



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 05:29 PM UTC

PDB ID : 6G9I / pdb_00006g9i
Title : Crystal structure of Ebolavirus glycoprotein in complex with clomipramine
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Deposited on : 2018-04-10
Resolution : 2.19 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

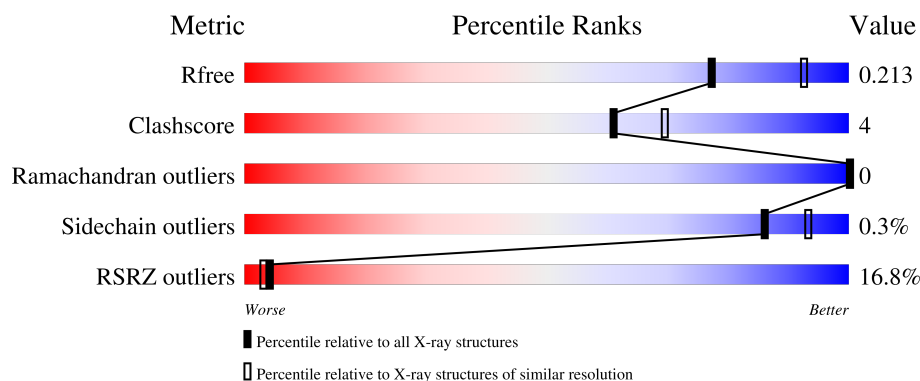
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 $\leq 5\%$. 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	330	11% 69% 7% 24%
2	B	168	16% 71% 7% 23%
3	C	4	25% 75%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3306 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 Envelope glycoprotein,Envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	7	0
			2003	1279	336	383	5			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLU	-	expression tag	UNP Q05320
A	29	THR	-	expression tag	UNP Q05320
A	30	GLY	-	expression tag	UNP Q05320
A	31	ARG	-	expression tag	UNP Q05320
A	42	ALA	THR	engineered mutation	UNP Q05320
A	471	UNK	-	linker	UNP Q05320
A	472	UNK	-	linker	UNP Q05320
A	473	UNK	-	linker	UNP Q05320
A	474	UNK	-	linker	UNP Q05320
A	475	UNK	-	linker	UNP Q05320
A	476	UNK	-	linker	UNP Q05320
A	477	UNK	-	linker	UNP Q05320
A	478	SER	-	linker	UNP Q05320
A	479	THR	THR	linker	UNP Q05320

- Molecule 2 is a protein called Envelope glycoprotein,Envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	130	Total	C	N	O	S	0	0	0
			1027	656	176	189	6			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	613	ALA	HIS	engineered mutation	UNP Q05320
B	633	GLY	-	linker	UNP Q05320

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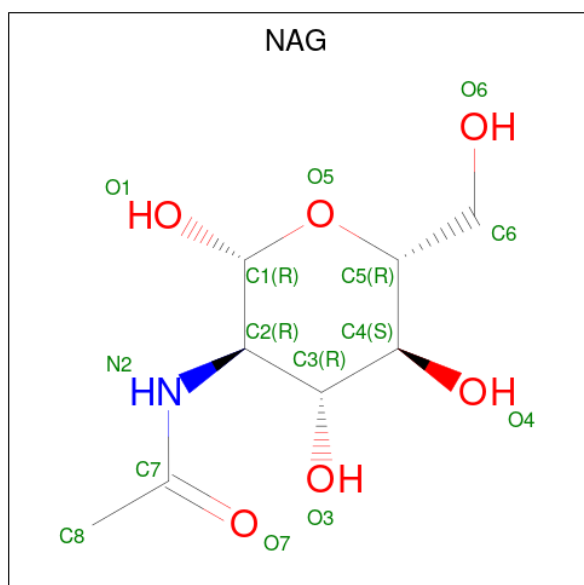
Chain	Residue	Modelled	Actual	Comment	Reference
B	634	SER	-	linker	UNP Q05320
B	635	GLY	-	linker	UNP Q05320
B	663	THR	-	expression tag	UNP M1E1E4
B	664	HIS	-	expression tag	UNP M1E1E4
B	665	HIS	-	expression tag	UNP M1E1E4
B	666	HIS	-	expression tag	UNP M1E1E4
B	667	HIS	-	expression tag	UNP M1E1E4
B	668	HIS	-	expression tag	UNP M1E1E4
B	669	HIS	-	expression tag	UNP M1E1E4

