



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:55 PM UTC

PDB ID : 4CD7 / pdb\_00004cd7  
Title : The structure of GH113 beta-mannanase AaManA from Alicyclobacillus acidocaldarius in complex with ManIFG and beta-1,4-mannobiose  
Authors : Williams, R.J.; Iglesias-Fernandez, J.; Stepper, J.; Jackson, A.; Thompson, A.J.; Lowe, E.C.; White, J.M.; Gilbert, H.J.; Rovira, C.; Davies, G.J.; Williams, S.J.  
Deposited on : 2013-10-30  
Resolution : 1.65 Å(reported)

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

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<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>.

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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

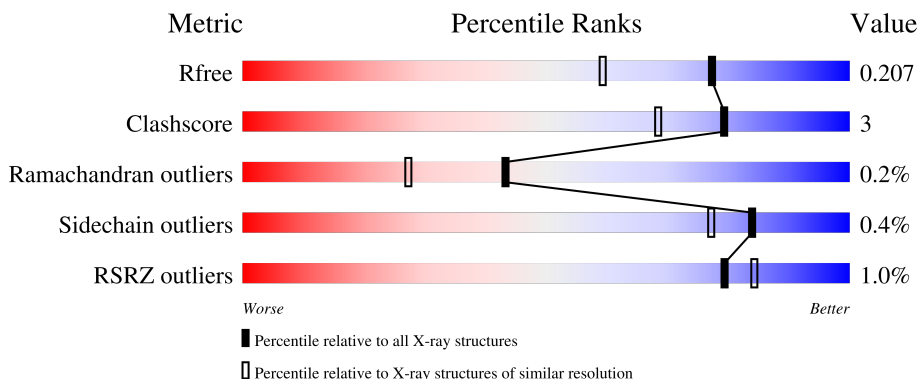
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	A	320	<div> <div></div> <div>92%</div> <div>6%</div> </div>
1	B	320	<div> <div></div> <div>93%</div> <div>5%</div> </div>
2	C	2	<div> <div></div> <div>100%</div> </div>
2	D	2	<div> <div></div> <div>100%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5595 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 ENDO-BETA-1,4-MANNANASE.

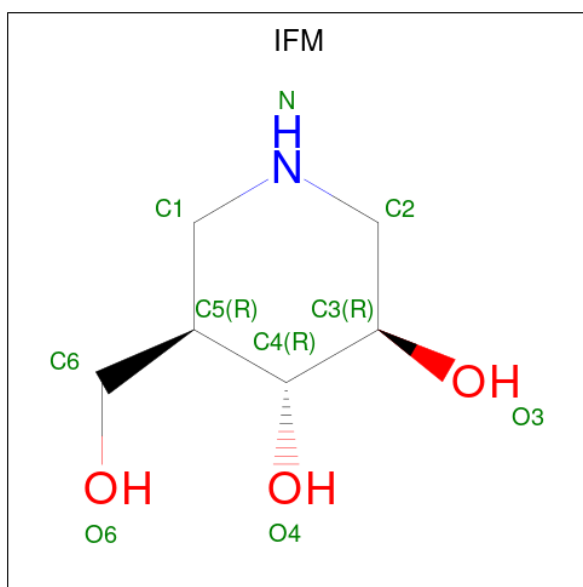
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	5	0
			2513	1600	429	461	23			
1	B	314	Total	C	N	O	S	0	6	0
			2514	1604	423	464	23			

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-alpha-D-mannopyranose.



