



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 3, 2023 – 02:23 am GMT

PDB ID : 1E4M  
Title : MYROSINASE FROM SINAPIS ALBA  
Authors : Burmeister, W.P.  
Deposited on : 2000-07-10  
Resolution : 1.20 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](mailto:validation@mail.wwpdb.org)

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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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

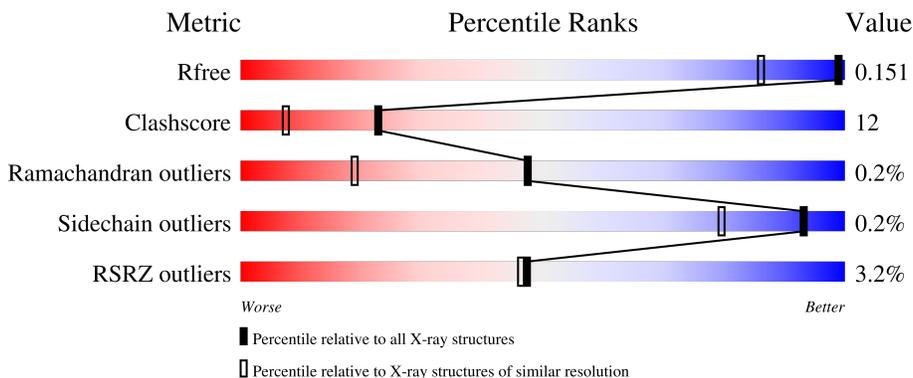
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.20 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))
$R_{free}$	130704	1223 (1.22-1.18)
Clashscore	141614	1286 (1.22-1.18)
Ramachandran outliers	138981	1240 (1.22-1.18)
Sidechain outliers	138945	1239 (1.22-1.18)
RSRZ outliers	127900	1200 (1.22-1.18)

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  $\geq 3$ , 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	M	501	
2	A	2	
3	B	5	
4	C	7	

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
4	BMA	C	3	-	-	X	-
4	MAN	C	6	X	-	X	X
5	NAG	M	961	X	-	-	X
5	NAG	M	971	-	-	-	X
5	NAG	M	991	-	-	-	X
7	SO4	M	1505	-	-	X	-
7	SO4	M	1507	-	X	-	-
7	SO4	M	1510	-	X	X	-
8	GOL	M	1513	-	X	-	-

## 2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 5201 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 MYROSINASE MA1.

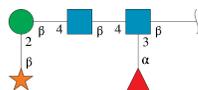
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	M	499	4082	2618	660	788	16	0	21	0

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



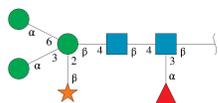
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	A	2	28	16	2	10	0	0	0

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



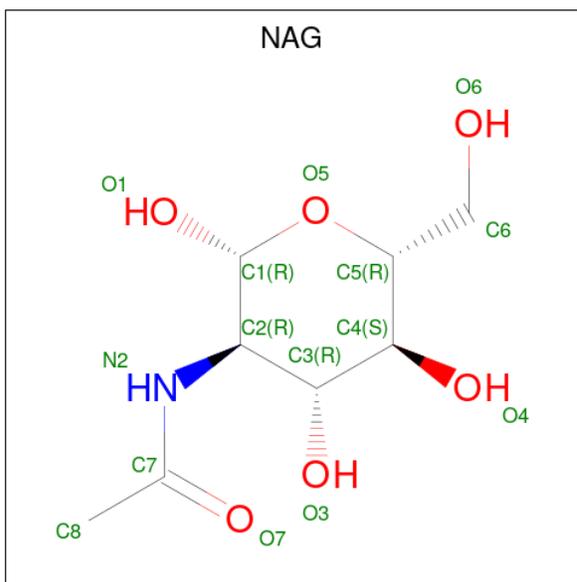
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	B	5	58	33	2	23	0	0	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	C	7	80	45	2	33	0	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).

