Full wwPDB X-ray Structure Validation Report (i)

Oct 8, 2023 – 10:08 AM EDT

PDB ID	:	6EAY
Title	:	Structural Basis for Broad Neutralization of Ebolaviruses by an Antibody Targeting the Glycoprotein Fusion Loop
Authors	:	Janus, B.M.; Ofek, G.
Deposited on	:	2018-08-03
Resolution	:	3.72 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
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 ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.72 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.
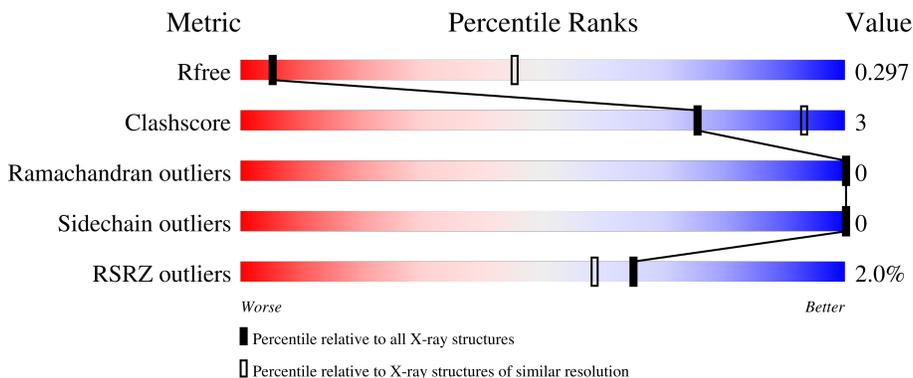
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1089 (3.90-3.54)
Clashscore	141614	1012 (3.88-3.56)
Ramachandran outliers	138981	1114 (3.90-3.54)
Sidechain outliers	138945	1110 (3.90-3.54)
RSRZ outliers	127900	1020 (3.90-3.54)

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	L	215	3% / 95% • •
2	H	237	3% / 81% • 15%
3	A	163	% / 64% 6% 31%
4	B	319	65% • 31%
5	C	8	50% 50%
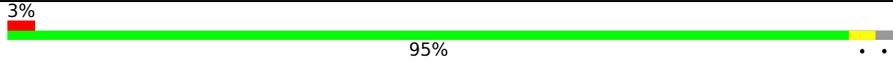
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	BMA	C	3	-	-	X	-
5	MAN	C	4	-	-	X	-

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 5376 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 CA45 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	0	0
			1481	927	251	298	5			

- Molecule 2 is a protein called CA45 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	202	Total	C	N	O	S	0	0	0
			1367	869	229	265	4			

- Molecule 3 is a protein called Envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	113	Total	C	N	O	S	0	0	0
			837	531	146	154	6			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	544	THR	ILE	conflict	UNP Q05320
A	638	GLY	-	expression tag	UNP Q05320
A	639	GLU	-	expression tag	UNP Q05320
A	640	ASN	-	expression tag	UNP Q05320
A	641	LEU	-	expression tag	UNP Q05320
A	642	TYR	-	expression tag	UNP Q05320
A	643	PHE	-	expression tag	UNP Q05320
A	644	GLN	-	expression tag	UNP Q05320
A	645	SER	-	expression tag	UNP Q05320
A	646	GLY	-	expression tag	UNP Q05320
A	647	SER	-	expression tag	UNP Q05320
A	648	ALA	-	expression tag	UNP Q05320
A	649	TRP	-	expression tag	UNP Q05320
A	650	SER	-	expression tag	UNP Q05320

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Chain	Residue	Modelled	Actual	Comment	Reference
A	651	HIS	-	expression tag	UNP Q05320
A	652	PRO	-	expression tag	UNP Q05320
A	653	GLN	-	expression tag	UNP Q05320
A	654	PHE	-	expression tag	UNP Q05320
A	655	GLU	-	expression tag	UNP Q05320
A	656	LYS	-	expression tag	UNP Q05320
A	657	HIS	-	expression tag	UNP Q05320
A	658	HIS	-	expression tag	UNP Q05320
A	659	HIS	-	expression tag	UNP Q05320
A	660	HIS	-	expression tag	UNP Q05320
A	661	HIS	-	expression tag	UNP Q05320
A	662	HIS	-	expression tag	UNP Q05320
A	663	HIS	-	expression tag	UNP Q05320
A	664	HIS	-	expression tag	UNP Q05320

- Molecule 4 is a protein called Envelope glycoprotein.

| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	B	221	1569	1001	266	297	5	0	0	0

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.
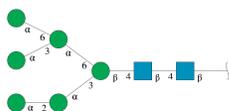
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	C	8	94	52	2	40	0	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).
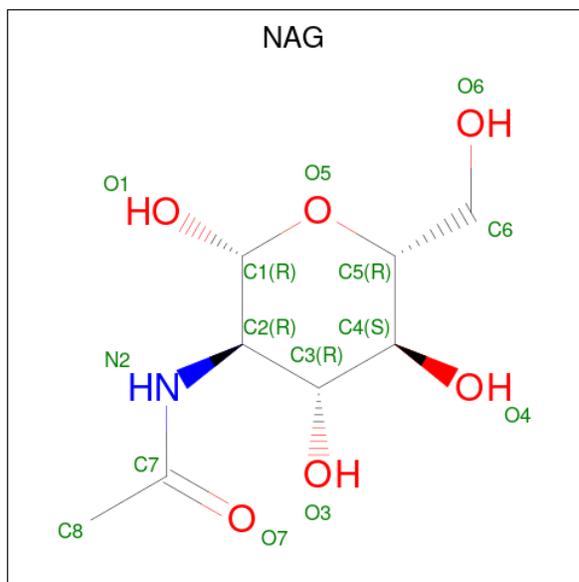
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

3 Residue-property plots ⓘ

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: CA45 light chain
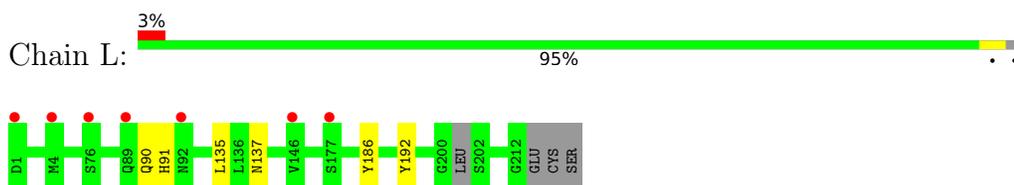
Chain L:

- Molecule 2: CA45 heavy chain

Chain H:
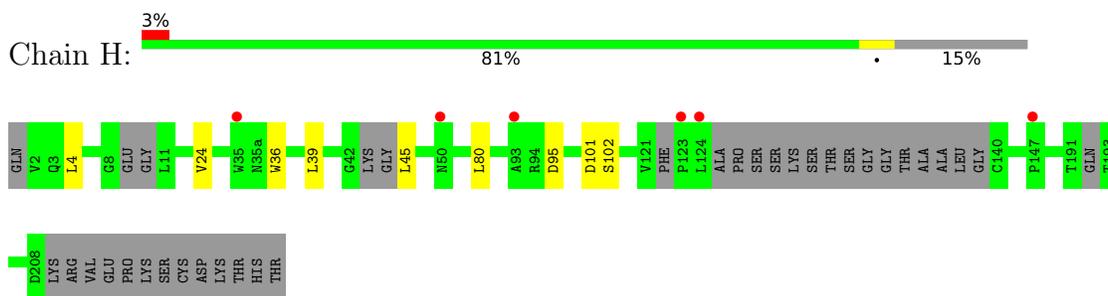
- Molecule 3: Envelope glycoprotein

Chain A:
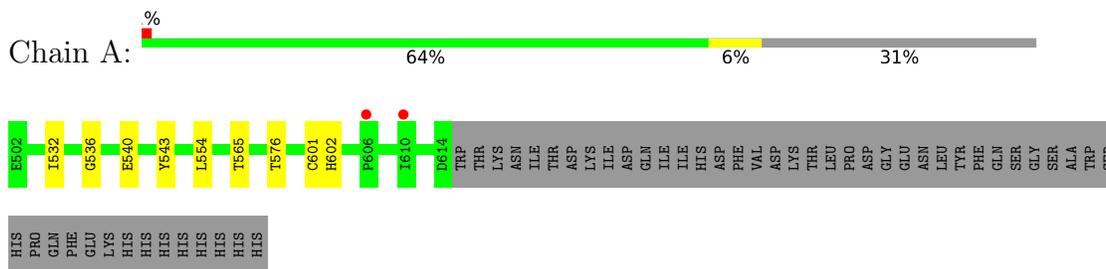
- Molecule 4: Envelope glycoprotein