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-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
3	C	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



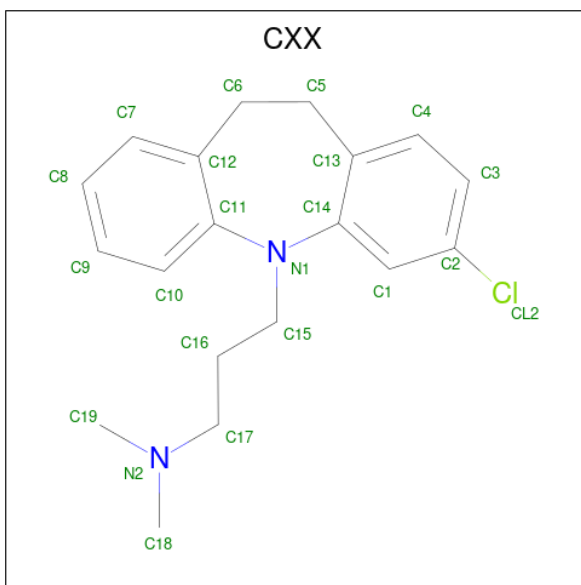
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is 3-(3-CHLORO-5H-DIBENZO[B,F]AZEPIN-5-YL)-N,N-DIMETHYLPROPAN-1-AMINE (CCD ID: CXX) (formula: $C_{19}H_{23}ClN_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	Cl	N	0	0
			22	19	1	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	77	Total	O	0	0
			77	77		
7	B	47	Total	O	0	0
			47	47		

4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	114.21Å 114.21Å 306.43Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	52.09 – 2.19 52.09 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.4 (52.09-2.19) 99.4 (52.09-2.19)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.18Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.190 , 0.208 0.196 , 0.213	Depositor DCC
R_{free} test set	2053 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3306	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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.

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: GOL, MAN, NAG, CXX, BMA

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	0.21	0/2014	0.38	0/2737
2	B	0.27	0/1052	0.48	0/1434
All	All	0.23	0/3066	0.42	0/4171

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	2003	0	1915	15	0
2	B	1027	0	997	13	0
3	C	50	0	43	0	0
4	A	56	0	52	0	0
5	A	12	0	16	0	0
5	B	12	0	16	0	0
6	B	22	0	23	0	0
7	A	77	0	0	0	0
7	B	47	0	0	1	0
All	All	3306	0	3062	26	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 4.

All (26) 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:269:THR:HG22	1:A:271:GLY:H	1.26	1.01
1:A:263:SER:HB3	1:A:265:LYS:HE2	1.55	0.87
2:B:617:LYS:HA	2:B:620:THR:HG22	1.74	0.70
2:B:616:THR:O	2:B:620:THR:HG22	1.96	0.65
1:A:106:GLU:HG3	1:A:290:PHE:CD1	2.37	0.59
2:B:617:LYS:O	2:B:617:LYS:HD3	2.06	0.56
2:B:617:LYS:HD3	2:B:621:ASP:HB3	1.87	0.56
2:B:612:PRO:O	2:B:616:THR:HG23	2.07	0.55
2:B:617:LYS:HA	2:B:620:THR:CG2	2.36	0.55
1:A:228:ASN:OD1	1:A:229:GLU:HG2	2.08	0.54
1:A:71:GLU:OE2	1:A:107:ASN:N	2.41	0.53
1:A:265:LYS:HB3	1:A:275:TRP:CZ2	2.46	0.51
2:B:596:ARG:NE	7:B:801:HOH:O	2.37	0.51
2:B:619:ILE:HA	2:B:622:LYS:HB2	1.92	0.51
1:A:263:SER:HB3	1:A:265:LYS:CE	2.37	0.50
1:A:51[B]:LEU:HD23	2:B:607:ASP:HA	1.96	0.46
2:B:617:LYS:HZ3	2:B:620:THR:HG23	1.81	0.46
1:A:188:GLN:CD	1:A:188:GLN:N	2.75	0.45
1:A:47[A]:ASP:O	1:A:51[A]:LEU:HG	2.17	0.44
1:A:277:VAL:HG13	1:A:281:ILE:HG12	1.99	0.44
2:B:622:LYS:CG	2:B:625:GLN:HE21	2.31	0.44
1:A:49[A]:ASP:HA	2:B:595:GLN:HG2	1.99	0.43
1:A:188:GLN:CD	1:A:188:GLN:H	2.27	0.42
1:A:248:PHE:HA	1:A:283:THR:HG21	2.00	0.42
1:A:64:ARG:HG3	1:A:186:LEU:HD11	2.03	0.41
2:B:617:LYS:CD	2:B:621:ASP:HB3	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	243/330 (74%)	240 (99%)	3 (1%)	0	100	100
2	B	128/168 (76%)	121 (94%)	7 (6%)	0	100	100
All	All	371/498 (74%)	361 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	214/273 (78%)	212 (99%)	2 (1%)	70	84
2	B	108/139 (78%)	108 (100%)	0	100	100
All	All	322/412 (78%)	320 (99%)	2 (1%)	86	89