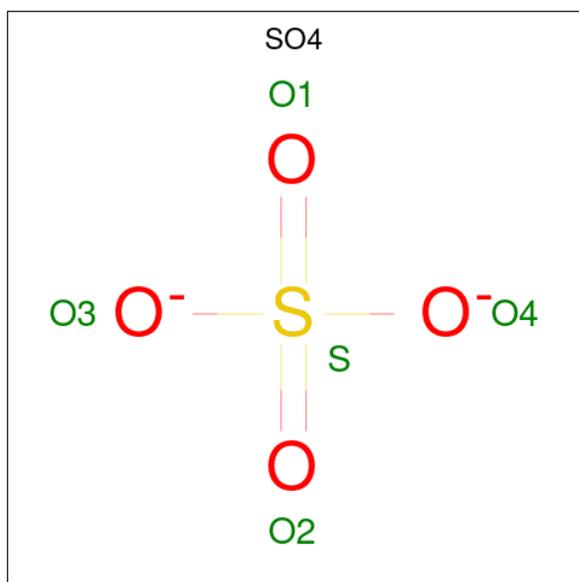


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	M	1	Total	Zn	0	0
			1	1		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	M	1	Total C O 6 3 3	0	0
8	M	1	Total C O 7 3 4	0	1
8	M	1	Total C O 6 3 3	0	0
8	M	1	Total C O 6 3 3	0	0
8	M	1	Total C O 6 3 3	0	0

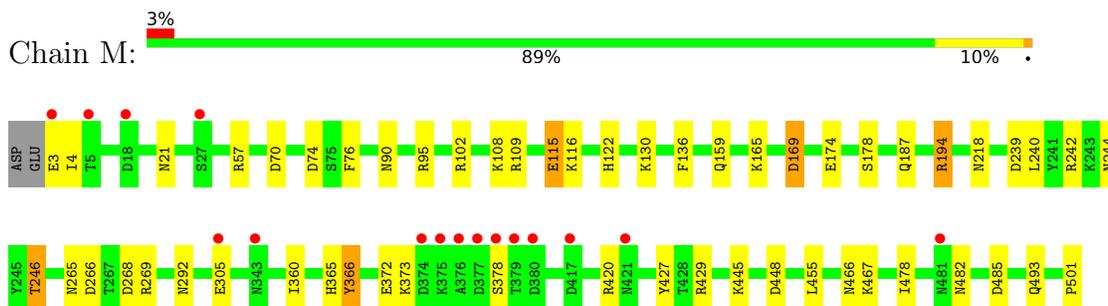
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	M	797	Total O 797 797	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.

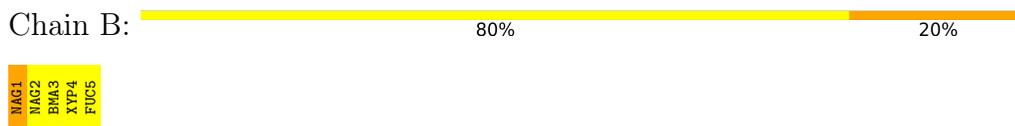
- Molecule 1: MYROSINASE MA1



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



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



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



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.30Å 137.20Å 80.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.20 9.99 – 1.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (10.00-1.20) 96.1 (9.99-1.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 1.20Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.124 , 0.142 0.137 , 0.151	Depositor DCC
$R_{free}$ test set	11150 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	8.1	Xtrriage
Anisotropy	0.110	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.50 , 56.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.012 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SO4, XYP, BMA, NAG, GOL, MAN, FUC, ZN

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	M	0.77	2/4290 (0.0%)	1.16	31/5833 (0.5%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	178	SER	CB-OG	6.28	1.50	1.42
1	M	501	PRO	N-CD	5.94	1.56	1.47

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	115	GLU	OE1-CD-OE2	-12.07	108.81	123.30
1	M	194	ARG	NE-CZ-NH2	-10.71	114.94	120.30
1	M	269	ARG	NE-CZ-NH1	9.32	124.96	120.30
1	M	109	ARG	NE-CZ-NH1	-9.27	115.67	120.30
1	M	268	ASP	CB-CG-OD1	8.34	125.80	118.30

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	M	4082	0	3834	69	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	28	0	24	3	0
3	B	58	0	42	3	0
4	C	80	0	57	18	0
5	M	84	0	77	14	0
6	M	1	0	0	0	0
7	M	40	0	0	7	0
8	M	31	0	37	0	0
9	M	797	0	0	30	0
All	All	5201	0	4071	90	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 12.

The worst 5 of 90 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:21:ASN:HD21	5:M:901:NAG:C1	0.93	1.57
1:M:244:ASN:HD21	5:M:931:NAG:C1	0.96	1.55
1:M:90:ASN:HD21	5:M:911:NAG:C1	0.90	1.52
1:M:360[B]:ILE:HD11	1:M:366[B]:TYR:CZ	1.53	1.41
1:M:360[B]:ILE:CD1	1:M:366[B]:TYR:CZ	2.13	1.31

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	M	518/501 (103%)	505 (98%)	12 (2%)	1 (0%)	47 19

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	187	GLN

### 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	M	456/437 (104%)	455 (100%)	1 (0%)	<b>93</b> <b>79</b>

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

Mol	Chain	Res	Type
1	M	3	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	M	90	ASN
1	M	159	GLN
1	M	244	ASN
1	M	365	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

