

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

#### Sep 11, 2023 – 01:26 PM EDT

PDB ID	:	8GLG
Title	:	Crystal Structure of Human CD1b in Complex with Phosphatidylethanolami
		ne C34:1
Authors	:	Shahine, A.
Deposited on		
Resolution	:	1.60  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:

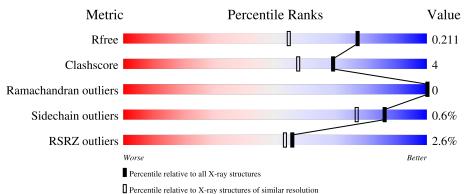
MolProbity	:	4.02b-467 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)		
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

# 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 1.60 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 <sub>free</sub>	130704	3398(1.60-1.60)
Clashscore	141614	3665(1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	300	<sup>2%</sup> 87%	6% 7%
2	В	101	5% 91%	8% •
3	С	7	71%	29%
4	D	4	100%	



#### 8 GLG

# 2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 3851 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 T-cell surface glycoprotein CD1b.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	280	Total 2232	C 1431	N 376	0 415	S 10	0	8	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	279	GLY	-	expression tag	UNP P29016
А	280	SER	-	expression tag	UNP P29016
А	281	GLY	-	expression tag	UNP P29016
А	282	LEU	-	expression tag	UNP P29016
А	283	ASN	-	expression tag	UNP P29016
А	284	ASP	-	expression tag	UNP P29016
А	285	ILE	-	expression tag	UNP P29016
А	286	PHE	-	expression tag	UNP P29016
А	287	GLU	-	expression tag	UNP P29016
А	288	ALA	-	expression tag	UNP P29016
А	289	GLN	-	expression tag	UNP P29016
А	290	LYS	-	expression tag	UNP P29016
А	291	ILE	-	expression tag	UNP P29016
А	292	GLU	-	expression tag	UNP P29016
А	293	TRP	-	expression tag	UNP P29016
А	294	HIS	-	expression tag	UNP P29016
А	295	GLU	-	expression tag	UNP P29016
А	296	HIS	-	expression tag	UNP P29016
А	297	HIS	-	expression tag	UNP P29016
А	298	HIS	-	expression tag	UNP P29016
А	299	HIS	-	expression tag	UNP P29016
А	300	HIS	-	expression tag	UNP P29016
А	301	HIS	-	expression tag	UNP P29016

There are 23 discrepancies between the modelled and reference sequences:

• Molecule 2 is a protein called Beta-2-microglobulin.



Μ	ol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	В	100	Total 842	C 537	N 142	O 161	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	5	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	1	PRO	-	expression tag	UNP P61769
В	2	LYS	-	expression tag	UNP P61769

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	С	7	Total 81	C 46	N 2	O 33	0	0	0

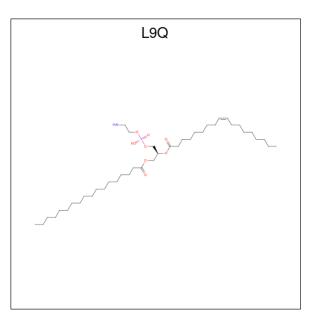
• Molecule 4 is an oligosaccharide called alpha-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-be ta-D-glucopyranose-(1-4)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyr anose.



Mol	Chain	Residues	Aton	ns	ZeroOcc	AltConf	Trace
4	D	4	TotalC4828	N O 2 18	0	0	0

• Molecule 5 is (1S)-2-{[(S)-(2-aminoethoxy)(hydroxy)phosphoryl]oxy}-1-[(octadecanoyl oxy)methyl]ethyl (9Z)-octadec-9-enoate (three-letter code: L9Q) (formula: C<sub>41</sub>H<sub>80</sub>NO<sub>8</sub>P) (labeled as "Ligand of Interest" by depositor).



