

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

Oct 6, 2021 – 07:17 am BST

PDB ID : 7ALT

Title : Structure of Drosophila Serrate C2-DSL-EGF1-EGF2

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Deposited on : 2020-10-07

Resolution : 2.03 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 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 : 2.23.2

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

Refmac: 5.8.0267

CCP4 : 7.1.010 (Gargrove)

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

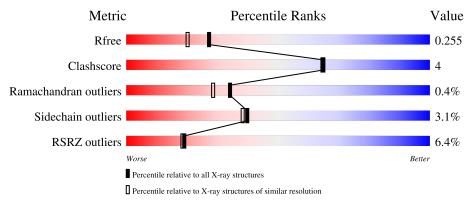
Validation Pipeline (wwPDB-VP) : 2.23.2

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.03 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$egin{aligned}  ext{Similar resolution} \ (\# ext{Entries, resolution range}(\mathring{ ext{A}})) \end{aligned}$		
$R_{free}$	130704	10434 (2.04-2.00)		
Clashscore	141614	11643 (2.04-2.00)		
Ramachandran outliers	138981	11493 (2.04-2.00)		
Sidechain outliers	138945	11492 (2.04-2.00)		
RSRZ outliers	127900	10220 (2.04-2.00)		

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	270	88%	10%	<del>.</del>
1	В	270	90%	8%	
2	С	2	100%		



## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8161 atoms, of which 3906 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 Protein serrate.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	270	Total 4004	C 1280	H 1944	N 357	O 396	S 27	0	0	0
1	В	265	Total 3930	C 1256	H 1911	N 350	O 386	S 27	0	0	0

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



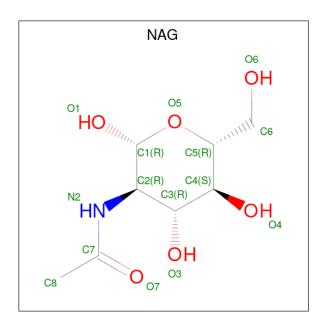
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	С	9	Total	С	Н	N	О	0	0	0
		2	53	16	25	2	10	U	0	U

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

$\mathbf{Mol}$	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	В	1	Total Ca 1 1	0	0

• Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
1	D	1	Total	С	Н	N	О	0	0
4 D	1	27	8	13	1	5	0	0	
1	В	1	Total	С	Н	N	О	0	0
4		1	27	8	13	1	5	U	U

### • Molecule 5 is water.

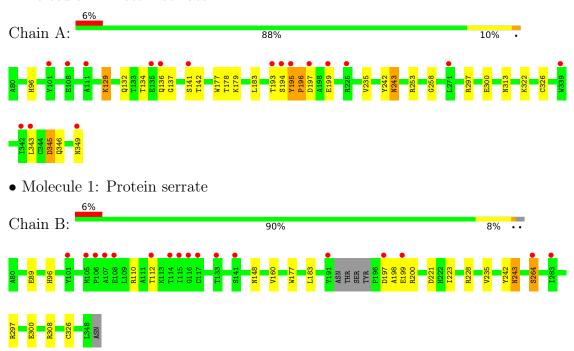
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	58	Total O 58 58	0	0
5	В	60	Total O 60 60	0	0



## 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: Protein serrate



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

Chain C: 100%



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	70.33Å 49.40Å 93.12Å	Donositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $110.25^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	45.61 - 2.03	Depositor
Resolution (A)	45.61 - 2.03	EDS
% Data completeness	98.9 (45.61-2.03)	Depositor
(in resolution range)	98.9 (45.61-2.03)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.27  (at  2.03Å)	Xtriage
Refinement program	PHENIX dev_3965, PHENIX dev_3965	Depositor
$R, R_{free}$	0.220 , $0.258$	Depositor
$\Pi, \Pi_{free}$	0.219 , $0.255$	DCC
$R_{free}$ test set	1996 reflections $(5.15\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.5	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8161	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 39.28 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.2484e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<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: NAG, 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).

