Full wwPDB X-ray Structure Validation Report (i)

Jan 3, 2024 – 09:02 pm GMT

PDB ID	:	5LK1
Title	:	Structure of hantavirus envelope glycoprotein Gc in postfusion conformation in presence of 200 mM KCL
Authors	:	Guardado-Calvo, P.; Rey, F.A.
Deposited on	:	2016-07-20
Resolution	:	1.70 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 (i)) were used in the production of this report:

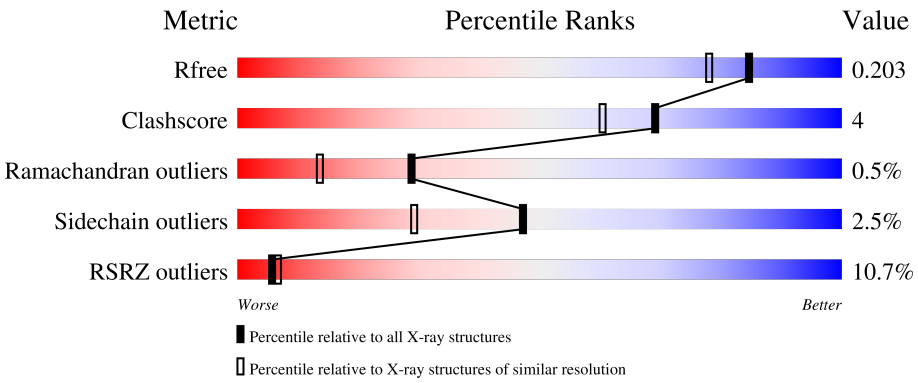
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	495	9% 74% 9% 17%
2	B	3	100%

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FUL	B	3	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3602 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 Envelopment polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	410	3247	2040	549	622	36	0	12	0

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	115	HIS	TRP	conflict	UNP P08668
A	458	GLY	-	expression tag	UNP P08668
A	459	GLY	-	expression tag	UNP P08668
A	460	SER	-	expression tag	UNP P08668
A	461	ASP	-	expression tag	UNP P08668
A	462	ASP	-	expression tag	UNP P08668
A	463	ASP	-	expression tag	UNP P08668
A	464	ASP	-	expression tag	UNP P08668
A	465	LYS	-	expression tag	UNP P08668
A	466	ALA	-	expression tag	UNP P08668
A	467	GLY	-	expression tag	UNP P08668
A	468	TRP	-	expression tag	UNP P08668
A	469	SER	-	expression tag	UNP P08668
A	470	HIS	-	expression tag	UNP P08668
A	471	PRO	-	expression tag	UNP P08668
A	472	GLN	-	expression tag	UNP P08668
A	473	PHE	-	expression tag	UNP P08668
A	474	GLU	-	expression tag	UNP P08668
A	475	LYS	-	expression tag	UNP P08668
A	476	GLY	-	expression tag	UNP P08668
A	477	GLY	-	expression tag	UNP P08668
A	478	GLY	-	expression tag	UNP P08668
A	479	SER	-	expression tag	UNP P08668
A	480	GLY	-	expression tag	UNP P08668
A	481	GLY	-	expression tag	UNP P08668
A	482	GLY	-	expression tag	UNP P08668
A	483	SER	-	expression tag	UNP P08668

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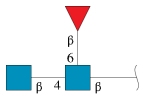
Chain	Residue	Modelled	Actual	Comment	Reference
A	484	GLY	-	expression tag	UNP P08668
A	485	GLY	-	expression tag	UNP P08668
A	486	GLY	-	expression tag	UNP P08668
A	487	SER	-	expression tag	UNP P08668
A	488	TRP	-	expression tag	UNP P08668
A	489	SER	-	expression tag	UNP P08668
A	490	HIS	-	expression tag	UNP P08668
A	491	PRO	-	expression tag	UNP P08668
A	492	GLN	-	expression tag	UNP P08668
A	493	PHE	-	expression tag	UNP P08668
A	494	GLU	-	expression tag	UNP P08668
A	495	LYS	-	expression tag	UNP P08668

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	38	22	2	14	0	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	K		
3	A	1	1	1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
4	A	1	1	1	0	0

- Molecule 5 is water.