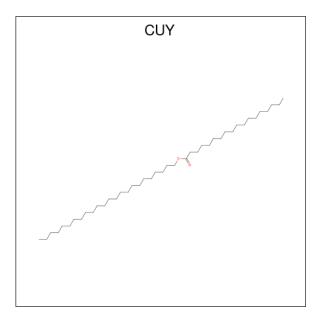


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
E.	Δ	1	Total	С	Ν	0	Р	0	0
9	A	1	49	39	1	8	1	0	0

• Molecule 6 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total Ni 1 1	0	0

• Molecule 7 is tetracosyl octa decanoate (three-letter code: CUY) (formula:  $C_{42}H_{84}O_2$ ) (labeled as "Lig and of Interest" by depositor).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
7	А	1	Total 35	C 33	O 2	0	0

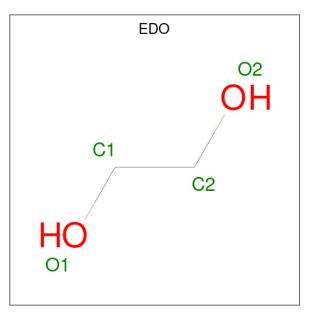
• Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	4	Total Cl 4 4	0	0

• Molecule 9 is IODIDE ION (three-letter code: IOD) (formula: I).

I	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	9	А	1	Total I 1 1	0	0
	9	В	1	Total I 1 1	0	0

• Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
10	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
10	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
10	В	1	Total 4	С 2	O 2	0	0

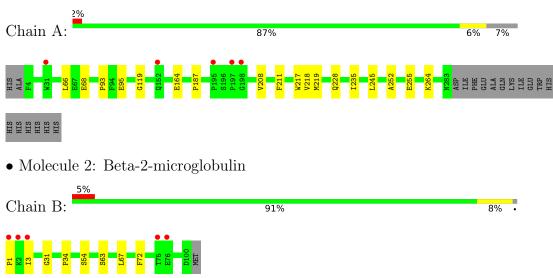
• Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	А	391	Total O 391 391	0	0
11	В	150	Total O 150 150	0	0



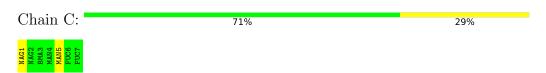
# 3 Residue-property plots (i)

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: T-cell surface glycoprotein CD1b

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



• Molecule 4: alpha-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)][alph a-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:

100%





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	58.07Å 80.53Å 92.98Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	36.95 - 1.60	Depositor
Resolution (A)	36.95 - 1.60	EDS
% Data completeness	98.6 (36.95-1.60)	Depositor
(in resolution range)	98.6 (36.95 - 1.60)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.21 (at 1.60 \text{\AA})$	Xtriage
Refinement program	BUSTER	Depositor
D D.	0.186 , $0.209$	Depositor
$R, R_{free}$	0.191 , $0.211$	DCC
$R_{free}$ test set	2854 reflections $(4.97%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	17.4	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.31,47.4	EDS
L-test for twinning <sup>2</sup>	$ \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	0.96	EDS
Total number of atoms	3851	wwPDB-VP
Average B, all atoms $(Å^2)$	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.50% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<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: MAN, CL, NAG, BMA, CUY, IOD, L9Q, NI, EDO, FUC

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	Bo	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.60	2/2306~(0.1%)	0.65	0/3133	
2	В	0.47	0/872	0.63	0/1188	
All	All	0.57	2/3178~(0.1%)	0.65	0/4321	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	164	GLU	CD-OE2	-5.52	1.19	1.25
1	А	95	GLU	CD-OE2	-5.04	1.20	1.25

There are no bond angle outliers.

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	2232	0	2142	16	0
2	В	842	0	787	7	0
3	С	81	0	70	0	0
4	D	48	0	43	0	0
5	А	49	0	72	3	0
6	А	1	0	0	0	0
7	А	35	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	А	4	0	0	2	0
9	А	1	0	0	0	0
9	В	1	0	0	0	0
10	А	4	0	6	0	0
10	В	12	0	17	6	0
11	А	391	0	0	6	0
11	В	150	0	0	0	0
All	All	3851	0	3137	24	0

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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 24 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:228:GLN:HG3	11:A:846:HOH:O	1.58	1.03
1:A:119:GLY:HA3	2:B:1:PRO:HA	1.40	1.01
8:A:604:CL:CL	11:A:868:HOH:O	2.21	0.94
8:A:605:CL:CL	11:A:846:HOH:O	2.28	0.87
2:B:67:LEU:HD23	10:B:203:EDO:H11	1.65	0.78

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	А	286/300~(95%)	283~(99%)	3(1%)	0	100 1	L00
2	В	103/101~(102%)	103 (100%)	0	0	100 1	L00
All	All	389/401~(97%)	386~(99%)	3 (1%)	0	100 1	L00

