



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 02:11 PM UTC

PDB ID : 6ZPS / pdb_00006zps
Title : Structure of Unliganded MgGH51 α -L-Arabinofuranosidase Crystal Type 3
Collected at 2.75 Å
Authors : McGregor, N.G.S.; Davies, G.J.
Deposited on : 2020-07-09
Resolution : 1.79 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

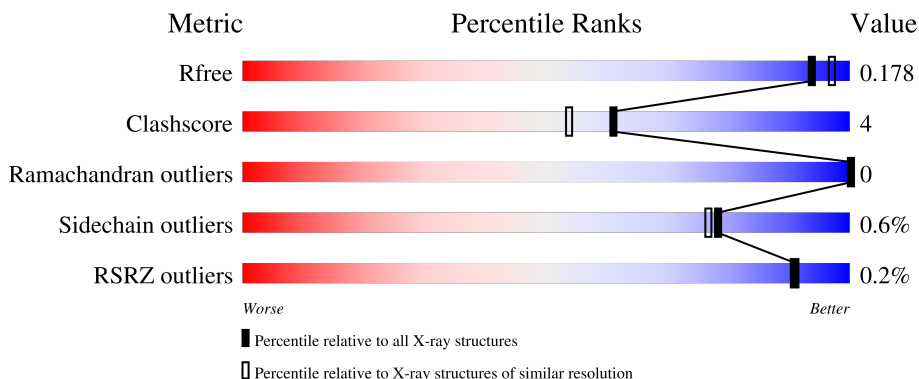
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.79 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AAA	627	94% 6%
2	A	6	17% 67% 17%
3	B	2	100%
3	D	2	100%
4	C	5	100%

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
7	SO4	AAA	723	-	-	-	X
7	SO4	AAA	726[B]	-	-	X	-
7	SO4	AAA	728[A]	-	-	X	-
8	CL	AAA	739	-	-	-	X
8	CL	AAA	742	-	-	-	X
8	CL	AAA	745	-	-	-	X
8	CL	AAA	746	-	-	-	X

2 Entry composition [i](#)

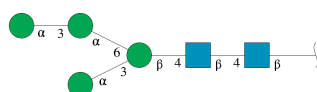
There are 9 unique types of molecules in this entry. The entry contains 10916 atoms, of which 4942 are hydrogens and 0 are deuteriums.

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 MgGH51.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	627	Total	C	H	N	O	S	317	22	0
			9667	3146	4750	818	946	7			

- Molecule 2 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.



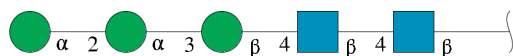
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	6	Total	C	H	N	O	17	0	0
			139	40	67	2	30			

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



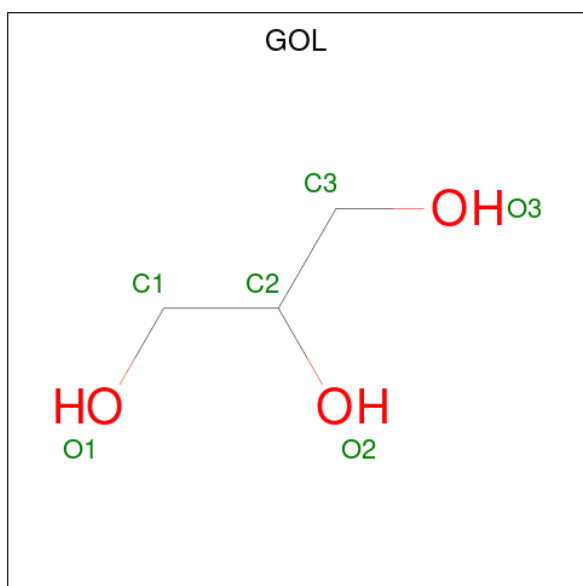
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	2	Total	C	H	N	O	5	0	0
			55	16	27	2	10			
3	D	2	Total	C	H	N	O	5	0	0
			55	16	27	2	10			

- Molecule 4 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
4	C	5	Total	C	H	N	O	14	0	0
			118	34	57	2	25			

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	AAA	1	Total	C	H	O	2	0
			14	3	8	3		

- Molecule 6 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	AAA	1	Total	C	H	O	0	0
			7	2	3	2		
6	AAA	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	1
			10	8	2		
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	1
			10	8	2		
7	AAA	1	Total	O	S	0	0
			5	4	1		
7	AAA	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	AAA	17	Total	Cl	0	0
			17	17		

- Molecule 9 is water.

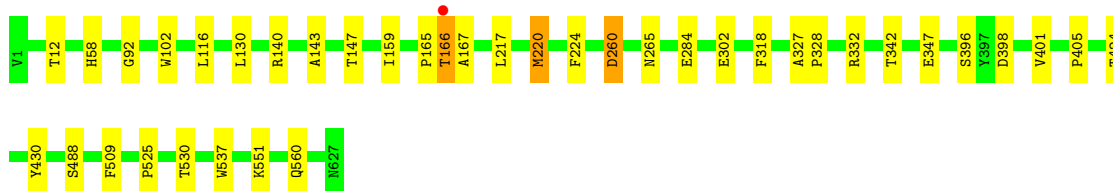
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	AAA	751	Total	O	0	21
			762	762		

3 Residue-property plots

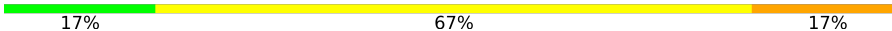
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

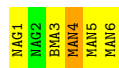
- Molecule 1: MgGH51

Chain AAA: 

