

Full wwPDB X-ray Structure Validation Report (i)

Sep 12, 2022 – 06:15 pm BST

PDB ID : 8AGK

Title: Botulinum neurotoxin subtype A6 cell binding domain in complex with GD1a

ganglioside

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Deposited on : 2022-07-20

Resolution : 1.50 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 : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.30

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

Refmac: 5.8.0267

CCP4 : 7.1.010 (Gargrove)

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

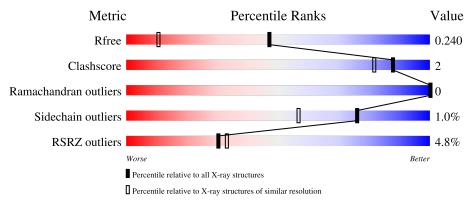
Validation Pipeline (wwPDB-VP) : 2.30

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 1.50 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
R_{free}	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	AAA	433	5%	90%		6%	5%
2	BBB	5	20%	40%	40%		



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3729 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.

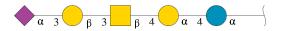
• Molecule 1 is a protein called Bont/A1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	AAA	413	Total 3423	C 2195	N 580	O 635	S 13	0	4	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual Comment		Reference
AAA	864	MET	-	initiating methionine	UNP C9WWY7
AAA	865	HIS	-	expression tag	UNP C9WWY7
AAA	866	HIS	-	expression tag	UNP C9WWY7
AAA	867	HIS	-	expression tag	UNP C9WWY7
AAA	868	HIS	-	expression tag	UNP C9WWY7
AAA	869	HIS	-	expression tag	UNP C9WWY7
AAA	870	HIS	-	expression tag	UNP C9WWY7

• Molecule 2 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galacto pyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-alpha-D-galactopyranose -(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	BBB	5	Total 68		N 2	0	0	0

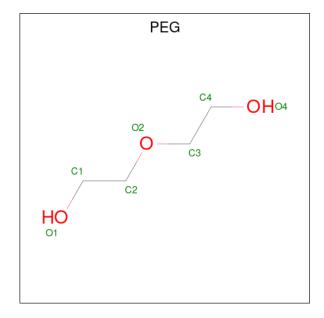
• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	1	Total C O 4 2 2	0	0
3	AAA	1	Total C O 4 2 2	0	0
3	AAA	1	Total C O 4 2 2	0	0
3	AAA	1	Total C O 4 2 2	0	0
3	AAA	1	Total C O 4 2 2	0	0

 $\bullet \ \ Molecule\ 4\ is\ DI(HYDROXYETHYL)ETHER\ (three-letter\ code:\ PEG)\ (formula:\ C_4H_{10}O_3).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	1	Total C O 7 4 3	0	0
4	AAA	1	Total C O 7 4 3	0	0
4	AAA	1	Total C O 7 4 3	0	0

• Molecule 5 is water.

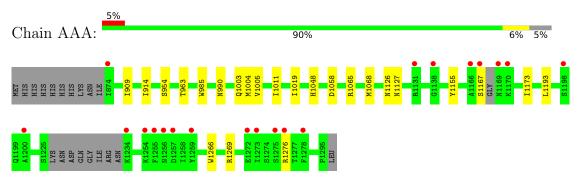
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAA	197	Total O 197 197	0	0



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: Bont/A1



• Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-alpha-D-galactopyranose-(1-4)-alpha-D-glucopyranose

Chain BBB: 20% 40% 40%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	44.31Å 83.64Å 58.31Å	Depositor
a, b, c, α , β , γ	90.00° 98.66° 90.00°	Depositor
Resolution (Å)	57.65 - 1.50	Depositor
resolution (A)	47.47 - 1.50	EDS
% Data completeness	99.9 (57.65-1.50)	Depositor
(in resolution range)	99.9 (47.47-1.50)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.14 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.203 , 0.236	Depositor
It, It free	0.210 , 0.240	DCC
R_{free} test set	3343 reflections (4.98%)	wwPDB-VP
Wilson B-factor (\mathring{A}^2)	17.3	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3729	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.95% 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: PEG, GLA, NGA, SIA, GAL, EDO, GLC

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	# Z > 5	
1	AAA	0.70	0/3503	0.84	1/4730 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
1	AAA	1155	TYR	CB-CG-CD2	-5.00	118.00	121.00

