

Full wwPDB X-ray Structure Validation Report (i)

Sep 2, 2023 – 02:57 PM EDT

PDB ID	:	3QDX
Title	:	Structure of the orthorhombic form of the Boletus edulis lectin in complex
		with T-antigen disaccharide and N,N-diacetyl chitobiose
Authors	:	Bovi, M.; Carrizo, M.E.; Capaldi, S.; Perduca, M.; Chiarelli, L.R.; Galliano,
		M.; Monaco, H.L.
Deposited on	:	2011-01-19
Resolution	:	1.70 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* 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:

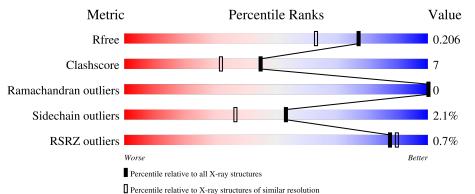
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.70 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	Qualit	y of chain		
1	А	143	% 		13%	-
1	В	143	% • 88%		11%	
2	С	2	50%	50%		
2	D	2	-	100%		•
3	Ε	2	50%	50%		-

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Mol	Chain	Length	Quality of chain			
3	F	2	50%	50%		



3QDX

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2440 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.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	143	Total	С	Ν	0	S	0	0	0
	A	140	1120	711	194	212	3			
1	Р	143	Total	С	Ν	0	S	0	0	0
	D	140	1120	711	194	212	3	0	0 0	0

• Molecule 1 is a protein called BOLETUS EDULIS LECTIN.

• Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-a lpha-D-galactopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	С	2	Total C N O 26 14 1 11	0	0	0
2	D	2	Total C N O 26 14 1 11	0	0	0

• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



Mo	l Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	Е	2	Total C N O 15 8 1 6	0	0	1
3	F	2	Total C N O 15 8 1 6	0	0	1

• Molecule 4 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	61	Total O 61 61	0	0
4	В	57	$\begin{array}{cc} \text{Total} & \text{O} \\ 57 & 57 \end{array}$	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.

.%			
Chain A:	87%	13%	-
ACE0 R7 R11 N12 F18 F18 G52	164 H71 R75 B78 D78 D78 B94 G95 F94 G95 F105 F123 F123 F123 F123 F123 F123 F123 F123		
• Molecule 1: B	OLETUS EDULIS LECTIN		
.%			
Chain B:	88%	11%	•
ACE0 T1 R7 N12 013 G14 N30 H41	164 H71 B78 D78 D78 D78 F122 F123 F123 F123 F123 F123 F123 F123		
• Molecule 2: be	eta-D-galactopyranose-(1-3)-2-acet	amido-2-deoxy-alpha-D-	galactopyranose
Chain C:	50%	50%	•
A2G1 GAL2			
• Molecule 2: be	eta-D-galactopyranose-(1-3)-2-acet	amido-2-deoxy-alpha-D-	galactopyranose
Chain D:	100%		-
A2G1 GAL2			
• Molecule 3: 2- opyranose	acetamido-2-deoxy-beta-D-glucop	yranose-(1-4)-2-acetamic	do-2-deoxy-beta-D-gluc
Chain E:	50%	50%	•

• Molecule 1: BOLETUS EDULIS LECTIN

NAG1 NAG2

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



Chain F: 50% 50%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	68.16Å 97.96Å 84.46Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 - 1.70	Depositor
Resolution (A)	46.64 - 1.70	EDS
% Data completeness	99.0 (40.00-1.70)	Depositor
(in resolution range)	$99.0 \ (46.64 - 1.70)$	EDS
R _{merge}	0.08	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.78 (at 1.70 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
D D.	0.177 , 0.208	Depositor
R, R_{free}	0.176 , 0.206	DCC
R_{free} test set	1567 reflections (5.03%)	wwPDB-VP
Wilson B-factor $(Å^2)$	11.3	Xtriage
Anisotropy	0.476	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.43, 54.2	EDS
L-test for twinning ²	$ \langle L \rangle = 0.48, \langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2440	wwPDB-VP
Average B, all atoms $(Å^2)$	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 18.12% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: ACE, NAG, A2G, GAL

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		lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.54	0/1143	0.63	0/1550	
1	В	0.52	0/1143	0.61	0/1550	
All	All	0.53	0/2286	0.62	0/3100	

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	А	1120	0	1098	17	0
1	В	1120	0	1098	13	0
2	С	26	0	21	0	0
2	D	26	0	21	0	0
3	Ε	15	0	13	0	0
3	F	15	0	13	0	0
4	А	61	0	0	2	0
4	В	57	0	0	4	0
All	All	2440	0	2264	30	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 7.



