

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

#### Aug 10, 2020 – 12:02 PM BST

PDB ID : 2VTC

Title: The structure of a glycoside hydrolase family 61 member, Cel61B from the

Hypocrea jecorina.

Authors: Karkehabadi, S.; Hansson, H.; Kim, S.; Piens, K.; Mitchinson, C.; Sandgren,

Μ.

Deposited on : 2008-05-14

Resolution : 1.60 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 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 : 2.13.1

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)

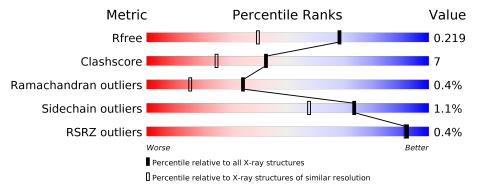
Validation Pipeline (wwPDB-VP) : 2.13.1

# 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 1.60 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 >=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	249	% 82%	8% • 8%			
1	В	249	84%	7% • 8%			
2	С	2	50%	50%			
2	D	2	50%	50%			



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4188 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 CEL61B.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	228	Total	С	N	О	S	0	0	0
1	1 A	220	1762	1129	299	329	5	U		
1	D	228	Total	С	N	О	S	0	0	0
1	D	220	1762	1129	299	329	5	0	0	U

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	С	2	Total C N O 28 16 2 10	0	0	0
2	D	2	Total C N O 28 16 2 10	0	0	0

• Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	2	Total Ni 2 2	0	0
3	A	1	Total Ni 1 1	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	295	Total O 295 295	0	0

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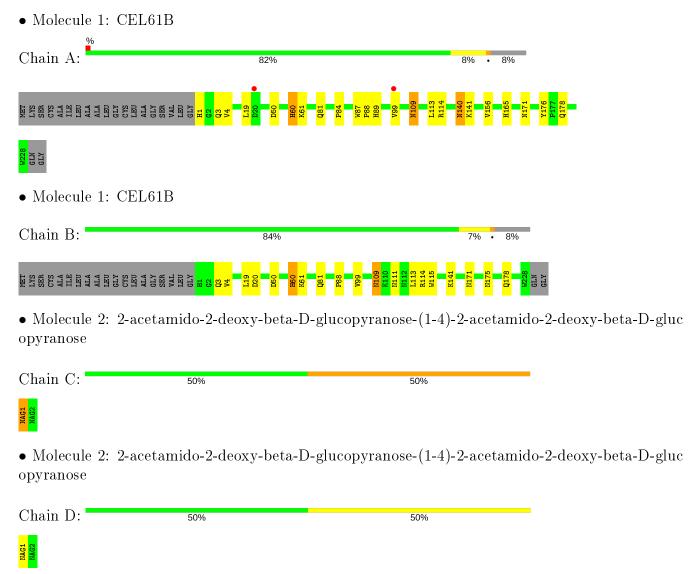
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	310	Total O 310 310	0	0



# 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.





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants	$101.44 ext{Å}$ $101.44 ext{Å}$ $102.70 ext{Å}$	Danagitan
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	50.00 - 1.60	Depositor
resolution (A)	50.72 - 1.60	EDS
% Data completeness	99.9 (50.00-1.60)	Depositor
(in resolution range)	99.9 (50.72-1.60)	EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.23~({\rm at}~1.60{\rm \AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
$R, R_{free}$	0.196 , $0.220$	Depositor
It, It free	0.196 , $0.219$	DCC
$R_{free}$ test set	3962  reflections  (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.7	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	$0.34 \; ,  43.1$	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.51, < L^2> = 0.34$	Xtriage
Estimated twinning fraction	0.029 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4188	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.10% 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.



 $<sup>^{1}</sup>$ 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: NI, NAG

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
IVIOI		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.60	0/1820	0.65	0/2501
1	В	0.63	0/1820	0.65	0/2501
All	All	0.62	0/3640	0.65	0/5002

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	В	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	88	PRO	Peptide
1	В	88	PRO	Peptide

### 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	1762	0	1676	23	0
1	В	1762	0	1676	24	0
2	С	28	0	25	1	0
2	D	28	0	25	0	0
3	A	1	0	0	1	0
3	В	2	0	0	0	0
4	A	295	0	0	7	0
4	В	310	0	0	1	0
All	All	4188	0	3402	48	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.

