



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2021 – 04:29 AM EDT

PDB ID : 3EDD  
Title : Structural base for cyclodextrin hydrolysis  
Authors : Buedenbender, S.; Schulz, G.E.  
Deposited on : 2008-09-03  
Resolution : 2.65 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.23.2  
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) : 2.23.2

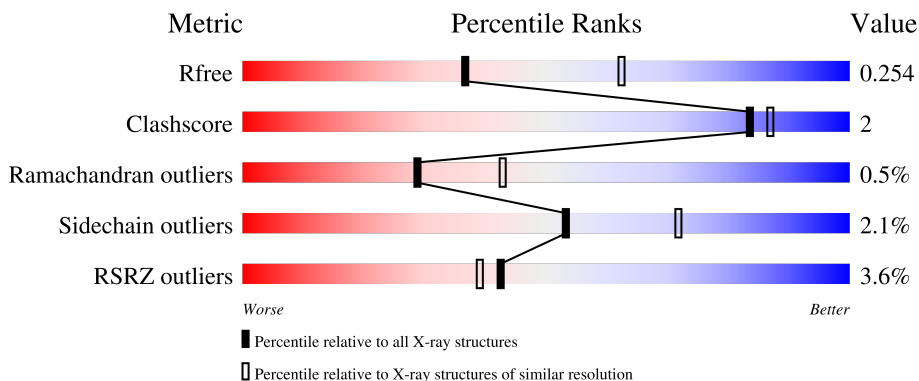
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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))
$R_{free}$	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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	601	 3% 92% 8%
1	B	601	 4% 90% 8%
2	C	6	 33% 67%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9731 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.

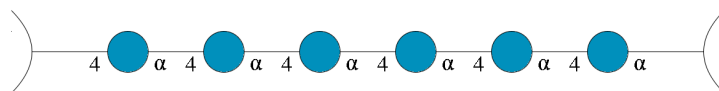
- Molecule 1 is a protein called Cyclomaltodextrinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	597	4770	3016	858	872	24	0	0	0
1	B	597	4770	3016	858	872	24	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	340	GLN	GLU	engineered mutation	UNP Q8KKG0
B	340	GLN	GLU	engineered mutation	UNP Q8KKG0

- Molecule 2 is an oligosaccharide called Cyclohexakis-(1-4)-( $\alpha$ -D-glucopyranose).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
			Total	O			
2	C	6	66	30	0	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		
3	B	2	Total	Ca	0	0
			2	2		

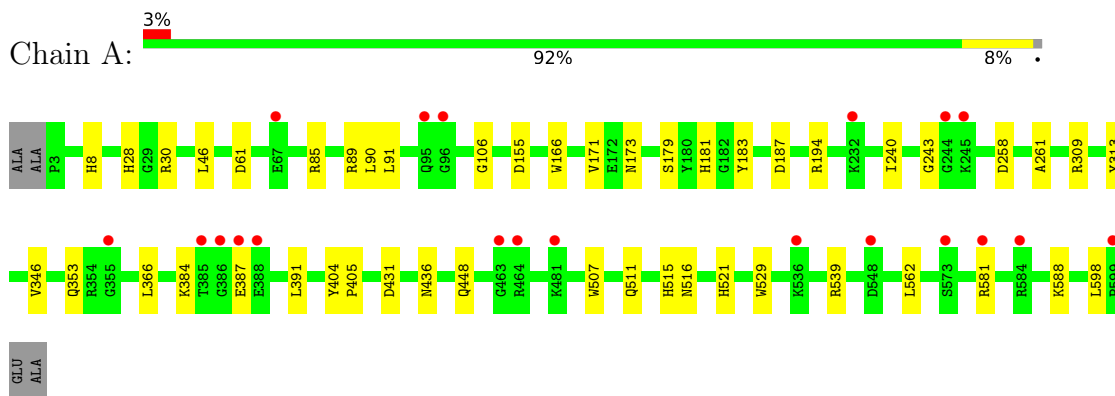
- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	65	Total 65	O 65	0	0
4	B	56	Total 56	O 56	0	0