	A.L. 0	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:10:GLN:HE22	1:A:18:PHE:H	1.12	0.97
1:A:95:GLN:NE2	1:A:102:ARG:HE	1.85	0.74
1:A:130:VAL:HG23	1:A:131:GLU:HG3	1.74	0.69
1:B:130:VAL:HG23	1:B:131:GLU:HG2	1.75	0.68
1:A:7:ARG:HE	1:A:138:ASN:HD21	1.46	0.64
1:B:1:THR:HG21	4:B:182:HOH:O	1.97	0.62
1:A:95:GLN:HE21	1:A:102:ARG:HE	1.47	0.61
1:B:41:HIS:HD2	4:B:177:HOH:O	1.83	0.60
1:A:123:PHE:CE2	1:A:141:PHE:CD1	2.91	0.59
1:A:7:ARG:HE	1:A:138:ASN:ND2	2.03	0.54
1:B:7:ARG:HE	1:B:138:ASN:HD21	1.56	0.54
1:A:123:PHE:HE2	1:A:141:PHE:CE1	2.26	0.53
1:A:123:PHE:CE2	1:A:141:PHE:CE1	2.98	0.52
1:B:7:ARG:HH21	1:B:138:ASN:HD21	1.57	0.52
1:A:64:ILE:C	1:A:64:ILE:HD12	2.33	0.49
1:B:7:ARG:HE	1:B:138:ASN:ND2	2.12	0.47
1:B:64:ILE:HG21	1:B:123:PHE:CZ	2.49	0.47
1:A:71:HIS:HE1	4:A:197:HOH:O	1.99	0.45
1:A:78:ASP:CG	1:A:105:THR:HG21	2.37	0.45
1:A:123:PHE:HE2	1:A:141:PHE:CD1	2.35	0.45
1:B:78:ASP:CG	1:B:105:THR:HG21	2.38	0.44
1:A:78:ASP:HB2	1:A:105:THR:HG21	2.00	0.44
1:B:1:THR:CG2	4:B:182:HOH:O	2.63	0.43
1:B:12:ASN:ND2	1:B:14:GLY:H	2.17	0.43
1:A:52:GLY:HA2	1:A:93:ASN:HD21	1.84	0.42
1:A:71:HIS:HD2	4:A:148:HOH:O	2.02	0.42
1:A:123:PHE:CE2	1:A:141:PHE:HD1	2.35	0.42
1:B:12:ASN:HD22	1:B:12:ASN:C	2.24	0.41
1:B:122:ARG:HB2	1:B:142:SER:HB3	2.02	0.41
1:B:71:HIS:HD2	4:B:150:HOH:O	2.04	0.40

All (30) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	А	141/143~(99%)	140 (99%)	1 (1%)	0	100	100
1	В	141/143~(99%)	140 (99%)	1 (1%)	0	100	100
All	All	282/286~(99%)	280 (99%)	2(1%)	0	100	100

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

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	А	120/120~(100%)	118 (98%)	2(2%)	60 46		
1	В	120/120~(100%)	117~(98%)	3~(2%)	47 29		
All	All	240/240~(100%)	235~(98%)	5(2%)	53 36		

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	12	ASN
1	А	75	ARG
1	В	12	ASN
1	В	30	ASN
1	В	75	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	10	GLN
1	А	12	ASN
1	А	41	HIS
1	А	71	HIS
1	А	93	ASN

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Mol	Chain	Res	Type
1	А	95	GLN
1	А	138	ASN
1	В	12	ASN
1	В	30	ASN
1	В	41	HIS
1	В	71	HIS
1	В	133	ASN
1	В	138	ASN

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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)

Of 8 monosaccharides modelled in this entry, 6 were used 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).