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	Rotameric Outliers	
1	А	236/247~(96%)	236 (100%)	0	100 100
2	В	94/96~(98%)	92~(98%)	2(2%)	53 29
All	All	330/343~(96%)	328~(99%)	2(1%)	86 77

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

Mol	Chain	Res	Type	
2	В	3	ILE	
2	В	72	PHE	

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)

11 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
IVIOI	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
3	NAG	С	1	1,3	$14,\!14,\!15$	0.40	0	$17,\!19,\!21$	0.96	1 (5%)
3	NAG	С	2	3	14,14,15	0.30	0	17,19,21	0.53	0
3	BMA	С	3	3	11,11,12	0.32	0	$15,\!15,\!17$	0.65	0
3	MAN	С	4	3	$11,\!11,\!12$	0.35	0	$15,\!15,\!17$	0.64	0
3	MAN	С	5	3	$11,\!11,\!12$	0.40	0	$15,\!15,\!17$	0.91	1 (6%)
3	FUC	С	6	3	10,10,11	0.38	0	14,14,16	0.57	0
3	FUC	С	7	3	10,10,11	0.45	0	$14,\!14,\!16$	0.73	0
4	NAG	D	1	4,1	14,14,15	0.30	0	17,19,21	0.63	0
4	FUC	D	2	4	$10,\!10,\!11$	0.39	0	$14,\!14,\!16$	0.72	0
4	NAG	D	3	4	$14,\!14,\!15$	0.29	0	17,19,21	0.45	0
4	FUC	D	4	4	$10,\!10,\!11$	0.39	0	$14,\!14,\!16$	0.56	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	С	1	1,3	-	1/6/23/26	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	FUC	С	6	3	-	-	0/1/1/1
3	FUC	С	7	3	-	-	0/1/1/1
4	NAG	D	1	4,1	-	0/6/23/26	0/1/1/1
4	FUC	D	2	4	-	-	0/1/1/1
4	NAG	D	3	4	-	0/6/23/26	0/1/1/1
4	FUC	D	4	4	-	_	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	С	5	MAN	C1-O5-C5	3.17	116.48	112.19
3	С	1	NAG	C1-O5-C5	2.74	115.90	112.19

There are no chirality outliers.

All (1) torsion outliers are listed below:



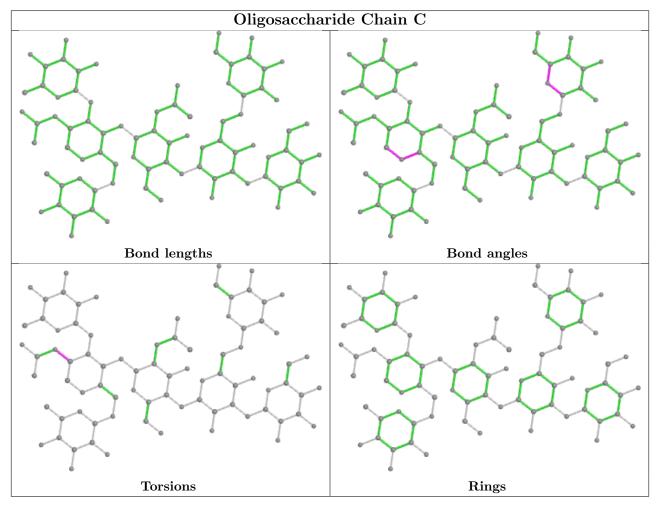
001	$\Omega$
0.01	ЬG

N	ſol	Chain	Res	Type	Atoms
	3	С	1	NAG	C3-C2-N2-C7

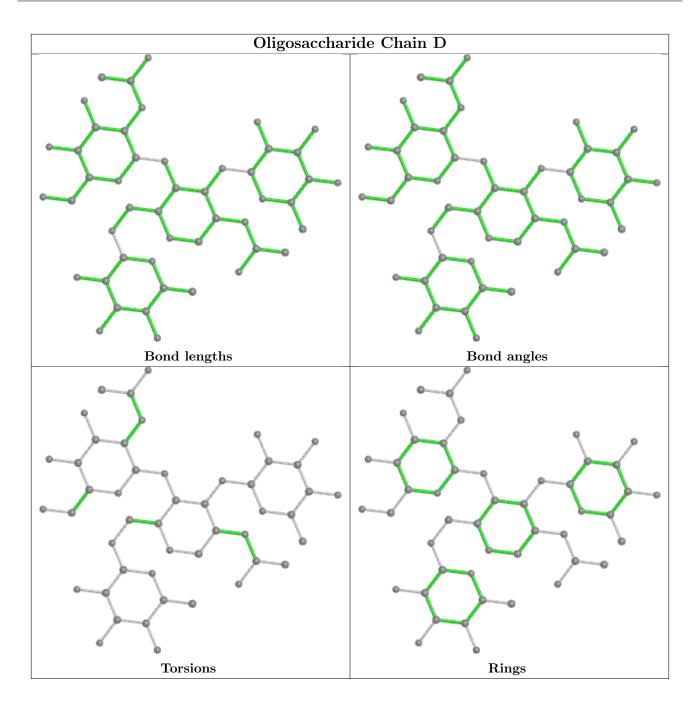
There are no ring outliers.

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 13 ligands modelled in this entry, 7 are monoatomic - leaving 6 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	Turne	Chain	Res	Link	Bo	ond leng	ths	Bond angles		
NIOI	Type	Chain	ries		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
5	L9Q	А	601	-	48,48,50	0.94	2 (4%)	$51,\!53,\!55$	1.12	5 (9%)
10	EDO	В	203	-	3,3,3	0.38	0	2,2,2	0.30	0
10	EDO	А	609	-	3,3,3	0.56	0	2,2,2	0.37	0
10	EDO	В	202	-	3,3,3	1.25	1 (33%)	2,2,2	0.58	0
10	EDO	В	204	-	3,3,3	0.52	0	2,2,2	0.35	0
7	CUY	А	603	-	34,34,43	0.64	1 (2%)	34,34,43	0.68	1 (2%)

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	L9Q	А	601	-	-	28/52/52/54	-
10	EDO	В	203	-	-	0/1/1/1	-
10	EDO	А	609	-	-	0/1/1/1	-
10	EDO	В	202	-	-	1/1/1/1	-
10	EDO	В	204	-	-	1/1/1/1	-
7	CUY	А	603	_	_	16/33/33/42	_

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
5	А	601	L9Q	O2-C31	2.64	1.41	1.34
7	А	603	CUY	OAQ-CAP	2.56	1.40	1.33
5	А	601	L9Q	O3-C11	2.16	1.39	1.33
10	В	202	EDO	O2-C2	-2.06	1.31	1.42

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

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
5	А	601	L9Q	O2-C31-C32	4.93	122.13	111.50
5	А	601	L9Q	O3-C11-C12	2.63	120.15	111.91
7	А	603	CUY	OAQ-CAP-CAO	2.44	119.58	111.91
5	А	601	L9Q	O2-C31-O31	-2.39	117.92	123.70
5	А	601	L9Q	C2-O2-C31	2.28	123.40	117.79

There are no chirality outliers.

5 of 46 torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
5	А	601	L9Q	C3-C2-O2-C31
5	А	601	L9Q	O31-C31-O2-C2
5	А	601	L9Q	C32-C31-O2-C2
5	А	601	L9Q	O4P-C4-C5-N
5	А	601	L9Q	C12-C11-O3-C3