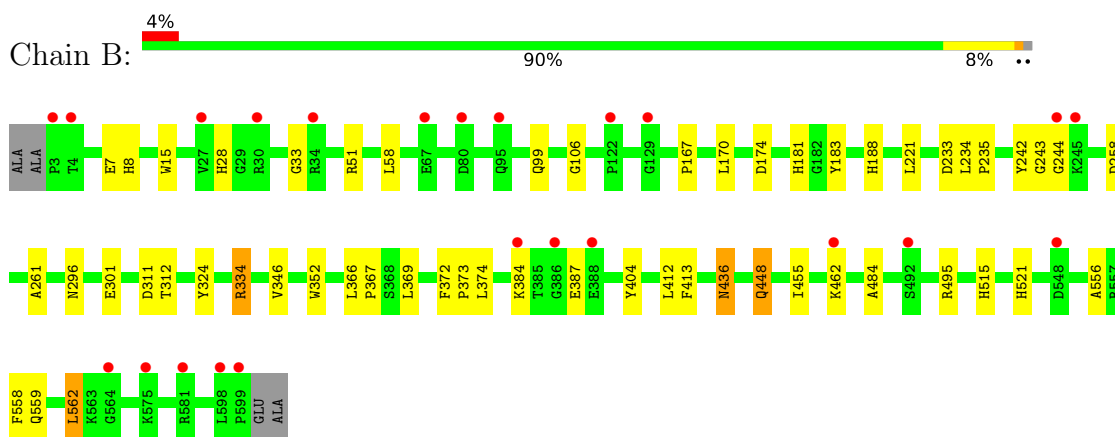
### 3 Residue-property plots [i](#)

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: Cyclomaltodextrinase



- Molecule 1: Cyclomaltodextrinase



- Molecule 2: Cyclohexakis-(1-4)-(alpha-D-glucopyranose)



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	183.76Å 183.76Å 233.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.61 – 2.65 19.61 – 2.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.61-2.65) 88.1 (19.61-2.65)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.30 (at 2.67Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.220 , 0.267 0.211 , 0.254	Depositor DCC
$R_{free}$ test set	2319 reflections (6.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.7	Xtrriage
Anisotropy	0.016	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 39.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.021 for $-2/3^*h-1/3^*k+2/3^*l,-1/3^*h-2/3^*k-2/3^*l,2/3^*h-2/3^*k+1/3^*l$ 0.011 for $-h,1/3^*h-1/3^*k+2/3^*l,2/3^*h+4/3^*k+1/3^*l$ 0.008 for $-1/3^*h+1/3^*k-2/3^*l,-k,-4/3^*h-2/3^*k+1/3^*l$	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9731	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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: GLC, CA

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	0.31	0/4904	0.48	0/6651
1	B	0.31	0/4904	0.47	0/6651
All	All	0.31	0/9808	0.47	0/13302

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	4770	0	4579	19	0
1	B	4770	0	4579	27	0
2	C	66	0	54	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	65	0	0	0	0
4	B	56	0	0	1	0
All	All	9731	0	9212	46	0