Mal	Trune	Chain	Dec	Link	Bo	Bond lengths			Bond angles		
Mol	Type	Chain	Res		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
2	A2G	С	1	2	15,15,15	1.05	0	21,21,21	1.04	1 (4%)	
2	GAL	С	2	2	11,11,12	0.62	0	$15,\!15,\!17$	0.87	0	
2	A2G	D	1	2	15,15,15	0.85	0	21,21,21	0.97	0	
2	GAL	D	2	2	11,11,12	0.50	0	$15,\!15,\!17$	0.91	0	
3	NAG	Е	2	3	14,14,15	0.82	1 (7%)	17,19,21	0.93	1 (5%)	
3	NAG	F	2	3	14,14,15	0.80	0	17,19,21	1.03	1 (5%)	

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.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A2G	С	1	2	-	0/6/26/26	0/1/1/1
2	GAL	С	2	2	-	1/2/19/22	0/1/1/1
2	A2G	D	1	2	-	0/6/26/26	0/1/1/1
2	GAL	D	2	2	-	0/2/19/22	0/1/1/1
3	NAG	Е	2	3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Ε	2	NAG	C8-C7	2.00	1.54	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	Е	2	NAG	O5-C5-C6	2.80	111.60	107.20
3	F	2	NAG	O5-C5-C6	2.69	111.42	107.20
2	С	1	A2G	C6-C5-C4	-2.31	107.60	113.00

There are no chirality outliers.

All (1) torsion outliers are listed below:

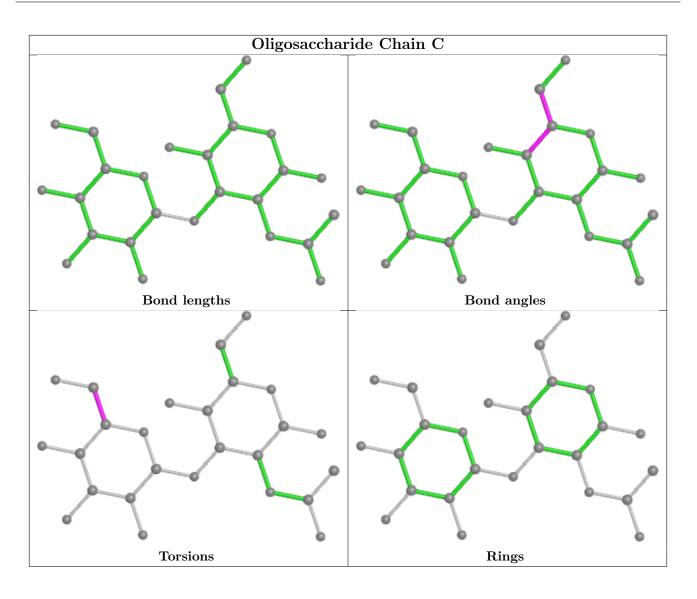
Mol	Chain	Res	Type	Atoms
2	С	2	GAL	C4-C5-C6-O6

There are no ring outliers.

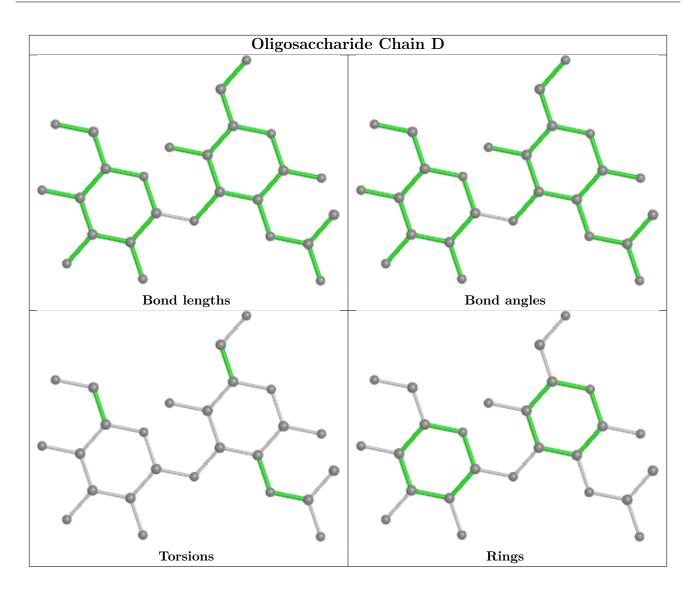
No monomer is involved in short contacts.