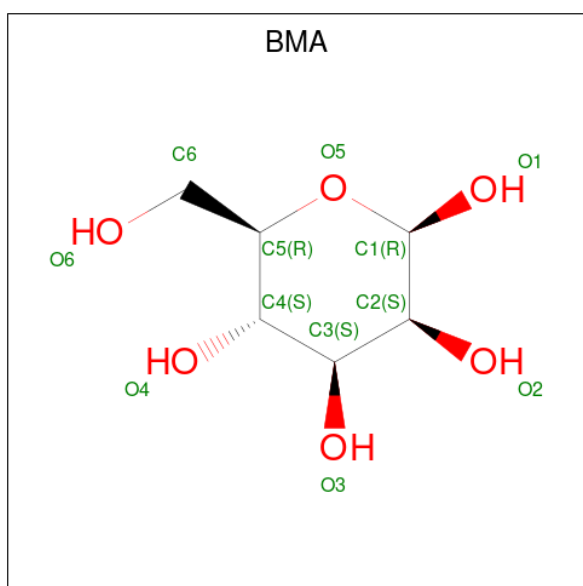
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	0	0	0
			23	12	11			
2	D	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is 5-HYDROXYMETHYL-3,4-DIHYDROXYPIPERIDINE (CCD ID: IFM) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	6	1	3		
3	B	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 4 is beta-D-mannopyranose (CCD ID: BMA) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	234	Total 239	O 239	0	5
5	B	236	Total 241	O 241	0	5



- Molecule 1: ENDO-BETA-1,4-MANNANASE



- 
- | Protein | Approx. Number of Amino Acids |
|---------|-------------------------------|
| MET     | 10                            |
| GLY     | 10                            |
| ARG     | 10                            |
| ILE     | 10                            |
| E5      | 10                            |
| S6      | 10                            |
| F20     | 10                            |
| V21     | 10                            |
| H57     | 10                            |
| P58     | 10                            |
| P94     | 10                            |
| W103    | 10                            |
| E110    | 10                            |
| M130    | 10                            |
| M131    | 10                            |
| N180    | 10                            |
| Y203    | 10                            |
| V232    | 10                            |
| M265    | 10                            |
| A311    | 10                            |
| A316    | 10                            |
| I317    | 10                            |
| A318    | 10                            |
| ASN     | 10                            |

- MAN1  
BMA2

- MAN1  
BMA2

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.47Å 76.59Å 140.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.11 – 1.65 70.11 – 1.65	Depositor EDS
% Data completeness (in resolution range)	97.3 (70.11-1.65) 97.4 (70.11-1.65)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.92 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0033	Depositor
R, $R_{free}$	0.151 , 0.196 0.166 , 0.207	Depositor DCC
$R_{free}$ test set	4466 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.0	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 34.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5595	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IFM, BMA, MAN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.71	0/2611	0.78	0/3551
1	B	0.71	0/2617	0.77	0/3562
All	All	0.71	0/5228	0.77	0/7113

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

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	2513	0	2340	11	0
1	B	2514	0	2323	16	0
2	C	23	0	21	1	0
2	D	23	0	21	1	0
3	A	10	0	12	1	0
3	B	10	0	12	1	0
4	A	11	0	10	0	0
4	B	11	0	10	0	0
5	A	239	0	0	3	2
5	B	241	0	0	5	2
All	All	5595	0	4749	27	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 3.

The worst 5 of 27 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:B:232:VAL:HG21	1:B:265:MET:SD	2.26	0.75
1:B:110:GLU:HG3	5:B:2125:HOH:O	1.87	0.75
1:A:256:ASP:OD2	1:A:260:ARG:NH1	2.22	0.73
1:A:60[A]:ASP:OD1	5:A:2060:HOH:O	2.15	0.65
1:B:130:MET:HE3	1:B:131:MET:CE	2.30	0.62

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)
5:A:2232:HOH:O	5:B:2215:HOH:O[4_545]	0.67	1.53
5:A:2133:HOH:O	5:B:2085:HOH:O[3_545]	1.93	0.27

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	317/320 (99%)	315 (99%)	2 (1%)	0	100	100
1	B	318/320 (99%)	314 (99%)	3 (1%)	1 (0%)	36	21
All	All	635/640 (99%)	629 (99%)	5 (1%)	1 (0%)	43	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	317	ILE