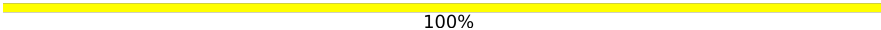


- Molecule 2: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain A: 

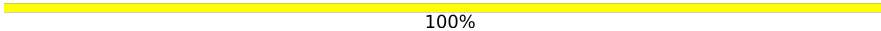


- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 



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

Chain D: 



- Molecule 4: 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 C:

100%

MAG1
MAG2
BGLA3
MAIN4
MAIN5

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	84.17Å 84.17Å 257.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.13 – 1.79 80.00 – 1.79	Depositor EDS
% Data completeness (in resolution range)	84.5 (80.13-1.79) 84.6 (80.00-1.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.144 , 0.178 0.144 , 0.178	Depositor DCC
R_{free} test set	3570 reflections (4.08%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10916	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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: GOL, MAN, SO4, NAG, CL, ACT, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AAA	1.09	2/5102 (0.0%)	1.15	5/6978 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	260	ASP	CG-OD2	5.76	1.36	1.25
1	AAA	260	ASP	CG-OD1	5.69	1.36	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	260	ASP	CB-CA-C	8.71	125.29	110.56
1	AAA	342	THR	CA-CB-OG1	-5.92	100.73	109.60
1	AAA	530	THR	CA-CB-OG1	-5.34	101.58	109.60
1	AAA	525	PRO	N-CA-CB	5.11	107.79	103.35
1	AAA	560	GLN	CB-CG-CD	-5.08	103.96	112.60

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	AAA	4917	4750	4748	33	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	72	67	61	0	1
3	B	28	27	25	0	0
3	D	28	27	25	0	0
4	C	61	57	52	0	0
5	AAA	6	8	8	0	0
6	AAA	8	6	6	0	0
7	AAA	75	0	0	7	0
8	AAA	17	0	0	8	0
9	AAA	762	0	0	19	0
All	All	5974	4942	4925	43	2

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 4.

The worst 5 of 43 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)
8:AAA:739:CL:CL	9:AAA:1445:HOH:O	1.92	1.21
8:AAA:748:CL:CL	9:AAA:1348:HOH:O	2.10	1.06
8:AAA:742:CL:CL	9:AAA:1335:HOH:O	2.09	1.04
8:AAA:745:CL:CL	9:AAA:1334:HOH:O	2.12	1.02
8:AAA:744:CL:CL	9:AAA:1365:HOH:O	2.18	0.98

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:302:GLU:H	2:A:4:MAN:HO2[7_555]	1.29	0.31
1:AAA:12:THR:HG1	1:AAA:92:GLY:H[7_545]	1.34	0.26

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	AAA	646/627 (103%)	638 (99%)	8 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	530/510 (104%)	525 (99%)	5 (1%)	70	67

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	166[A]	THR
1	AAA	166[B]	THR
1	AAA	220[A]	MET
1	AAA	220[B]	MET
1	AAA	265	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

15 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	$\# Z > 2$
2	NAG	A	1	2,1	14,14,15	0.99	0	17,19,21	1.25	3 (17%)
2	NAG	A	2	2	14,14,15	1.02	0	17,19,21	0.76	0
2	BMA	A	3	2	11,11,12	0.77	0	15,15,17	0.85	1 (6%)
2	MAN	A	4	2	11,11,12	1.00	1 (9%)	15,15,17	1.51	2 (13%)
2	MAN	A	5	2	11,11,12	1.15	1 (9%)	15,15,17	1.88	6 (40%)
2	MAN	A	6	2	11,11,12	0.89	0	15,15,17	1.24	1 (6%)
3	NAG	B	1	3,1	14,14,15	0.89	1 (7%)	17,19,21	1.37	2 (11%)
3	NAG	B	2	3	14,14,15	0.93	1 (7%)	17,19,21	1.22	3 (17%)
4	NAG	C	1	4,1	14,14,15	1.19	1 (7%)	17,19,21	1.42	3 (17%)
4	NAG	C	2	4	14,14,15	0.75	0	17,19,21	1.49	2 (11%)
4	BMA	C	3	4	11,11,12	1.02	0	15,15,17	1.84	4 (26%)
4	MAN	C	4	4	11,11,12	1.22	2 (18%)	15,15,17	1.64	2 (13%)
4	MAN	C	5	4	11,11,12	0.94	0	15,15,17	1.74	4 (26%)
3	NAG	D	1	3,1	14,14,15	0.68	0	17,19,21	1.73	3 (17%)
3	NAG	D	2	3	14,14,15	0.86	1 (7%)	17,19,21	1.34	3 (17%)

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
2	NAG	A	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	A	2	2	-	1/6/23/26	0/1/1/1
2	BMA	A	3	2	-	0/2/19/22	0/1/1/1
2	MAN	A	4	2	-	0/2/19/22	0/1/1/1
2	MAN	A	5	2	-	1/2/19/22	0/1/1/1
2	MAN	A	6	2	-	0/2/19/22	0/1/1/1
3	NAG	B	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	B	2	3	-	0/6/23/26	0/1/1/1
4	NAG	C	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	C	2	4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	C	3	4	-	0/2/19/22	0/1/1/1
4	MAN	C	4	4	-	0/2/19/22	0/1/1/1
4	MAN	C	5	4	-	2/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5	MAN	O5-C5	3.20	1.49	1.43
4	C	1	NAG	O5-C1	2.72	1.48	1.43
4	C	4	MAN	C2-C3	2.48	1.56	1.52
2	A	4	MAN	O4-C4	2.38	1.48	1.43
3	D	2	NAG	O5-C1	-2.37	1.39	1.43