All (48) 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:99:VAL:HG13	1:B:115:TRP:CE3	1.98	0.99
1:B:99:VAL:HG12	1:B:114:ARG:O	1.61	0.98
1:B:60:HIS:HD2	1:B:61:LYS:H	1.27	0.82
3:A:1231:NI:NI	4:A:2230:HOH:O	1.21	0.81
1:A:99:VAL:HG23	1:A:114:ARG:O	1.82	0.80
1:B:60:HIS:CD2	1:B:61:LYS:H	2.02	0.78
1:B:4:VAL:H	1:B:178:GLN:HE21	1.32	0.77
1:A:87:TRP:H	1:A:140:ASN:HD21	1.31	0.77
1:A:1:HIS:ND1	4:A:2230:HOH:O	2.21	0.73
1:A:60:HIS:CD2	1:A:61:LYS:H	2.08	0.72
1:A:60:HIS:HD2	1:A:61:LYS:H	1.37	0.72
1:B:20:ASP:OD1	4:B:2046:HOH:O	2.07	0.72
1:A:4:VAL:H	1:A:178:GLN:HE21	1.37	0.72
1:B:99:VAL:HG12	1:B:114:ARG:C	2.10	0.71
1:B:99:VAL:HG13	1:B:115:TRP:CD2	2.27	0.69
1:B:3:GLN:HE22	1:B:19:LEU:H	1.46	0.64
1:B:99:VAL:CG1	1:B:115:TRP:CD2	2.81	0.64
1:A:3:GLN:HE22	1:A:19:LEU:H	1.50	0.60
1:A:81:GLN:HE22	1:A:141:LYS:NZ	1.99	0.60
1:B:109:ASN:HD22	1:B:109:ASN:C	2.06	0.59
1:B:50:ASP:H	1:B:171:ASN:HD21	1.51	0.57
1:A:99:VAL:HG21	1:A:113:LEU:HB3	1.86	0.56
1:B:99:VAL:HG22	1:B:115:TRP:CZ3	2.40	0.56
1:A:99:VAL:CG2	4:A:2149:HOH:O	2.53	0.56
1:B:99:VAL:HG12	1:B:115:TRP:HA	1.88	0.55
1:A:50:ASP:H	1:A:171:ASN:HD21	1.56	0.53

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A 4 a rea 1	A 4 0 mg 2	Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \; ({\rm \AA})$	$overlap (\AA)$
1:A:99:VAL:HG22	4:A:2149:HOH:O	2.08	0.52
1:A:165:HIS:HE1	4:A:2229:HOH:O	1.92	0.52
1:B:50:ASP:H	1:B:171:ASN:ND2	2.07	0.52
1:B:81:GLN:NE2	1:B:141:LYS:HE3	2.26	0.51
1:A:176:TYR:OH	4:A:2230:HOH:O	2.17	0.50
1:A:50:ASP:H	1:A:171:ASN:ND2	2.09	0.50
1:A:99:VAL:CG1	1:A:113:LEU:HD22	2.42	0.49
1:A:109:ASN:C	1:A:109:ASN:HD22	2.17	0.48
1:B:99:VAL:CG1	1:B:115:TRP:HA	2.44	0.47
1:A:99:VAL:CG2	1:A:114:ARG:H	2.28	0.47
1:B:4:VAL:H	1:B:178:GLN:NE2	2.08	0.46
1:A:84:PRO:HA	2:C:1:NAG:O6	2.16	0.45
1:B:81:GLN:HE22	1:B:141:LYS:NZ	2.14	0.45
1:B:99:VAL:CG2	1:B:113:LEU:HD22	2.47	0.45
1:B:99:VAL:CG1	1:B:115:TRP:CE3	2.84	0.44
1:B:60:HIS:CD2	1:B:61:LYS:N	2.81	0.43
1:A:99:VAL:HG12	1:A:156:VAL:HB	2.00	0.43
1:A:87:TRP:NE1	1:A:89:HIS:HB2	2.34	0.43
1:A:89:HIS:NE2	4:A:2230:HOH:O	2.36	0.42
1:B:99:VAL:HG11	1:B:115:TRP:CD2	2.54	0.42
1:A:4:VAL:H	1:A:178:GLN:NE2	2.12	0.41
1:B:109:ASN:HD22	1:B:111:ASN:H	1.69	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	Percer	$_{ m tiles}$
1	A	$226/249 \ (91\%)$	225 (100%)	0	1 (0%)	34	15
1	В	$226/249 \ (91\%)$	224 (99%)	1 (0%)	1 (0%)	34	15
All	All	452/498 (91%)	449 (99%)	1 (0%)	2 (0%)	34	15



