

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

#### Mar 23, 2024 – 10:36 PM EDT

PDB ID : 1GAH

Title: GLUCOAMYLASE-471 COMPLEXED WITH ACARBOSE

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Deposited on : 1996-03-06

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 : 2.36.1

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

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)
oteins) : Engh & Huber (200)

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

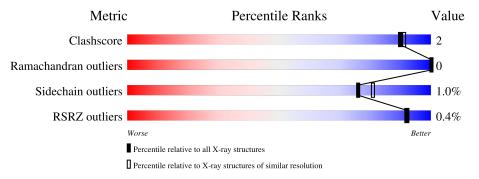
Validation Pipeline (wwPDB-VP) : 2.36.1

## 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 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
TVICTIC	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
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	471	94%	5%
2	В	5	60% 40%	
3	С	9	89%	11%
4	D	3	67% 33%	

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:



$\mathbf{M}$	ol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	3	MAN	C	9	-	-	-	X
4	:	GLC	D	1[B]	X	-	-	-



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6756 atoms, of which 2219 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.

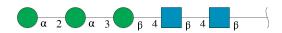
• Molecule 1 is a protein called GLUCOAMYLASE-471.

N	Aol	Chain	Residues		4	Atom	ıs			ZeroOcc	AltConf	Trace
	1	A	471	Total 4409	C 2269	H 781	N 594	O 757	S 8	0	9	0
				4403	2203	101	554	101	O			

There are 3 discrepancies between the modelled and reference sequences:

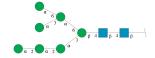
Chain	Residue	Modelled	Actual	Comment	Reference
A	58	LEU	ILE	conflict	UNP P22832
A	60	ILE	LEU	conflict	UNP P22832
A	117	THR	ALA	conflict	UNP P22832

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	B	5	Total	С	Н	N	О	0	0	0
	Ъ	9	118	34	57	2	25	U	0	

• Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-4)-2-acetamido-2-deox y-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



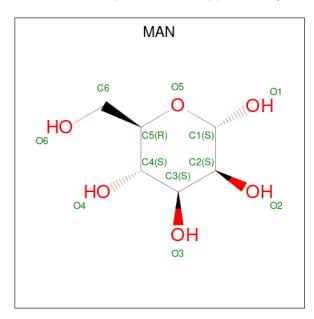


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	С	0	Total	С	Н	N	О	0	0	0
0		9	202	58	97	2	45	U	0	U

• Molecule 4 is an oligosaccharide called 4,6-dideoxy-4- $\{[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose e-(1-4)-alpha-D-glucopyranose.$ 

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
4	D	3	Total 131	C 37	H 64	N 1	O 29	0	2	0

• Molecule 5 is alpha-D-mannopyranose (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	A	Ator	ns		ZeroOcc	AltConf
5	A	1	Total	С	Н	О	0	1
	11	1	44	12	22	10		1
5	A	1	Total	$\mathbf{C}$	Η	O	0	1
	11	1	44	12	22	10	0	1
5	A	1	Total	$\mathbf{C}$	Η	O	0	0
	Λ	1	22	6	11	5		U
5	A	1	Total	С	Η	O	0	0
	Λ	1	22	6	11	5	0	U
5	A	1	Total	С	Η	O	0	0
	Λ	1	22	6	11	5	U	U
5	A	1	Total	С	Н	О	0	0
	Λ	1	22	6	11	5		U
5	A	1	Total	С	Н	О	0	0
	Λ	1	22	6	11	5		U



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C H O 22 6 11 5	0	0
5	A	1	Total C H O 22 6 11 5	0	0
5	A	1	Total C H O 22 6 11 5	0	0

#### • Molecule 6 is water.

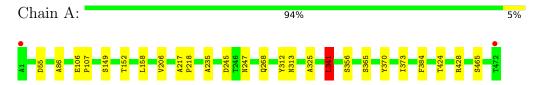
Mol	Chain	Residues	A	toms		ZeroOcc	AltConf
6	A	531	Total 1632	H 1088	O 544	0	14