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4	MAN	O6-C6-C5	-4.32	96.61	111.33
3	D	1	NAG	O7-C7-N2	3.72	128.56	121.98
4	C	2	NAG	O6-C6-C5	-3.55	99.25	111.33
4	C	3	BMA	C1-O5-C5	-3.55	107.43	112.19
4	C	4	MAN	C1-O5-C5	3.51	116.89	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

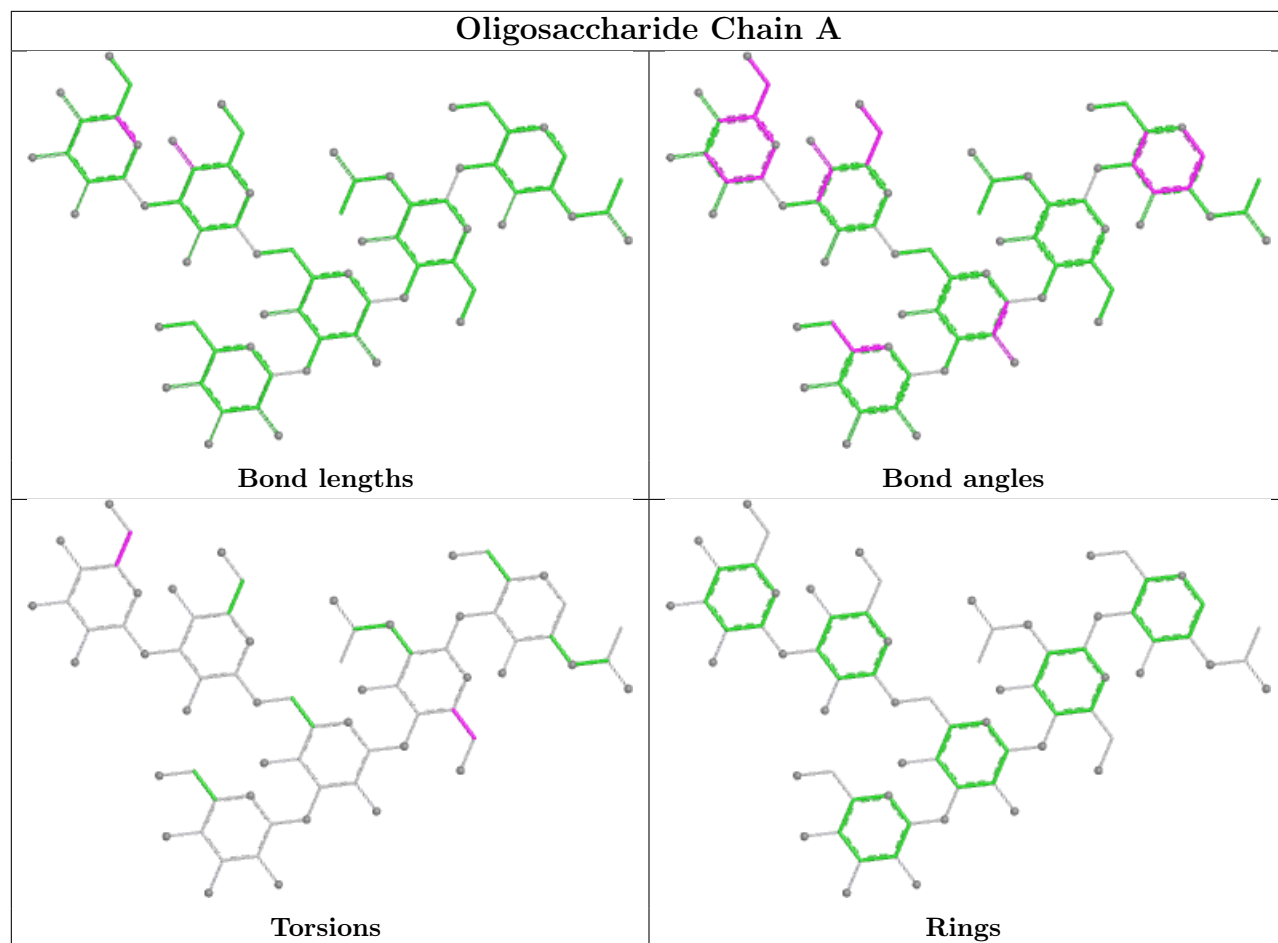
Mol	Chain	Res	Type	Atoms
2	A	5	MAN	O5-C5-C6-O6
4	C	5	MAN	C4-C5-C6-O6
4	C	5	MAN	O5-C5-C6-O6
2	A	2	NAG	O5-C5-C6-O6