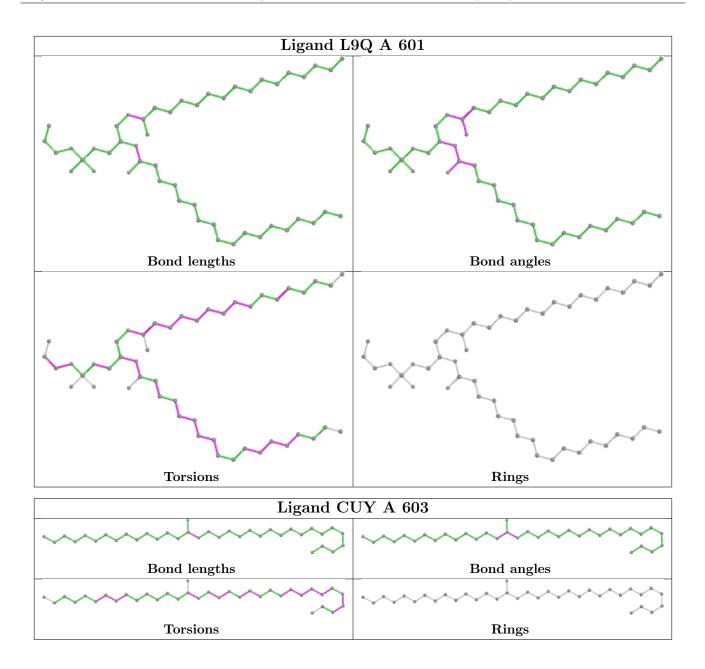
There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	А	601	L9Q	3	0
10	В	203	EDO	3	0
10	В	202	EDO	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	280/300~(93%)	-0.30	5 (1%) 68 67	10, 19, 39, 63	0
2	В	100/101~(99%)	-0.12	5 (5%) 28 26	11, 25, 49, 72	0
All	All	380/401~(94%)	-0.25	10 (2%) 56 53	10, 20, 43, 72	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	1	PRO	4.1
1	А	31	TRP	4.0
1	А	195	PRO	3.2
2	В	75	THR	2.9
2	В	2	LYS	2.8

## 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	$B-factors(Å^2)$	Q < 0.9
4	NAG	D	3	14/15	0.66	0.23	54,57,60,62	0
4	FUC	D	2	10/11	0.78	0.35	60,66,67,67	0
4	NAG	D	1	14/15	0.82	0.14	39,45,49,55	0
4	FUC	D	4	10/11	0.83	0.25	$50,\!53,\!55,\!55$	0
3	FUC	С	6	10/11	0.89	0.13	23,28,31,31	0

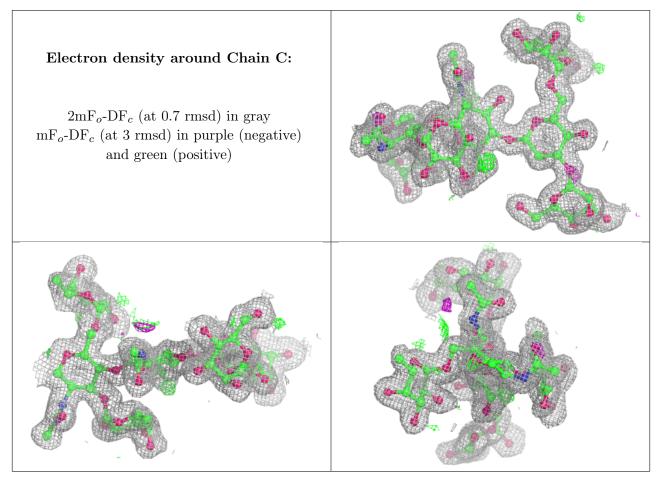
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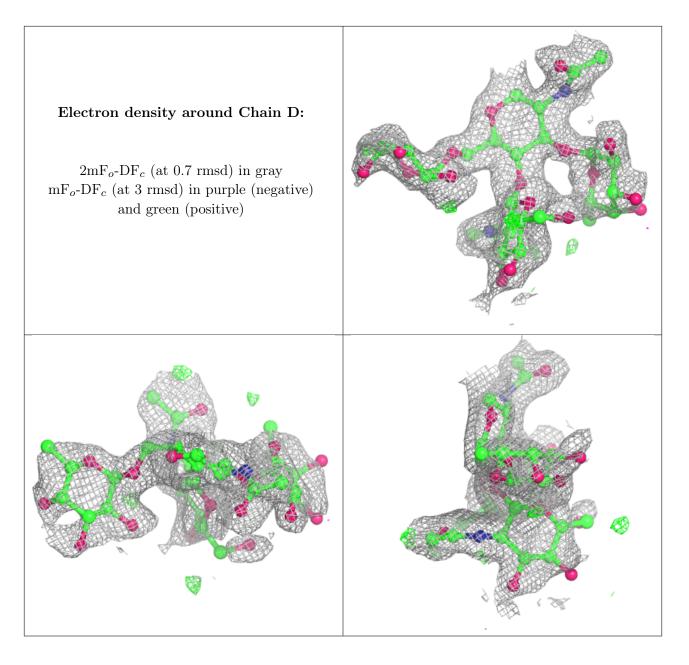
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MAN	С	5	11/12	0.91	0.10	$16,\!17,\!20,\!21$	0
3	MAN	С	4	11/12	0.91	0.09	23,25,29,29	0
3	FUC	С	7	10/11	0.93	0.10	20,24,26,26	0
3	NAG	С	2	14/15	0.95	0.06	$16,\!18,\!20,\!25$	0
3	BMA	С	3	11/12	0.95	0.07	$16,\!17,\!20,\!20$	0
3	NAG	С	1	14/15	0.96	0.07	14,15,17,18	0