14 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	3.27	5 (35%)	17,19,21	3.37	8 (47%)
2	NAG	A	2	2	14,14,15	3.23	2 (14%)	17,19,21	5.32	7 (41%)
3	NAG	B	1	1,3	14,14,15	0.47	0	17,19,21	1.96	4 (23%)
3	NAG	B	2	3	14,14,15	1.00	1 (7%)	17,19,21	1.07	1 (5%)
3	BMA	B	3	3	11,11,12	1.74	2 (18%)	15,15,17	1.53	3 (20%)
3	XYP	B	4	3	9,9,10	0.94	0	10,12,14	2.25	4 (40%)
3	FUC	B	5	3	10,10,11	1.54	1 (10%)	14,14,16	1.93	4 (28%)
4	NAG	C	1	4,1	14,14,15	1.71	3 (21%)	17,19,21	2.57	4 (23%)
4	NAG	C	2	4	14,14,15	1.34	2 (14%)	17,19,21	1.57	3 (17%)
4	BMA	C	3	4	11,11,12	2.12	2 (18%)	15,15,17	4.87	9 (60%)
4	XYP	C	4	4	9,9,10	1.48	3 (33%)	10,12,14	1.84	4 (40%)
4	MAN	C	5	4	11,11,12	1.48	3 (27%)	15,15,17	2.34	7 (46%)
4	MAN	C	6	4	11,11,12	2.67	4 (36%)	15,15,17	6.53	11 (73%)
4	FUC	C	7	4	10,10,11	2.10	4 (40%)	14,14,16	1.54	1 (7%)

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FUC	C	7	4	-	-	0/1/1/1

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2	NAG	C4-C5	9.31	1.72	1.53
2	A	1	NAG	O7-C7	-7.35	1.06	1.23
2	A	1	NAG	C4-C5	-7.21	1.37	1.53
2	A	2	NAG	C6-C5	6.72	1.74	1.51
4	C	6	MAN	O5-C5	6.01	1.55	1.43

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	6	MAN	C1-O5-C5	-13.79	93.51	112.19
2	A	2	NAG	C1-O5-C5	-13.44	93.98	112.19
4	C	6	MAN	C6-C5-C4	12.67	142.68	113.00
2	A	2	NAG	C6-C5-C4	-9.90	89.81	113.00
4	C	3	BMA	O4-C4-C5	9.43	132.72	109.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	6	MAN	C5

All (2) torsion outliers are listed below:

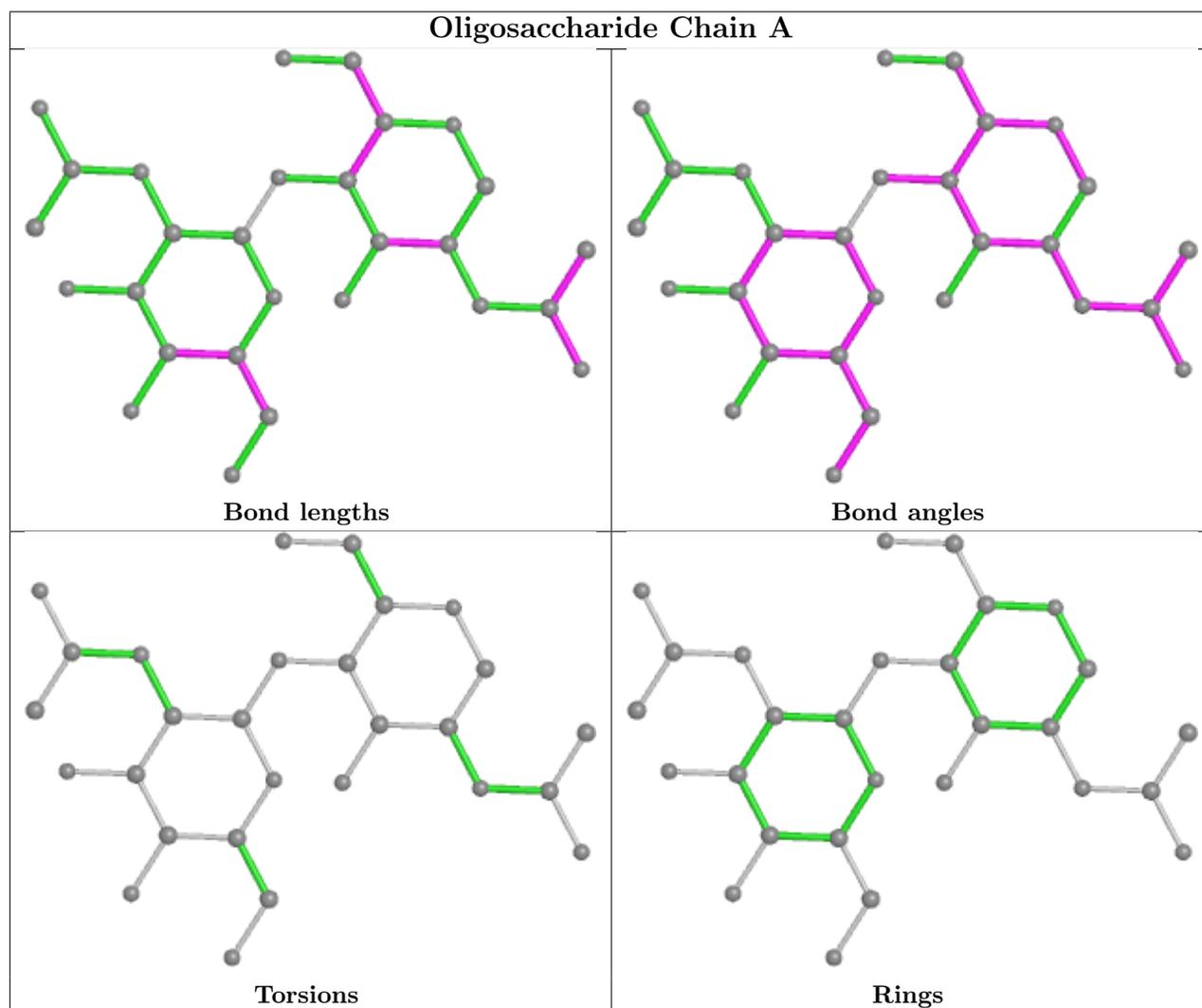
Mol	Chain	Res	Type	Atoms
4	C	6	MAN	O5-C5-C6-O6
4	C	3	BMA	C4-C5-C6-O6