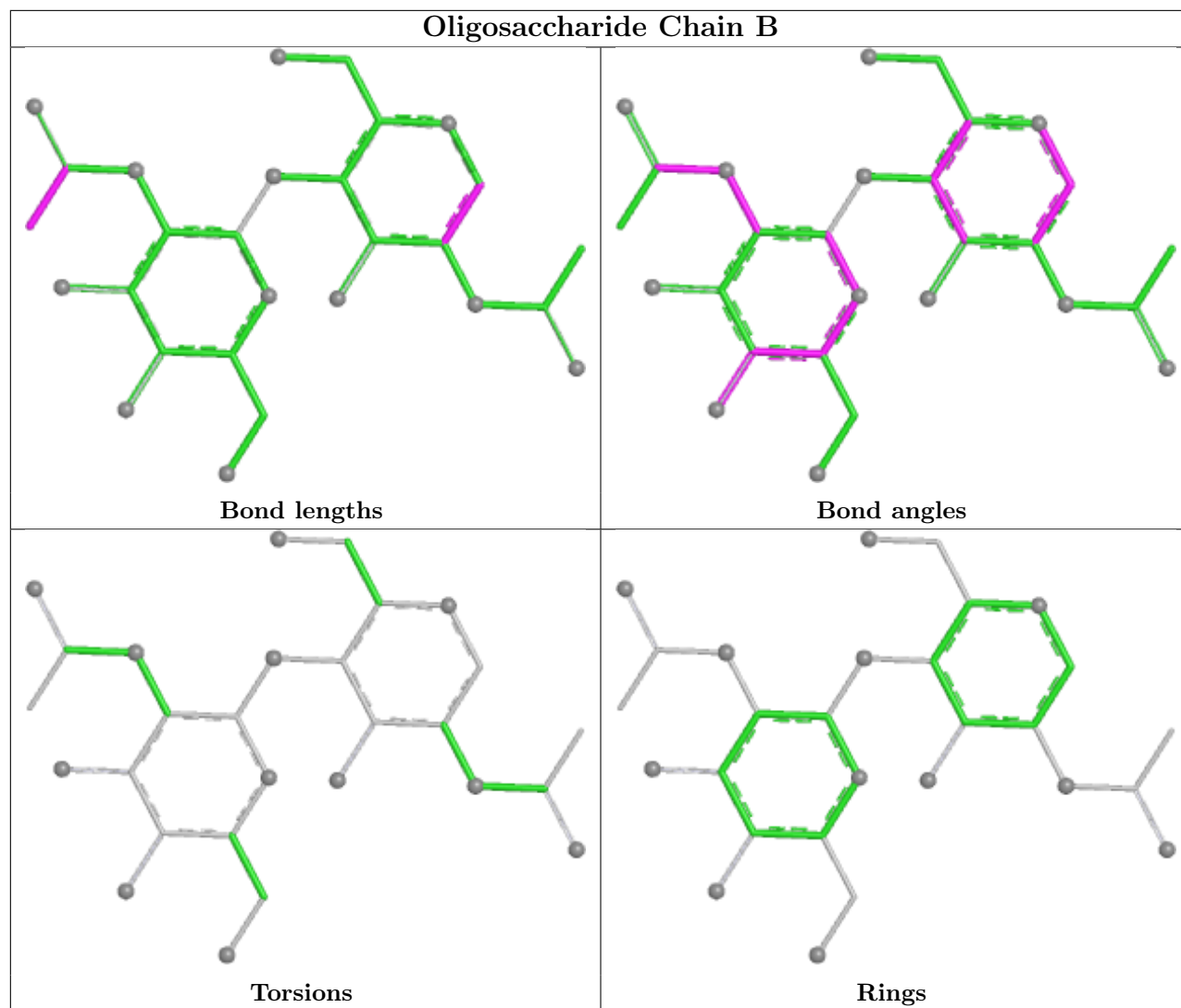
There are no ring outliers.

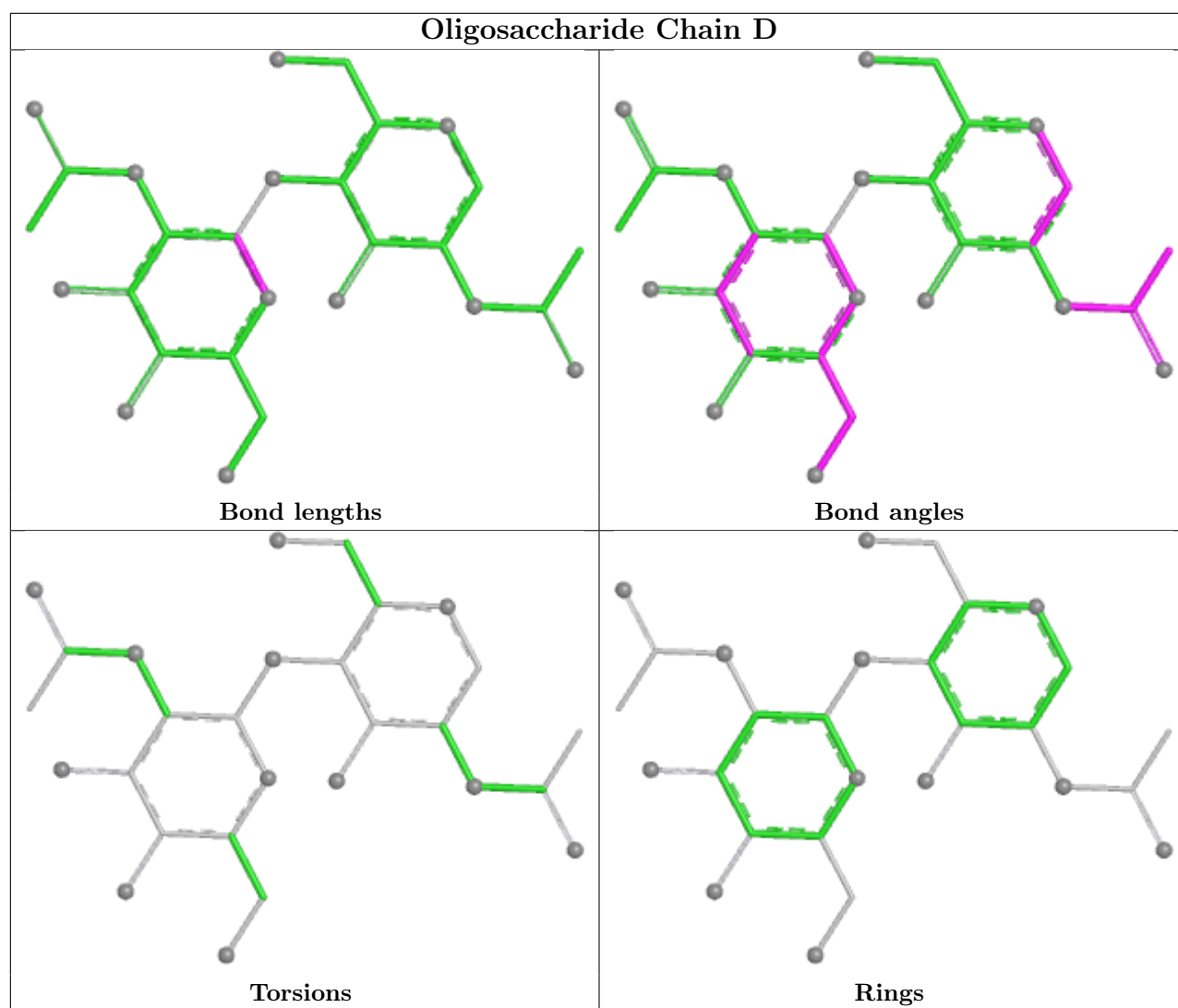
1 monomer is involved in 1 short contact:

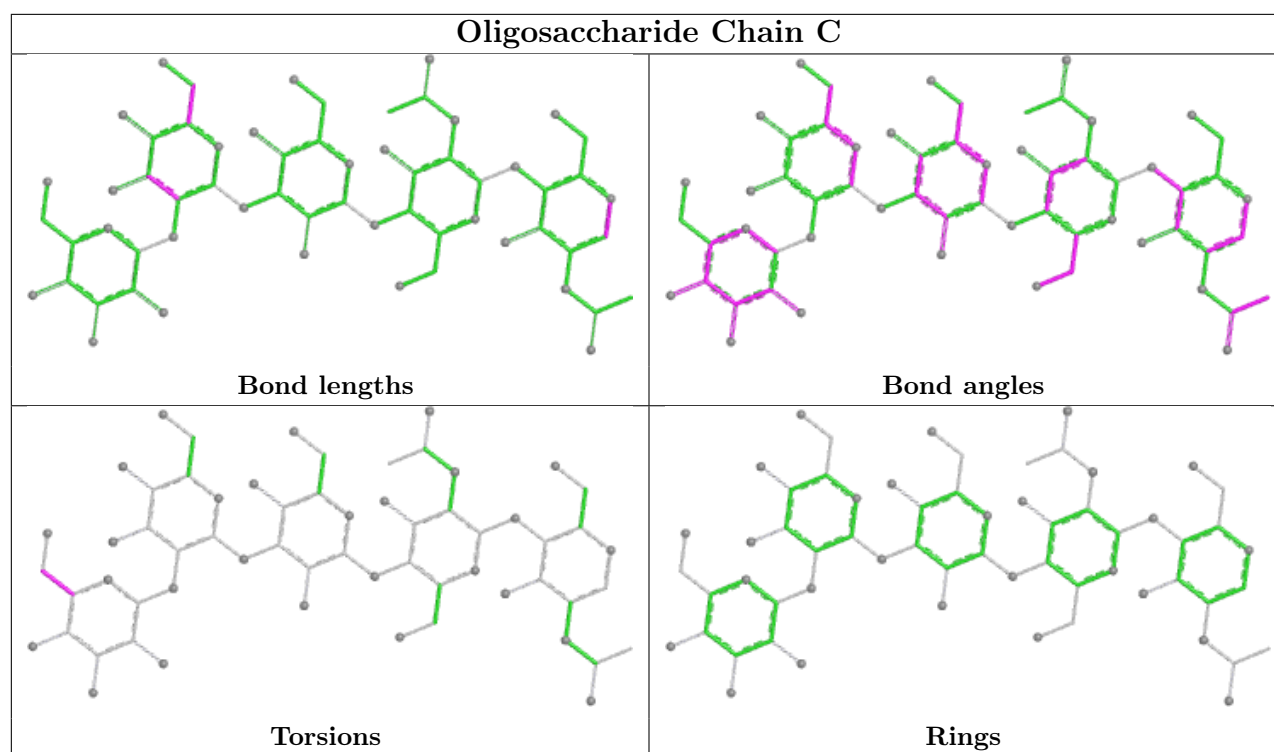
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	4	MAN	0	1

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](#)

Of 35 ligands modelled in this entry, 17 are monoatomic - leaving 18 for Mogul analysis.

