

wwPDB X-ray Structure Validation Summary Report (i)

Oct 18, 2023 – 05:31 PM EDT

:	1K7C
:	Rhamnogalacturonan acetylesterase with seven N-linked carbohydrate residues
	distributed at two N-glycosylation sites refined at 1.12 A resolution
:	Molgaard, A.; Larsen, S.
:	2001-10-19
:	1.12 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:

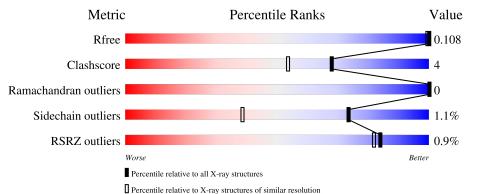
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.12 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	1168 (1.14-1.10)
Clashscore	141614	1205 (1.14-1.10)
Ramachandran outliers	138981	1168 (1.14-1.10)
Sidechain outliers	138945	1165 (1.14-1.10)
RSRZ outliers	127900	1146 (1.14-1.10)

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	А	233	% • 90%	8% •	,		
2	В	6	17%	83%	•		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MAN	В	3	Х	-	-	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2219 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 rhamnogalacturonan acetylesterase.

Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
1	А	233	Total 1784	C 1120	N 284	0 375	${ m S}{ m 5}$	0	14	0

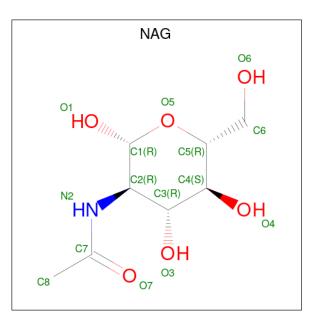
• Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyran ose-(1-6)]alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



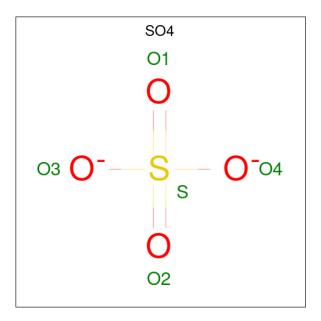
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	В	6	$\begin{array}{ccccc} Total & C & N & O \\ 72 & 40 & 2 & 30 \end{array}$	0	0	0

• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	Α	ton	ns		ZeroOcc	AltConf
3	А	1	Total 14	C 8	N 1	O 5	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

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Mol	Chain	Residues	Ator	\mathbf{ms}		ZeroOcc	AltConf
4	А	1	Total 5	0 4	S 1	0	0

• Molecule 5 is water.

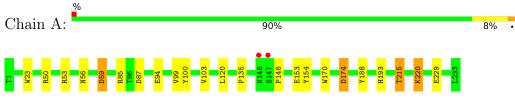
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	329	Total O 329 329	0	0



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: rhamnogalacturonan acetylesterase



 $\label{eq:mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-$

Chain B:	17%	83%	
NAG1 NAG2 MAN3 MAN4 MAN5 MAN5 MAN6			



4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	52.17Å 56.92Å 71.69Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	40.00 - 1.12	Depositor	
	35.84 - 1.12	EDS	
% Data completeness	97.8 (40.00-1.12)	Depositor	
(in resolution range)	95.7 (35.84-1.12)	EDS	
R _{merge}	(Not available)	Depositor	
R _{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$0.62 (at 1.12 \text{\AA})$	Xtriage	
Refinement program	SHELXL-97	Depositor	
D D.	0.103 , 0.134	Depositor	
R, R_{free}	0.104 , 0.108	DCC	
R_{free} test set	4026 reflections $(5.00%)$	wwPDB-VP	
Wilson B-factor $(Å^2)$	11.1	Xtriage	
Anisotropy	0.126	Xtriage	
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.38, 66.6	EDS	
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.98	EDS	
Total number of atoms	2219	wwPDB-VP	
Average B, all atoms $(Å^2)$	17.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.56% 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: SO4, MAN, 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		lengths		ond angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.80	0/1879	1.19	23/2566~(0.9%)

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	188	TYR	CB-CG-CD2	6.19	124.72	121.00
1	А	87	ASP	CB-CG-OD2	6.14	123.83	118.30
1	А	50	ARG	NE-CZ-NH1	-6.12	117.24	120.30
1	А	153[A]	GLU	OE1-CD-OE2	-6.09	116.00	123.30
1	А	153[B]	GLU	OE1-CD-OE2	-6.09	116.00	123.30