### 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	254/257 (99%)	253 (100%)	1 (0%)	84	77
1	B	254/257 (99%)	253 (100%)	1 (0%)	84	77
All	All	508/514 (99%)	506 (100%)	2 (0%)	84	77

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	180	ASN
1	B	180	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	319	ASN
1	B	182	ASN
1	B	258	GLN
1	A	188	HIS
1	A	182	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](#)

4 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	MAN	C	1	2	12,12,12	0.55	0	17,17,17	1.84	4 (23%)
2	BMA	C	2	2	11,11,12	0.30	0	15,15,17	0.77	0
2	MAN	D	1	2	12,12,12	0.56	0	17,17,17	2.08	6 (35%)
2	BMA	D	2	2	11,11,12	0.50	0	15,15,17	0.94	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
2	MAN	C	1	2	-	2/2/22/22	0/1/1/1
2	BMA	C	2	2	-	0/2/19/22	0/1/1/1
2	MAN	D	1	2	-	2/2/22/22	0/1/1/1
2	BMA	D	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	MAN	O1-C1-O5	5.40	126.46	110.41
2	D	1	MAN	O1-C1-O5	3.93	122.09	110.41
2	D	1	MAN	C1-C2-C3	-3.68	102.86	110.36
2	D	1	MAN	O5-C1-C2	3.38	116.23	110.30
2	D	1	MAN	C1-O5-C5	-2.74	108.36	113.65

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	MAN	O5-C5-C6-O6
2	D	1	MAN	C4-C5-C6-O6

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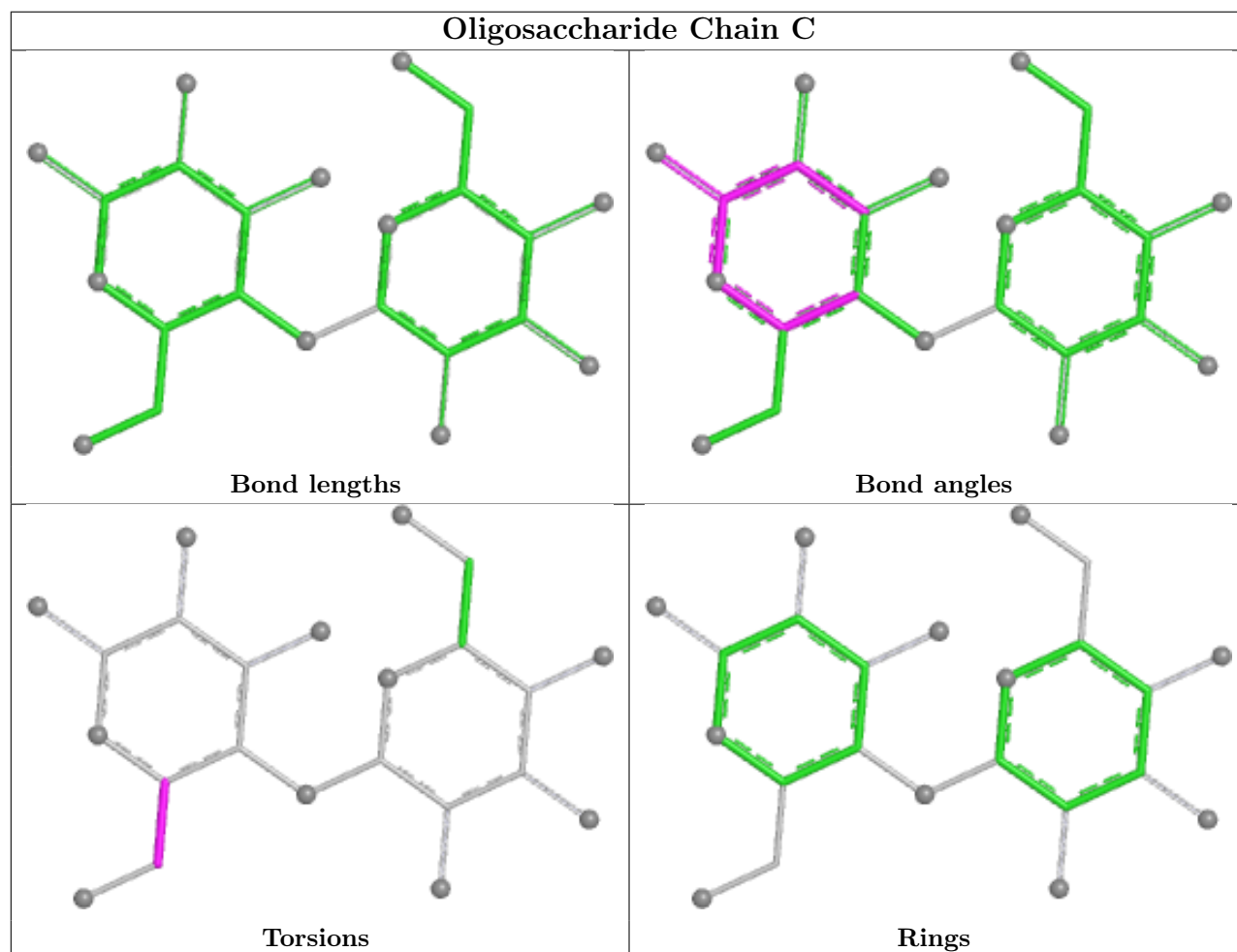
Mol	Chain	Res	Type	Atoms
2	C	1	MAN	C4-C5-C6-O6
2	C	1	MAN	O5-C5-C6-O6