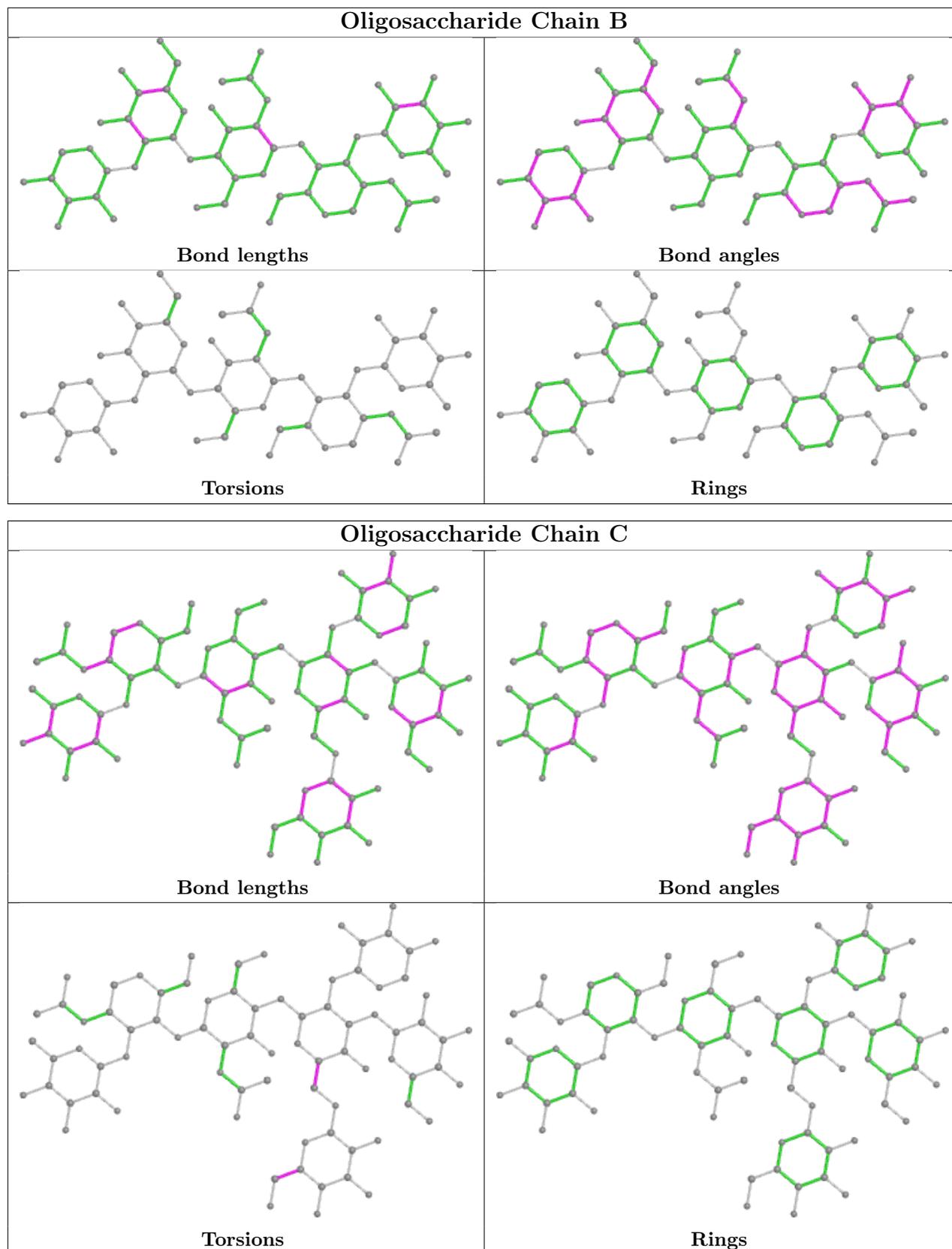
There are no ring outliers.