Mal	Clasia	Bo	nd lengths	Bond angles		
Mol   Chain		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.30	0/2108	0.57	0/2862	
1	В	0.37	$2/2065 \ (0.1\%)$	0.62	1/2800 (0.0%)	
All	All	0.34	$2/4173 \ (0.0\%)$	0.59	1/5662 (0.0%)	

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(A)
1	В	264	SER	CB-OG	7.53	1.52	1.42
1	В	264	SER	CA-CB	5.85	1.61	1.52

#### All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	264	SER	N-CA-CB	8.86	123.79	110.50

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	2060	1944	1943	20	0
1	В	2019	1911	1909	13	0
2	С	28	25	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	В	28	26	26	0	0
5	A	58	0	0	1	0
5	В	60	0	0	1	2
All	All	4255	3906	3903	33	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 4.

The worst 5 of 33 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:297:ARG:NH1	1:A:300:GLU:OE1	2.04	0.90
1:B:197:ASP:O	1:B:200:ARG:HG2	1.84	0.77
1:B:221:ASP:OD2	1:B:228:ARG:NH2	2.20	0.75
1:A:195:TYR:HB3	1:A:196:PRO:CD	2.28	0.63
1:B:297:ARG:NH2	1:B:300:GLU:OE1	2.35	0.57

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)
5:B:501:HOH:O	5:B:505:HOH:O[1_445]	1.76	0.44
5:B:533:HOH:O	5:B:543:HOH:O[2_746]	2.13	0.07

## 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 Outlier		s Percentiles		
1	A	268/270 (99%)	251 (94%)	15 (6%)	2 (1%)	22 15		

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	В	261/270 (97%)	246 (94%)	15 (6%)	0	100	100
All	All	529/540 (98%)	497 (94%)	30 (6%)	2 (0%)	34	28

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

Mol	Chain	Res	Type
1	A	195	TYR
1	A	196	PRO

#### 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	227/227 (100%)	218 (96%)	9 (4%)	31 28		
1	В	222/227 (98%)	217 (98%)	5 (2%)	50 51		
All	All	449/454 (99%)	435 (97%)	14 (3%)	40 38		

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	345	ASP
1	A	349	ASN
1	В	326	CYS
1	В	243	ASN
1	В	264	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	256	GLN
1	В	256	GLN
1	В	346	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)

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).

Mol Type Cl	Chain	Chain Res	Res Link	Bond lengths			В	ond ang	les	
	Chain			Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
2	NAG	С	1	2,1	14,14,15	0.47	0	17,19,21	1.11	2 (11%)
2	NAG	С	2	2	14,14,15	1.12	2 (14%)	17,19,21	1.24	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	С	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	С	2	2	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

$\mathbf{Mol}$	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}( ext{\AA})$
2	С	2	NAG	O5-C1	3.54	1.49	1.43
2	С	2	NAG	C1-C2	2.15	1.55	1.52

All (3) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	С	2	NAG	C1-O5-C5	4.79	118.68	112.19
2	С	1	NAG	O5-C1-C2	-2.24	107.75	111.29
2	С	1	NAG	C3-C4-C5	2.05	113.90	110.24

There are no chirality outliers.

All (4) torsion outliers are listed below:

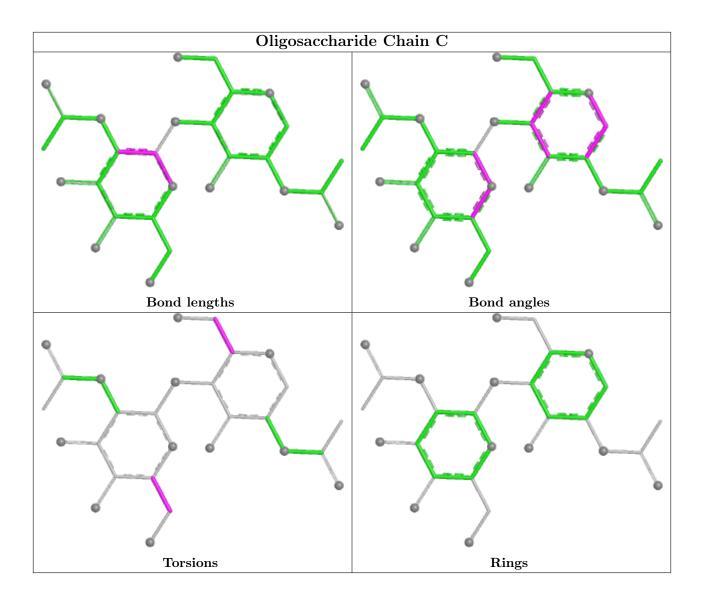
Mol	Chain	Res	Type	Atoms
2	С	1	NAG	C4-C5-C6-O6
2	С	1	NAG	O5-C5-C6-O6
2	С	2	NAG	C4-C5-C6-O6
2	С	2	NAG	O5-C5-C6-O6