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	А	1784	0	1672	11	1
2	В	72	0	61	0	0
3	А	14	0	12	0	0
4	А	20	0	0	2	0
5	А	329	0	0	11	1
All	All	2219	0	1745	14	1



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 14 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:220[A]:LYS:HE3	5:A:1137:HOH:O	1.41	1.17
1:A:59[B]:ASP:OD2	5:A:1171:HOH:O	1.86	0.93
1:A:229[B]:GLU:OE1	5:A:1155:HOH:O	1.99	0.80
1:A:215[A]:THR:HG22	5:A:1093:HOH:O	1.96	0.66
1:A:170:TRP:HH2	5:A:1195:HOH:O	1.87	0.58

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:59[A]:ASP:OD1	5:A:1206:HOH:O[4_456]	2.15	0.05

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	Percentil	es
1	А	245/233~(105%)	241 (98%)	4 (2%)	0	100 10	0

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	Analysed Rotameric Outliers		Percentiles	
1	А	198/184~(108%)	196~(99%)	2(1%)	76 42	

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	174	ASP
1	А	193	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

6 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	Turne	Chain	Res	Link	Bo	ond leng	\mathbf{ths}	B	ond ang	les
Mol	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
2	NAG	В	1	2,1	14,14,15	2.66	4 (28%)	17,19,21	2.63	<mark>6 (35%)</mark>
2	NAG	В	2	2	14,14,15	2.23	5 (35%)	17,19,21	2.11	7 (41%)
2	MAN	В	3	2	11,11,12	1.27	2 (18%)	15,15,17	1.04	1 (6%)
2	MAN	В	4	2	11,11,12	1.16	1 (9%)	$15,\!15,\!17$	1.32	2 (13%)
2	MAN	В	5	2	11,11,12	1.25	1 (9%)	15,15,17	1.78	4 (26%)
2	MAN	В	6	2	11,11,12	1.18	0	$15,\!15,\!17$	1.02	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	В	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	В	2	2	-	0/6/23/26	0/1/1/1
2	MAN	В	3	2	1/1/4/5	0/2/19/22	0/1/1/1
2	MAN	В	4	2	-	0/2/19/22	0/1/1/1
2	MAN	В	5	2	-	0/2/19/22	0/1/1/1
2	MAN	В	6	2	-	0/2/19/22	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	В	1	NAG	C2-N2	7.30	1.58	1.46
2	В	2	NAG	C2-N2	4.62	1.54	1.46
2	В	1	NAG	O5-C1	4.34	1.50	1.43
2	В	2	NAG	C8-C7	4.34	1.59	1.50
2	В	1	NAG	C8-C7	4.23	1.59	1.50

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	В	1	NAG	C2-N2-C7	-6.41	113.78	122.90
2	В	2	NAG	O3-C3-C2	-4.46	100.24	109.47
2	В	1	NAG	C1-C2-N2	-4.44	102.90	110.49
2	В	1	NAG	O4-C4-C3	-4.40	100.19	110.35
2	В	5	MAN	C1-O5-C5	4.38	118.12	112.19

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	В	3	MAN	C1

There are no torsion outliers.

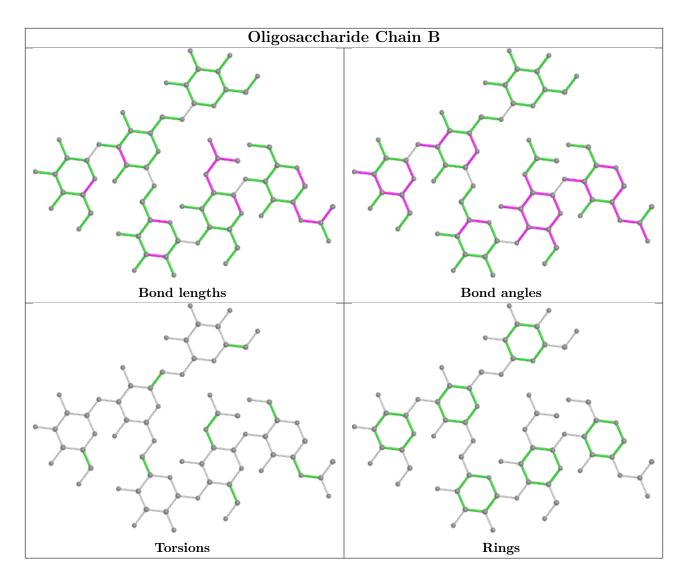
There are no ring outliers.