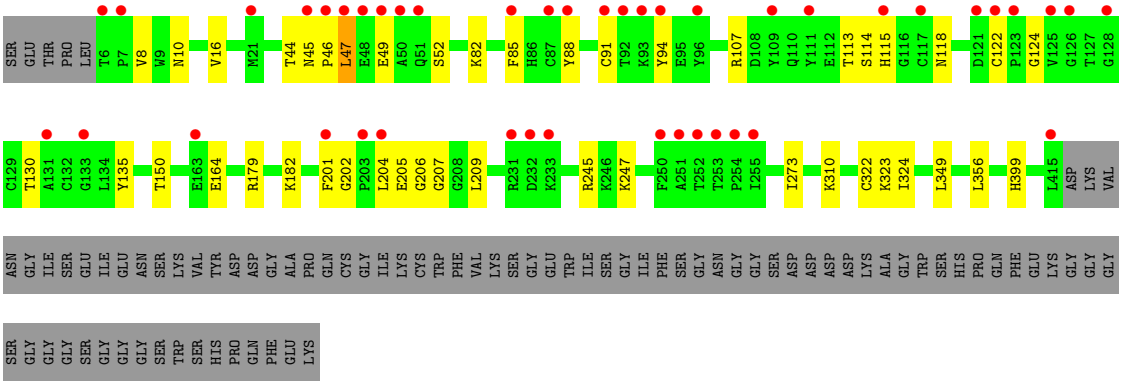
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	315	315	315	0	0

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.

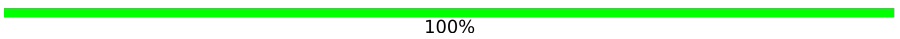
• Molecule 1: Envelopment polyprotein

Chain A:



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

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	107.29Å 107.29Å 127.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.55 – 1.70 37.55 – 1.70	Depositor EDS
% Data completeness (in resolution range)	94.5 (37.55-1.70) 94.5 (37.55-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.88 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.177 , 0.203 0.179 , 0.203	Depositor DCC
R_{free} test set	2800 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	16.4	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 28.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	0.060 for -2/3*h-1/3*k+2/3*l,-1/3*h-2/3*k-2/3*l,2/3*h-2/3*k+1/3*l 0.056 for -h,1/3*h-1/3*k+2/3*l,2/3*h+4/3*k+1/3*l 0.057 for -1/3*h+1/3*k-2/3*l,-k,-4/3*h-2/3*k+1/3*l 0.055 for -h,2/3*h+1/3*k-2/3*l,-2/3*h-4/3*k-1/3*l 0.055 for 1/3*h+2/3*k+2/3*l,-k,4/3*h+2/3*k-1/3*l 0.058 for -1/3*h-2/3*k-2/3*l,-2/3*h-1/3*k+2/3*l,-2/3*h+2/3*k-1/3*l 0.165 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3602	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]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.

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: FUL, NA, K, NAG

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	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.52	0/3339	0.66	0/4521

There are no bond length outliers.