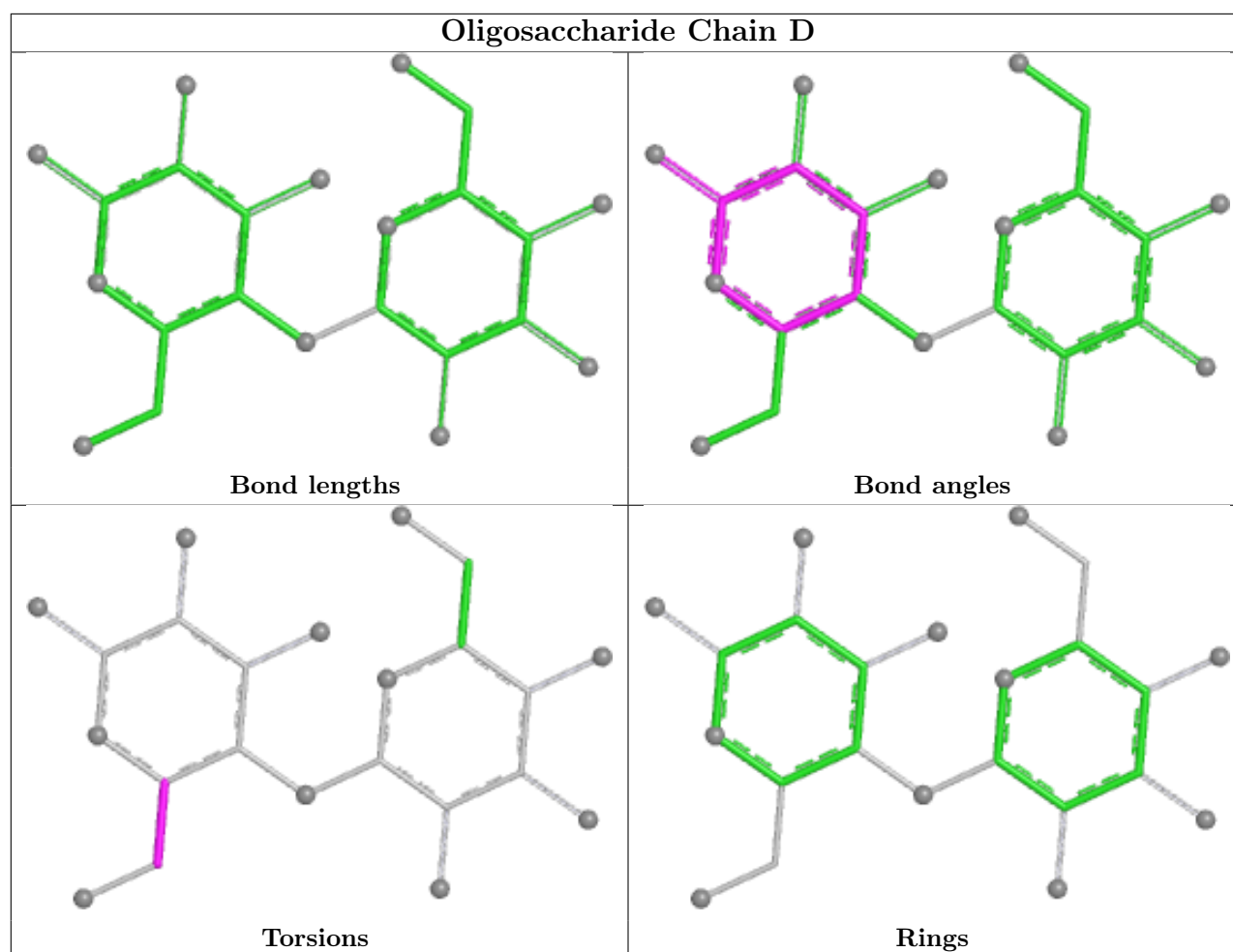
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	BMA	1	0
2	C	2	BMA	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 [i](#)

