

# wwPDB X-ray Structure Validation Summary Report (i)

Nov 15, 2023 – 01:59 PM JST

PDB ID : 6J9Y

Title: Crystal structure of ABC transporter alpha-glycoside-binding protein in

complex with maltose

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Deposited on : 2019-01-24

Resolution : 1.63 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 (i) 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 (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

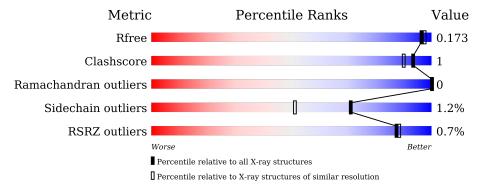
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.63 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
$R_{free}$	130704	3122 (1.66-1.62)
Clashscore	141614	3268 (1.66-1.62)
Ramachandran outliers	138981	3215 (1.66-1.62)
Sidechain outliers	138945	3215 (1.66-1.62)
RSRZ outliers	127900	3079 (1.66-1.62)

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 <=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	408	90%	8%				
2	В	2	100%					



## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3893 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 ABC transporter, periplasmic substrate-binding protein.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	404	Total	С	N	O	S	0	9	0
			3274	2079	592	595	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	403	HIS	-	expression tag	UNP Q5SLD7
A	404	HIS	-	expression tag	UNP Q5SLD7
A	405	HIS	-	expression tag	UNP Q5SLD7
A	406	HIS	-	expression tag	UNP Q5SLD7
A	407	HIS	-	expression tag	UNP Q5SLD7
A	408	HIS	-	expression tag	UNP Q5SLD7

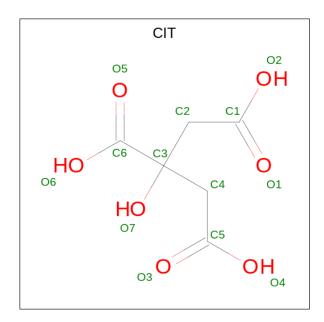
• Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



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

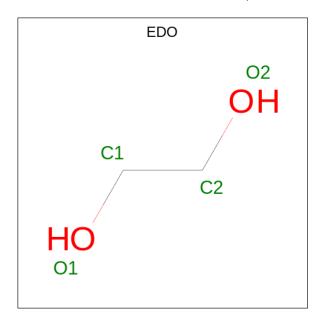
• Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 13	C 6	O 7	0	0

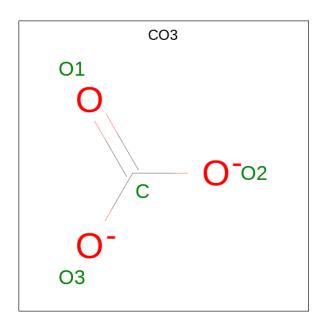
 $\bullet$  Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $\mathrm{C_2H_6O_2}).$ 



Mol	Chain	Residues	Atoms	3	ZeroOcc	AltConf
4	A	1	Total C 4 2	O 2	0	0

 $\bullet$  Molecule 5 is CARBONATE ION (three-letter code: CO3) (formula: CO3).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 4	C 1	O 3	0	0

#### • Molecule 6 is water.

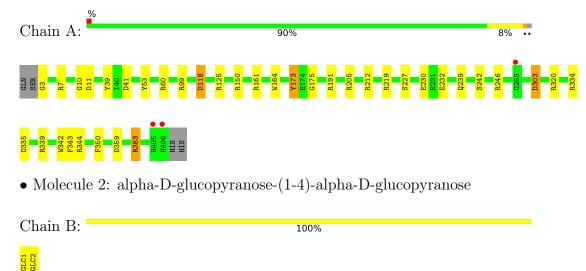
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	575	Total O 575 575	0	0



## 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: ABC transporter, periplasmic substrate-binding protein





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	85.24Å 85.24Å 145.68Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.57 - 1.63	Depositor
rtesolution (A)	46.44 - 1.63	EDS
% Data completeness	100.0 (73.57-1.63)	Depositor
(in resolution range)	100.0 (46.44-1.63)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.39 (at 1.63Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
D D.	0.137 , 0.163	Depositor
$R, R_{free}$	0.147 , $0.173$	DCC
$R_{free}$ test set	3303 reflections $(4.88%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.0	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 47.9	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.51, < L^2>=0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3893	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 4.33% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: CIT, CO3, GLC, EDO

