

Full wwPDB X-ray Structure Validation Report (i)

Nov 22, 2023 – 06:11 PM JST

PDB ID : 7WHE

Title : The mutant crystal structure of b-1,4-Xylanase (XynAF1_R246K) with xylo-

biose

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Deposited on : 2021-12-30

Resolution : 1.75 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:

Mol Probity : 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)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

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

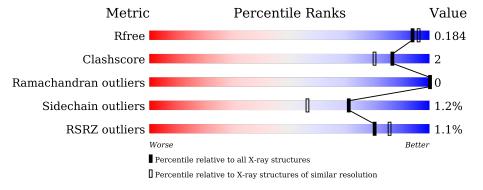
Validation Pipeline (wwPDB-VP) : 2.36

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 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	329	92%			
1	В	329	91%	6% •		
2	С	2	50%			



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5390 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 Beta-xylanase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	319	Total	С	N	О	S	0	1	0
_	11	010	2422	1544	397	471	10		1	
1	D	319	Total	С	N	О	S	0	1	0
1	D	319	2425	1545	398	472	10	0	1	U

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLU	-	expression tag	UNP A0A229WLM4
A	2	ALA	-	expression tag	UNP A0A229WLM4
A	3	GLU	-	expression tag	UNP A0A229WLM4
A	4	ALA	-	expression tag	UNP A0A229WLM4
A	246	LYS	ARG	engineered mutation	UNP A0A229WLM4
В	1	GLU	-	expression tag	UNP A0A229WLM4
В	2	ALA	-	expression tag	UNP A0A229WLM4
В	3	GLU	-	expression tag	UNP A0A229WLM4
В	4	ALA	-	expression tag	UNP A0A229WLM4
В	246	LYS	ARG	engineered mutation	UNP A0A229WLM4

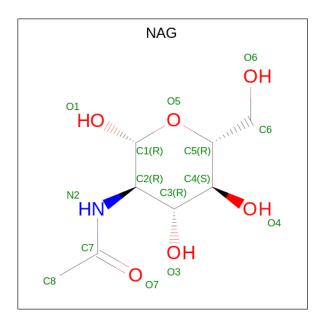
• Molecule 2 is an oligosaccharide called beta-D-xylopyranose-(1-4)-alpha-D-xylopyranose.



Mol	Chain	Residues	At	$\overline{\text{oms}}$		ZeroOcc	AltConf	Trace
2	С	2	Total 19	C 10	O 9	0	0	0

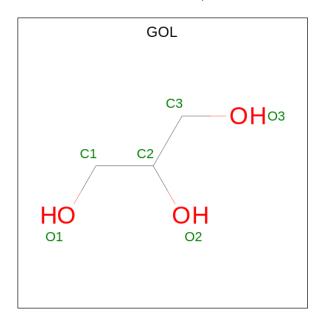
• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf		
3	A	1	Total 14	C 8	N 1	O 5	0	0

 \bullet Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $\mathrm{C_3H_8O_3}).$



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0

$\bullet\,$ Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	268	Total O 268 268	0	0
5	В	212	Total O 212 212	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: Beta-xylanase

Chain A:

92%

• Molecule 1: Beta-xylanase

Chain B:

91%

6%

• Molecule 2: beta-D-xylopyranose-(1-4)-alpha-D-xylopyranose

Chain C:

50%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants	68.06Å 85.85Å 97.70Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.11 - 1.75	Depositor
Resolution (A)	30.10 - 1.75	EDS
% Data completeness	99.7 (30.11-1.75)	Depositor
(in resolution range)	99.8 (30.10-1.75)	EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.16 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
D D.	0.151 , 0.184	Depositor
R, R_{free}	0.151 , 0.184	DCC
R_{free} test set	2873 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	17.9	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 46.1	EDS
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5390	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.46% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: XYS, XYP, NAG, GOL

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			nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.52	$1/2487 \ (0.0\%)$	0.82	1/3398 (0.0%)	
1	В	0.49	$1/2487 \ (0.0\%)$	0.77	0/3398	
All	All	0.50	$2/4974 \ (0.0\%)$	0.80	1/6796 (0.0%)	

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	139	GLU	CD-OE2	-5.38	1.19	1.25
1	В	139	GLU	CD-OE2	-5.27	1.19	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	144	ARG	CG-CD-NE	-6.28	98.61	111.80

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	18	TYR	Peptide
1	В	18	TYR	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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	2422	0	2330	8	0
1	В	2425	0	2330	12	0
2	С	19	0	9	1	0
3	A	14	0	13	0	0
4	A	24	0	32	2	0
4	В	6	0	8	2	0
5	A	268	0	0	0	1
5	В	212	0	0	1	1
All	All	5390	0	4722	20	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 2.