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

Mol	Chain	Res	Type
1	A	50[A]	LYS
1	A	50[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
2	B	625	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

4 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	C	1	3,2	14,14,15	0.20	0	17,19,21	0.81	1 (5%)
3	NAG	C	2	3	14,14,15	0.25	0	17,19,21	0.76	1 (5%)
3	BMA	C	3	3	11,11,12	0.86	0	15,15,17	0.77	0
3	MAN	C	4	3	11,11,12	0.78	0	15,15,17	1.50	2 (13%)

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	C	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4	MAN	C1-O5-C5	4.39	118.07	112.19
3	C	1	NAG	C1-O5-C5	2.48	115.50	112.19
3	C	4	MAN	O2-C2-C3	-2.43	105.11	110.15
3	C	2	NAG	C1-O5-C5	2.36	115.34	112.19

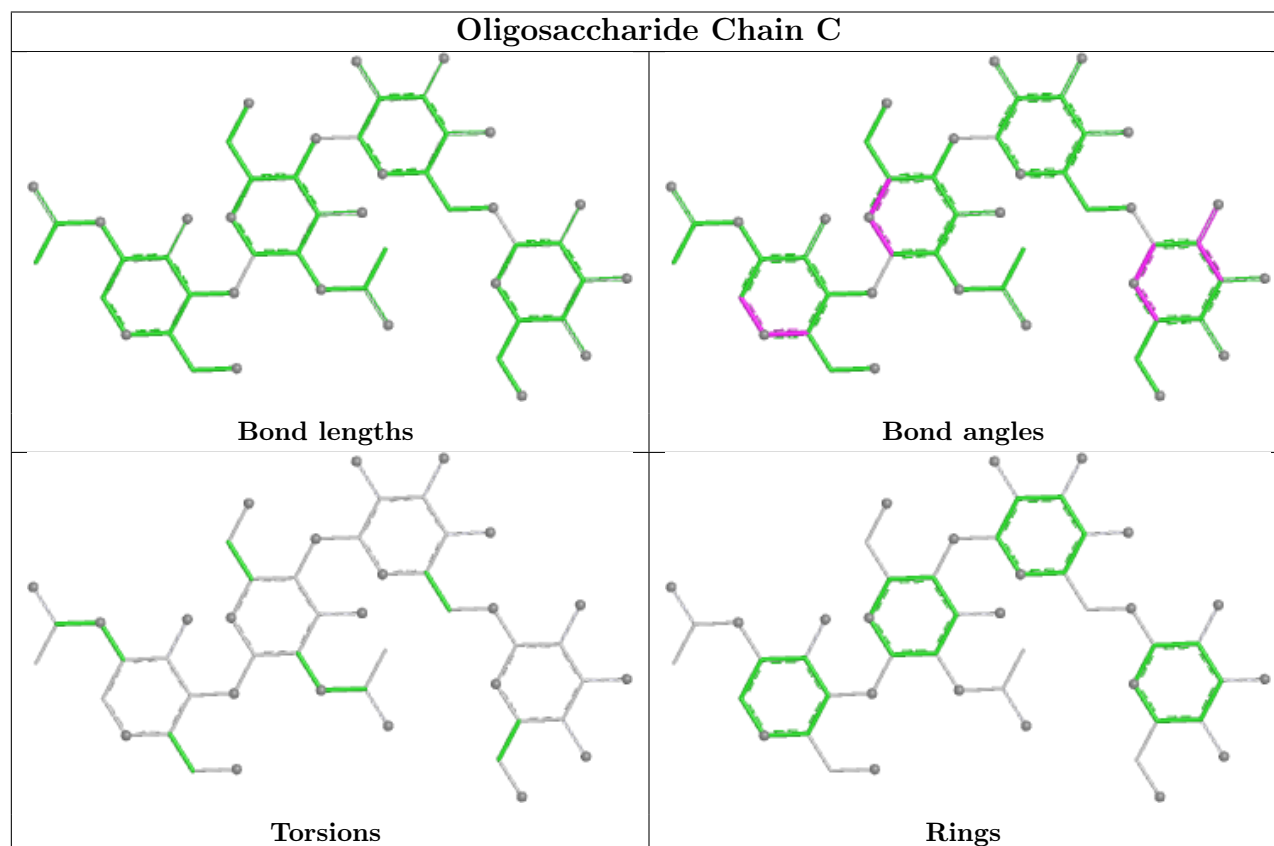
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry [i](#)