Chain B:
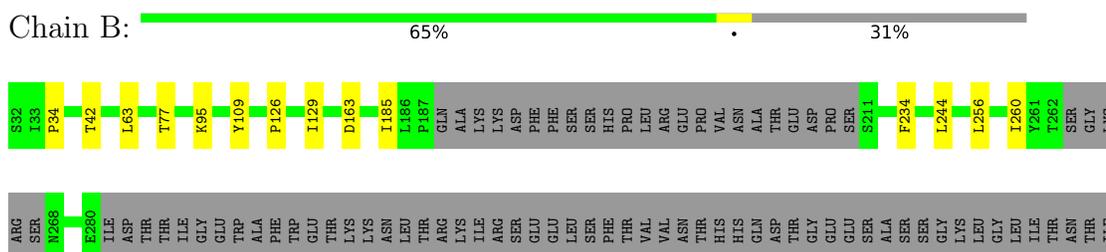
ALA GLY VAL ALA GLY LEU ILE THR GLY GLY ARG ARG THR ARG ARG

• Molecule 5: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyran ose-(1-3)-[alpha-D-mannopyranose-(1-6)]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-glucopyranos e

Chain C:

50%   50%

NAG1 NAG2 BMA3 MAN4 MAN5 MAN6 MAN7 MAN8

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	153.43Å　153.43Å　335.86Å 90.00°　　90.00°　　120.00°	Depositor
Resolution (Å)	45.13　–　3.72 76.71　–　3.72	Depositor EDS
% Data completeness (in resolution range)	86.0 (45.13-3.72) 80.5 (76.71-3.72)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.76 (at 3.67Å)	Xtriage
Refinement program	PHENIX (1.14_3228: ???)	Depositor
R, R_{free}	0.259　,　0.297 0.258　,　0.297	Depositor DCC
R_{free} test set	696 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	88.0	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 53.5	EDS
L-test for twinning[2]	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	5376	wwPDB-VP
Average B, all atoms (Å^2)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, BMA, 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	L	0.24	0/1511	0.44	0/2068
2	H	0.24	0/1402	0.46	0/1933
3	A	0.25	0/857	0.43	0/1172
4	B	0.25	0/1607	0.43	0/2199
All	All	0.24	0/5377	0.44	0/7372

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 ⓘ

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	L	1481	0	1322	3	0
2	H	1367	0	1131	6	0
3	A	837	0	767	7	0
4	B	1569	0	1348	9	0
5	C	94	0	79	8	0
6	B	28	0	26	0	0
All	All	5376	0	4673	29	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 3.

All (29) 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)
5:C:3:BMA:H2	5:C:4:MAN:H5	1.70	0.72
5:C:3:BMA:C3	5:C:4:MAN:H5	2.27	0.65
3:A:565:THR:HG23	4:B:34:PRO:HD2	1.79	0.64
5:C:3:BMA:C2	5:C:4:MAN:H5	2.28	0.63
5:C:3:BMA:H3	5:C:4:MAN:H5	1.82	0.61
3:A:601:CYS:SG	3:A:602:HIS:N	2.78	0.57
2:H:39:LEU:HB3	2:H:45:LEU:HD23	1.87	0.56
4:B:126:PRO:HD2	4:B:129:ILE:HD12	1.88	0.56
4:B:77:THR:O	4:B:109:TYR:OH	2.25	0.54
3:A:543:TYR:OH	4:B:163:ASP:OD1	2.26	0.52
5:C:2:NAG:O3	5:C:3:BMA:O5	2.25	0.52
4:B:256:LEU:O	4:B:260:ILE:N	2.43	0.51
3:A:532:ILE:O	3:A:536:GLY:N	2.43	0.51
2:H:101:ASP:OD1	2:H:102:SER:N	2.43	0.50
2:H:4:LEU:HD22	2:H:24:VAL:HG22	1.94	0.50
2:H:36:TRP:CG	2:H:80:LEU:HD12	2.47	0.50
2:H:95:ASP:N	2:H:95:ASP:OD1	2.47	0.47
5:C:2:NAG:H83	5:C:6:MAN:O4	2.13	0.47
2:H:36:TRP:CD2	2:H:80:LEU:HD12	2.51	0.46
5:C:3:BMA:H3	5:C:4:MAN:C5	2.46	0.46
4:B:234:PHE:HB2	4:B:244:LEU:HD21	1.99	0.45
1:L:90:GLN:O	1:L:91:HIS:ND1	2.50	0.44
3:A:554:LEU:HD12	4:B:42:THR:HA	2.00	0.44
4:B:63:LEU:HD23	4:B:185:ILE:HG12	1.99	0.43
1:L:135:LEU:HD21	1:L:137:ASN:HB2	2.02	0.42
3:A:576:THR:O	4:B:95:LYS:NZ	2.47	0.41
3:A:540:GLU:N	3:A:540:GLU:OE1	2.53	0.41
5:C:3:BMA:C3	5:C:4:MAN:C5	2.97	0.40
1:L:186:TYR:O	1:L:192:TYR:OH	2.38	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	L	207/215 (96%)	198 (96%)	9 (4%)	0	100	100
2	H	190/237 (80%)	187 (98%)	3 (2%)	0	100	100
3	A	111/163 (68%)	105 (95%)	6 (5%)	0	100	100
4	B	215/319 (67%)	206 (96%)	9 (4%)	0	100	100
All	All	723/934 (77%)	696 (96%)	27 (4%)	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	L	144/186 (77%)	144 (100%)	0	100	100
2	H	120/202 (59%)	120 (100%)	0	100	100
3	A	79/139 (57%)	79 (100%)	0	100	100
4	B	139/271 (51%)	139 (100%)	0	100	100
All	All	482/798 (60%)	482 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