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

All (46) 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:A:181:HIS:HD2	1:A:183:TYR:H	1.30	0.77
1:B:258:ASP:HB3	1:B:261:ALA:HB2	1.71	0.71
1:B:181:HIS:HD2	1:B:183:TYR:H	1.42	0.67
1:A:166:TRP:CZ2	1:A:309:ARG:HD3	2.30	0.67
1:A:258:ASP:HB3	1:A:261:ALA:HB2	1.80	0.64
1:B:8:HIS:HB2	1:B:28:HIS:HB3	1.81	0.61
1:A:8:HIS:HB2	1:A:28:HIS:HB3	1.84	0.59
1:B:296:ASN:ND2	1:B:324:TYR:OH	2.36	0.56
1:B:384:LYS:HB3	1:B:387:GLU:HB2	1.90	0.52
1:A:173:ASN:O	1:A:179:SER:HB2	2.11	0.50
1:A:166:TRP:CE2	1:A:309:ARG:HD3	2.46	0.50
1:B:33:GLY:HA2	1:B:58:LEU:HB2	1.93	0.49
1:B:7:GLU:HG3	1:B:8:HIS:CD2	2.48	0.49
1:B:346:VAL:HG13	1:B:404:TYR:CE2	2.47	0.49
1:A:353:GLN:HE21	1:A:405:PRO:HD2	1.78	0.49
1:A:171:VAL:HG13	1:A:187:ASP:O	2.15	0.46
1:A:346:VAL:HG13	1:A:404:TYR:CE2	2.50	0.46
1:A:384:LYS:HB3	1:A:387:GLU:HB2	1.97	0.46
1:A:507:TRP:O	1:A:511:GLN:HG2	2.16	0.46
1:B:556:ALA:HA	1:B:559:GLN:HG2	1.97	0.46
1:B:167:PRO:HB2	1:B:170:LEU:HD11	1.97	0.45
1:B:33:GLY:O	1:B:51:ARG:HD3	2.16	0.45
1:B:436:ASN:HD22	1:B:436:ASN:C	2.20	0.45
1:B:413:PHE:HB3	1:B:448:GLN:HB3	1.97	0.45
1:A:166:TRP:CZ2	1:A:309:ARG:CD	2.98	0.45
1:A:391:LEU:HD13	1:A:529:TRP:HB2	1.99	0.44
1:A:539:ARG:HD3	1:A:598:LEU:HD13	1.99	0.44
1:B:15:TRP:CD2	1:B:301:GLU:HG2	2.53	0.43
1:B:558:PHE:HB2	1:B:562:LEU:HD23	2.00	0.43
1:B:374:LEU:HD23	1:B:412:LEU:HD13	2.01	0.42
1:B:311:ASP:O	1:B:312:THR:C	2.58	0.42
1:B:352:TRP:HB2	1:B:369:LEU:HD21	2.02	0.42
1:A:313:TYR:CZ	1:A:366:LEU:HD22	2.54	0.42
1:B:188:HIS:HE1	4:B:805:HOH:O	2.02	0.42
1:B:372:PHE:N	1:B:373:PRO:CD	2.83	0.42
1:B:221:LEU:HD21	1:B:296:ASN:ND2	2.34	0.41
1:A:106:GLY:HA2	1:A:515:HIS:CD2	2.56	0.41
1:A:431:ASP:HB3	1:A:588:LYS:O	2.21	0.41
1:B:181:HIS:CD2	1:B:183:TYR:H	2.29	0.41
1:B:366:LEU:HA	1:B:367:PRO:HD3	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:GLN:NE2	1:B:334:ARG:HD2	2.35	0.41
1:B:234:LEU:HA	1:B:235:PRO:HD3	1.89	0.41
1:A:89:ARG:HH11	1:A:91:LEU:HD11	1.86	0.41
1:B:106:GLY:HA2	1:B:515:HIS:CD2	2.55	0.41
1:A:353:GLN:HE22	1:A:404:TYR:HB3	1.86	0.40
1:B:455:ILE:HD13	1:B:484:ALA:HB2	2.03	0.40

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	595/601 (99%)	570 (96%)	24 (4%)	1 (0%)	47 64
1	B	595/601 (99%)	570 (96%)	20 (3%)	5 (1%)	19 29
All	All	1190/1202 (99%)	1140 (96%)	44 (4%)	6 (0%)	29 43

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	243	GLY
1	B	233	ASP
1	B	242	TYR
1	A	243	GLY
1	B	174	ASP
1	B	244	GLY

### 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	492/493 (100%)	478 (97%)	14 (3%)	43	61
1	B	492/493 (100%)	485 (99%)	7 (1%)	67	81
All	All	984/986 (100%)	963 (98%)	21 (2%)	53	72

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	46	LEU
1	A	61	ASP
1	A	85	ARG
1	A	90	LEU
1	A	155	ASP
1	A	194	ARG
1	A	240	ILE
1	A	436	ASN
1	A	448	GLN
1	A	516	ASN
1	A	521	HIS
1	A	562	LEU
1	A	581	ARG
1	B	334	ARG
1	B	436	ASN
1	B	448	GLN
1	B	462	LYS
1	B	495	ARG
1	B	521	HIS
1	B	562	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	111	GLN
1	A	181	HIS
1	A	188	HIS
1	A	217	GLN
1	A	257	GLN

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Mol	Chain	Res	Type
1	A	290	ASN
1	A	296	ASN
1	A	353	GLN
1	A	358	ASN
1	A	436	ASN
1	A	448	GLN
1	A	498	GLN
1	B	8	HIS
1	B	99	GLN
1	B	111	GLN
1	B	181	HIS
1	B	188	HIS
1	B	217	GLN
1	B	257	GLN
1	B	283	GLN
1	B	296	ASN
1	B	353	GLN
1	B	358	ASN
1	B	436	ASN
1	B	448	GLN
1	B	521	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](#)

