Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 07:25 AM EDT

PDB ID	:	6MU3
Title	:	Anti-HIV-1 Fab 2G12 + Man7 re-refinement
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Deposited on	:	2018-10-22
Resolution	:	2.33 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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
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-RAY DIFFRACTION

The reported resolution of this entry is 2.33 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6681 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 Fab 2G12, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	1	0
			1626	1023	275	323	5			
1	K	211	Total	C	N	O	S	0	1	0
			1621	1020	272	323	6			

- Molecule 2 is a protein called Fab 2G12, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	218	Total	C	N	O	S	0	1	0
			1635	1030	278	319	8			
2	M	216	Total	C	N	O	S	0	1	0
			1627	1026	276	317	8			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	A	4	Total	C	O	0	0	0
			45	24	21			
3	B	4	Total	C	O	0	0	0
			45	24	21			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	31	Total	O	0	0
			31	31		
4	H	17	Total	O	0	0
			17	17		
4	K	18	Total	O	0	0
			18	18		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	M	16	Total O 16 16	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	44.82Å 131.09Å 169.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.43 – 2.33	Depositor
% Data completeness (in resolution range)	99.3 (40.43-2.33)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.12 (at 2.31Å)	Xtriage
Refinement program	PHENIX (1.12_2829)	Depositor
R, R_{free}	0.201 , 0.234	Depositor
Wilson B-factor (Å^2)	47.3	Xtriage
Anisotropy	0.625	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6681	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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.

4 Model quality

4.1 Standard geometry

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles

4.3.1 Protein backbone

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains

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

4.5 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	$\#\|Z\|>2$
3	BMA	A	1	3	12,12,12	0.51	0	17,17,17	0.68	0
3	MAN	A	2	3	11,11,12	0.76	0	15,15,17	1.01	2 (13%)
3	MAN	A	3	3	11,11,12	0.70	0	15,15,17	1.26	2 (13%)
3	MAN	A	4	3	11,11,12	0.52	0	15,15,17	1.18	2 (13%)
3	BMA	B	1	3	12,12,12	0.62	0	17,17,17	0.72	1 (5%)
3	MAN	B	2	3	11,11,12	0.76	0	15,15,17	1.16	3 (20%)
3	MAN	B	3	3	11,11,12	0.90	0	15,15,17	1.14	2 (13%)
3	MAN	B	4	3	11,11,12	0.49	0	15,15,17	1.23	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	BMA	A	1	3	-	0/2/22/22	0/1/1/1
3	MAN	A	2	3	-	0/2/19/22	0/1/1/1
3	MAN	A	3	3	-	1/2/19/22	0/1/1/1
3	MAN	A	4	3	-	0/2/19/22	0/1/1/1
3	BMA	B	1	3	-	1/2/22/22	0/1/1/1
3	MAN	B	2	3	-	0/2/19/22	0/1/1/1
3	MAN	B	3	3	-	0/2/19/22	0/1/1/1
3	MAN	B	4	3	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	3	MAN	C1-O5-C5	3.83	117.39	112.19
3	A	4	MAN	C1-O5-C5	3.52	116.96	112.19
3	B	4	MAN	C1-O5-C5	3.45	116.86	112.19
3	B	2	MAN	C1-O5-C5	2.72	115.88	112.19
3	B	3	MAN	C1-O5-C5	2.70	115.85	112.19
3	A	2	MAN	C1-O5-C5	2.61	115.73	112.19
3	B	3	MAN	O2-C2-C3	-2.57	104.99	110.14
3	A	3	MAN	O2-C2-C3	-2.37	105.40	110.14
3	B	4	MAN	O2-C2-C3	-2.35	105.43	110.14
3	A	2	MAN	O2-C2-C3	-2.23	105.68	110.14
3	A	4	MAN	O2-C2-C3	-2.20	105.72	110.14
3	B	2	MAN	O2-C2-C3	-2.20	105.73	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1	BMA	O2-C2-C3	-2.12	105.46	110.35
3	B	2	MAN	C1-C2-C3	-2.07	107.12	109.67

There are no chirality outliers.