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

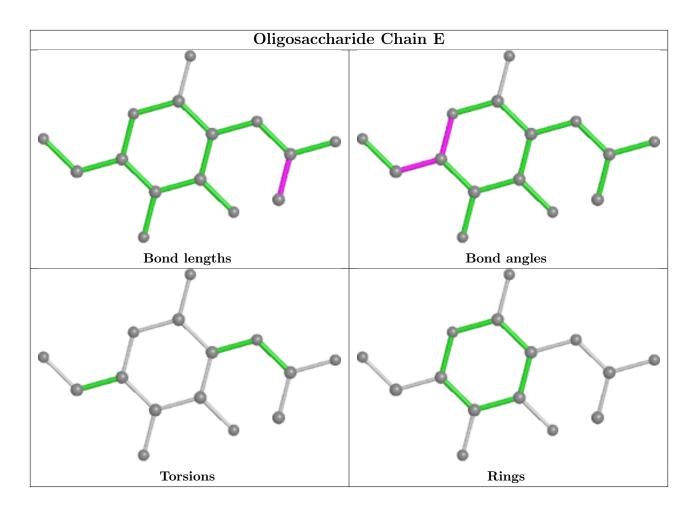






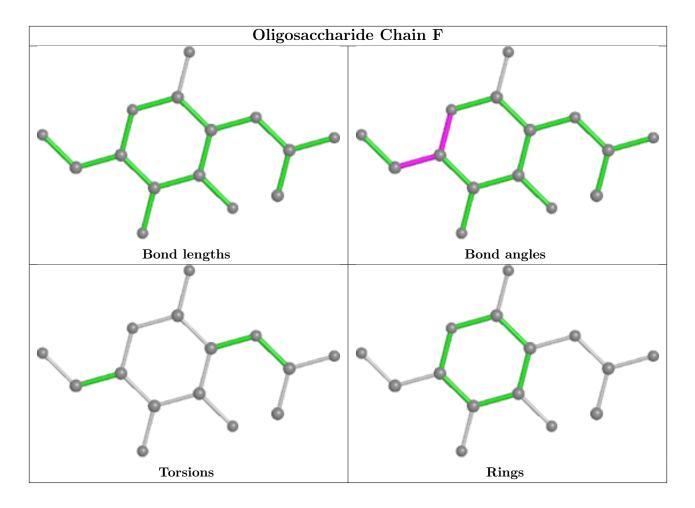












5.6 Ligand geometry (i)

There are no ligands in this entry.

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>2		$\mathbf{OWAB}(\mathbf{A}^2)$	Q < 0.9
1	А	142/143~(99%)	-0.08	1 (0%) 87	90	5, 9, 19, 30	0
1	В	142/143~(99%)	-0.00	1 (0%) 87	90	5, 10, 20, 26	0
All	All	284/286~(99%)	-0.04	2 (0%) 87	90	5, 10, 20, 30	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	142	SER	4.0
1	В	142	SER	2.1

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

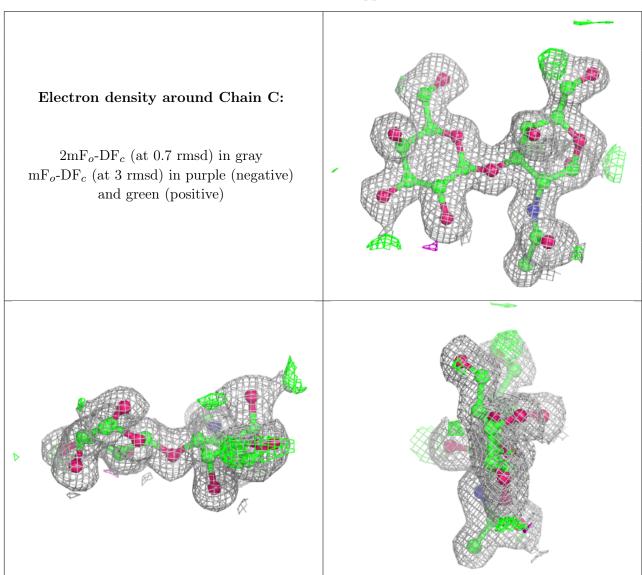
There are no non-standard protein/DNA/RNA residues in this entry.

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.