8 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	#$|Z| > 2$
5	NAG	C	1	5,3	14,14,15	0.38	0	17,19,21	0.43	0
5	NAG	C	2	5	14,14,15	0.35	0	17,19,21	0.46	0
5	BMA	C	3	5	11,11,12	0.44	0	15,15,17	0.89	0
5	MAN	C	4	5	11,11,12	0.30	0	15,15,17	0.64	0
5	MAN	C	5	5	11,11,12	0.24	0	15,15,17	0.58	0
5	MAN	C	6	5	11,11,12	0.63	0	15,15,17	0.75	0
5	MAN	C	7	5	11,11,12	0.37	0	15,15,17	0.69	0
5	MAN	C	8	5	11,11,12	0.34	0	15,15,17	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
5	NAG	C	1	5,3	-	0/6/23/26	0/1/1/1
5	NAG	C	2	5	-	2/6/23/26	0/1/1/1
5	BMA	C	3	5	-	0/2/19/22	0/1/1/1
5	MAN	C	4	5	-	0/2/19/22	0/1/1/1
5	MAN	C	5	5	-	0/2/19/22	0/1/1/1
5	MAN	C	6	5	-	2/2/19/22	0/1/1/1
5	MAN	C	7	5	-	0/2/19/22	0/1/1/1
5	MAN	C	8	5	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	8	MAN	O5-C5-C6-O6
5	C	8	MAN	C4-C5-C6-O6
5	C	2	NAG	O5-C5-C6-O6
5	C	6	MAN	C4-C5-C6-O6
5	C	6	MAN	O5-C5-C6-O6
5	C	2	NAG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	6	MAN	1	0
5	C	3	BMA	7	0
5	C	4	MAN	6	0
5	C	2	NAG	2	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.