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	Boı	nd lengths	Во	ond angles
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	1.13	$6/3388 \; (0.2\%)$	1.19	34/4605 (0.7%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$Ideal(\AA)$
1	A	60	ARG	CZ-NH2	6.32	1.41	1.33
1	A	342	TRP	CE3-CZ3	5.89	1.48	1.38
1	A	232	GLU	CD-OE2	5.77	1.31	1.25
1	A	11	ASP	N-CA	5.38	1.57	1.46
1	A	239	GLN	CG-CD	5.14	1.62	1.51

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	A	334	ARG	NE-CZ-NH2	-12.10	114.25	120.30
1	A	344	ARG	NE-CZ-NH2	-9.84	115.38	120.30
1	A	334	ARG	NE-CZ-NH1	9.76	125.18	120.30
1	A	39	TYR	CB-CG-CD1	-9.52	115.29	121.00
1	A	7	ARG	NE-CZ-NH2	-8.38	116.11	120.30

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	A	3274	0	3220	8	0
2	В	23	0	21	0	0
3	A	13	0	5	0	0
4	A	4	0	6	0	0
5	A	4	0	0	1	0
6	A	575	0	0	7	2
All	All	3893	0	3252	9	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 1.

The worst 5 of 9 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$	
1:A:303[B]:ASP:OD2	6:A:601:HOH:O	1.91	0.89	
1:A:10:GLY:O	6:A:602:HOH:O	1.91	0.88	
5:A:504:CO3:O3	6:A:603:HOH:O	1.99	0.80	
1:A:3:GLY:N	6:A:610:HOH:O	2.35	0.60	
1:A:227[A]:SER:OG	6:A:604:HOH:O	2.18	0.56	

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
6:A:822:HOH:O	6:A:822:HOH:O[7_555]	1.51	0.69
6:A:1154:HOH:O	6:A:1159:HOH:O[6_444]	2.08	0.12

#### 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	411/408 (101%)	404 (98%)	7 (2%)	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	Percenti	les
1	A	338/333 (102%)	334 (99%)	4 (1%)	71 5	1

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\operatorname{Res}$	Type
1	A	118	ASP
1	A	161	ARG
1	A	173	TYR
1	A	246	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	404	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)

2 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).

Mal	Mol Type	Chain	Dog	Link	Bo	Bond lengths			Bond angles		
IVIOI	Type Chain Res		Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2		
2	GLC	В	1	2	12,12,12	1.79	3 (25%)	17,17,17	2.04	8 (47%)	
2	GLC	В	2	2	11,11,12	0.91	0	15,15,17	1.34	2 (13%)	

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	В	1	2	-	0/2/22/22	0/1/1/1
2	GLC	В	2	2	-	0/2/19/22	0/1/1/1

#### All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\textup{\AA})$	$Ideal(\AA)$
2	В	1	GLC	O2-C2	2.80	1.49	1.43
2	В	1	GLC	C1-C2	-2.44	1.46	1.52
2	В	1	GLC	C3-C2	-2.36	1.46	1.52

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

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	1	GLC	O4-C4-C5	-3.43	100.79	109.30
2	В	1	GLC	C3-C4-C5	-2.91	105.05	110.24
2	В	1	GLC	O5-C5-C4	2.76	114.72	109.69
2	В	1	GLC	O6-C6-C5	-2.71	102.00	111.29
2	В	1	GLC	O4-C4-C3	-2.66	104.20	110.35

There are no chirality outliers.

There are no torsion outliers.