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	A	3247	0	3089	24	0
2	B	38	0	34	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	315	0	0	2	1
All	All	3602	0	3123	24	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (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:202:GLY:H	1:A:204:LEU:HG	1.47	0.78
1:A:201:PHE:H	1:A:204:LEU:HD12	1.58	0.68
1:A:45:ASN:O	1:A:47:LEU:N	2.26	0.67
1:A:44:THR:O	1:A:310:LYS:NZ	2.35	0.59
1:A:209:LEU:HD11	1:A:273:ILE:HD11	1.85	0.59
1:A:44:THR:HG22	1:A:52:SER:HB3	1.85	0.58
1:A:113:THR:HB	1:A:118:ASN:HD21	1.69	0.57
1:A:201:PHE:N	1:A:204:LEU:HD12	2.21	0.55
1:A:324:ILE:HD12	1:A:399:HIS:CE1	2.43	0.53
1:A:82:LYS:HE2	1:A:135:TYR:OH	2.10	0.51
1:A:88:TYR:O	1:A:94:TYR:OH	2.21	0.51
1:A:204:LEU:HB3	1:A:207:GLY:O	2.12	0.48
1:A:164:GLU:OE2	1:A:179:ARG:NH2	2.46	0.48
1:A:322:CYS:HB3	1:A:349:LEU:HD11	1.98	0.46
1:A:118:ASN:ND2	1:A:124:GLY:O	2.47	0.46
1:A:150[A]:THR:HG21	5:A:661:HOH:O	2.16	0.46
1:A:10:ASN:HA	1:A:356:LEU:O	2.16	0.45
1:A:204:LEU:HD13	1:A:207:GLY:O	2.17	0.45
1:A:202:GLY:N	1:A:204:LEU:HG	2.24	0.43
1:A:16:VAL:HG22	1:A:182:LYS:HD3	1.99	0.43
1:A:205:GLU:N	1:A:205:GLU:OE1	2.52	0.43
1:A:323:LYS:NZ	5:A:601:HOH:O	2.27	0.41
1:A:247:LYS:HB3	1:A:247:LYS:HE2	1.77	0.40
1:A:85:PHE:HD1	1:A:130:THR:HG1	1.69	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:765:HOH:O	5:A:828:HOH:O[2_675]	2.17	0.03

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	420/495 (85%)	406 (97%)	12 (3%)	2 (0%)	29 13

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	PRO
1	A	206	GLY

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	366/419 (87%)	356 (97%)	10 (3%)	44 26

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	VAL
1	A	47	LEU
1	A	49	GLU
1	A	91[A]	CYS
1	A	91[B]	CYS
1	A	107	ARG
1	A	114	SER
1	A	115	HIS
1	A	122	CYS
1	A	245	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)

3 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	B	1	1,2	14,14,15	0.58	0	17,19,21	0.66	0
2	NAG	B	2	2	14,14,15	0.35	0	17,19,21	0.52	0
2	FUL	B	3	2	10,10,11	0.93	0	14,14,16	0.76	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	FUL	B	3	2	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