Oligosaccharide Chain C

Bond lengths

Bond angles

Torsions

Rings
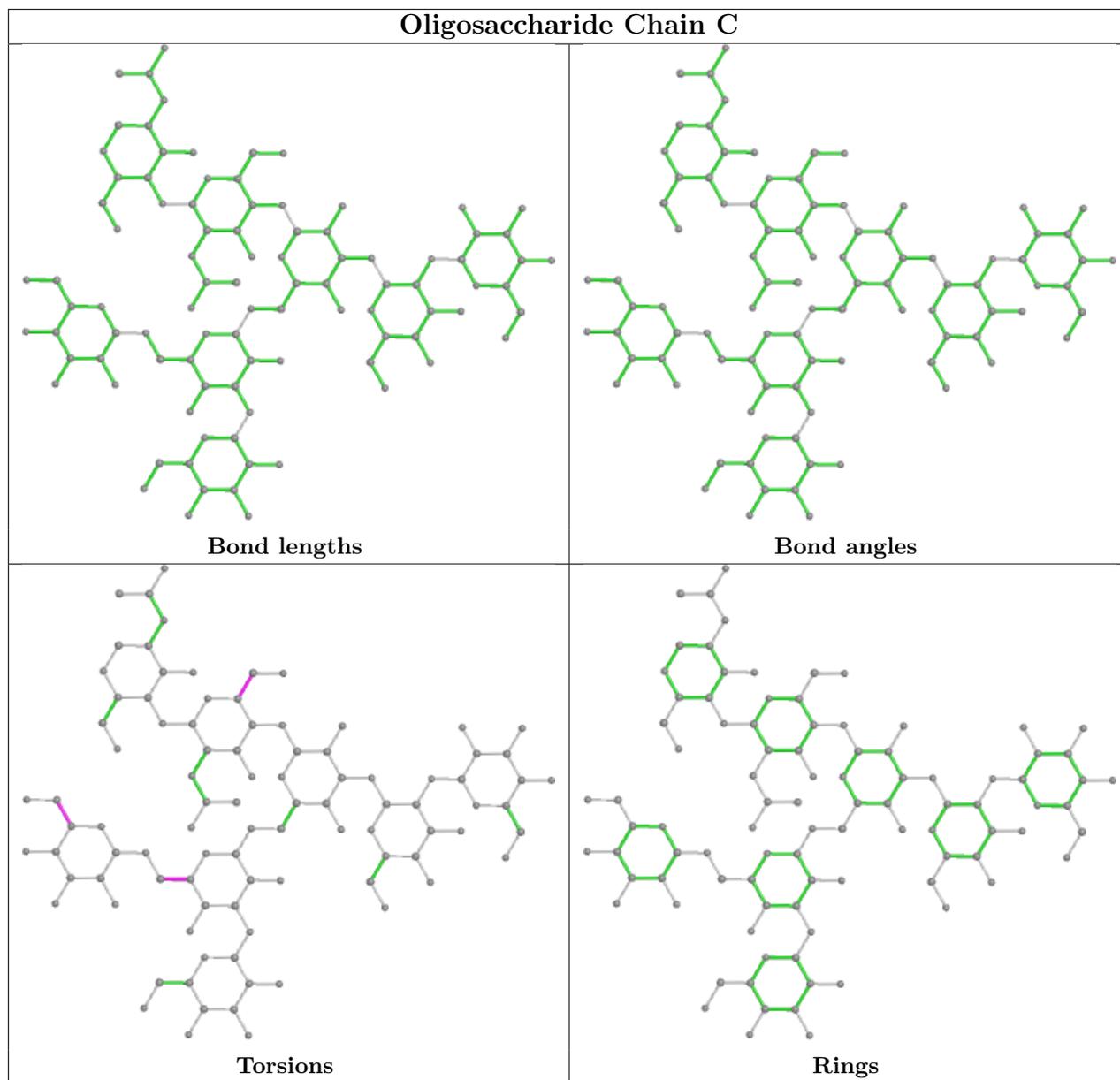
5.6 Ligand geometry ⓘ

2 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	$\#|Z| > 2$
6	NAG	B	401	4	14,14,15	0.27	0	17,19,21	0.44	0
6	NAG	B	402	4	14,14,15	0.26	0	17,19,21	0.43	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
6	NAG	B	401	4	-	3/6/23/26	0/1/1/1
6	NAG	B	402	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	402	NAG	O5-C5-C6-O6
6	B	402	NAG	C4-C5-C6-O6
6	B	401	NAG	C8-C7-N2-C2
6	B	401	NAG	O7-C7-N2-C2
6	B	401	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

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	L	211/215 (98%)	0.29	7 (3%)	46	38	86, 122, 185, 214	0
2	H	202/237 (85%)	0.27	6 (2%)	50	40	94, 127, 161, 174	0
3	A	113/163 (69%)	0.13	2 (1%)	68	62	65, 89, 180, 198	0
4	B	221/319 (69%)	-0.06	0	100	100	58, 88, 133, 160	0
All	All	747/934 (79%)	0.16	15 (2%)	65	58	58, 112, 169, 214	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	89	GLN	3.0
2	H	123	PRO	2.5
2	H	35	TRP	2.5
3	A	606	PRO	2.4
1	L	92	ASN	2.4
2	H	93	ALA	2.3
1	L	76	SER	2.3
2	H	147	PRO	2.2
1	L	1	ASP	2.2
1	L	4	MET	2.2
3	A	610	ILE	2.2
1	L	146	VAL	2.1
1	L	177	SER	2.1
2	H	50	ASN	2.0
2	H	124	LEU	2.0