9 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	A	604	1	14,14,15	0.32	0	17,19,21	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CXX	B	707	-	24,24,24	0.76	1 (4%)	33,33,33	1.16	3 (9%)
5	GOL	A	606	-	5,5,5	1.09	0	5,5,5	0.82	0
5	GOL	B	701	-	5,5,5	1.01	0	5,5,5	1.03	0
5	GOL	B	702	-	5,5,5	1.01	0	5,5,5	0.98	0
4	NAG	A	603	1	14,14,15	1.15	1 (7%)	17,19,21	1.21	1 (5%)
4	NAG	A	602	1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	A	601	1	14,14,15	0.26	0	17,19,21	0.54	0
5	GOL	A	605	-	5,5,5	0.94	0	5,5,5	0.99	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
4	NAG	A	604	1	-	0/6/23/26	0/1/1/1
6	CXX	B	707	-	-	1/6/19/19	0/3/3/3
5	GOL	A	606	-	-	4/4/4/4	-
5	GOL	B	701	-	-	2/4/4/4	-
5	GOL	B	702	-	-	2/4/4/4	-
4	NAG	A	603	1	-	0/6/23/26	0/1/1/1
4	NAG	A	602	1	-	0/6/23/26	0/1/1/1
4	NAG	A	601	1	-	0/6/23/26	0/1/1/1
5	GOL	A	605	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	NAG	O5-C1	3.76	1.50	1.43
6	B	707	CXX	C2-CL2	2.50	1.80	1.74

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	NAG	C1-O5-C5	4.75	118.56	112.19
6	B	707	CXX	C14-N1-C11	2.41	122.18	116.29
6	B	707	CXX	C13-C14-N1	2.26	124.65	120.06
6	B	707	CXX	C5-C6-C12	-2.06	106.67	115.54

There are no chirality outliers.