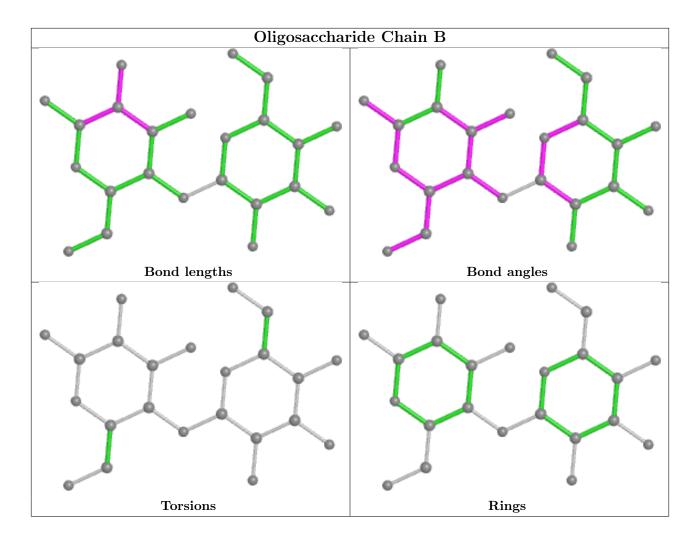
There are no ring outliers.

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.



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#### Ligand geometry (i) 5.6

3 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		
WIOI	Type		Ites	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
5	CO3	A	504	-	2,3,3	1.63	0	2,3,3	1.01	0
4	EDO	A	503	-	3,3,3	0.31	0	2,2,2	1.14	0
3	CIT	A	502	-	12,12,12	1.74	3 (25%)	17,17,17	1.69	5 (29%)

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.

$\mathbf{Mol}$	Type	Chain	$\operatorname{Res}$	Link	Chirals	Torsions	Rings
4	EDO	A	503	-	-	1/1/1/1	-
3	CIT	A	502	-	-	6/16/16/16	-

#### All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
3	A	502	CIT	C3-C6	-3.35	1.49	1.53
3	A	502	CIT	C2-C3	-3.17	1.49	1.53
3	A	502	CIT	O3-C5	2.62	1.30	1.22

#### All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
3	A	502	CIT	O5-C6-C3	-3.16	117.77	122.25
3	A	502	CIT	O7-C3-C2	-2.69	103.12	109.40
3	A	502	CIT	C4-C3-C2	2.28	115.10	109.16
3	A	502	CIT	C4-C3-C6	-2.20	105.37	110.11
3	A	502	CIT	O1-C1-C2	-2.00	117.09	122.94

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	CIT	O7-C3-C6-O5
3	A	502	CIT	C2-C3-C6-O5
3	A	502	CIT	C4-C3-C6-O6
3	A	502	CIT	C4-C3-C6-O5
3	A	502	CIT	O7-C3-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	504	CO3	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,  $95^{th}$  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>	# RSRZ > 2		$OWAB(A^2)$	Q<0.9
1	A	404/408 (99%)	-0.14	3 (0%)	87 88	8, 13, 30, 58	0

All (3) RSRZ outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	RSRZ
1	A	406	HIS	4.9
1	A	405	HIS	2.6
1	A	259	GLY	2.1

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

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

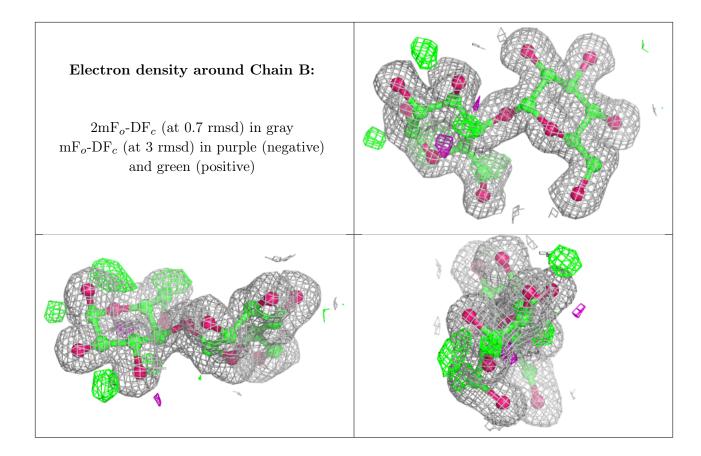
## 6.3 Carbohydrates (i)

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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	GLC	В	1	12/12	0.94	0.09	9,15,18,20	0
2	GLC	В	2	11/12	0.98	0.09	7,8,9,9	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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	EDO	A	503	4/4	0.85	0.11	38,41,48,55	0
3	CIT	A	502	13/13	0.91	0.11	14,23,36,37	0
5	CO3	A	504	4/4	0.92	0.31	32,36,47,51	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