## 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: GLUCOAMYLASE-471



 $\bullet \ \, Molecule \ 2: \ alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamid$ 

Chain B: 60% 40%

NAG1 NAG2 BMA3 MAN4

 $\bullet \ \, \text{Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)] alpha-D-mannopyranose-(1-6)] beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyran$ 

Chain C: 89% 11%

NAG1
NAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9

• Molecule 4: 4,6-dideoxy-4-{[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl|amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D: 67% 33%





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	116.80Å 104.10Å 48.40Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 - 2.00	Depositor
Resolution (A)	10.00 - 2.00	EDS
% Data completeness	84.7 (10.00-2.00)	Depositor
(in resolution range)	84.8 (10.00-2.00)	EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.46 (at 2.01Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
D D.	0.131 , 0.159	Depositor
$R, R_{free}$	0.128 , (Not available)	DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	10.3	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33, 62.6	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.46, < L^2> = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6756	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.21% 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: GLC, NAG, AC1, BMA, MAN

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	Chain	Bond	lengths	Bond angles		
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.43	0/3718	0.64	1/5088 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mo	l Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	341	LEU	CA-CB-CG	5.92	128.91	115.30

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	A	3628	781	3351	14	0
2	В	61	57	52	0	0
3	С	105	97	88	0	0
4	D	67	64	50	0	0
5	A	132	132	120	0	0
6	A	544	1088	0	4	0
All	All	4537	2219	3661	14	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 (14) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)	
1:A:152[B]:THR:HG22	1:A:206:VAL:HB	1.64	0.79	
1:A:152[B]:THR:HG21	6:A:809:HOH:O	2.00	0.61	
1:A:268:GLN:HA	6:A:817:HOH:O	2.02	0.58	
1:A:465:SER:HA	6:A:1005:HOH:O	2.09	0.51	
1:A:235:ALA:HB2	1:A:245:ASP:HB3	1.93	0.49	
1:A:424:THR:O	1:A:428:ARG:HG2	2.13	0.49	
1:A:341:LEU:HD11	1:A:373:ILE:HG21	1.98	0.46	
1:A:325:ALA:HB2	1:A:384:PHE:HB2	1.99	0.45	
1:A:365:SER:HA	1:A:370:TYR:CG	2.53	0.44	
1:A:106:GLU:HA	1:A:107:PRO:HD3	1.87	0.43	
1:A:312:TYR:O	1:A:313:ASN:HB2	2.19	0.42	
1:A:86:ALA:HA	1:A:158:LEU:HD21	2.03	0.41	
1:A:217:ALA:HB3	1:A:218:PRO:HD3	2.03	0.41	
1:A:149:SER:HB2	6:A:970:HOH:O	2.21	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	Percentiles	
1	A	478/471 (102%)	463 (97%)	15 (3%)	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 side chain 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	395/386 (102%)	391 (99%)	4 (1%)	76 81	

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

Mol	Chain	Res	Type
1	A	55	ASP
1	A	247	ASN
1	A	341	LEU
1	A	356	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	168	GLN
1	A	426	ASN
1	A	427	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)

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

### 5.5 Carbohydrates (i)

19 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	Chain	Res	Link	Во	ond leng	ths	В	ond ang	les
IVIOI	Type	Chain	rtes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	В	1	2,1	14,14,15	0.51	0	17,19,21	0.68	0
2	NAG	В	2	2	14,14,15	0.42	0	17,19,21	0.55	0
2	BMA	В	3	2	11,11,12	0.60	0	15,15,17	0.79	1 (6%)
2	MAN	В	4	2	11,11,12	0.62	0	15,15,17	0.61	0
2	MAN	В	5	2	11,11,12	0.83	0	15,15,17	0.98	1 (6%)
3	NAG	С	1	1,3	14,14,15	0.53	0	17,19,21	0.50	0
3	NAG	С	2	3	14,14,15	0.38	0	17,19,21	0.57	0
3	BMA	С	3	3	11,11,12	0.32	0	15,15,17	0.54	0
3	MAN	С	4	3	11,11,12	0.44	0	15,15,17	0.72	0
3	MAN	С	5	3	11,11,12	0.48	0	15,15,17	0.75	0
3	MAN	С	6	3	11,11,12	0.50	0	15,15,17	0.67	0
3	MAN	С	7	3	11,11,12	0.52	0	15,15,17	0.56	0
3	MAN	С	8	3	11,11,12	0.51	0	15,15,17	0.72	0
3	MAN	С	9	3	11,11,12	0.53	0	15,15,17	0.61	1 (6%)
4	GLC	D	1[A]	4	12,12,12	0.31	0	17,17,17	0.41	0
4	GLC	D	1[B]	4	12,12,12	0.40	0	17,17,17	0.45	0
4	GLC	D	2[A]	4	11,11,12	0.66	0	15,15,17	0.63	0
4	GLC	D	2[B]	4	11,11,12	0.70	0	15,15,17	0.72	0
4	AC1	D	3	4	21,22,23	0.96	1 (4%)	22,32,34	1.20	2 (9%)

