



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 08:26 pm GMT

PDB ID : 1D3C  
Title : MICHAELIS COMPLEX OF BACILLUS CIRCULANS STRAIN 251  
CYCLODEXTRIN GLYCOSYLTRANSFERASE WITH GAMMA-  
CYCLODEXTRIN  
Authors : Uitdehaag, J.C.M.; Kalk, K.H.; van der Veen, B.A.; Dijkhuizen, L.; Dijkstra,  
B.W.  
Deposited on : 1999-09-29  
Resolution : 1.78 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)

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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

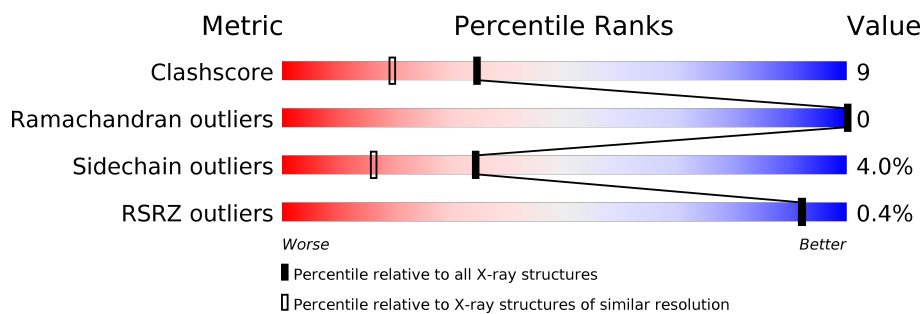
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 1.78 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))
Clashscore	122126	8858 (1.80-1.76)
Ramachandran outliers	120053	8764 (1.80-1.76)
Sidechain outliers	120020	8763 (1.80-1.76)
RSRZ outliers	108989	7741 (1.80-1.76)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	686	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6201 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.

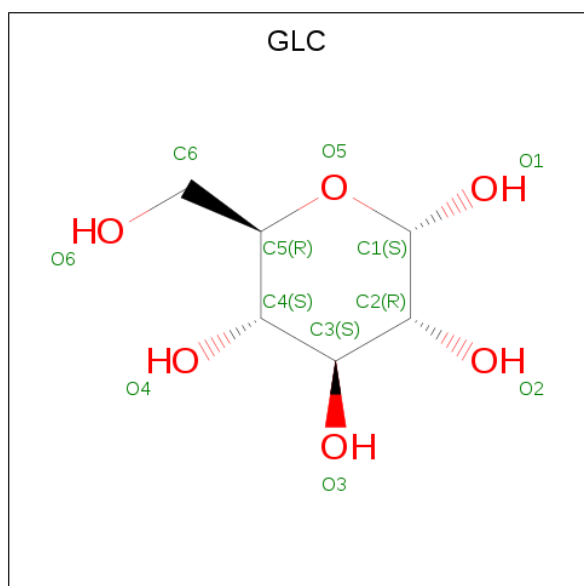
- Molecule 1 is a protein called CYCLODEXTRIN GLYCOSYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	686	5264	3321	902	1025	16	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	229	ASN	ASP	ENGINEERED	UNP P43379
A	257	GLN	GLU	ENGINEERED	UNP P43379

- Molecule 2 is ALPHA-D-GLUCOSE (three-letter code: GLC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	11	6	5	0	0
2	A	1	12	6	6	0	0

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

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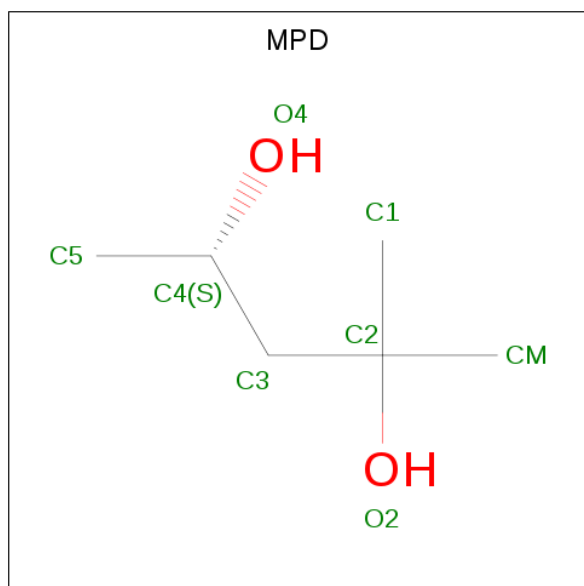
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			11	6	5		
2	A	1	Total	C	O	0	0
			11	6	5		
2	A	1	Total	C	O	0	0
			11	6	5		