All (4) torsion outliers are listed below:

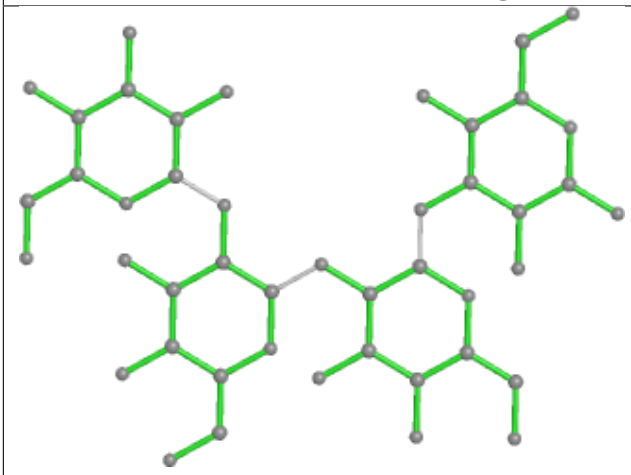
Mol	Chain	Res	Type	Atoms
3	B	1	BMA	O5-C5-C6-O6
3	B	4	MAN	C4-C5-C6-O6
3	B	4	MAN	O5-C5-C6-O6
3	A	3	MAN	O5-C5-C6-O6

There are no ring outliers.

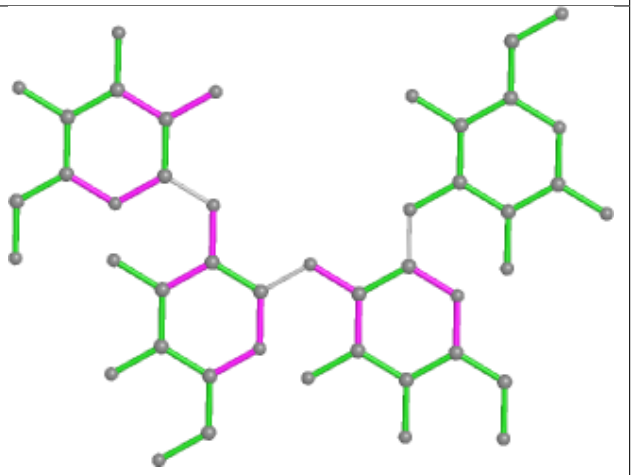
No monomer is involved in short contacts.