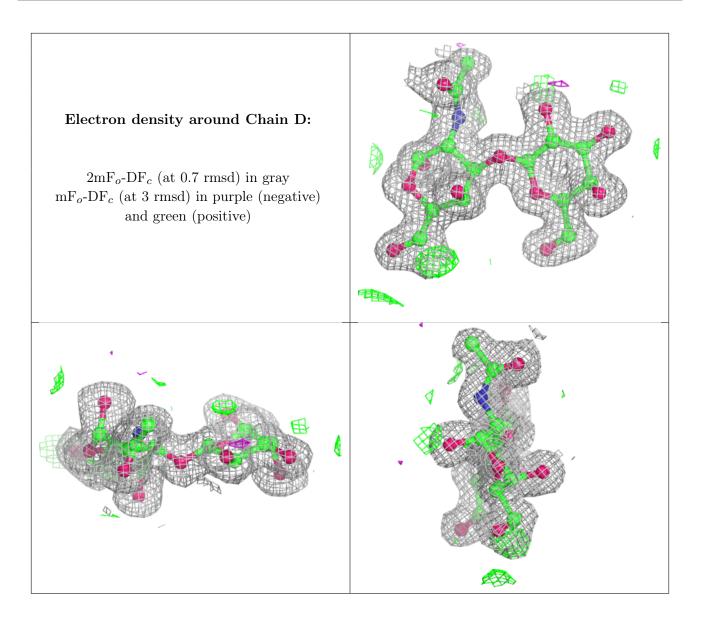
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
3	NAG	F	1	1/15	0.79	0.11	22,22,22,22	0
3	NAG	Е	1	1/15	0.89	0.11	16, 16, 16, 16	0
2	A2G	С	1	15/15	0.94	0.10	5, 9, 15, 19	0
3	NAG	F	2	14/15	0.94	0.14	14,19,25,25	0
2	A2G	D	1	15/15	0.95	0.09	7,10,15,24	0
3	NAG	Е	2	14/15	0.95	0.13	9,12,18,20	0
2	GAL	D	2	11/12	0.96	0.08	9,11,13,19	0
2	GAL	С	2	11/12	0.97	0.08	9,11,14,20	0



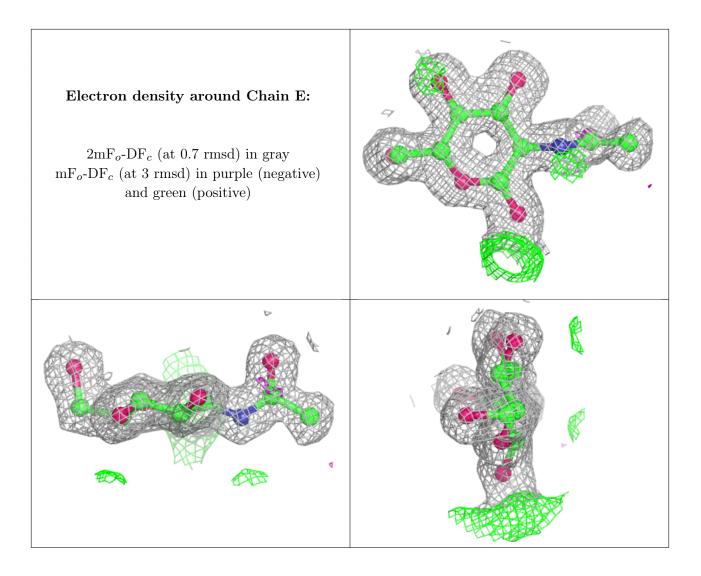


The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

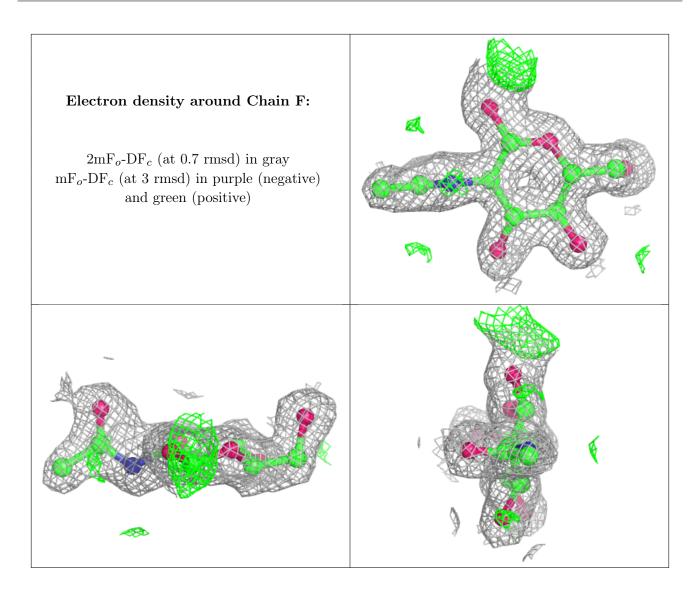












6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