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

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

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		

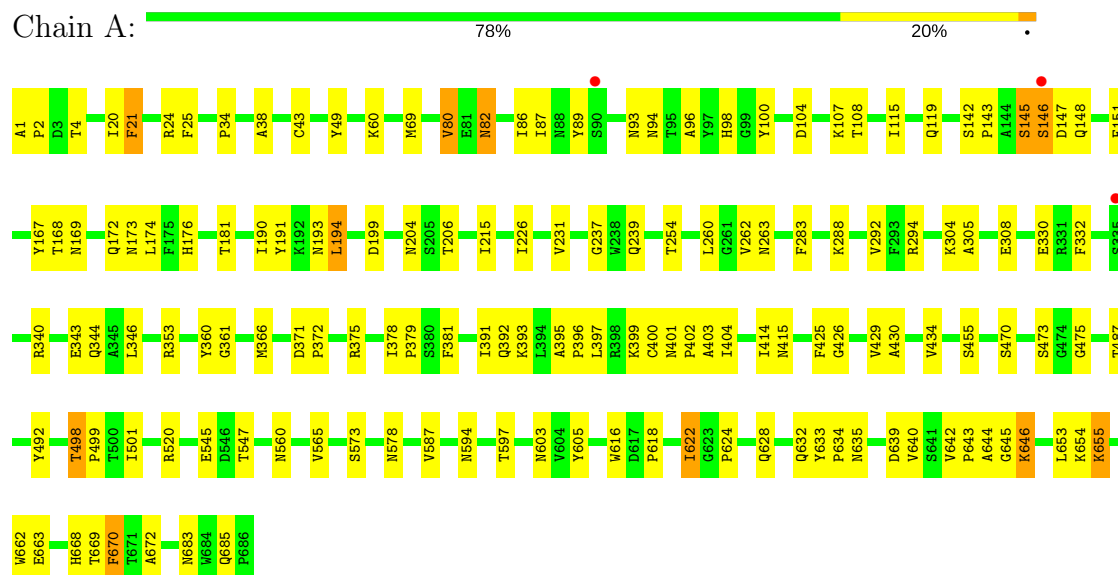
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	639	Total	O	0	0
			639	639		

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

These plots are drawn for all protein, RNA and DNA 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: CYCLODEXTRIN GLYCOSYLTRANSFERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.79Å 109.53Å 65.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.78 80.21 – 1.78	Depositor EDS
% Data completeness (in resolution range)	97.7 (8.00-1.78) 96.1 (80.21-1.78)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.28 (at 1.78Å)	Xtriage
Refinement program	TNT	Depositor
R, $R_{free}$	0.220 , 0.258 0.213 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.2	Xtriage
Anisotropy	0.509	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 98.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: CA, GLC, MPD

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	0.37	0/5394	0.51	0/7352

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	5264	0	5029	92	0
2	A	287	0	236	8	0
3	A	3	0	0	0	0
4	A	8	0	14	0	0
5	A	639	0	0	13	0
All	All	6201	0	5279	98	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 9.

The worst 5 of 98 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:304:LYS:O	1:A:308:GLU:HG3	1.85	0.77
1:A:146:SER:HB2	1:A:167:TYR:CE2	2.20	0.76
1:A:146:SER:HB2	1:A:167:TYR:HE2	1.48	0.76
1:A:20:ILE:HG23	5:A:1281:HOH:O	1.88	0.73
2:A:698:GLC:H61	2:A:699:GLC:O5	1.92	0.70

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	684/686 (100%)	657 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	556/556 (100%)	534 (96%)	22 (4%)	34	16

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	194	LEU
1	A	392	GLN

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Mol	Chain	Res	Type
1	A	655	LYS
1	A	346	LEU
1	A	353	ARG