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	BMA	В	3	2	-	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	-	2/2/19/22	0/1/1/1
3	NAG	С	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	С	2	3	-	0/6/23/26	0/1/1/1
3	BMA	С	3	3	-	0/2/19/22	0/1/1/1
3	MAN	С	4	3	-	0/2/19/22	0/1/1/1
3	MAN	С	5	3	-	0/2/19/22	0/1/1/1
3	MAN	С	6	3	-	2/2/19/22	0/1/1/1
3	MAN	С	7	3	-	0/2/19/22	0/1/1/1
3	MAN	С	8	3	-	0/2/19/22	0/1/1/1
3	MAN	С	9	3	-	0/2/19/22	0/1/1/1
4	GLC	D	1[A]	4	-	0/2/22/22	0/1/1/1



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GLC	D	1[B]	4	1/1/5/5	0/2/22/22	0/1/1/1
4	GLC	D	2[A]	4	-	0/2/19/22	0/1/1/1
4	GLC	D	2[B]	4	-	0/2/19/22	0/1/1/1
4	AC1	D	3	4	-	1/6/43/46	0/2/2/2

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

$\mathbf{Mol}$	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(Å)	$\operatorname{Ideal}( ext{\AA})$
4	D	3	AC1	C7B-C5B	2.83	1.36	1.32

#### All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathbf{Ideal}(^{o})$
4	D	3	AC1	C2-C3-C4	-3.39	107.64	110.63
2	В	5	MAN	C1-C2-C3	2.74	113.04	109.67
4	D	3	AC1	O4-C4A-C3B	-2.43	105.52	110.53
2	В	3	BMA	C1-C2-C3	-2.17	107.00	109.67
3	С	9	MAN	C1-O5-C5	2.07	115.00	112.19

#### All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	D	1[B]	GLC	C1

#### All (5) torsion outliers are listed below:

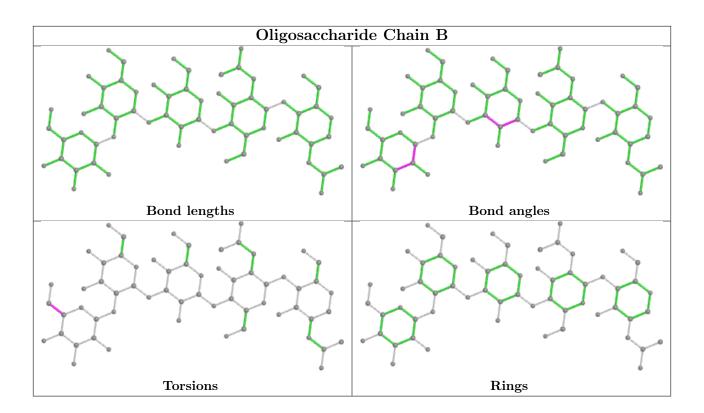
Mol	Chain	Res	Type	Atoms
2	В	5	MAN	C4-C5-C6-O6
2	В	5	MAN	O5-C5-C6-O6
3	С	6	MAN	O5-C5-C6-O6
4	D	3	AC1	C5-C4-N4A-C1B
3	С	6	MAN	C4-C5-C6-O6

There are no ring outliers.