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

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
5	MAN	C	5	11/12	0.70	0.22	131,131,131,131	0
5	MAN	C	7	11/12	0.84	0.24	118,118,118,118	0
5	NAG	C	2	14/15	0.88	0.19	78,87,91,101	0
5	MAN	C	8	11/12	0.88	0.25	99,99,99,99	0
5	MAN	C	4	11/12	0.89	0.21	115,115,115,115	0
5	MAN	C	6	11/12	0.90	0.17	100,100,100,100	0
5	BMA	C	3	11/12	0.92	0.14	93,98,105,107	0
5	NAG	C	1	14/15	0.93	0.24	59,63,69,79	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.
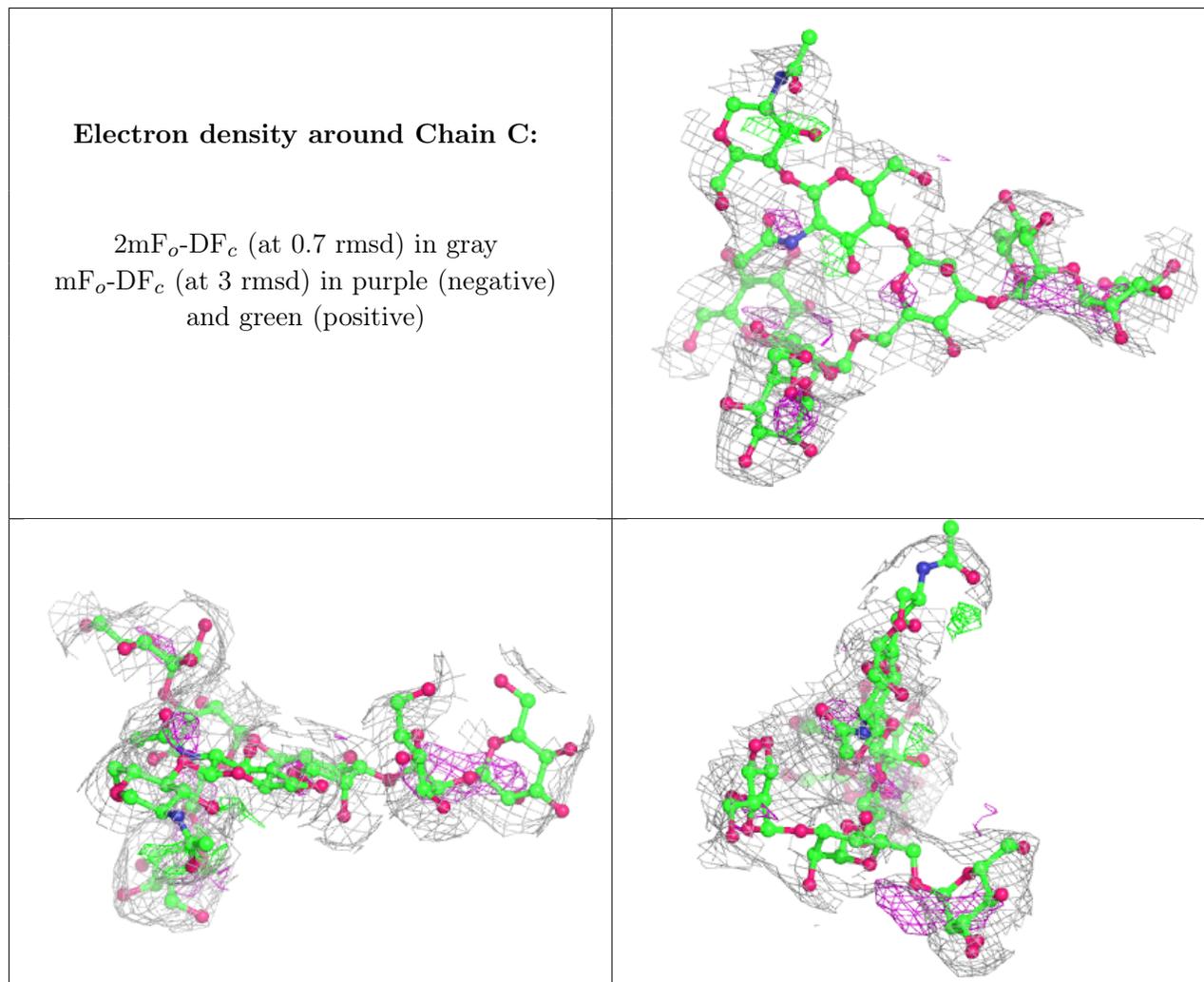
Electron density around Chain C:

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

6.4 Ligands ⓘ

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
6	NAG	B	401	14/15	0.84	0.24	114,114,114,114	0
6	NAG	B	402	14/15	0.88	0.19	108,108,108,108	0

6.5 Other polymers ⓘ

There are no such residues in this entry.