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

Mol	Chain	Res	Type
1	A	120	ASN
1	A	479	ASN
1	A	560	ASN
1	A	578	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](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 3 are monoatomic - leaving 27 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	$\# Z  > 2$
2	GLC	A	690	2	11,11,12	0.41	0	15,15,17	0.89	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GLC	A	691	2	12,12,12	0.33	0	17,17,17	0.63	0
2	GLC	A	692	2	11,11,12	0.94	1 (9%)	15,15,17	1.08	1 (6%)
2	GLC	A	693	2	11,11,12	1.68	2 (18%)	15,15,17	1.27	1 (6%)
2	GLC	A	694	2	11,11,12	1.67	1 (9%)	15,15,17	1.04	0
2	GLC	A	695	2	11,11,12	2.16	4 (36%)	15,15,17	1.45	3 (20%)
2	GLC	A	696	2	11,11,12	0.90	0	15,15,17	1.04	2 (13%)
2	GLC	A	697	2	11,11,12	0.84	0	15,15,17	1.20	2 (13%)
2	GLC	A	698	2	11,11,12	1.28	1 (9%)	15,15,17	1.36	3 (20%)
2	GLC	A	699	2	11,11,12	1.50	2 (18%)	15,15,17	0.96	1 (6%)
2	GLC	A	700	2	11,11,12	1.61	3 (27%)	15,15,17	1.00	1 (6%)
2	GLC	A	701	2	11,11,12	2.08	1 (9%)	15,15,17	1.16	0
2	GLC	A	702	2	11,11,12	0.96	0	15,15,17	0.97	1 (6%)
2	GLC	A	703	2	11,11,12	0.83	0	15,15,17	0.95	0
2	GLC	A	704	2	11,11,12	1.71	3 (27%)	15,15,17	1.08	1 (6%)
2	GLC	A	705	2	11,11,12	1.08	2 (18%)	15,15,17	1.00	0
2	GLC	A	706	2	11,11,12	1.33	1 (9%)	15,15,17	0.88	0
2	GLC	A	707	2	11,11,12	1.56	1 (9%)	15,15,17	0.98	2 (13%)
2	GLC	A	708	2	11,11,12	1.24	1 (9%)	15,15,17	1.44	2 (13%)
2	GLC	A	709	2	11,11,12	0.75	0	15,15,17	0.83	1 (6%)
2	GLC	A	710	2	11,11,12	1.19	1 (9%)	15,15,17	1.09	1 (6%)
2	GLC	A	711	2	11,11,12	0.86	0	15,15,17	1.18	2 (13%)
2	GLC	A	712	2	11,11,12	1.21	1 (9%)	15,15,17	0.99	1 (6%)
2	GLC	A	713	2	11,11,12	2.11	3 (27%)	15,15,17	1.05	0
2	GLC	A	714	2	11,11,12	1.17	1 (9%)	15,15,17	0.74	0
2	GLC	A	715	2	11,11,12	1.34	2 (18%)	15,15,17	0.96	0
4	MPD	A	716	-	7,7,7	1.15	1 (14%)	9,10,10	0.77	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	GLC	A	690	2	-	0/2/18/22	0/1/1/1
2	GLC	A	691	2	-	0/2/22/22	0/1/1/1
2	GLC	A	692	2	-	0/2/18/22	0/1/1/1
2	GLC	A	693	2	-	0/2/18/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	A	694	2	-	0/2/18/22	0/1/1/1
2	GLC	A	695	2	-	0/2/18/22	0/1/1/1
2	GLC	A	696	2	-	0/2/18/22	0/1/1/1
2	GLC	A	697	2	-	0/2/18/22	0/1/1/1
2	GLC	A	698	2	-	0/2/18/22	0/1/1/1
2	GLC	A	699	2	-	0/2/18/22	0/1/1/1
2	GLC	A	700	2	-	0/2/18/22	0/1/1/1
2	GLC	A	701	2	-	0/2/18/22	0/1/1/1
2	GLC	A	702	2	-	0/2/18/22	0/1/1/1
2	GLC	A	703	2	-	0/2/18/22	0/1/1/1
2	GLC	A	704	2	-	0/2/18/22	0/1/1/1
2	GLC	A	705	2	-	0/2/18/22	0/1/1/1
2	GLC	A	706	2	-	0/2/18/22	0/1/1/1
2	GLC	A	707	2	-	0/2/18/22	0/1/1/1
2	GLC	A	708	2	-	0/2/18/22	0/1/1/1
2	GLC	A	709	2	-	0/2/18/22	0/1/1/1
2	GLC	A	710	2	-	0/2/18/22	0/1/1/1
2	GLC	A	711	2	-	0/2/18/22	0/1/1/1
2	GLC	A	712	2	-	0/2/18/22	0/1/1/1
2	GLC	A	713	2	-	0/2/18/22	0/1/1/1
2	GLC	A	714	2	-	0/2/18/22	0/1/1/1
2	GLC	A	715	2	-	0/2/18/22	0/1/1/1
4	MPD	A	716	-	-	0/5/5/5	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	GLC	C3-C2	-6.57	1.42	1.52
2	A	713	GLC	C3-C2	-5.70	1.44	1.52
2	A	695	GLC	C3-C2	-4.49	1.45	1.52
2	A	707	GLC	O2-C2	-3.96	1.33	1.43
2	A	693	GLC	C3-C2	-3.71	1.47	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	697	GLC	C3-C4-C5	-2.97	106.31	111.26
2	A	698	GLC	C3-C4-C5	-2.78	106.63	111.26
2	A	708	GLC	C3-C4-C5	-2.71	106.75	111.26
2	A	695	GLC	C3-C4-C5	-2.69	106.77	111.26
2	A	695	GLC	C4-C3-C2	-2.54	107.25	110.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	698	GLC	3	0
2	A	699	GLC	2	0
2	A	702	GLC	1	0
2	A	703	GLC	1	0
2	A	704	GLC	1	0
2	A	707	GLC	1	0
2	A	710	GLC	1	0
2	A	715	GLC	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	686/686 (100%)	-0.29	3 (0%) 92 92	7, 15, 26, 67	10 (1%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	SER	2.8
1	A	90	SER	2.2
1	A	335	SER	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](#)