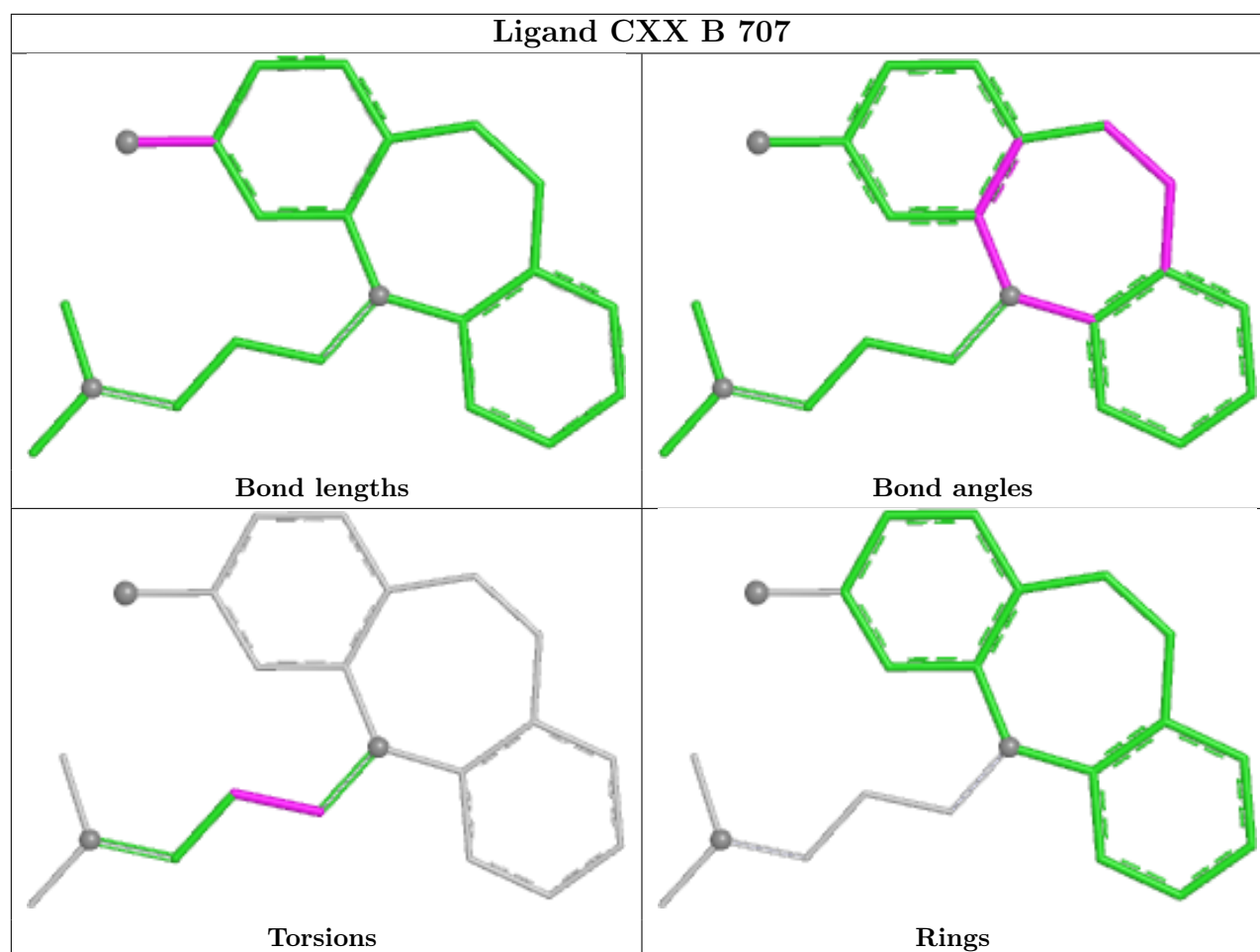
All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	606	GOL	O1-C1-C2-C3
5	A	606	GOL	C1-C2-C3-O3
5	B	702	GOL	C1-C2-C3-O3
5	B	702	GOL	O2-C2-C3-O3
5	A	605	GOL	O1-C1-C2-C3
5	A	605	GOL	C1-C2-C3-O3
5	B	701	GOL	O1-C1-C2-C3
5	A	606	GOL	O1-C1-C2-O2
5	A	606	GOL	O2-C2-C3-O3
5	B	701	GOL	O1-C1-C2-O2
6	B	707	CXX	N1-C15-C16-C17
5	A	605	GOL	O2-C2-C3-O3
5	A	605	GOL	O1-C1-C2-O2

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 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 than 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	310:VAL	C	471:UNK	N	10.77

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	244/330 (73%)	0.83	36 (14%) 5 4	36, 61, 131, 169	7 (2%)
2	B	130/168 (77%)	1.01	27 (20%) 2 2	42, 59, 185, 201	0
All	All	374/498 (75%)	0.89	63 (16%) 4 3	36, 60, 161, 201	7 (1%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	49[A]	ASP	10.1
1	A	48[A]	VAL	9.1
2	B	626	ILE	8.9
1	A	189	ALA	8.1
1	A	51[A]	LEU	8.0
2	B	615	TRP	7.8
2	B	522	ASP	7.7
1	A	310	VAL	7.5
2	B	623	ILE	7.0
2	B	631	VAL	6.9
2	B	627	ILE	6.5
1	A	293	THR	5.7
2	B	525	ALA	5.6
2	B	620	THR	5.5
1	A	283	THR	5.2
2	B	521	GLN	5.2
1	A	288	TRP	4.9
1	A	305	LEU	4.9
1	A	307	PHE	4.8
1	A	269	THR	4.7
1	A	309	VAL	4.5
1	A	47[A]	ASP	4.3
2	B	616	THR	4.2
1	A	39	HIS	4.2