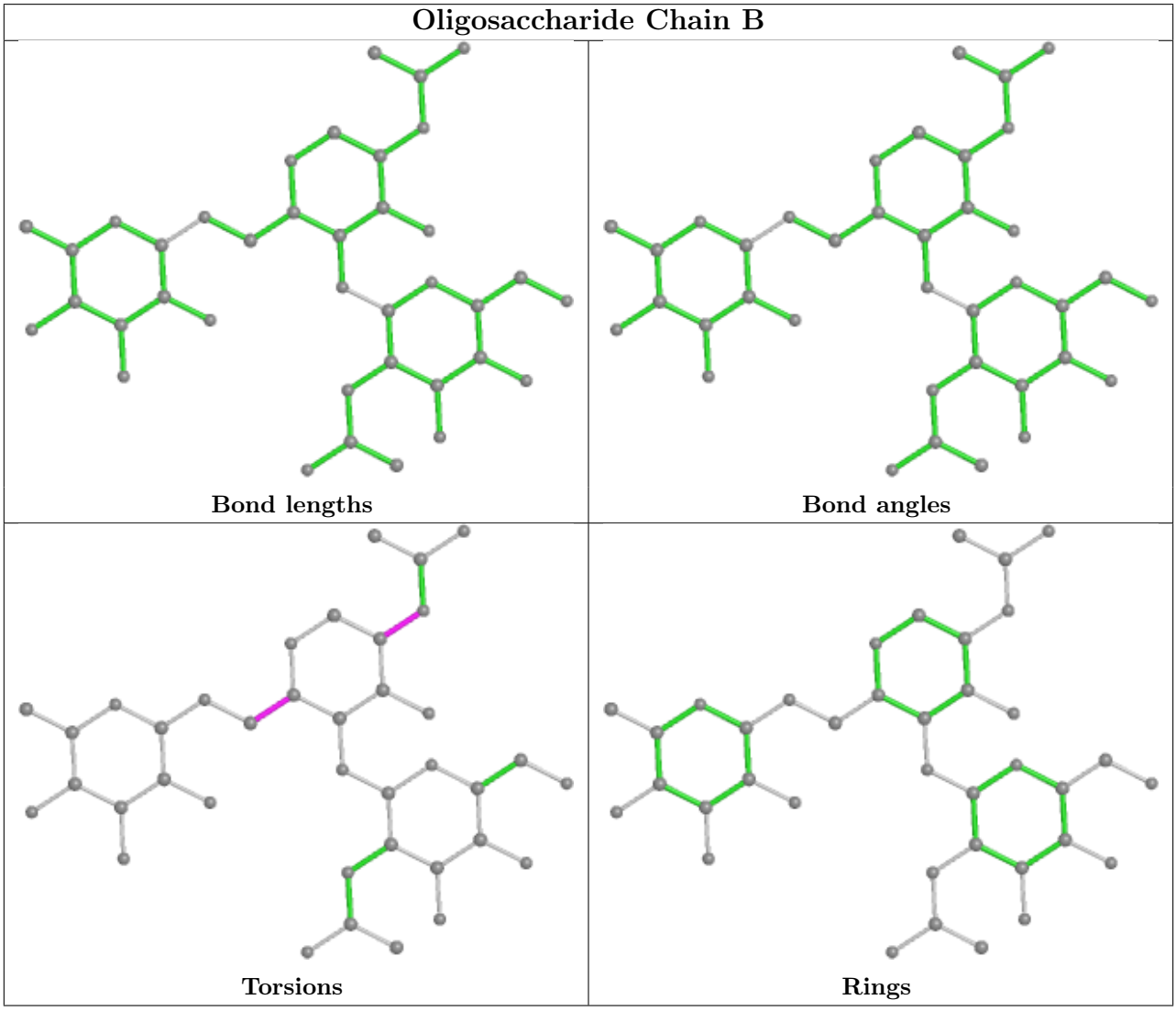
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
2	B	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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	410/495 (82%)	0.00	44 (10%) 6 7	10, 21, 95, 126	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	47	LEU	10.1
1	A	204	LEU	8.0
1	A	122	CYS	6.7
1	A	115	HIS	6.6
1	A	250	PHE	5.8
1	A	92	THR	5.2
1	A	109	TYR	4.8
1	A	46	PRO	4.8
1	A	233	LYS	4.7
1	A	125	VAL	4.7
1	A	128	GLY	4.3
1	A	6	THR	4.2
1	A	88	TYR	4.2
1	A	126	GLY	4.1
1	A	117	CYS	4.1
1	A	203	PRO	4.0
1	A	50	ALA	4.0
1	A	254	PRO	3.9
1	A	232	ASP	3.8
1	A	91[A]	CYS	3.6
1	A	7	PRO	3.6
1	A	48	GLU	3.6
1	A	123	PRO	3.6
1	A	255	ILE	3.2
1	A	49	GLU	3.1
1	A	45	ASN	3.1
1	A	415	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	121	ASP	2.9
1	A	21	MET	2.8
1	A	201	PHE	2.8
1	A	51	GLN	2.8
1	A	111	TYR	2.7
1	A	163	GLU	2.6
1	A	94	TYR	2.6
1	A	87	CYS	2.6
1	A	251	ALA	2.5
1	A	85	PHE	2.5
1	A	133	GLY	2.4
1	A	231	ARG	2.2
1	A	131	ALA	2.1
1	A	253	THR	2.1
1	A	93	LYS	2.1
1	A	252	THR	2.1
1	A	96	TYR	2.0

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)