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	AAA	3423	0	3408	13	0
2	BBB	68	0	58	2	0
3	AAA	20	0	30	1	0
4	AAA	21	0	29	2	0
5	AAA	197	0	0	1	0
All	All	3729	0	3525	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	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:909:ILE:HG23	1:AAA:1173:ILE:HD11	1.78	0.63
4:AAA:1306:PEG:H42	5:AAA:1500:HOH:O	2.02	0.58
1:AAA:1266:TRP:CE3	2:BBB:4:GAL:H5	2.43	0.54
1:AAA:1276:ARG:NH1	2:BBB:5:SIA:O9	2.40	0.54
1:AAA:1003:GLN:HA	1:AAA:1011:ILE:HD11	1.90	0.54
1:AAA:909:ILE:CG2	1:AAA:1173:ILE:HD11	2.39	0.51
1:AAA:1126:ASN:OD1	1:AAA:1127:ASN:N	2.44	0.50
1:AAA:1193:LEU:HD23	1:AAA:1193:LEU:C	2.33	0.49
1:AAA:985:TRP:CD2	1:AAA:1019:ILE:HG21	2.47	0.48
1:AAA:954:SER:HB2	3:AAA:1309:EDO:H11	1.95	0.48
1:AAA:963:THR:HB	1:AAA:1058:ASP:HB3	1.99	0.45
1:AAA:1005:VAL:HG21	4:AAA:1306:PEG:H21	2.00	0.44
1:AAA:914:ILE:O	1:AAA:1068:MET:HA	2.19	0.43
1:AAA:990:ASN:HD21	1:AAA:1048:HIS:HB3	1.84	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	AAA	411/433 (95%)	397 (97%)	14 (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	AAA	386/400 (96%)	382 (99%)	4 (1%)	76 57	

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

Mol	Chain	Res	Type
1	AAA	1004	MET
1	AAA	1065	ARG
1	AAA	1167	SER
1	AAA	1269	ARG

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)

5 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	Chain	Res	Link	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	BBB	1	2	12,12,12	0.81	0	17,17,17	0.91	1 (5%)
2	GLA	BBB	2	2	11,11,12	0.82	0	15,15,17	2.63	7 (46%)
2	NGA	BBB	3	2	14,14,15	0.38	0	17,19,21	0.86	0



Mol Type Chair	Chain	nain Res	Link	Вс	nd leng	ths	Bond angles			
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GAL	BBB	4	2	11,11,12	0.42	0	15,15,17	1.24	2 (13%)
2	SIA	BBB	5	2	20,20,21	0.69	0	24,28,31	1.00	1 (4%)

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	GLC	BBB	1	2	-	0/2/22/22	0/1/1/1
2	GLA	BBB	2	2	-	2/2/19/22	0/1/1/1
2	NGA	BBB	3	2	-	0/6/23/26	0/1/1/1
2	GAL	BBB	4	2	-	0/2/19/22	0/1/1/1
2	SIA	BBB	5	2	-	2/18/34/38	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	BBB	2	GLA	C1-C2-C3	5.93	116.96	109.67
2	BBB	2	GLA	O5-C1-C2	4.56	117.81	110.77
2	BBB	2	GLA	C1-O5-C5	4.12	117.78	112.19
2	BBB	2	GLA	O5-C5-C6	3.06	112.01	107.20
2	BBB	2	GLA	O2-C2-C3	-2.78	104.56	110.14
2	BBB	5	SIA	C6-O6-C2	2.34	116.34	111.34
2	BBB	4	GAL	O5-C1-C2	-2.24	107.31	110.77
2	BBB	1	GLC	C3-C4-C5	2.16	114.10	110.24
2	BBB	4	GAL	C1-O5-C5	-2.14	109.30	112.19
2	BBB	2	GLA	C3-C4-C5	-2.11	106.47	110.24
2	BBB	2	GLA	O3-C3-C2	2.04	113.89	109.99

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	BBB	5	SIA	C11-C10-N5-C5
2	BBB	5	SIA	O10-C10-N5-C5
2	BBB	2	GLA	O5-C5-C6-O6
2	BBB	2	GLA	C4-C5-C6-O6

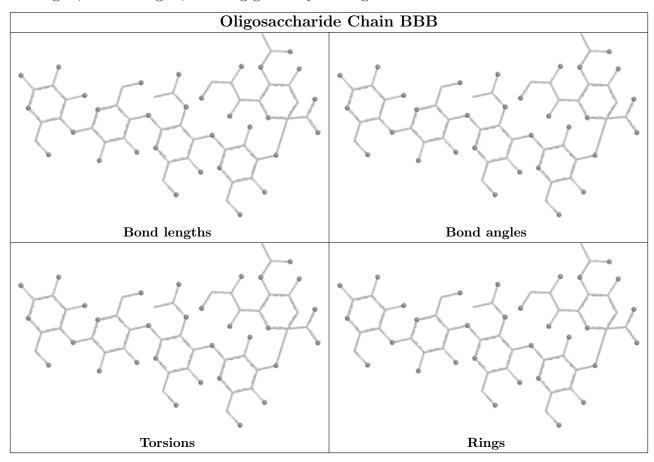


There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	5	SIA	1	0
2	BBB	4	GAL	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)