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

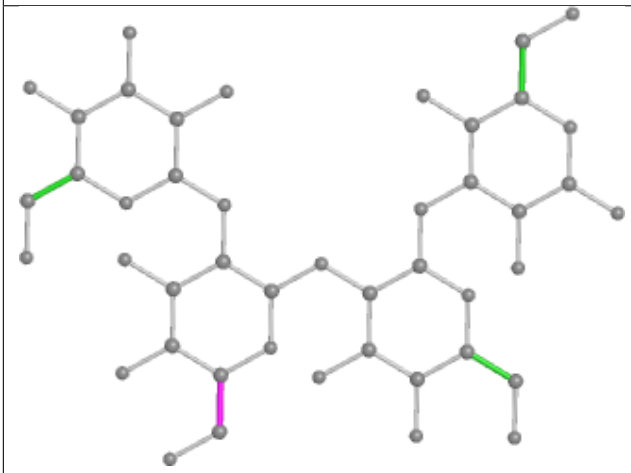
Oligosaccharide Chain A



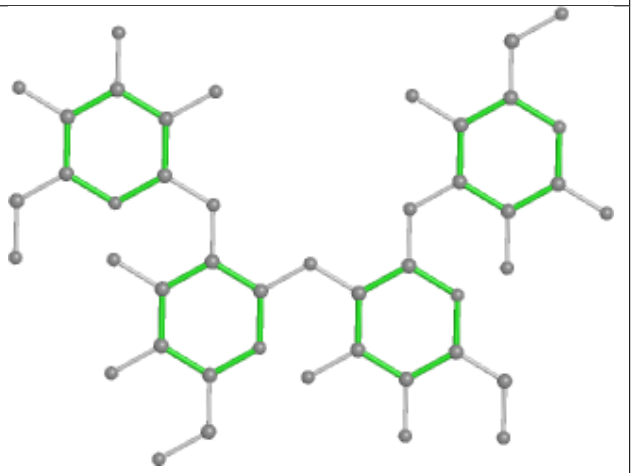
Bond lengths



Bond angles

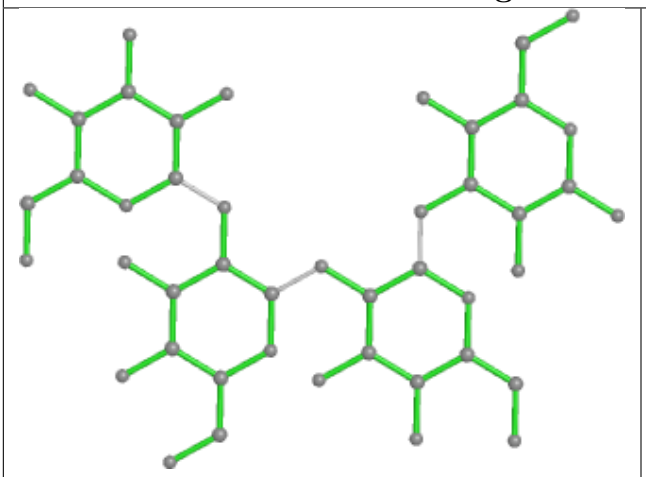


Torsions

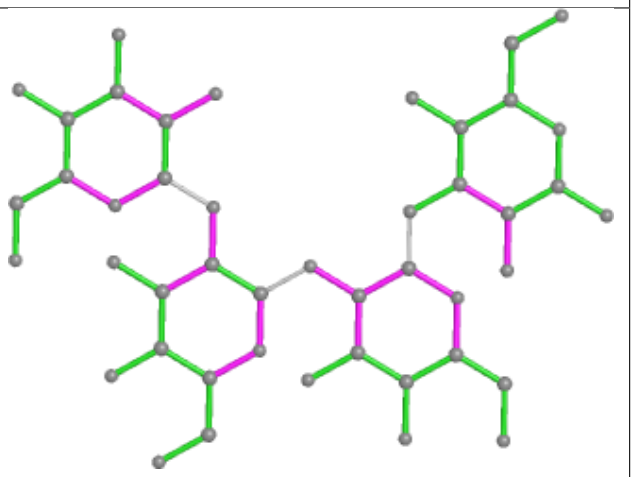


Rings

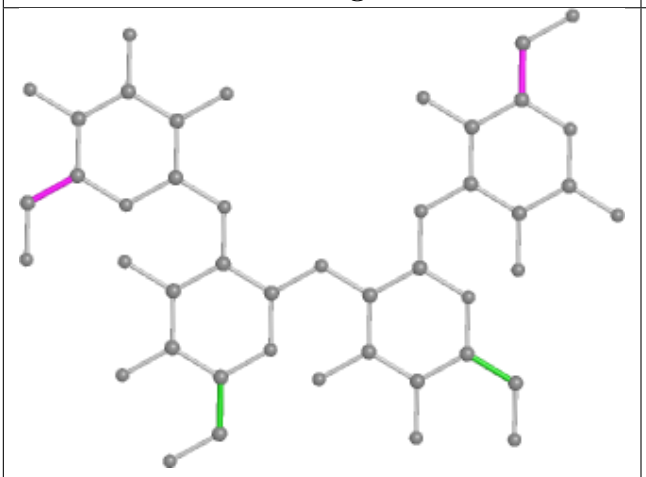
Oligosaccharide Chain B



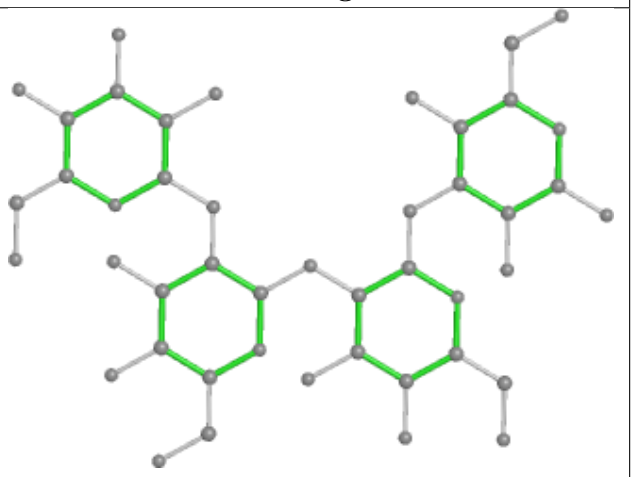
Bond lengths



Bond angles



Torsions



Rings

4.6 Ligand geometry

There are no ligands in this entry.

4.7 Other polymers

There are no such residues in this entry.

4.8 Polymer linkage issues

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.