All (20) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)
1:A:283:ASP:OD2	4:A:602:GOL:H32	1.77	0.85
1:B:283:ASP:HB2	4:B:601:GOL:H12	1.82	0.61
1:B:249:LEU:HB3	1:B:250:PRO:HA	1.84	0.60
1:B:62:ASN:HD22	1:B:114:ASN:HD21	1.49	0.59
1:A:214:ILE:HD13	1:A:246:LYS:HG2	1.83	0.59
1:B:62:ASN:ND2	1:B:114:ASN:HD21	2.04	0.56
1:B:290:TRP:CZ3	2:C:1:XYS:H51	2.47	0.49
1:B:49:GLY:HA3	4:B:601:GOL:H32	1.94	0.49
1:A:214:ILE:HD13	1:A:246:LYS:CG	2.42	0.49
1:B:290:TRP:CZ2	1:B:292:PRO:HB3	2.48	0.49
1:A:214:ILE:CD1	1:A:246:LYS:CG	2.91	0.48
1:A:90:TRP:CE2	1:A:92:SER:HB3	2.50	0.47
1:B:214:ILE:HD13	1:B:246:LYS:CG	2.46	0.46
1:B:181:GLU:HA	1:B:209:LEU:HD23	1.97	0.46

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Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	$ ext{overlap} \ (ext{Å})$
1:A:282:TRP:CD1	4:A:602:GOL:H11	2.50	0.45
1:B:145:ASN:OD1	1:B:150:GLN:NE2	2.53	0.42
1:B:300:ALA:N	1:B:301:PRO:HD3	2.34	0.42
1:A:300:ALA:N	1:A:301:PRO:HD3	2.36	0.41
1:B:200:TYR:OH	5:B:701:HOH:O	2.17	0.41
1:A:57:THR:O	1:A:64:PHE:HA	2.21	0.41

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
5:A:883:HOH:O	5:B:891:HOH:O[2_555]	2.12	0.08

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	Perce	ntiles
1	A	318/329 (97%)	311 (98%)	7 (2%)	0	100	100
1	В	318/329 (97%)	312 (98%)	6 (2%)	0	100	100
All	All	$636/658 \ (97\%)$	623 (98%)	13 (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	Perce	ntiles
1	A	$252/257 \ (98\%)$	249 (99%)	3 (1%)	71	56
1	В	252/257~(98%)	249 (99%)	3 (1%)	71	56
All	All	504/514 (98%)	498 (99%)	6 (1%)	71	56

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	SER
1	A	283	ASP
1	A	285	THR
1	В	109	LEU
1	В	283	ASP
1	В	285	THR

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

Mol	Chain	Res	Type
1	В	62	ASN
1	В	145	ASN
1	В	150	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	Trus	Chain	Res	Link	Bond lengths			Bond angles		
IVIOI	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	XYS	С	1	2	10,10,10	0.81	1 (10%)	14,14,14	1.07	1 (7%)
2	XYP	С	2	2	9,9,10	0.41	0	10,12,14	0.79	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	XYS	С	1	2	-	-	0/1/1/1
2	XYP	С	2	2	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
2	С	1	XYS	O5-C1	2.15	1.46	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
2	С	1	XYS	O3-C3-C4	-2.30	105.59	109.99

There are no chirality outliers.

There are no torsion outliers.