5 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	3	BMA	10	0
4	C	1	NAG	3	0
2	A	1	NAG	3	0
4	C	6	MAN	12	0
3	B	1	NAG	3	0

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





## 5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 1 is monoatomic - leaving 20 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
8	GOL	M	1512[B]	-	5,5,5	0.96	0	5,5,5	2.70	1 (20%)
7	SO4	M	1509	-	4,4,4	0.67	0	6,6,6	0.24	0
5	NAG	M	911	1	14,14,15	1.27	1 (7%)	17,19,21	2.06	4 (23%)
8	GOL	M	1515	-	5,5,5	0.61	0	5,5,5	1.12	1 (20%)
8	GOL	M	1511	-	5,5,5	0.46	0	5,5,5	0.73	0
5	NAG	M	991	1	14,14,15	1.26	1 (7%)	17,19,21	1.91	4 (23%)
7	SO4	M	1506	-	4,4,4	0.25	0	6,6,6	0.30	0
5	NAG	M	931	1	14,14,15	1.91	5 (35%)	17,19,21	8.60	9 (52%)
8	GOL	M	1513	-	5,5,5	2.59	2 (40%)	5,5,5	1.74	2 (40%)
7	SO4	M	1508	-	4,4,4	0.87	0	6,6,6	1.05	0
7	SO4	M	1504	-	4,4,4	0.52	0	6,6,6	0.43	0
8	GOL	M	1512[A]	-	5,5,5	1.04	0	5,5,5	0.99	0
5	NAG	M	961	1	14,14,15	1.40	2 (14%)	17,19,21	2.47	5 (29%)
5	NAG	M	971	1	14,14,15	1.33	1 (7%)	17,19,21	2.04	6 (35%)
7	SO4	M	1505	7	4,4,4	1.08	1 (25%)	6,6,6	1.30	1 (16%)
5	NAG	M	901	1	14,14,15	1.14	1 (7%)	17,19,21	2.14	4 (23%)
7	SO4	M	1503	-	4,4,4	0.72	0	6,6,6	1.15	0
7	SO4	M	1507	-	4,4,4	1.59	1 (25%)	6,6,6	2.16	3 (50%)
8	GOL	M	1514	-	5,5,5	0.34	0	5,5,5	0.88	0
7	SO4	M	1510	7	4,4,4	1.23	1 (25%)	6,6,6	2.56	4 (66%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GOL	M	1511	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	M	961	1	1/1/5/7	0/6/23/26	0/1/1/1
5	NAG	M	971	1	-	4/6/23/26	0/1/1/1
5	NAG	M	931	1	-	2/6/23/26	0/1/1/1
8	GOL	M	1512[B]	-	-	2/4/4/4	-
5	NAG	M	901	1	-	0/6/23/26	0/1/1/1
8	GOL	M	1514	-	-	0/4/4/4	-
5	NAG	M	911	1	-	0/6/23/26	0/1/1/1
8	GOL	M	1513	-	-	3/4/4/4	-
8	GOL	M	1515	-	-	0/4/4/4	-
8	GOL	M	1512[A]	-	-	0/4/4/4	-
5	NAG	M	991	1	-	0/6/23/26	0/1/1/1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	931	NAG	O7-C7	-4.19	1.13	1.23
8	M	1513	GOL	O1-C1	4.01	1.59	1.42
5	M	971	NAG	O7-C7	-3.96	1.14	1.23
5	M	991	NAG	O7-C7	-3.74	1.14	1.23
5	M	911	NAG	O7-C7	-3.65	1.15	1.23