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	$\# Z > 2$
6	ACT	AAA	708	-	3,3,3	1.20	0	3,3,3	1.06	0
7	SO4	AAA	719	-	4,4,4	0.36	0	6,6,6	0.10	0
7	SO4	AAA	726[B]	-	4,4,4	0.34	0	6,6,6	0.11	0
7	SO4	AAA	728[A]	-	4,4,4	0.47	0	6,6,6	0.20	0
5	GOL	AAA	707	-	5,5,5	0.20	0	5,5,5	0.42	0
7	SO4	AAA	718	-	4,4,4	0.30	0	6,6,6	0.28	0
7	SO4	AAA	720	-	4,4,4	0.47	0	6,6,6	0.19	0
7	SO4	AAA	726[A]	-	4,4,4	0.32	0	6,6,6	0.07	0
7	SO4	AAA	730	-	4,4,4	0.33	0	6,6,6	0.17	0
7	SO4	AAA	722	-	4,4,4	0.24	0	6,6,6	0.16	0
7	SO4	AAA	721	-	4,4,4	0.41	0	6,6,6	0.13	0
6	ACT	AAA	731	-	3,3,3	1.00	0	3,3,3	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SO4	AAA	725	-	4,4,4	0.40	0	6,6,6	0.14	0
7	SO4	AAA	728[B]	-	4,4,4	0.36	0	6,6,6	0.12	0
7	SO4	AAA	723	-	4,4,4	0.37	0	6,6,6	0.18	0
7	SO4	AAA	727	-	4,4,4	0.27	0	6,6,6	0.24	0
7	SO4	AAA	729	-	4,4,4	0.66	0	6,6,6	0.26	0
7	SO4	AAA	724	-	4,4,4	0.34	0	6,6,6	0.12	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
5	GOL	AAA	707	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	AAA	726[B]	SO4	2	0
7	AAA	728[A]	SO4	3	0
7	AAA	722	SO4	1	0
7	AAA	724	SO4	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	AAA	627/627 (100%)	-0.72	1 (0%) 91 91	9, 18, 27, 41	22 (3%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	166[A]	THR	6.6

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.

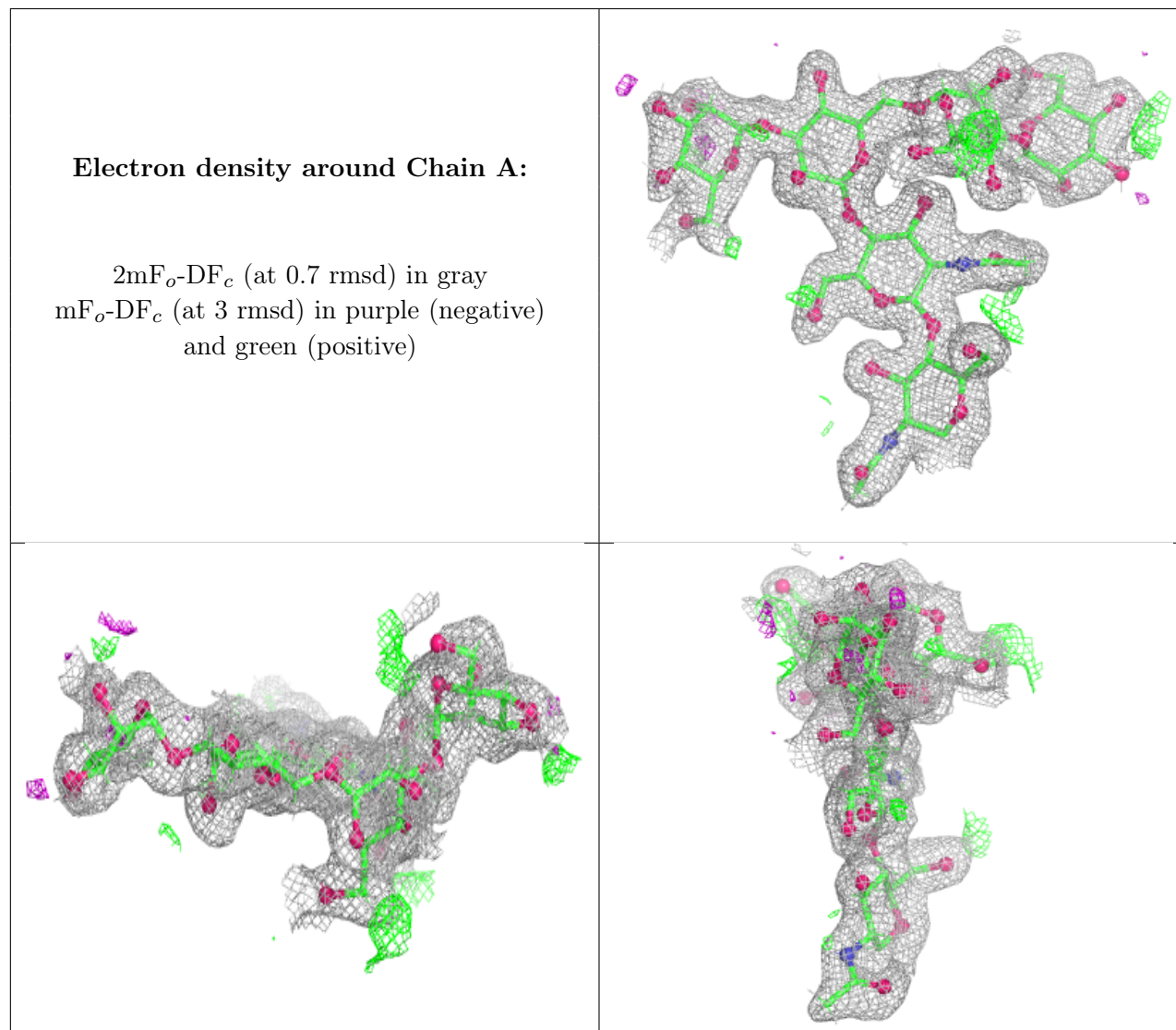
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	A	1	14/15	-	-	22,25,31,31	2
2	NAG	A	2	14/15	-	-	23,26,32,34	2
2	BMA	A	3	11/12	-	-	24,31,33,39	2
2	MAN	A	4	11/12	-	-	20,26,31,38	3
2	MAN	A	5	11/12	-	-	38,44,60,61	4
2	MAN	A	6	11/12	-	-	39,49,54,56	4
4	NAG	C	2	14/15	0.82	0.11	22,24,28,31	2
3	NAG	D	2	14/15	0.94	0.07	32,42,51,52	3
3	NAG	B	2	14/15	0.96	0.06	38,45,62,70	3
4	NAG	C	1	14/15	0.97	0.05	18,21,29,30	2
3	NAG	D	1	14/15	0.97	0.05	19,24,28,29	2

