

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

### Dec 17, 2023 – 02:20 PM EST

PDB ID : 1QH6

Title : CATALYSIS AND SPECIFICITY IN ENZYMATIC GLYCOSIDE HYDRO-

LASES: A 2,5B CONFORMATION FOR THE GLYCOSYL-ENZYME INTERMIDIATE REVEALED BY THE STRUCTURE OF THE BACILLUS

AGARADHAERENS FAMILY 11 XYLANASE

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Deposited on : 1999-05-11

Resolution : 2.00 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 : 2.36

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)

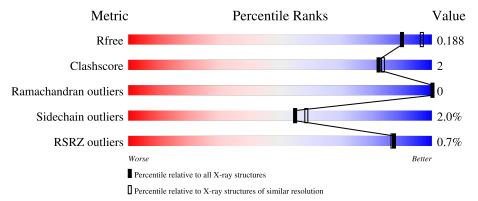
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

## 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 2.00 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	Similar resolution
Metric	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	207	93%	6%	<del>-</del>
1	В	207	91%	8%	<del>-</del>
2	С	2	100%		_
2	D	2	100%		

 $\begin{tabular}{lll} Validation Pipeline (wwPDB-VP) & : & 2.36 \end{tabular}$ 



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3874 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 XYLANASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	207	Total 1641	C 1032	11	O 316	S 7	0	2	0
1	В	207	Total 1658	C 1038		O 323	S 7	0	9	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	С	9	Total	С	F	О	0 0	0	0
			18	10	1	7	0	U	0
2	D	9	Total	С	F	О	0	0	0
2	ע	2	18	10	1	7	U	0	

• Molecule 3 is water.

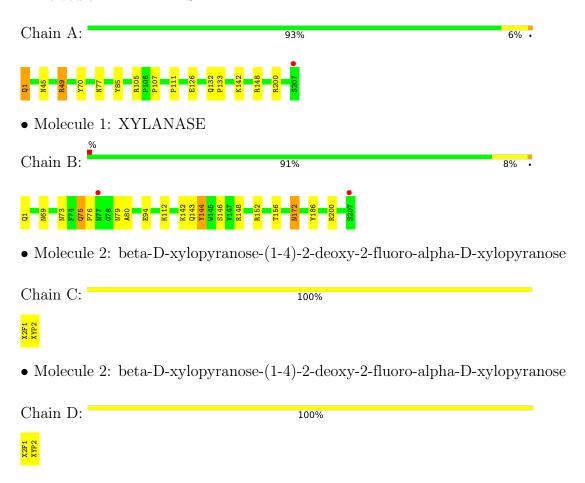
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	283	Total O 283 283	0	0
3	В	256	Total O 256 256	0	0



## 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: XYLANASE





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	71.91Å 74.83Å 78.35Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	20.00 - 2.00	Depositor
Resolution (A)	19.83 - 2.00	EDS
% Data completeness	97.6 (20.00-2.00)	Depositor
(in resolution range)	97.7 (19.83-2.00)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	6.80	Depositor
$< I/\sigma(I) > 1$	7.64 (at 2.01Å)	Xtriage
Refinement program	REFMAC	Depositor
D.D.	0.142 , 0.189	Depositor
$R, R_{free}$	0.144 , $0.188$	DCC
$R_{free}$ test set	893 reflections (3.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	12.8	Xtriage
Anisotropy	0.332	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36 , 72.2	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.015 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3874	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.44% 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>&</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: XYP, X2F, PCA

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	Chain	RMSZ $ \# Z  > 5$		RMSZ		
1	A	0.56	0/1688	1.26	9/2294~(0.4%)	
1	В	0.54	0/1740	1.28	9/2367 (0.4%)	
All	All	0.55	0/3428	1.27	18/4661 (0.4%)	

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	148	ARG	NE-CZ-NH1	12.73	126.67	120.30
1	A	200	ARG	NE-CZ-NH2	-11.66	114.47	120.30
1	A	1	PCA	O-C-N	-11.36	104.53	122.70
1	A	148	ARG	NE-CZ-NH1	10.33	125.47	120.30
1	В	1	PCA	C-N-CA	8.54	143.05	121.70
1	В	200	ARG	NE-CZ-NH1	8.53	124.56	120.30
1	В	1	PCA	O-C-N	-8.52	109.08	122.70
1	В	200	ARG	NE-CZ-NH2	-7.39	116.60	120.30
1	В	146	SER	N-CA-CB	6.22	119.84	110.50
1	A	1	PCA	C-N-CA	6.15	137.07	121.70
1	A	49	ARG	CG-CD-NE	6.07	124.55	111.80
1	A	105	ARG	NE-CZ-NH2	5.92	123.26	120.30
1	В	144	TYR	CB-CG-CD1	5.84	124.51	121.00
1	В	152	ARG	NE-CZ-NH2	-5.57	117.52	120.30

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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	В	148	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	A	70	TYR	CB-CG-CD1	5.43	124.26	121.00
1	A	200	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	85	TYR	CA-CB-CG	5.11	123.12	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	PCA	Mainchain

### 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	1641	0	1547	5	0
1	В	1658	0	1562	11	0
2	С	18	0	6	0	0
2	D	18	0	6	0	0
3	A	283	0	0	2	0
3	В	256	0	0	2	0
All	All	3874	0	3121	16	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 2.