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	931	NAG	C2-N2-C7	27.98	162.74	122.90
5	M	931	NAG	O5-C1-C2	12.68	131.30	111.29
5	M	931	NAG	C8-C7-N2	11.36	135.34	116.10
5	M	931	NAG	O7-C7-N2	-9.25	104.95	121.95
5	M	961	NAG	C1-O5-C5	7.68	122.59	112.19

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	M	961	NAG	C1

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	M	931	NAG	C8-C7-N2-C2
5	M	931	NAG	O7-C7-N2-C2
8	M	1511	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
8	M	1511	GOL	O1-C1-C2-C3
8	M	1513	GOL	O1-C1-C2-C3

There are no ring outliers.

5 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	911	NAG	5	0
5	M	931	NAG	4	0
7	M	1505	SO4	5	0
5	M	901	NAG	5	0
7	M	1510	SO4	7	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	M	499/501 (99%)	-0.17	16 (3%) 47 46	5, 9, 22, 46	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	376	ALA	9.1
1	M	417	ASP	4.6
1	M	3	GLU	4.5
1	M	380	ASP	4.4
1	M	375	LYS	4.3

### 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, 95<sup>th</sup> 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.

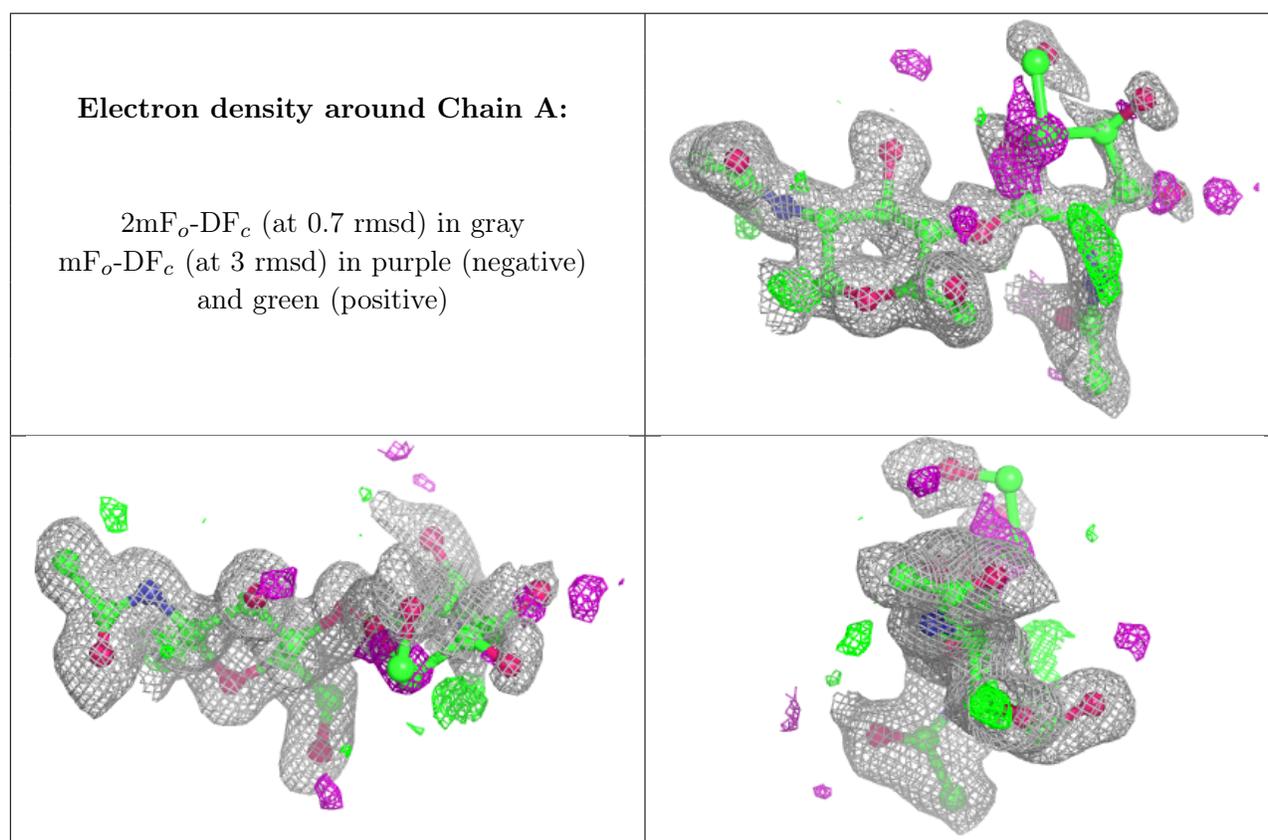
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	A	2	14/15	0.66	0.34	28,34,39,41	0
4	XYP	C	4	9/10	0.66	0.29	27,30,33,36	0
3	XYP	B	4	9/10	0.70	0.32	35,37,39,40	0
4	MAN	C	6	11/12	0.72	0.43	30,35,40,45	0
3	BMA	B	3	11/12	0.73	0.33	29,33,35,38	0
4	MAN	C	5	11/12	0.82	0.28	19,26,32,32	0
4	BMA	C	3	11/12	0.92	0.10	16,21,25,25	0