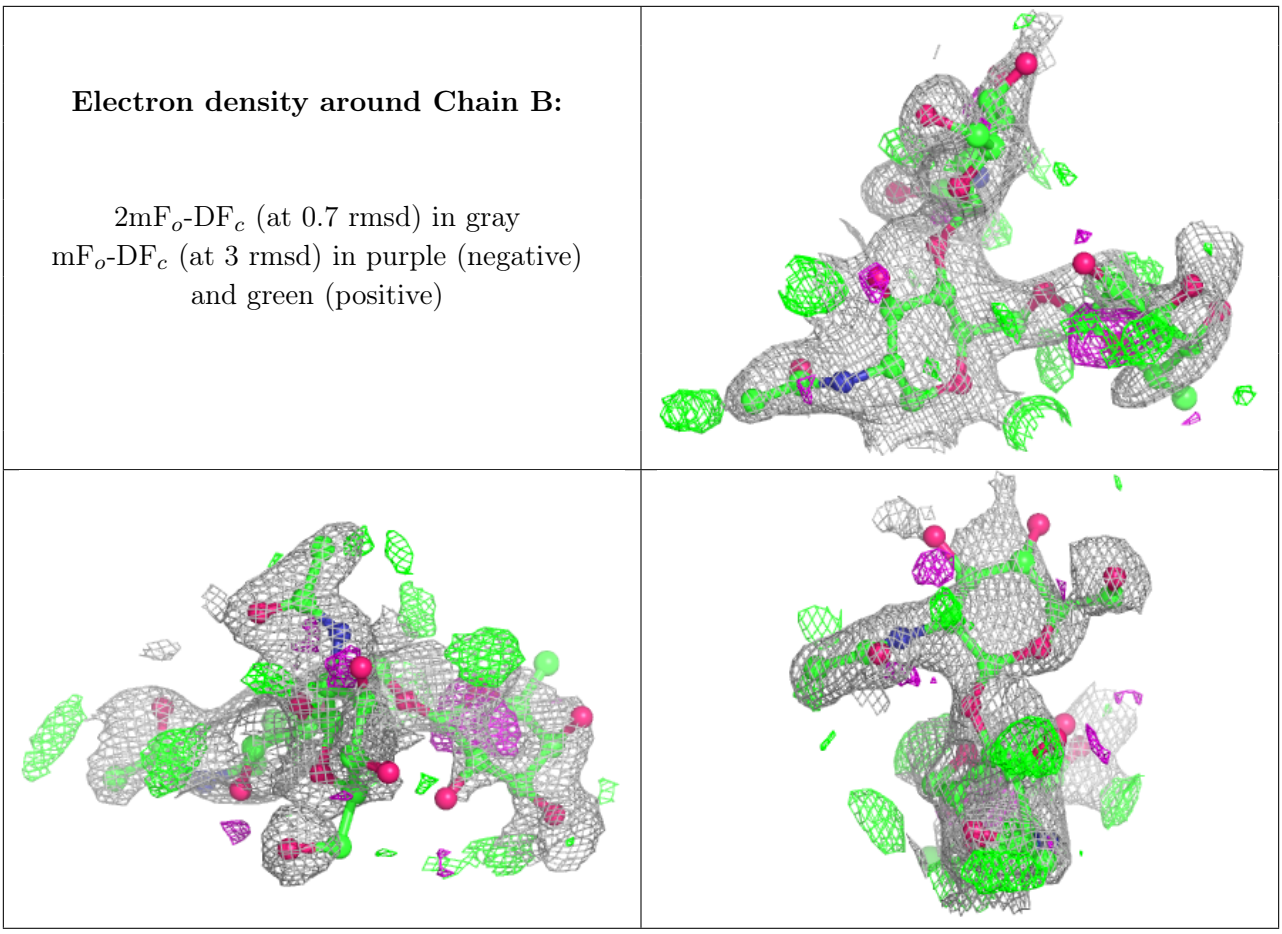
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	FUL	B	3	10/11	0.48	0.42	66,69,72,74	0
2	NAG	B	2	14/15	0.72	0.24	43,55,60,67	0
2	NAG	B	1	14/15	0.85	0.16	38,49,57,64	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.

Electron density around Chain B:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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, 95th 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
3	K	A	504	1/1	0.99	0.03	23,23,23,23	0
4	NA	A	505	1/1	0.99	0.07	16,16,16,16	1

6.5 Other polymers (i)

There are no such residues in this entry.