All (16) 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:73[A]:ASN:ND2	1:B:75:GLN:OE1	2.04	0.91
1:B:73[A]:ASN:CG	1:B:75:GLN:OE1	2.16	0.83
1:B:69[A]:ASN:OD1	3:B:1130:HOH:O	2.03	0.76
1:B:73[A]:ASN:OD1	1:B:75:GLN:OE1	2.12	0.67
1:A:132:GLN:HB3	1:A:133:PRO:HD2	1.82	0.61
1:B:172:ASN:HD22	1:B:172:ASN:H	1.50	0.58

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Atom-1	Atom-2	$egin{aligned}  ext{Interatomic} \  ext{distance} & ( ext{Å}) \end{aligned}$	Clash overlap (Å)
1:B:69[B]:ASN:ND2	1:B:156:THR:OG1	2.46	0.48
1:B:142:LYS:HG2	3:B:1165:HOH:O	2.12	0.48
1:B:142:LYS:HE3	1:B:144:TYR:OH	2.14	0.48
1:B:79:ASN:HB3	1:B:186:TYR:O	2.16	0.45
1:A:142:LYS:HD3	3:A:1101:HOH:O	2.16	0.45
1:A:126:GLU:HG2	1:A:142:LYS:HE2	1.99	0.45
1:B:76:PRO:HB3	1:B:80:ALA:HB3	1.99	0.45
1:A:142:LYS:NZ	3:A:1101:HOH:O	2.46	0.42
1:B:94:GLU:O	1:B:143:GLN:HA	2.20	0.42
1:A:49:ARG:HH11	1:A:49:ARG:HD3	1.72	0.41

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	Perce	${f ntiles}$
1	A	207/207 (100%)	203 (98%)	4 (2%)	0	100	100
1	В	$214/207 \ (103\%)$	208 (97%)	6 (3%)	0	100	100
All	All	421/414 (102%)	411 (98%)	10 (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	Percentiles		
1	A	176/174~(101%)	171 (97%)	5 (3%)	43 44		
1	В	183/174 (105%)	180 (98%)	3 (2%)	62 67		
All	All	359/348 (103%)	351 (98%)	8 (2%)	55 55		

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	77[A]	ASN
1	A	77[B]	ASN
1	A	107	PRO
1	A	111	PRO
1	В	75	GLN
1	В	112	LYS
1	В	172	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	132	GLN
1	A	193	ASN
1	В	65	ASN
1	В	172	ASN

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	Des	T inle	В	ond leng	$_{ m gths}$	В	ond ang	gles
MIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
1	PCA	A	1	1	7,8,9	1.34	2 (28%)	9,10,12	2.74	2 (22%)
1	PCA	В	1	1	7,8,9	1.39	1 (14%)	9,10,12	1.67	2 (22%)

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
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1
1	PCA	В	1	1	-	0/0/11/13	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	$Observed(\AA)$	$Ideal(\AA)$
1	В	1	PCA	CG-CD	2.69	1.57	1.50
1	A	1	PCA	CG-CD	2.19	1.56	1.50
1	A	1	PCA	O-C	2.09	1.28	1.19

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	1	PCA	CB-CA-C	-5.81	104.71	112.70
1	A	1	PCA	OE-CD-CG	-5.04	117.97	126.76
1	В	1	PCA	CB-CA-C	-3.24	108.25	112.70
1	В	1	PCA	CB-CG-CD	-2.66	100.11	104.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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	Trino	Type Chain Res		Link	В	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
2	X2F	С	1	2,1	9,9,10	0.91	0	7,12,14	2.75	3 (42%)	
2	XYP	С	2	2	9,9,10	1.12	0	10,12,14	1.60	3 (30%)	
2	X2F	D	1	2,1	9,9,10	1.18	0	7,12,14	2.60	2 (28%)	
2	XYP	D	2	2	9,9,10	0.86	0	10,12,14	1.41	2 (20%)	

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	X2F	С	1	2,1	-	-	0/1/1/1
2	XYP	С	2	2	-	-	0/1/1/1
2	X2F	D	1	2,1	-	-	0/1/1/1
2	XYP	D	2	2	-	-	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	С	1	X2F	C5-O5-C1	4.56	118.53	111.52
2	D	1	X2F	C5-O5-C1	4.50	118.44	111.52
2	D	1	X2F	C5-C4-C3	4.32	114.98	109.67
2	С	1	X2F	C5-C4-C3	3.89	114.44	109.67
2	С	1	X2F	O3-C3-C4	3.66	117.00	109.99
2	С	2	XYP	C4-C3-C2	-3.27	107.04	110.92
2	D	2	XYP	O4-C4-C3	-2.79	104.54	110.14
2	С	2	XYP	O4-C4-C3	-2.62	104.89	110.14
2	D	2	XYP	O4-C4-C5	2.36	113.98	109.15
2	С	2	XYP	C5-C4-C3	-2.28	106.87	109.67

There are no chirality outliers.