6 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	GLC	C	1	2	11,11,12	0.79	0	15,15,17	1.66	5 (33%)
2	GLC	C	2	2	11,11,12	0.82	0	15,15,17	1.02	1 (6%)
2	GLC	C	3	2	11,11,12	0.83	0	15,15,17	1.02	0
2	GLC	C	4	2	11,11,12	0.85	0	15,15,17	1.41	2 (13%)
2	GLC	C	5	2	11,11,12	0.92	0	15,15,17	0.69	0
2	GLC	C	6	2	11,11,12	0.76	0	15,15,17	1.66	5 (33%)

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	GLC	C	1	2	-	2/2/19/22	0/1/1/1
2	GLC	C	2	2	-	2/2/19/22	0/1/1/1
2	GLC	C	3	2	-	1/2/19/22	0/1/1/1
2	GLC	C	4	2	-	0/2/19/22	0/1/1/1
2	GLC	C	5	2	-	2/2/19/22	0/1/1/1
2	GLC	C	6	2	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	6	GLC	C3-C4-C5	3.32	116.16	110.24
2	C	1	GLC	C3-C4-C5	2.92	115.45	110.24
2	C	6	GLC	C1-C2-C3	2.84	113.15	109.67
2	C	4	GLC	O4-C4-C3	-2.81	103.84	110.35
2	C	1	GLC	O4-C4-C3	-2.78	103.92	110.35
2	C	4	GLC	C3-C4-C5	2.73	115.11	110.24
2	C	2	GLC	O5-C1-C2	-2.51	106.89	110.77
2	C	1	GLC	C1-O5-C5	2.42	115.48	112.19
2	C	6	GLC	O4-C4-C3	-2.38	104.85	110.35
2	C	6	GLC	C2-C3-C4	2.22	114.74	110.89
2	C	1	GLC	C1-C2-C3	2.05	112.18	109.67
2	C	6	GLC	C1-O5-C5	2.01	114.92	112.19
2	C	1	GLC	O5-C5-C4	2.01	115.71	110.83

There are no chirality outliers.

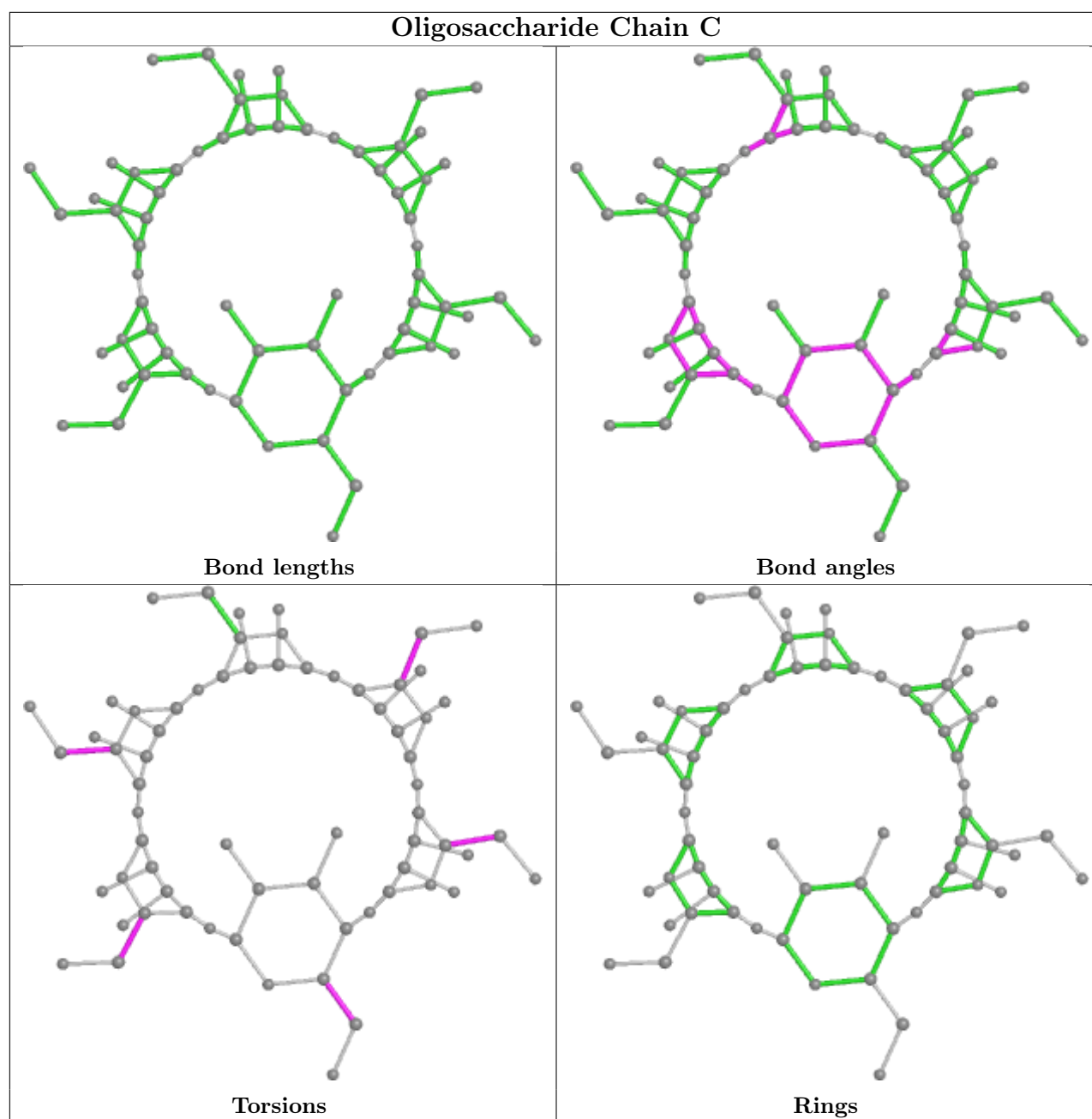
All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	GLC	O5-C5-C6-O6
2	C	6	GLC	O5-C5-C6-O6
2	C	1	GLC	O5-C5-C6-O6
2	C	5	GLC	O5-C5-C6-O6
2	C	1	GLC	C4-C5-C6-O6
2	C	2	GLC	C4-C5-C6-O6
2	C	6	GLC	C4-C5-C6-O6
2	C	5	GLC	C4-C5-C6-O6
2	C	3	GLC	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 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