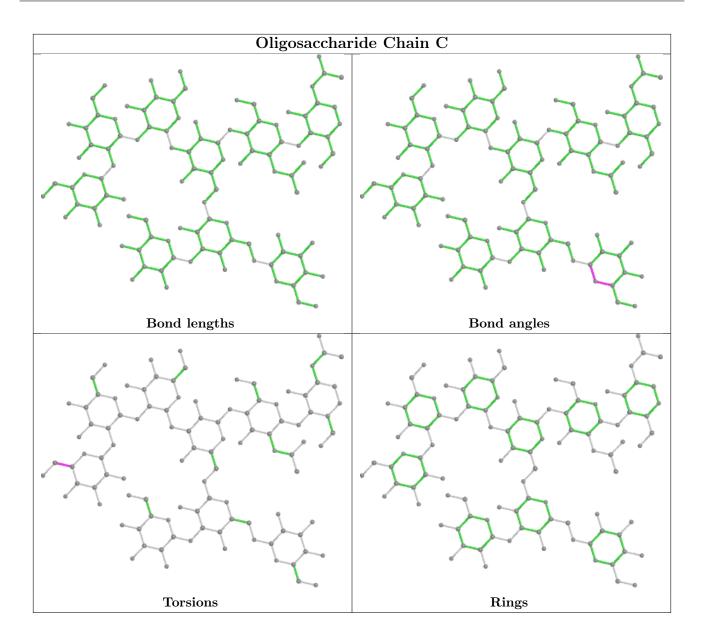
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

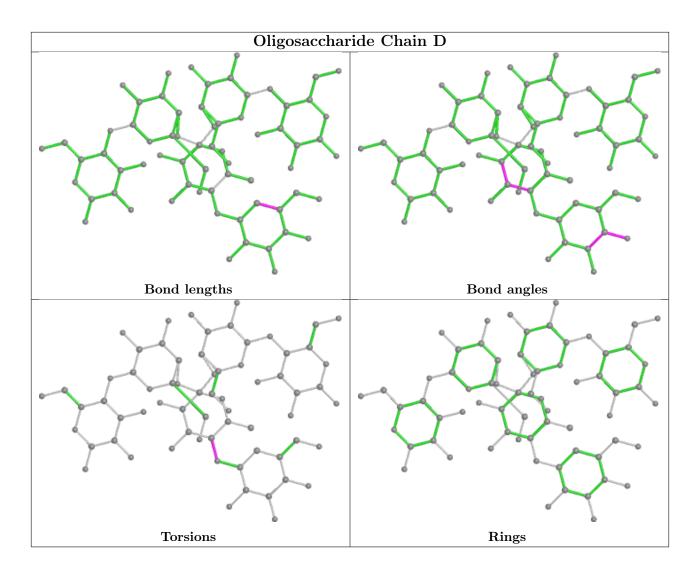












## 5.6 Ligand geometry (i)

12 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	Tuna	Chain	Res	Link	Bond lengths			Bond angles		
MIOI	Type				Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	MAN	A	473[B]	1	11,11,12	0.46	0	15,15,17	0.68	0
5	MAN	A	477	1	11,11,12	0.46	0	15,15,17	0.64	0
5	MAN	A	476	1	11,11,12	0.45	0	15,15,17	0.70	1 (6%)
5	MAN	A	481	1	11,11,12	0.35	0	15,15,17	0.57	0



Mol	Tuno	Chain	Res	Link	Во	ond leng	ths	Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	MAN	A	474[A]	1	11,11,12	0.44	0	15,15,17	0.60	0
5	MAN	A	478	1	11,11,12	0.70	0	15,15,17	0.82	0
5	MAN	A	475	1	11,11,12	0.35	0	15,15,17	0.49	0
5	MAN	A	479	1	11,11,12	0.44	0	15,15,17	0.50	0
5	MAN	A	480	1	11,11,12	0.47	0	15,15,17	0.59	0
5	MAN	A	474[B]	1	11,11,12	0.43	0	15,15,17	0.52	0
5	MAN	A	473[A]	1	11,11,12	0.48	0	15,15,17	0.62	0
5	MAN	A	482	1	11,11,12	0.71	0	15,15,17	1.06	1 (6%)