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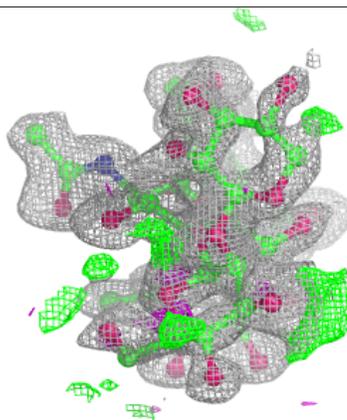
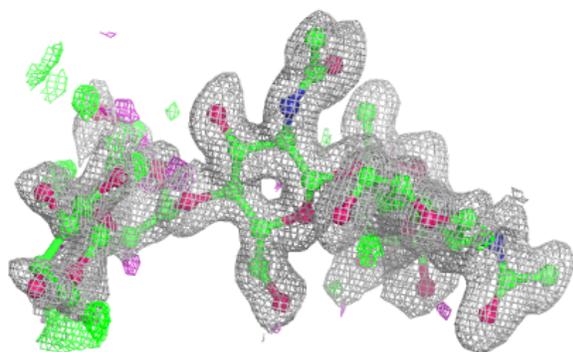
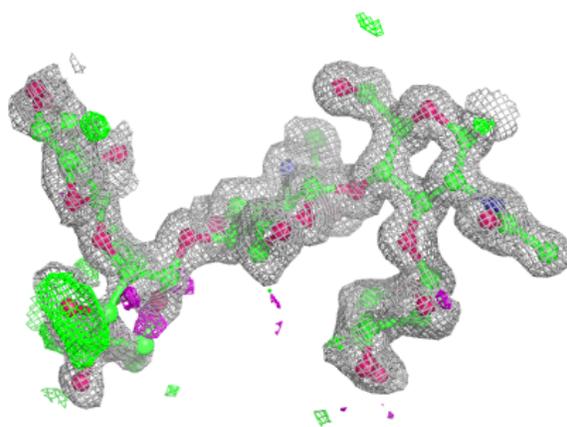
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	FUC	B	5	10/11	0.93	0.18	20,25,29,31	0
4	FUC	C	7	10/11	0.94	0.12	12,14,16,18	0
3	NAG	B	2	14/15	0.95	0.09	18,21,25,30	0
2	NAG	A	1	14/15	0.96	0.08	12,17,23,24	0
4	NAG	C	2	14/15	0.97	0.08	14,16,23,25	0
4	NAG	C	1	14/15	0.97	0.07	12,13,17,21	0
3	NAG	B	1	14/15	0.98	0.05	13,15,17,19	0