### 6.1 Protein, DNA and RNA chains

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	597/601 (99%)	-0.10	20 (3%) 45 41	31, 43, 57, 65	0
1	B	597/601 (99%)	-0.02	23 (3%) 39 35	36, 48, 63, 70	0
All	All	1194/1202 (99%)	-0.06	43 (3%) 42 39	31, 45, 62, 70	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	PRO	5.3
1	A	386	GLY	4.0
1	B	244	GLY	3.7
1	B	599	PRO	3.6
1	B	386	GLY	3.5
1	A	581	ARG	3.4
1	B	548	ASP	3.2
1	B	4	THR	3.2
1	B	129	GLY	3.2
1	B	80	ASP	3.1
1	B	492	SER	3.0
1	B	245	LYS	2.9
1	A	244	GLY	2.9
1	A	599	PRO	2.8
1	A	388	GLU	2.7
1	A	95	GLN	2.7
1	B	462	LYS	2.7
1	B	67	GLU	2.6
1	A	385	THR	2.6
1	B	581	ARG	2.5
1	B	384	LYS	2.5
1	B	388	GLU	2.4
1	A	584	ARG	2.4
1	A	245	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	548	ASP	2.4
1	B	122	PRO	2.3
1	B	27	VAL	2.3
1	A	463	GLY	2.3
1	B	34	ARG	2.3
1	A	464	ARG	2.2
1	B	575	LYS	2.2
1	A	96	GLY	2.1
1	B	30	ARG	2.1
1	A	355	GLY	2.1
1	A	481	LYS	2.1
1	B	95	GLN	2.1
1	B	598	LEU	2.0
1	B	564	GLY	2.0
1	A	536	LYS	2.0
1	A	232	LYS	2.0
1	A	573	SER	2.0
1	A	387	GLU	2.0
1	A	67	GLU	2.0