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Mol	Chain	Res	Type	RSRZ
2	B	630	PHE	4.1
1	A	211	SER	4.1
2	B	527	ILE	3.9
1	A	188	GLN	3.8
1	A	308	THR	3.8
2	B	613	ALA	3.7
2	B	524	GLY	3.6
1	A	306	SER	3.6
1	A	290	PHE	3.6
1	A	214	TYR	3.5
2	B	523	GLU	3.5
1	A	52[A]	VAL	3.5
2	B	619	ILE	3.4
2	B	614	ASP	3.2
1	A	46[A]	SER	3.2
1	A	270	THR	3.2
1	A	50[A]	LYS	3.2
1	A	281	ILE	3.0
1	A	277	VAL	2.9
2	B	604	LEU	2.9
1	A	272	LYS	2.8
2	B	526	ALA	2.7
1	A	264	GLY	2.7
2	B	617	LYS	2.6
1	A	255	GLN	2.6
1	A	54	ARG	2.6
1	A	275	TRP	2.5
1	A	289	ALA	2.3
2	B	503	ALA	2.3
2	B	618	ASN	2.3
1	A	287	GLU	2.2
1	A	251	GLN	2.1
1	A	115	LYS	2.1
2	B	556	CYS	2.1
2	B	551	GLN	2.1
2	B	625	GLN	2.1
2	B	606	PRO	2.1
2	B	622	LYS	2.1
1	A	228	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

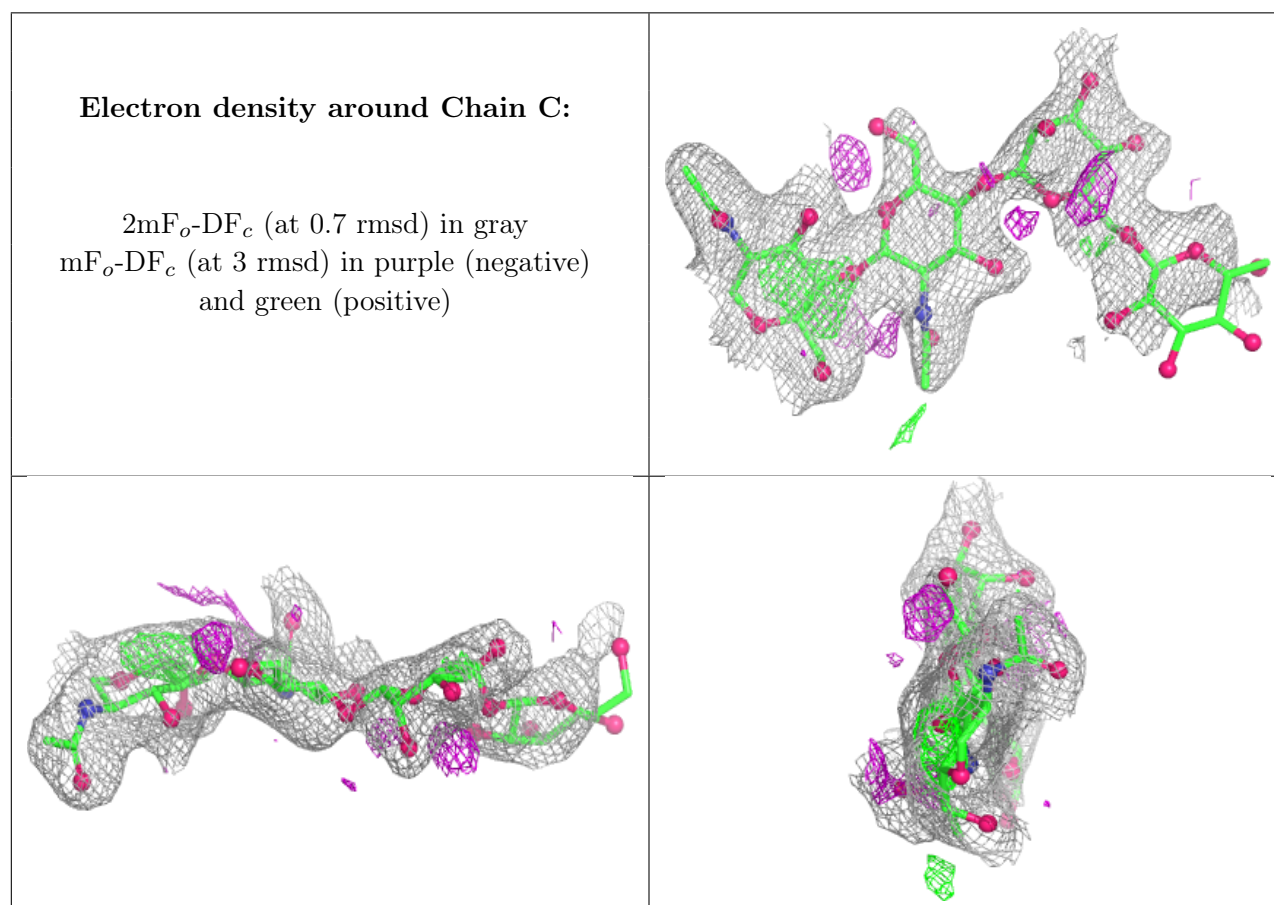
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
3	BMA	C	3	11/12	0.24	0.23	192,195,205,208	0
3	MAN	C	4	11/12	0.30	0.17	210,212,217,220	0
3	NAG	C	2	14/15	0.84	0.25	127,139,162,186	0
3	NAG	C	1	14/15	0.94	0.11	45,59,71,100	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