All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	HIS
1	В	60	HIS

#### 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	Analysed Rotameric Ou		Percentiles
1	A	186/199~(94%)	184 (99%)	2 (1%)	73 57
1	В	186/199 (94%)	184 (99%)	2 (1%)	73 57
All	All	372/398 (94%)	368 (99%)	4 (1%)	73 57

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

Mol	Chain	Res	Type
1	A	109	ASN
1	A	140	ASN
1	В	109	ASN
1	В	175	ASN

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

Mol	Chain	Res	Type
1	A	3	GLN
1	A	5	GLN
1	A	15	GLN
1	A	60	HIS
1	A	77	ASN
1	A	81	GLN
1	A	109	ASN
1	A	140	ASN
1	A	165	HIS
1	A	171	ASN
1	A	174	GLN

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Mol	Chain	Res	Type
1	A	175	ASN
1	A	178	GLN
1	В	3	GLN
1	В	5	GLN
1	В	15	GLN
1	В	30	HIS
1	В	33	ASN
1	В	60	HIS
1	В	77	ASN
1	В	81	GLN
1	В	109	ASN
1	В	111	ASN
1	В	171	ASN
1	В	174	GLN
1	В	175	ASN
1	В	178	GLN

#### 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	Mol Type Chain Res		m Res	Pos	Pos	Pos	Pos	Pos	Ros	Pos	Pos	Dog	Link	Bo	ond leng	${ m ths}$	В	ond ang	cles
WIOI	туре	Chain	rtes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2									
2	NAG	С	1	1,2	14,14,15	0.56	0	17,19,21	0.98	1 (5%)									
2	NAG	С	2	2	14,14,15	0.48	0	17,19,21	0.92	0									



Mol	Type	ype Chain Res Link		Link	Bo	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2	
2	NAG	D	1	1,2	14,14,15	0.54	0	17,19,21	1.15	2 (11%)	
2	NAG	D	2	2	14,14,15	0.56	0	17,19,21	1.04	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	NAG	С	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	С	2	2	-	0/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	С	1	NAG	O5-C1-C2	-3.13	106.35	111.29
2	D	1	NAG	O5-C1-C2	-2.54	107.28	111.29
2	D	1	NAG	C1-O5-C5	2.41	115.46	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

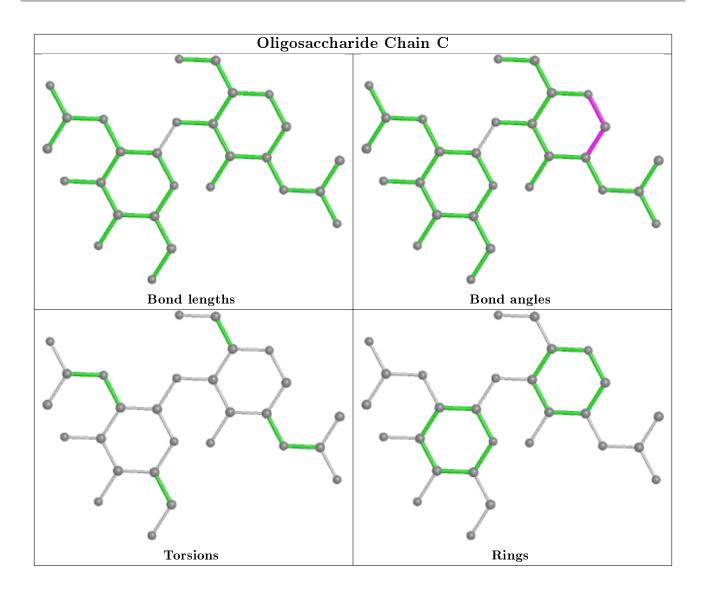
There are no ring outliers.

1 monomer is involved in 1 short contact:

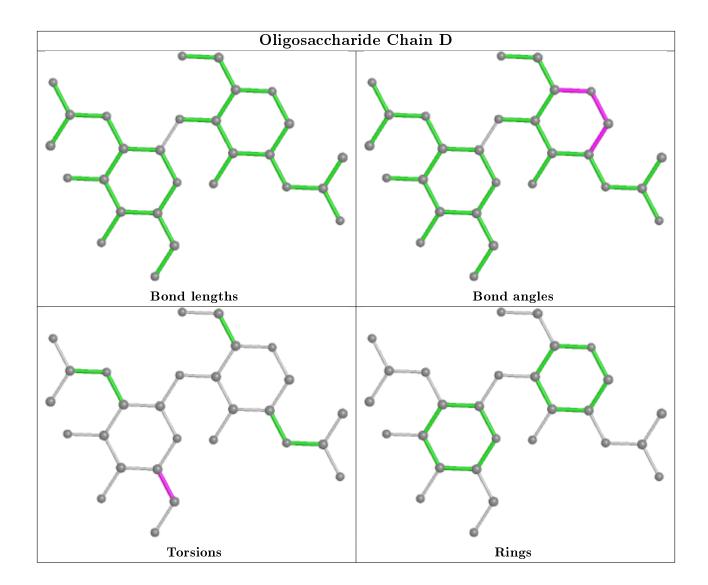
Mol	Chain	${f Res}$	Type	Clashes	Symm-Clashes
2	С	1	NAG	1	0

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)

Of 3 ligands modelled in this entry, 3 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 (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 $>$	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	A	228/249 (91%)	-0.29	2 (0%) 84 84	14, 22, 32, 39	0
1	В	228/249 (91%)	-0.41	0 100 100	12, 19, 28, 37	0
All	All	456/498 (91%)	-0.35	2 (0%) 92 92	12, 20, 31, 39	0

#### All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	99	VAL	2.6
1	A	20	ASP	2.2

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

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

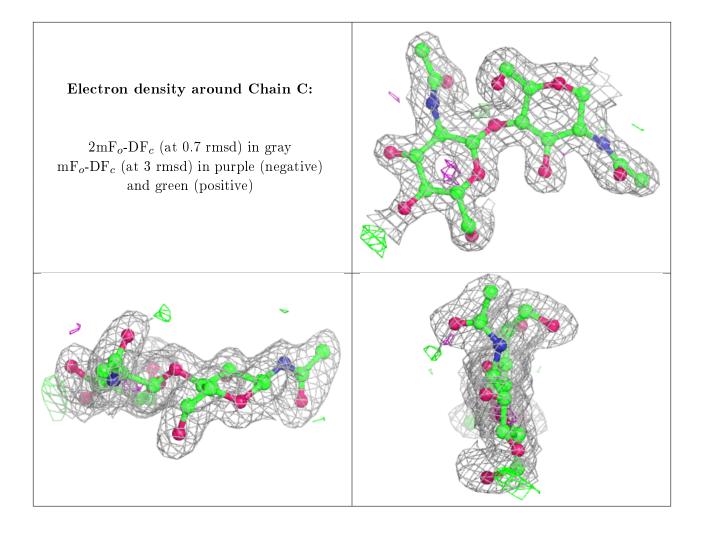
## 6.3 Carbohydrates (i)

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.

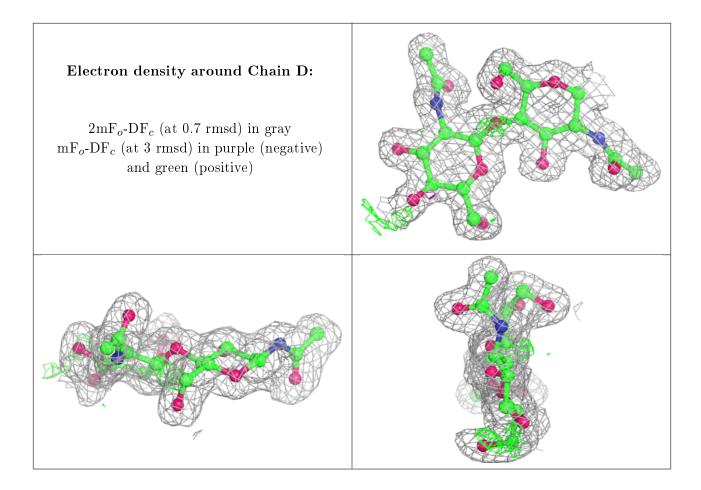
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	NAG	С	2	14/15	0.80	0.14	30,38,40,42	0
2	NAG	С	1	14/15	0.87	0.08	25,30,32,33	0
2	NAG	D	2	14/15	0.88	0.09	25,28,34,35	0
2	NAG	D	1	14/15	0.96	0.07	20,22,24,25	0

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	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
3	NI	В	1232	1/1	0.95	0.04	36,36,36,36	0
3	NI	A	1231	1/1	0.99	0.04	23,23,23,23	0
3	NI	В	1231	1/1	0.99	0.06	17,17,17,17	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