There are no carbohydrates in this entry.

### 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
2	GLC	A	704	11/12	0.46	0.26	47,50,55,56	0
2	GLC	A	703	11/12	0.53	0.40	57,59,64,67	0
2	GLC	A	712	11/12	0.56	0.20	50,51,57,59	0
2	GLC	A	713	11/12	0.57	0.32	51,52,58,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLC	A	711	11/12	0.58	0.23	45,48,53,56	0
2	GLC	A	701	11/12	0.58	0.22	51,57,62,65	0
2	GLC	A	702	11/12	0.61	0.28	59,61,67,70	0
2	GLC	A	714	11/12	0.70	0.23	42,45,50,52	0
4	MPD	A	716	8/8	0.73	0.21	23,25,27,28	0
2	GLC	A	710	11/12	0.77	0.18	39,42,47,49	0
2	GLC	A	692	11/12	0.80	0.15	29,31,34,37	0
2	GLC	A	705	11/12	0.81	0.12	33,36,41,44	0
2	GLC	A	699	11/12	0.82	0.13	34,35,39,42	0
2	GLC	A	700	11/12	0.83	0.16	34,43,49,53	0
2	GLC	A	709	11/12	0.84	0.12	31,34,39,42	0
2	GLC	A	715	11/12	0.87	0.11	31,33,39,39	0
2	GLC	A	698	11/12	0.88	0.14	32,35,41,44	0
2	GLC	A	708	11/12	0.88	0.11	26,27,31,33	0
2	GLC	A	697	11/12	0.90	0.12	24,27,33,36	0
2	GLC	A	707	11/12	0.91	0.12	23,25,30,32	0
2	GLC	A	693	11/12	0.91	0.11	20,21,27,30	0
2	GLC	A	695	11/12	0.93	0.09	15,16,21,23	0
2	GLC	A	696	11/12	0.93	0.10	18,19,23,26	0
2	GLC	A	694	11/12	0.94	0.08	13,14,18,21	0
2	GLC	A	691	12/12	0.94	0.09	16,17,22,27	0
2	GLC	A	706	11/12	0.94	0.10	22,23,30,31	0
2	GLC	A	690	11/12	0.95	0.09	12,13,17,22	0
3	CA	A	687	1/1	0.99	0.05	19,19,19,19	0
3	CA	A	688	1/1	1.00	0.05	12,12,12,12	0
3	CA	A	689	1/1	1.00	0.03	22,22,22,22	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.