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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
5	L9Q	А	601	49/51	0.72	0.19	$31,\!43,\!54,\!58$	0
10	EDO	А	609	4/4	0.79	0.22	$50,\!52,\!54,\!55$	0
7	CUY	А	603	35/44	0.83	0.18	26,31,36,37	0
10	EDO	В	204	4/4	0.84	0.20	40,42,43,44	0

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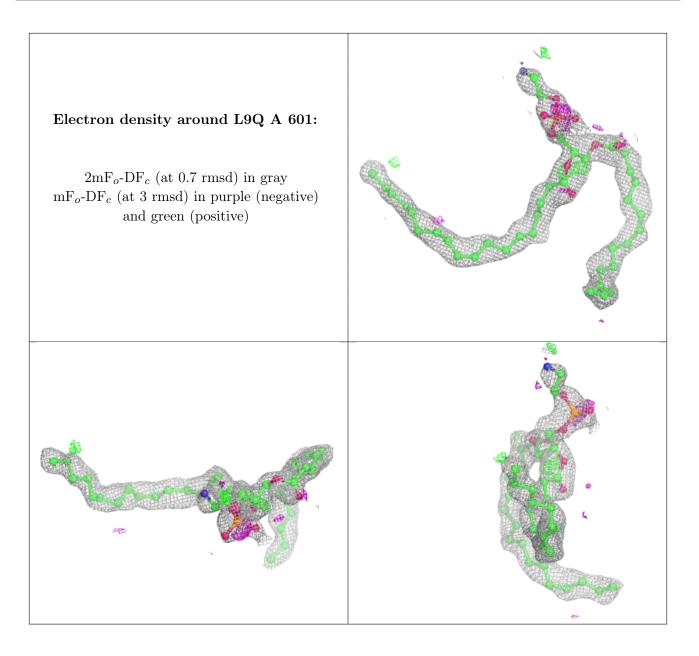


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
10	EDO	В	203	4/4	0.92	0.19	$34,\!35,\!39,\!43$	0
8	CL	А	606	1/1	0.92	0.06	28,28,28,28	0
9	IOD	В	201	1/1	0.95	0.08	30,30,30,30	1
10	EDO	В	202	4/4	0.95	0.20	12,17,27,33	0
8	CL	А	607	1/1	0.97	0.20	12,12,12,12	0
6	NI	А	602	1/1	0.97	0.08	25,25,25,25	0
8	CL	А	604	1/1	0.98	0.06	20,20,20,20	0
9	IOD	А	608	1/1	0.99	0.09	$15,\!15,\!15,\!15$	1
8	CL	А	605	1/1	0.99	0.05	21,21,21,21	0

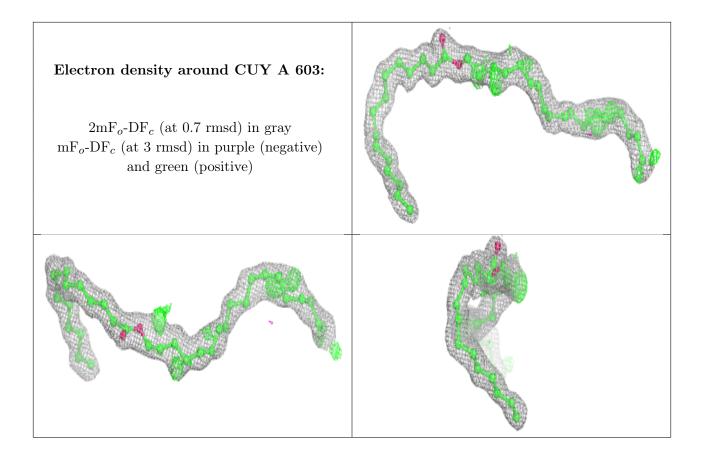
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The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.









## 6.5 Other polymers (i)

There are no such residues in this entry.