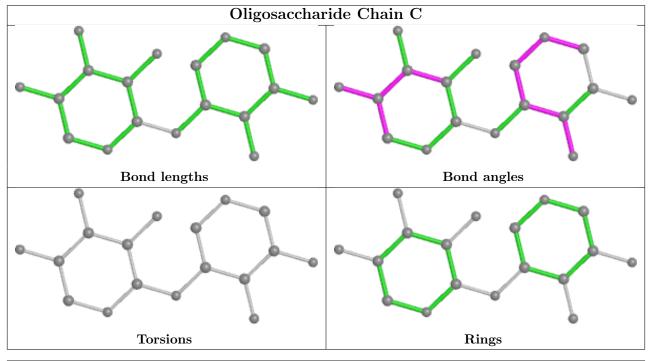
There are no torsion outliers.

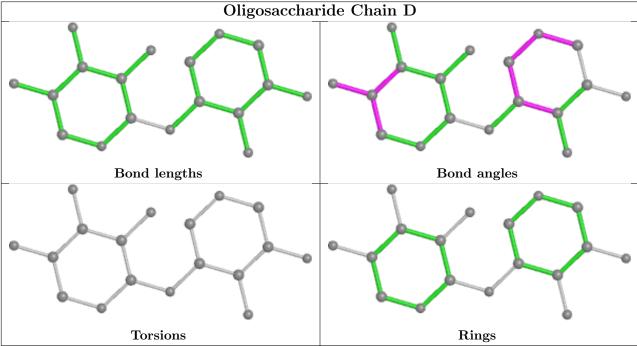
There are no ring outliers.

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)

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	$\langle { m RSRZ} \rangle$	# RSRZ > 2		$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9	
1	A	206/207 (99%)	-0.69	1 (0%)	91	90	6, 11, 20, 46	0
1	В	206/207 (99%)	-0.54	2 (0%)	82	81	7, 14, 24, 49	0
All	All	412/414 (99%)	-0.61	3 (0%)	87	87	6, 13, 23, 49	0

#### All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	77[A]	ASN	3.1
1	A	207	SER	3.0
1	В	207	SER	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains (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
1	PCA	В	1	8/9	0.85	0.21	15,25,29,30	0
1	PCA	A	1	8/9	0.95	0.12	14,19,19,20	0

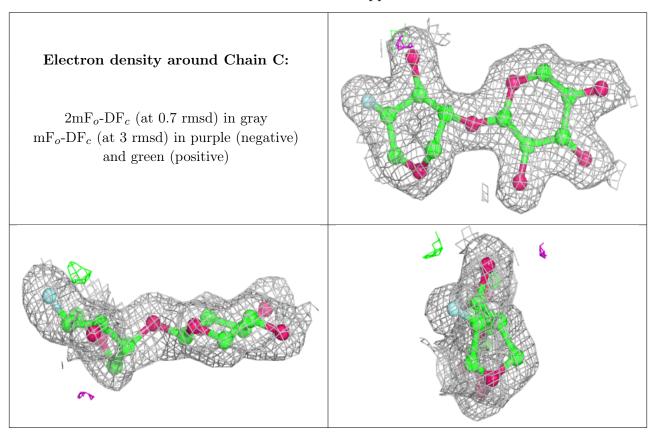
### 6.3 Carbohydrates (i)

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.

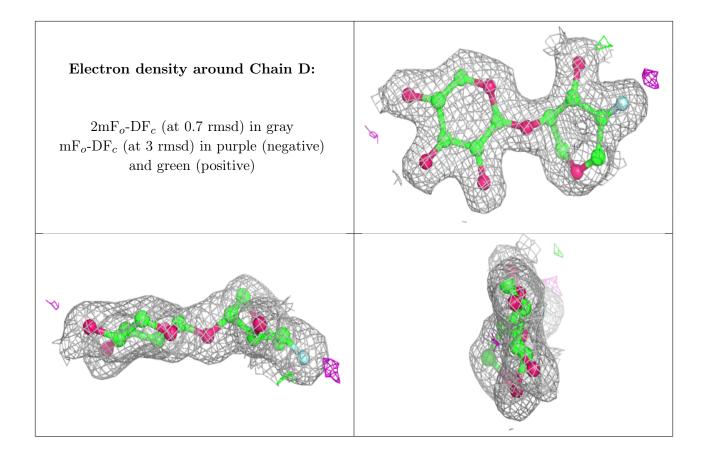


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	XYP	D	2	9/10	0.97	0.08	8,10,12,12	0
2	X2F	D	1	9/10	0.98	0.08	9,10,12,12	0
2	XYP	С	2	9/10	0.98	0.06	8,10,11,12	0
2	X2F	С	1	9/10	0.99	0.06	7,8,9,11	0

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.