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.







5.6 Ligand geometry (i)

5 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).

Mal	Mol Type Chair		Res	Link	Bo	Bond lengths			Bond angles		
	туре	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2	
4	SO4	А	303	-	4,4,4	0.99	0	$6,\!6,\!6$	0.28	0	
4	SO4	А	304	-	4,4,4	0.97	0	$6,\!6,\!6$	0.07	0	
4	SO4	А	306	-	4,4,4	1.00	0	$6,\!6,\!6$	0.09	0	
3	NAG	А	302	1	14,14,15	2.30	4 (28%)	17,19,21	1.90	6 (35%)	



Mal	Mol Type Chain R		Res	Link	Bond lengths			Bond angles		
	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
4	SO4	А	305	-	4,4,4	1.08	0	$6,\!6,\!6$	0.17	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
3	NAG	А	302	1	-	1/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	302	NAG	C8-C7	4.81	1.60	1.50
3	А	302	NAG	C2-N2	4.33	1.53	1.46
3	А	302	NAG	O5-C1	3.84	1.49	1.43
3	А	302	NAG	C7-N2	-2.16	1.26	1.34

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

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	302	NAG	C4-C3-C2	-3.49	105.91	111.02
3	А	302	NAG	C2-N2-C7	3.25	127.53	122.90
3	А	302	NAG	O4-C4-C3	-3.15	103.08	110.35
3	А	302	NAG	C1-O5-C5	-2.50	108.80	112.19
3	А	302	NAG	O7-C7-N2	-2.24	117.84	121.95

There are no chirality outliers.

All (1) torsion outliers are listed below:

\mathbf{N}	lol	Chain	Res	Type	Atoms
	3	А	302	NAG	O7-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	303	SO4	1	0
4	А	306	SO4	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>2	$OWAB(Å^2)$	Q<0.9
1	А	233/233~(100%)	-0.15	2 (0%) 84 82	8, 13, 24, 33	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	А	147[A]	SER	2.1	
1	А	146	ASN	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.

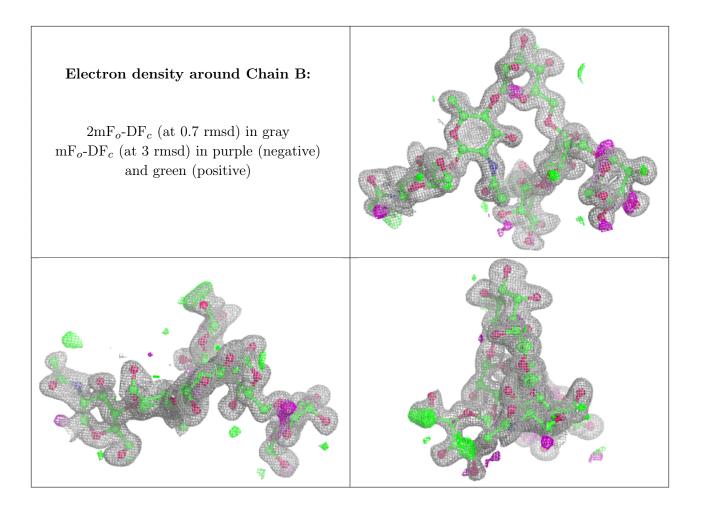
6.3 Carbohydrates (i)

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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	MAN	В	5	11/12	0.86	0.23	$23,\!28,\!39,\!48$	0
2	NAG	В	2	14/15	0.92	0.14	23,27,39,44	0
2	MAN	В	3	11/12	0.95	0.14	17,22,30,33	0
2	MAN	В	4	11/12	0.95	0.13	14,17,20,22	0
2	NAG	В	1	14/15	0.95	0.15	17,22,32,33	0
2	MAN	В	6	11/12	0.96	0.14	13,14,17,18	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	B-factors(Å ²)	Q<0.9
4	SO4	А	306	5/5	0.88	0.16	33,37,42,45	5
4	SO4	А	304	5/5	0.91	0.26	67,74,80,87	0
3	NAG	А	302	14/15	0.92	0.17	31,36,40,51	0
4	SO4	А	303	5/5	0.97	0.06	15,17,21,21	5
4	SO4	А	305	5/5	0.98	0.16	47,51,59,61	0

6.5 Other polymers (i)

There are no such residues in this entry.