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

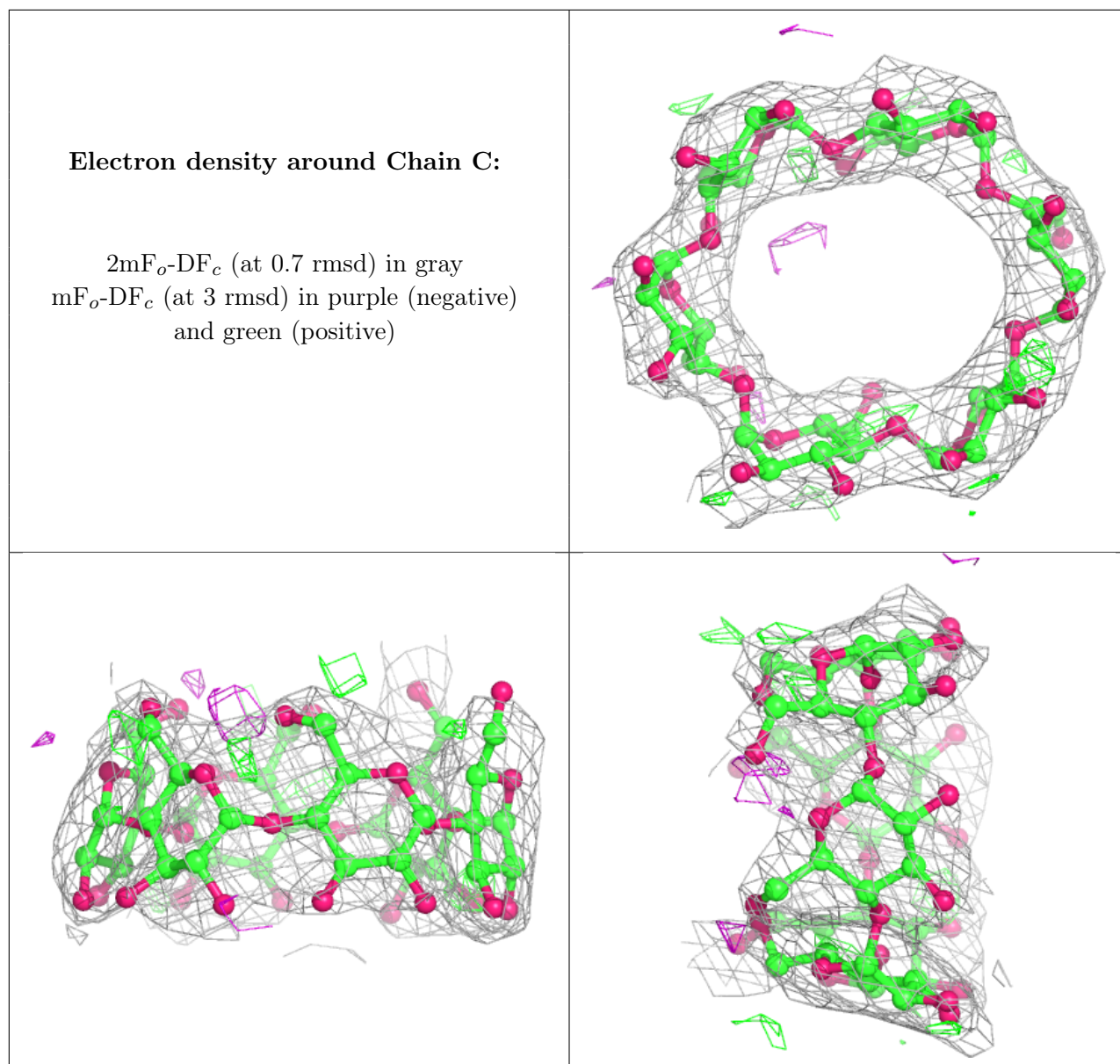
There are no non-standard protein/DNA/RNA residues in this entry.

## 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	GLC	C	3	11/12	0.86	0.22	55,55,56,56	11
2	GLC	C	5	11/12	0.87	0.17	58,58,58,58	11
2	GLC	C	4	11/12	0.89	0.22	57,57,58,58	11
2	GLC	C	6	11/12	0.90	0.18	56,57,57,57	11
2	GLC	C	1	11/12	0.91	0.24	54,54,55,55	11
2	GLC	C	2	11/12	0.91	0.17	54,54,54,55	11

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(Å <sup>2</sup> )	Q<0.9
3	CA	A	700	1/1	0.89	0.09	40,40,40,40	0
3	CA	A	701	1/1	0.91	0.18	49,49,49,49	0
3	CA	B	701	1/1	0.94	0.16	53,53,53,53	0
3	CA	B	700	1/1	0.95	0.12	68,68,68,68	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.