4 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	$\# Z  > 2$
3	IFM	B	500	4	10,10,10	0.79	0	9,13,13	3.33	2 (22%)
3	IFM	A	500	4	10,10,10	0.80	1 (10%)	9,13,13	3.28	2 (22%)
4	BMA	B	501	3	11,11,12	0.31	0	15,15,17	1.11	1 (6%)
4	BMA	A	501	3	11,11,12	0.42	0	15,15,17	1.12	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
3	IFM	B	500	4	-	0/2/16/16	0/1/1/1
3	IFM	A	500	4	-	0/2/16/16	0/1/1/1
4	BMA	B	501	3	-	0/2/19/22	0/1/1/1
4	BMA	A	501	3	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	IFM	C2-C3	2.12	1.54	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	IFM	C1-N-C2	8.94	122.15	111.78
3	B	500	IFM	C1-N-C2	8.76	121.94	111.78
3	B	500	IFM	C2-C3-C4	3.92	115.04	110.25
3	A	500	IFM	C2-C3-C4	3.20	114.16	110.25
4	A	501	BMA	C1-C2-C3	-3.08	105.15	109.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	500	IFM	1	0
3	A	500	IFM	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, 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	A	314/320 (98%)	-0.49	2 (0%) 85 90	8, 12, 29, 42	5 (1%)
1	B	314/320 (98%)	-0.44	4 (1%) 75 80	6, 13, 32, 42	7 (2%)
All	All	628/640 (98%)	-0.47	6 (0%) 79 84	6, 13, 30, 42	12 (1%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	318	ALA	3.2
1	B	5	GLU	3.0
1	A	8	PHE	2.8
1	B	316	ALA	2.8
1	A	319	ASN	2.4