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, 2 are monoatomic - leaving 2 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	s Link	Bo	ond leng	$ ag{ths}$	В	ond ang	eles
	Туре				Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	В	401	1	14,14,15	0.78	1 (7%)	17,19,21	1.15	2 (11%)
4	NAG	В	402	1	14,14,15	1.21	1 (7%)	17,19,21	0.86	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	В	401	1	-	2/6/23/26	0/1/1/1
4	NAG	В	402	1	-	2/6/23/26	0/1/1/1

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
4	В	402	NAG	O5-C1	3.91	1.50	1.43
4	В	401	NAG	O5-C1	-2.09	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
4	В	401	NAG	C1-O5-C5	3.19	116.51	112.19
4	В	401	NAG	C3-C4-C5	2.80	115.23	110.24
4	В	402	NAG	O5-C1-C2	-2.31	107.64	111.29

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	401	NAG	C1-C2-N2-C7
4	В	402	NAG	C4-C5-C6-O6
4	В	402	NAG	O5-C5-C6-O6
4	В	401	NAG	C3-C2-N2-C7

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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(\AA^2)$	Q < 0.9
1	A	270/270 (100%)	0.61	17 (6%) 20 19	23, 35, 77, 113	0
1	В	$265/270\ (98\%)$	0.62	17 (6%) 19 18	25, 39, 61, 103	0
All	All	535/540~(99%)	0.61	34 (6%) 19 18	23, 37, 67, 113	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	115	ILE	7.6
1	В	108	GLU	5.5
1	A	194	SER	4.4
1	A	108	GLU	4.4
1	В	106	PRO	4.1

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

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

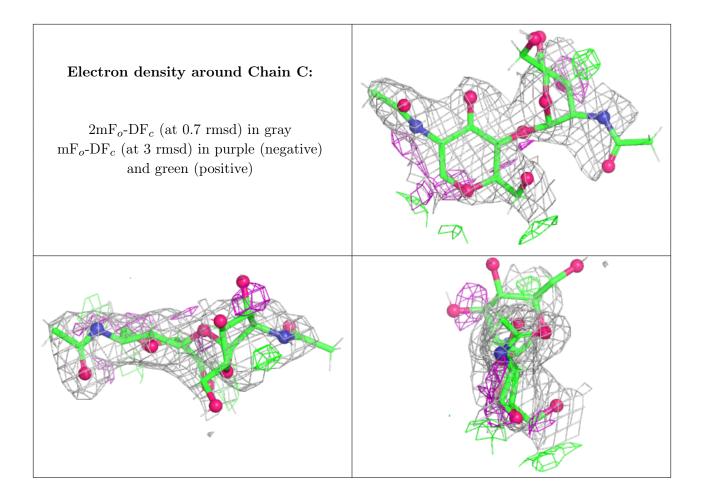
### 6.3 Carbohydrates (i)

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	NAG	С	2	14/15	0.69	0.38	70,89,113,113	0
2	NAG	С	1	14/15	0.83	0.20	40,58,73,76	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	$\operatorname{B-factors}(\mathring{\mathbf{A}}^2)$	Q < 0.9
4	NAG	В	402	14/15	0.72	0.20	46,64,83,87	0
4	NAG	В	401	14/15	0.76	0.26	66,81,98,103	0
3	CA	В	403	1/1	0.87	0.13	54,54,54,54	0
3	CA	A	401	1/1	0.95	0.14	43,43,43,43	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