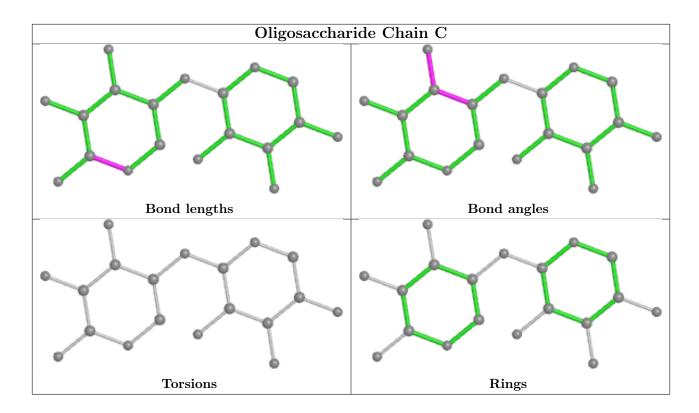
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	С	1	XYS	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)

6 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	Mol Type Chain Res		Link	Вс	ond leng	$ ag{ths}$	Bond angles			
MIOI	Mol Type Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
4	GOL	A	603	-	5,5,5	0.25	0	5,5,5	0.41	0
4	GOL	A	605	-	5,5,5	0.24	0	5,5,5	0.39	0
3	NAG	A	601	1	14,14,15	1.07	1 (7%)	17,19,21	1.05	0
4	GOL	A	602	-	5,5,5	0.17	0	5,5,5	0.30	0
4	GOL	В	601	-	5,5,5	0.14	0	5,5,5	0.28	0
4	GOL	A	604	-	5,5,5	0.08	0	5,5,5	0.39	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
4	GOL	A	603	-	-	0/4/4/4	-
4	GOL	A	605	-	-	1/4/4/4	-
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1
4	GOL	A	602	-	-	2/4/4/4	-
4	GOL	В	601	-	-	0/4/4/4	-
4	GOL	A	604	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
3	A	601	NAG	C1-C2	2.17	1.55	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	602	GOL	C1-C2-C3-O3
4	A	605	GOL	O1-C1-C2-C3
4	A	602	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	602	GOL	2	0
4	В	601	GOL	2	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	A	319/329 (96%)	-0.28	3 (0%) 84 89	11, 15, 23, 35	0
1	В	319/329 (96%)	-0.15	4 (1%) 77 83	12, 17, 29, 42	0
All	All	638/658 (96%)	-0.21	7 (1%) 80 86	11, 16, 27, 42	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	323	ALA	3.0
1	A	5	ALA	3.0
1	В	5	ALA	2.9
1	В	293	SER	2.9
1	В	294	VAL	2.6
1	A	243	LEU	2.1
1	В	296	GLN	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.

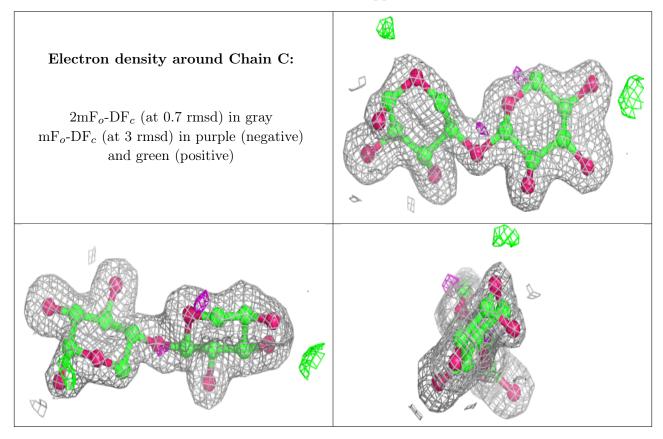
6.3 Carbohydrates (i)

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	XYP	С	2	9/10	0.89	0.10	24,26,30,30	0
2	XYS	С	1	10/10	0.91	0.14	16,30,32,35	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	GOL	A	602	6/6	0.81	0.21	38,41,43,44	0
4	GOL	A	604	6/6	0.87	0.16	39,41,43,50	0
4	GOL	A	603	6/6	0.90	0.12	24,28,32,36	0
4	GOL	A	605	6/6	0.91	0.16	17,26,35,41	0
4	GOL	В	601	6/6	0.92	0.15	31,32,36,39	0
3	NAG	A	601	14/15	0.96	0.08	17,20,26,27	0

6.5 Other polymers (i)

There are no such residues in this entry.