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

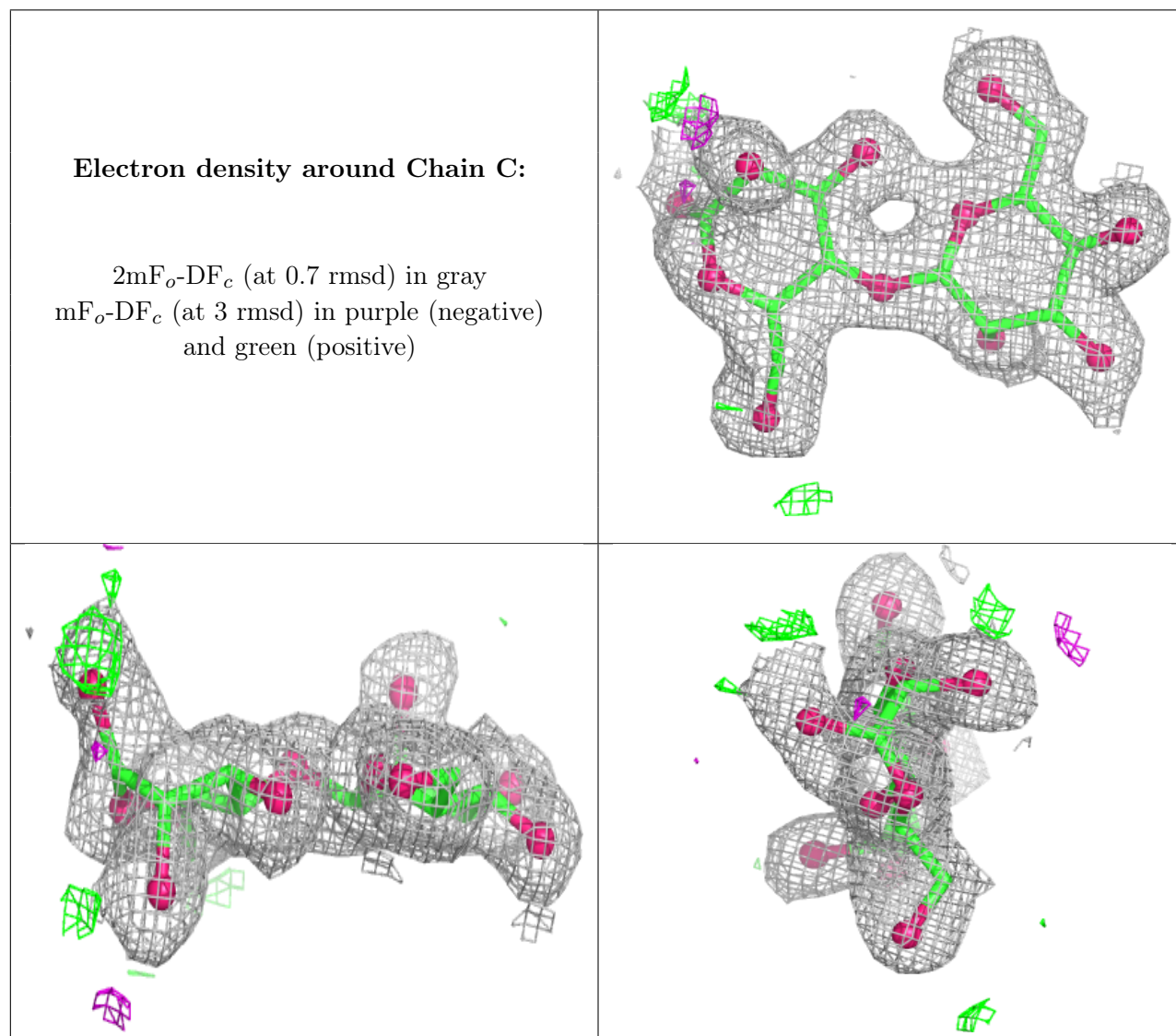
There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