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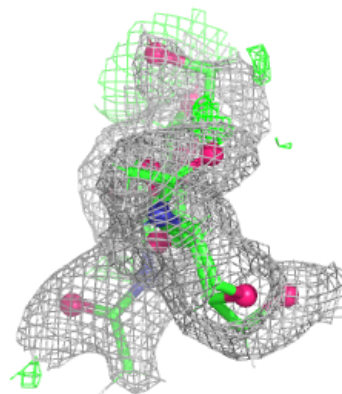
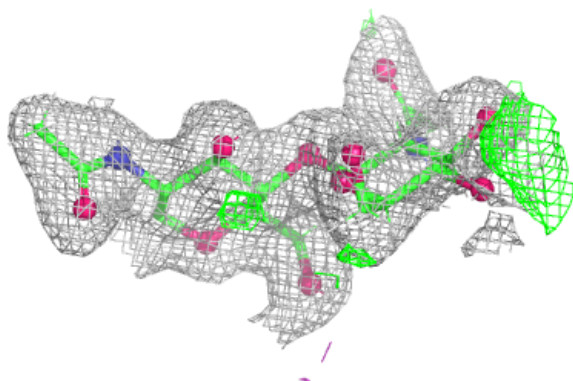
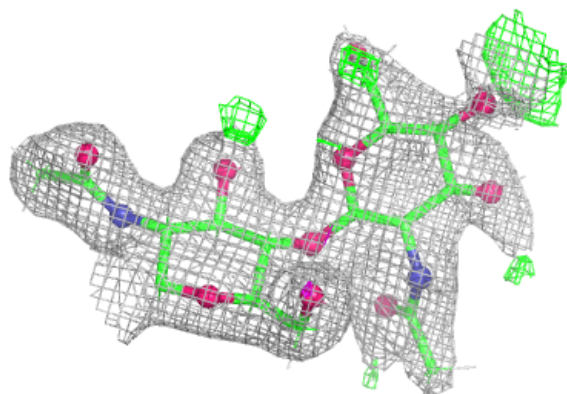
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	B	1	14/15	0.98	0.05	24,27,32,36	2
4	BMA	C	3	11/12	-	-	31,46,58,65	3
4	MAN	C	4	11/12	-	-	29,34,37,38	3
4	MAN	C	5	11/12	-	-	30,35,47,67	4

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.

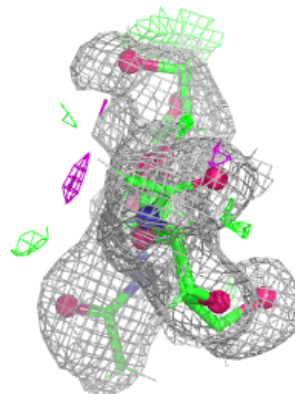
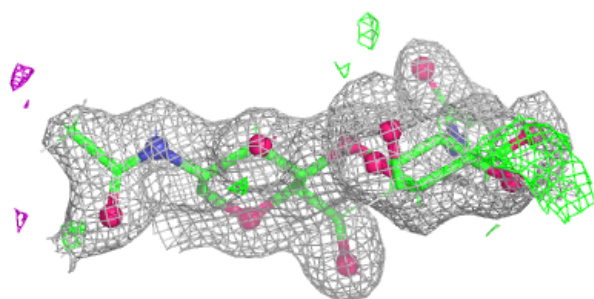
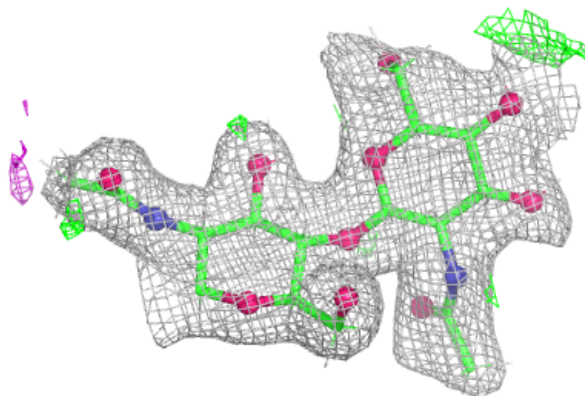