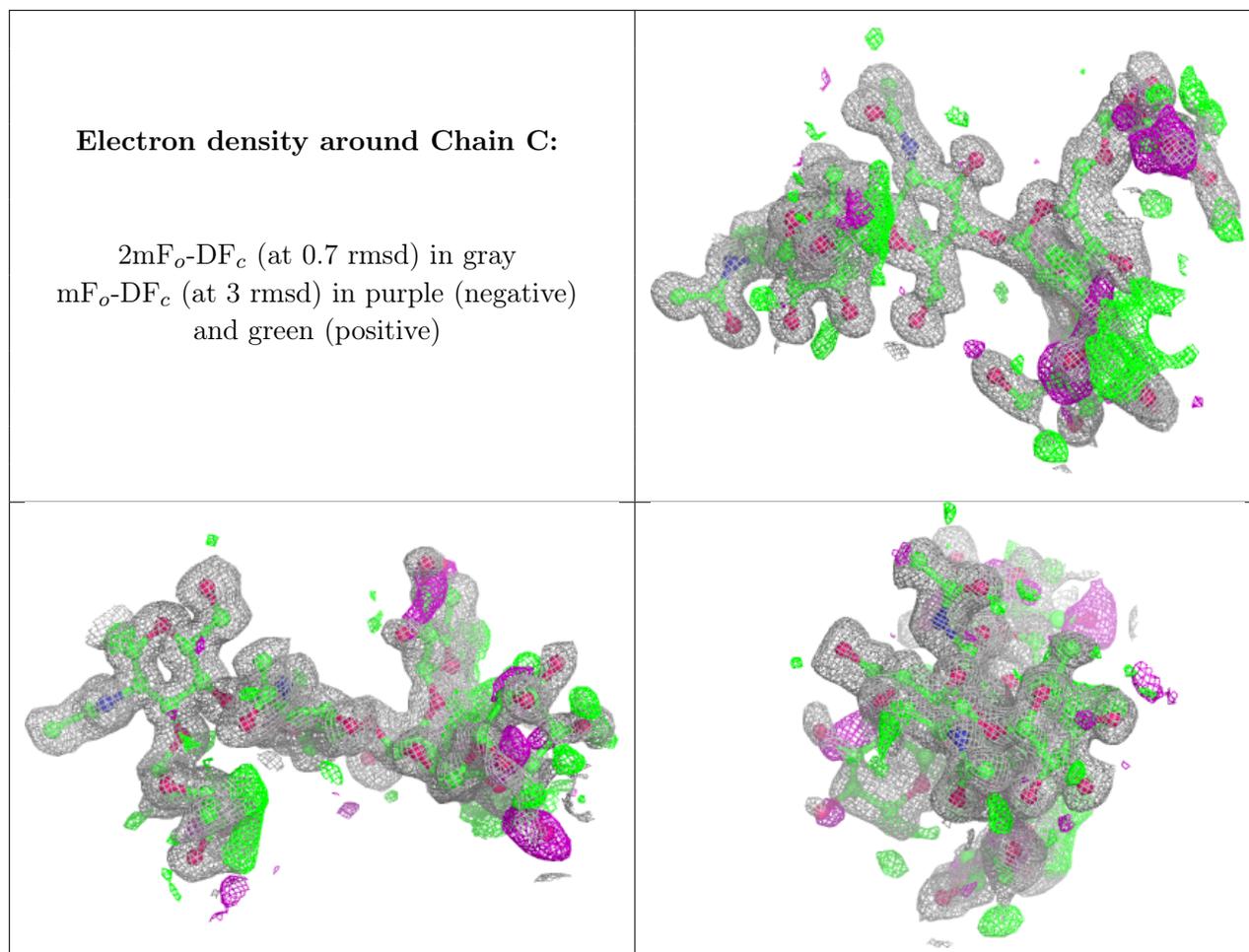
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



**Electron density around Chain B:**

$2mF_o-DF_c$  (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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	NAG	M	971	14/15	0.40	0.52	48,55,56,57	0
5	NAG	M	961	14/15	0.56	0.48	30,37,45,45	0
8	GOL	M	1511	6/6	0.56	0.30	30,35,35,36	6
7	SO4	M	1508	5/5	0.58	0.29	20,26,27,29	5
8	GOL	M	1514	6/6	0.72	0.26	24,24,26,28	6
5	NAG	M	931	14/15	0.74	0.33	28,35,40,40	0
5	NAG	M	991	14/15	0.75	0.40	27,31,39,40	0
7	SO4	M	1505	5/5	0.80	0.23	18,21,24,26	5
7	SO4	M	1509	5/5	0.83	0.22	30,31,31,32	5
7	SO4	M	1510	5/5	0.83	0.35	32,33,36,38	1
5	NAG	M	901	14/15	0.85	0.16	26,29,32,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	SO4	M	1507	5/5	0.90	0.20	22,23,26,27	5
8	GOL	M	1513	6/6	0.91	0.18	9,16,21,23	6
5	NAG	M	911	14/15	0.91	0.17	18,20,24,24	0
8	GOL	M	1512[B]	6/6	0.93	0.13	8,12,12,15	2
7	SO4	M	1504	5/5	0.93	0.19	17,21,25,26	5
8	GOL	M	1512[A]	6/6	0.93	0.13	6,11,12,12	2
7	SO4	M	1503	5/5	0.97	0.16	16,18,23,25	5
8	GOL	M	1515	6/6	0.97	0.08	9,11,15,15	0
7	SO4	M	1506	5/5	0.99	0.05	13,14,19,21	0
6	ZN	M	1502	1/1	1.00	0.03	5,5,5,5	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.