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
5	MAN	A	473[B]	1	-	2/2/19/22	0/1/1/1
5	MAN	A	477	1	-	0/2/19/22	0/1/1/1
5	MAN	A	476	1	-	0/2/19/22	0/1/1/1
5	MAN	A	481	1	-	0/2/19/22	0/1/1/1
5	MAN	A	474[A]	1	-	0/2/19/22	0/1/1/1
5	MAN	A	478	1	-	0/2/19/22	0/1/1/1
5	MAN	A	475	1	-	0/2/19/22	0/1/1/1
5	MAN	A	479	1	-	0/2/19/22	0/1/1/1
5	MAN	A	480	1	-	0/2/19/22	0/1/1/1
5	MAN	A	474[B]	1	-	0/2/19/22	0/1/1/1
5	MAN	A	473[A]	1	-	1/2/19/22	0/1/1/1
5	MAN	A	482	1	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^o)$
5	A	482	MAN	C1-C2-C3	3.09	113.46	109.67
5	A	476	MAN	C1-O5-C5	2.21	115.18	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	473[B]	MAN	O5-C5-C6-O6
5	A	473[B]	MAN	C4-C5-C6-O6



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Mol	Chain	Res	Type	Atoms
5	A	482	MAN	O5-C5-C6-O6
5	A	473[A]	MAN	O5-C5-C6-O6

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></rsrz>	# RSRZ > 2		$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	A	471/471 (100%)	-0.93	2 (0%) 92	92	3, 8, 22, 71	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	ALA	6.9
1	A	472	THR	3.8

#### 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.

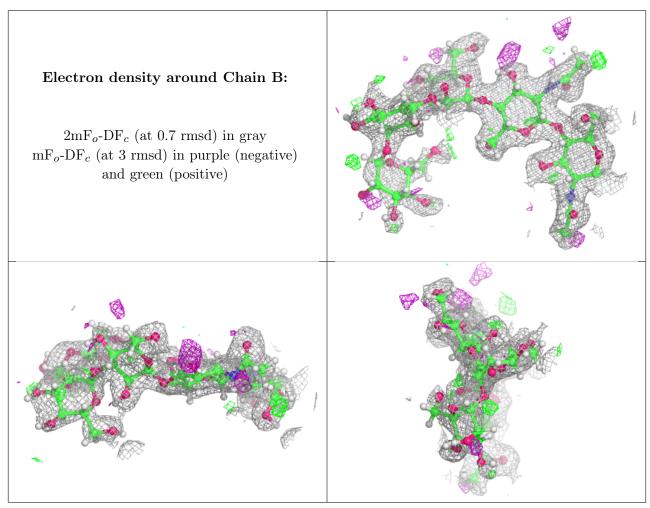
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	MAN	С	9	11/12	0.71	0.47	60,67,70,73	0
2	MAN	В	5	11/12	0.72	0.31	53,55,58,58	0
2	BMA	В	3	11/12	0.83	0.18	30,38,41,41	0
3	MAN	С	6	11/12	0.86	0.23	50,55,58,61	0
2	MAN	В	4	11/12	0.86	0.17	44,48,53,53	0
3	MAN	С	4	11/12	0.89	0.21	34,39,44,44	0
4	GLC	D	1[A]	12/12	0.89	0.17	19,22,24,26	23
4	GLC	D	1[B]	12/12	0.89	0.17	13,21,24,25	23
3	MAN	С	5	11/12	0.91	0.14	28,33,38,44	0
3	MAN	С	7	11/12	0.93	0.12	18,28,41,53	0