8 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	Tuno	Chain	Chain Res Link			ond leng	$_{ m gths}$	Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	AAA	1305	-	3,3,3	0.10	0	2,2,2	0.11	0
3	EDO	AAA	1308	-	3,3,3	0.16	0	2,2,2	0.10	0
4	PEG	AAA	1303	-	6,6,6	0.39	0	5,5,5	0.16	0
4	PEG	AAA	1307	-	6,6,6	0.22	0	5,5,5	0.33	0
4	PEG	AAA	1306	-	6,6,6	1.09	0	5,5,5	0.71	0
3	EDO	AAA	1302	-	3,3,3	0.47	0	2,2,2	0.18	0
3	EDO	AAA	1304	-	3,3,3	0.10	0	2,2,2	0.26	0
3	EDO	AAA	1309	-	3,3,3	0.23	0	2,2,2	0.74	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	EDO	AAA	1305	-	-	1/1/1/1	-
3	EDO	AAA	1308	-	-	1/1/1/1	-
4	PEG	AAA	1303	-	-	1/4/4/4	-
4	PEG	AAA	1307	-	-	2/4/4/4	-
4	PEG	AAA	1306	-	-	1/4/4/4	-
3	EDO	AAA	1302	-	-	1/1/1/1	-
3	EDO	AAA	1304	-	-	1/1/1/1	-
3	EDO	AAA	1309	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	AAA	1307	PEG	O1-C1-C2-O2
3	AAA	1302	EDO	O1-C1-C2-O2
3	AAA	1304	EDO	O1-C1-C2-O2
3	AAA	1308	EDO	O1-C1-C2-O2
4	AAA	1307	PEG	C4-C3-O2-C2
4	AAA	1306	PEG	O2-C3-C4-O4
4	AAA	1303	PEG	C4-C3-O2-C2
3	AAA	1305	EDO	O1-C1-C2-O2

There are no ring outliers.



2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	1306	PEG	2	0
3	AAA	1309	EDO	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q<0.9	
1	AAA	413/433 (95%)	0.13	20 (4%)	30	33	15, 25, 50, 85	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	1257	ASP	5.8
1	AAA	1276	ARG	4.4
1	AAA	1273	ILE	4.2
1	AAA	1200	ALA	3.9
1	AAA	874	ILE	3.6
1	AAA	1275	SER	3.6
1	AAA	1259	TYR	3.1
1	AAA	1234	LYS	2.6
1	AAA	1256	ASN	2.6
1	AAA	1272	GLU	2.5
1	AAA	1278	PHE	2.5
1	AAA	1167	SER	2.4
1	AAA	1255	PHE	2.4
1	AAA	1131	ARG	2.4
1	AAA	1170	LYS	2.4
1	AAA	1166	ALA	2.3
1	AAA	1138	GLY	2.3
1	AAA	1169	ASN	2.2
1	AAA	1198	SER	2.2
1	AAA	1254	LYS	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.

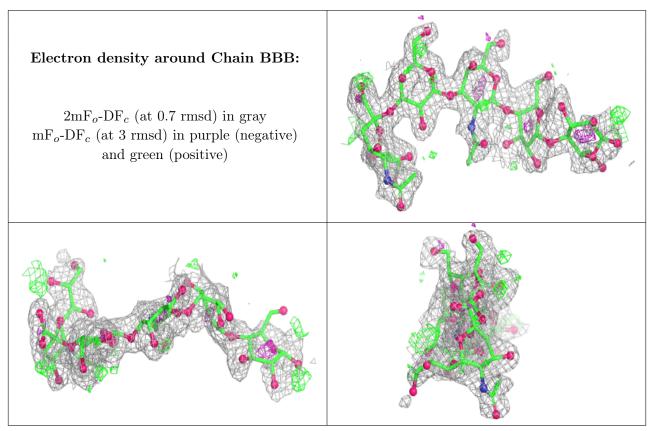


6.3 Carbohydrates (i)

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
2	GLC	BBB	1	12/12	0.58	0.25	66,75,77,78	0
2	GLA	BBB	2	11/12	0.76	0.12	57,61,65,67	0
2	NGA	BBB	3	14/15	0.82	0.18	36,47,51,52	0
2	SIA	BBB	5	20/21	0.86	0.18	38,49,64,65	0
2	GAL	BBB	4	11/12	0.89	0.09	31,36,38,39	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
3	EDO	AAA	1304	4/4	0.83	0.16	45,47,48,49	0
4	PEG	AAA	1303	7/7	0.83	0.11	35,41,48,53	0
4	PEG	AAA	1307	7/7	0.84	0.18	29,44,52,52	0
3	EDO	AAA	1308	4/4	0.85	0.25	39,49,55,64	0
3	EDO	AAA	1302	4/4	0.85	0.15	29,29,34,40	0
3	EDO	AAA	1305	4/4	0.85	0.12	55,56,58,61	0
4	PEG	AAA	1306	7/7	0.87	0.15	24,31,34,36	0
3	EDO	AAA	1309	4/4	0.91	0.16	29,30,31,32	0

6.5 Other polymers (i)

There are no such residues in this entry.