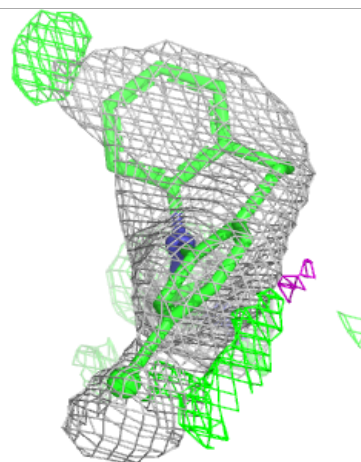
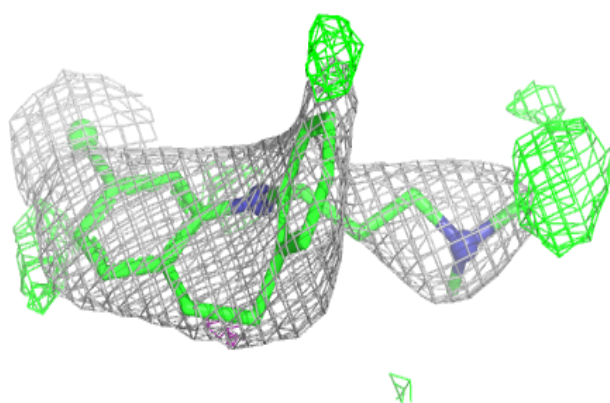
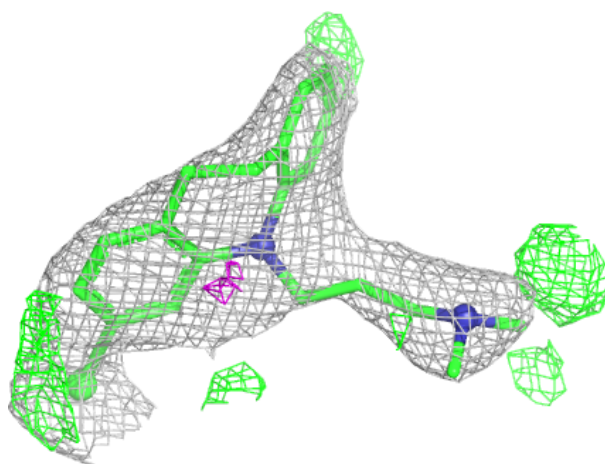
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	603	14/15	0.50	0.18	136,145,149,151	0
4	NAG	A	604	14/15	0.65	0.22	121,138,143,146	0
5	GOL	B	702	6/6	0.65	0.34	118,121,123,124	0
5	GOL	A	605	6/6	0.79	0.22	79,97,105,110	0
4	NAG	A	602	14/15	0.84	0.15	95,113,121,123	0
6	CXX	B	707	22/22	0.84	0.26	96,102,110,134	0
5	GOL	A	606	6/6	0.90	0.19	68,80,87,88	0
5	GOL	B	701	6/6	0.91	0.16	71,85,93,96	0
4	NAG	A	601	14/15	0.93	0.12	58,79,89,91	0

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.

Electron density around CXX B 707:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.