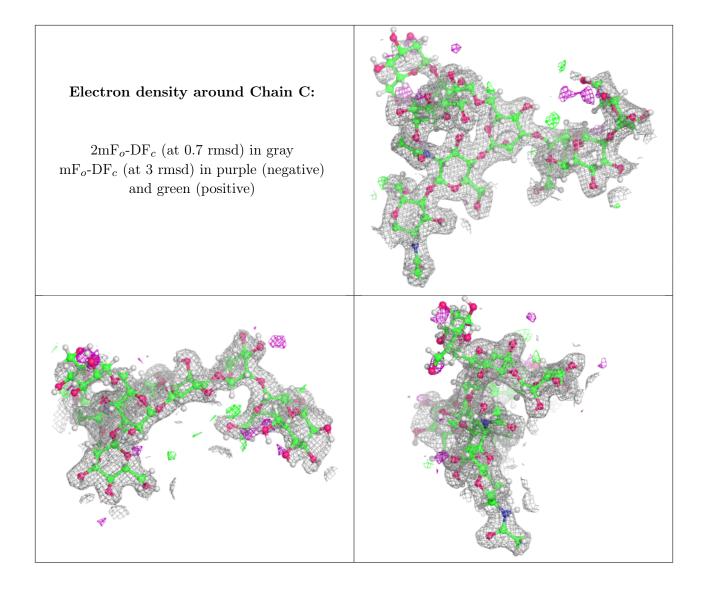
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	NAG	В	2	14/15	0.95	0.09	11,16,21,25	0
3	NAG	С	2	14/15	0.96	0.09	16,18,19,21	0
3	BMA	С	3	11/12	0.96	0.10	20,24,28,31	0
3	NAG	С	1	14/15	0.96	0.08	16,17,23,25	0
4	GLC	D	2[A]	11/12	0.97	0.12	10,12,15,17	21
4	GLC	D	2[B]	11/12	0.97	0.12	3,6,13,13	21
3	MAN	С	8	11/12	0.98	0.08	15,17,19,19	0
2	NAG	В	1	14/15	0.98	0.06	3,6,7,9	0
4	AC1	D	3	21/22	0.99	0.05	3,4,7,8	0

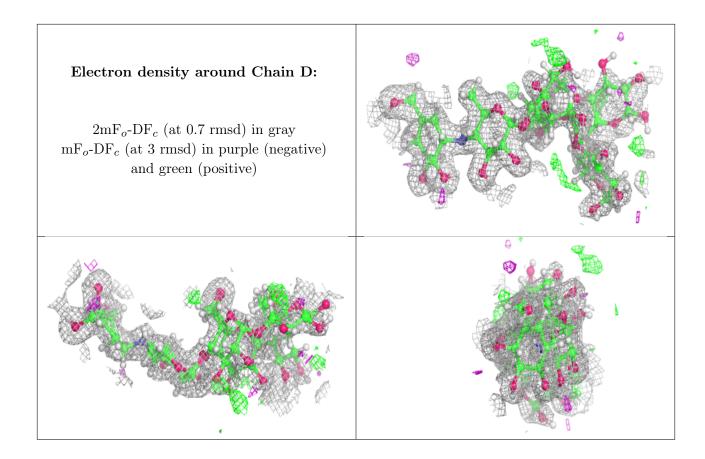
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.











## 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
5	MAN	A	482	11/12	0.79	0.30	56,61,63,66	0
5	MAN	A	477	11/12	0.86	0.17	29,37,41,46	0
5	MAN	A	473[A]	11/12	0.90	0.18	17,20,22,25	22
5	MAN	A	473[B]	11/12	0.90	0.18	20,23,26,28	22
5	MAN	A	481	11/12	0.92	0.13	19,25,29,35	0
5	MAN	A	476	11/12	0.92	0.16	29,32,35,35	0
5	MAN	A	478	11/12	0.95	0.12	14,19,20,25	0
5	MAN	A	480	11/12	0.96	0.09	7,16,21,26	0
5	MAN	A	475	11/12	0.97	0.11	15,21,23,24	0
5	MAN	A	474[B]	11/12	0.98	0.09	12,14,17,17	22
5	MAN	A	474[A]	11/12	0.98	0.09	17,18,20,22	22
5	MAN	A	479	11/12	0.99	0.05	4,8,10,11	0



# 6.5 Other polymers (i)

There are no such residues in this entry.