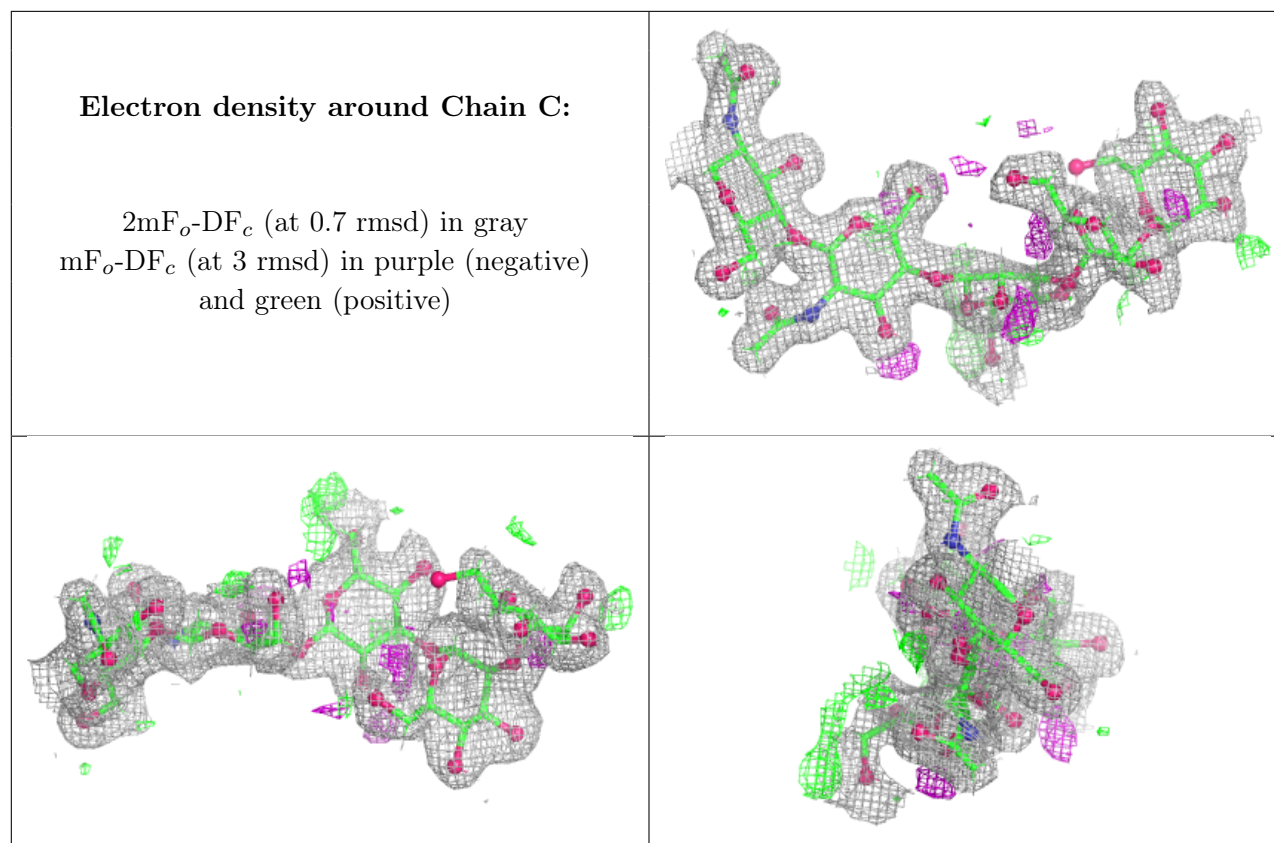
Electron density around Chain B:

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

**Electron density around Chain D:**

$2mF_o-DF_c$ (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
7	SO4	AAA	720	5/5	0.58	0.38	19,26,30,30	5
7	SO4	AAA	724	5/5	0.59	0.38	25,25,28,29	5
8	CL	AAA	739	1/1	0.68	0.48	52,52,52,52	1
8	CL	AAA	746	1/1	0.71	0.55	39,39,39,39	1
8	CL	AAA	745	1/1	0.74	0.60	45,45,45,45	1
7	SO4	AAA	721	5/5	0.75	0.36	33,33,35,36	5
7	SO4	AAA	723	5/5	0.75	0.45	26,27,28,29	5
7	SO4	AAA	722	5/5	0.76	0.19	21,21,22,26	5
8	CL	AAA	742	1/1	0.78	0.73	38,38,38,38	1
8	CL	AAA	744	1/1	0.80	0.50	46,46,46,46	1
8	CL	AAA	741	1/1	0.80	0.51	49,49,49,49	1
8	CL	AAA	733	1/1	0.80	0.36	40,40,40,40	1
6	ACT	AAA	731	4/4	0.81	0.46	32,34,34,35	7
8	CL	AAA	748	1/1	0.81	0.47	42,42,42,42	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	CL	AAA	747	1/1	0.82	0.60	40,40,40,40	1
7	SO4	AAA	727	5/5	0.82	0.16	26,40,46,47	5
8	CL	AAA	732	1/1	0.83	0.53	39,39,39,39	1
8	CL	AAA	737	1/1	0.85	0.33	49,49,49,49	1
7	SO4	AAA	726[B]	5/5	0.85	0.14	43,48,50,51	5
7	SO4	AAA	726[A]	5/5	0.85	0.14	40,45,47,48	5
7	SO4	AAA	729	5/5	0.86	0.12	15,24,26,28	5
7	SO4	AAA	728[A]	5/5	0.87	0.30	25,26,30,31	5
7	SO4	AAA	728[B]	5/5	0.87	0.30	31,35,37,37	5
8	CL	AAA	743	1/1	0.88	0.46	32,32,32,32	1
8	CL	AAA	738	1/1	0.89	0.36	46,46,46,46	1
7	SO4	AAA	719	5/5	0.90	0.15	35,36,40,42	5
8	CL	AAA	735	1/1	0.91	0.33	54,54,54,54	1
8	CL	AAA	734	1/1	0.91	0.27	47,47,47,47	1
8	CL	AAA	740	1/1	0.92	0.41	45,45,45,45	1
6	ACT	AAA	708	4/4	0.93	0.11	29,31,33,37	0
7	SO4	AAA	725	5/5	0.94	0.10	40,41,48,56	5
5	GOL	AAA	707	6/6	0.95	0.08	22,35,41,42	2
7	SO4	AAA	718	5/5	0.96	0.08	26,41,46,52	0
7	SO4	AAA	730	5/5	0.97	0.06	32,35,37,37	4
8	CL	AAA	736	1/1	0.99	0.05	20,20,20,20	1

6.5 Other polymers

There are no such residues in this entry.