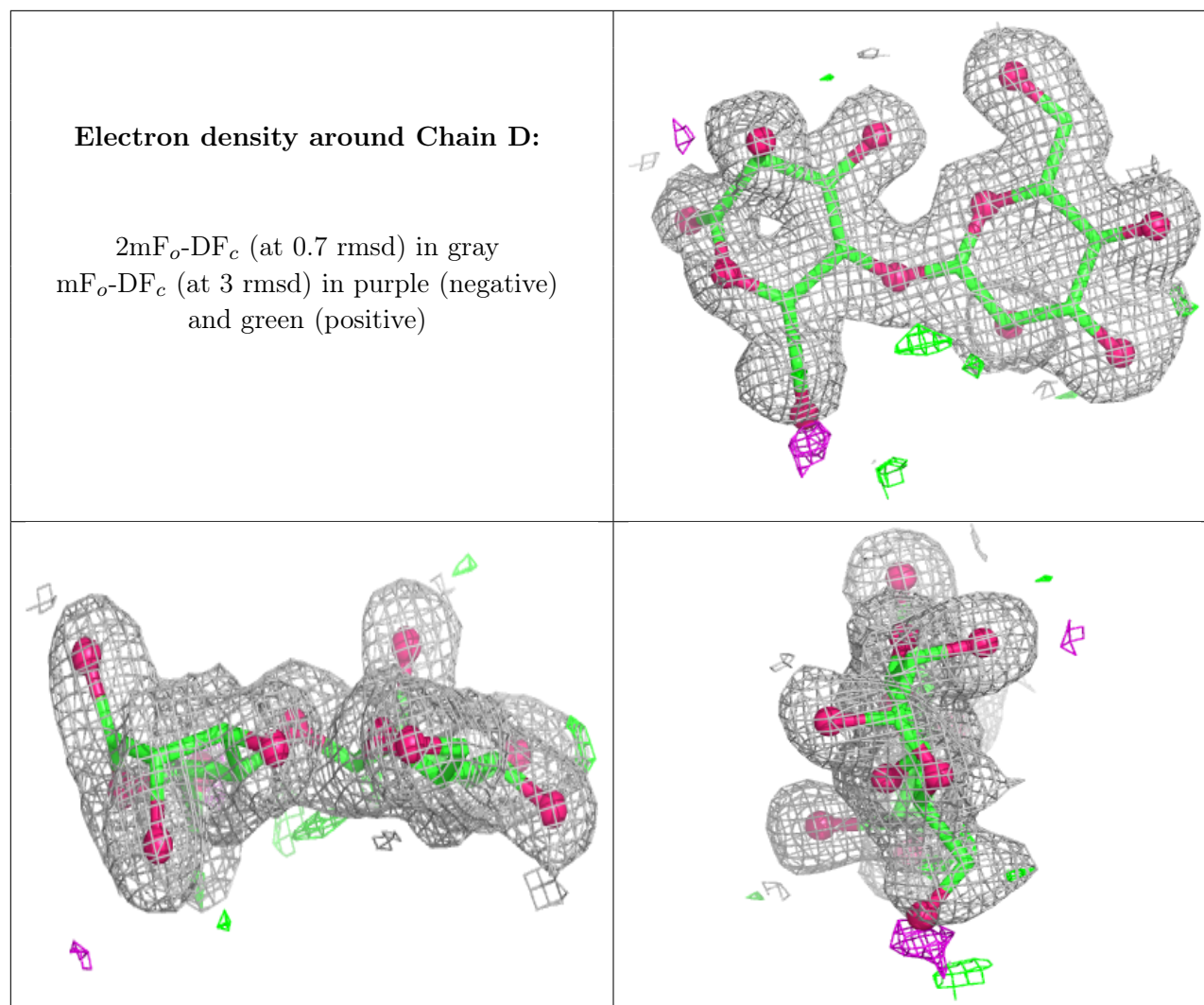
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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	MAN	C	1	12/12	0.91	0.10	22,30,41,43	0
2	MAN	D	1	12/12	0.92	0.09	20,22,27,40	0
2	BMA	D	2	11/12	0.96	0.07	17,20,23,25	0
2	BMA	C	2	11/12	0.97	0.06	21,26,29,31	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.







## 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( $\text{\AA}^2$ )	Q<0.9
3	IFM	B	500	10/10	0.93	0.07	17,19,22,25	0
4	BMA	A	501	11/12	0.93	0.08	24,27,32,34	0
4	BMA	B	501	11/12	0.95	0.06	19,24,26,31	0
3	IFM	A	500	10/10	0.96	0.06	15,21,23,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.