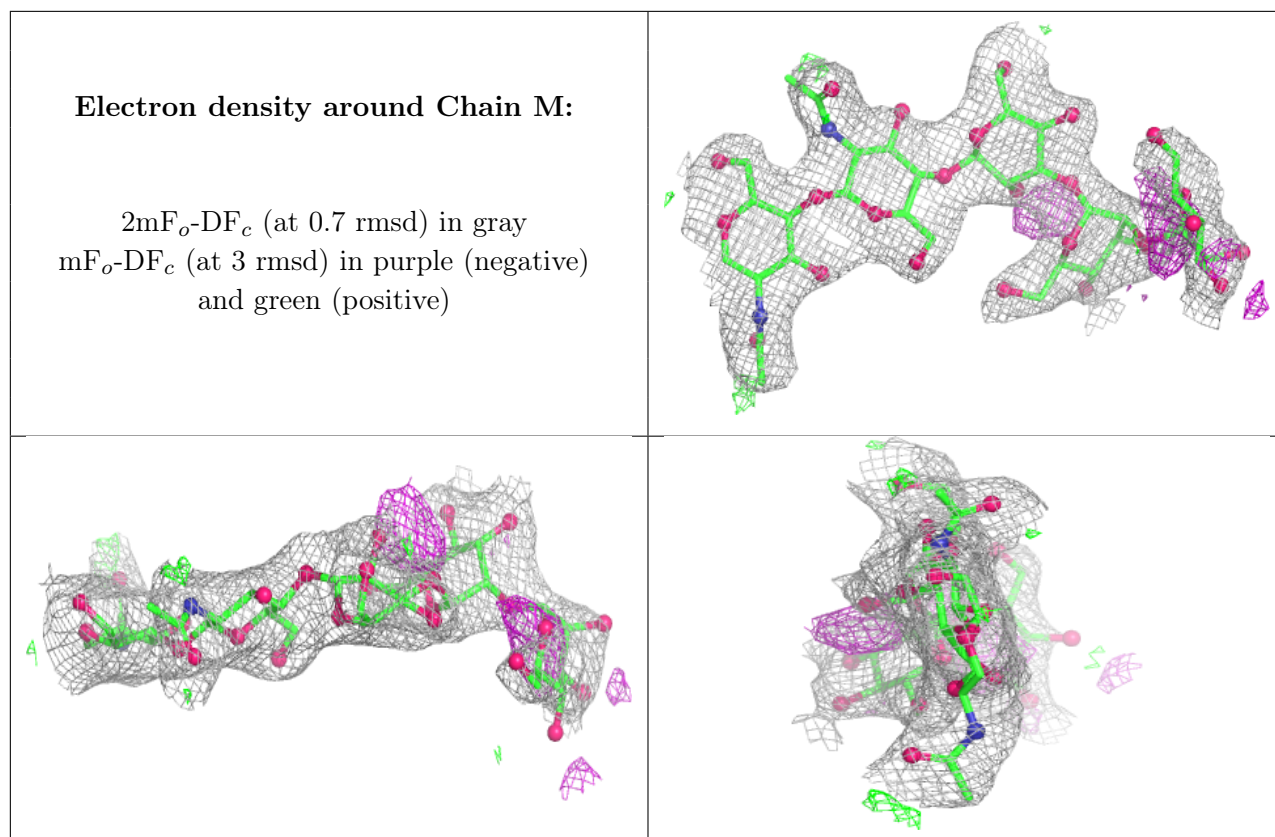
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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
11	NAG	A	524	14/15	0.29	0.16	118,135,139,142	0
11	NAG	A	521	14/15	0.37	0.15	99,114,127,131	0
11	NAG	G	502	14/15	0.46	0.18	101,124,133,135	0
11	NAG	A	501	14/15	0.56	0.14	109,134,144,150	0
11	NAG	A	512	14/15	0.63	0.11	103,120,126,128	0
11	NAG	G	525	14/15	0.67	0.16	94,108,114,117	0
11	NAG	G	514	14/15	0.71	0.14	87,100,115,123	0
13	ACT	B	303	4/4	0.74	0.23	82,88,90,90	0
11	NAG	G	526	14/15	0.78	0.15	54,86,110,111	0
12	EDO	G	537	4/4	0.79	0.36	64,66,68,73	0
11	NAG	A	523	14/15	0.80	0.12	88,101,104,107	0
12	EDO	L	303	4/4	0.81	0.26	76,89,97,97	0
11	NAG	G	527	14/15	0.82	0.12	67,88,105,107	0
12	EDO	B	302	4/4	0.85	0.14	94,94,95,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
12	EDO	A	534	4/4	0.85	0.31	99,99,101,103	0
12	EDO	L	302	4/4	0.86	0.20	73,74,75,76	0
12	EDO	H	301	4/4	0.87	0.17	57,62,64,70	0
12	EDO	B	301	4/4	0.88	0.20	78,84,87,88	0
11	NAG	G	501	14/15	0.89	0.10	81,98,119,122	0
11	NAG	A	522	14/15	0.90	0.10	67,76,82,89	0
11	NAG	C	301	14/15	0.93	0.08	57,62,72,76	0
11	NAG	L	301	14/15	0.95	0.06	34,57,68,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.