



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2023 – 06:01 AM EDT

PDB ID : 6UTB  
Title : CRYSTAL STRUCTURE OF UNLIGANDED HIV-1 LM/HT CLADE A/E  
CRF01 GP120 CORE  
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Deposited on : 2019-10-29  
Resolution : 2.50 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](mailto: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>.

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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)  
Xtrriage (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

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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

There are 4 unique types of molecules in this entry. The entry contains 2875 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 HIV-1 LM/HT Clade A/E CRF01 gp120 core.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	341	2674	1680	461	510	23	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	VAL	-	expression tag	UNP A0A0M3KKW9
A	43	PRO	-	expression tag	UNP A0A0M3KKW9
A	61	TYR	HIS	engineered mutation	UNP A0A0M3KKW9
A	105	HIS	GLN	engineered mutation	UNP A0A0M3KKW9
A	108	ILE	VAL	engineered mutation	UNP A0A0M3KKW9
A	375	THR	HIS	engineered mutation	UNP A0A0M3KKW9
A	474	ASP	ASN	engineered mutation	UNP A0A0M3KKW9
A	475	MET	ILE	engineered mutation	UNP A0A0M3KKW9
A	476	ARG	LYS	engineered mutation	UNP A0A0M3KKW9

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula:  $C_8H_{18}N_2O_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	15	8	2	4	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	46	46	46	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, $\alpha$ , $\beta$ , $\gamma$	66.90Å 67.69Å 86.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.51 – 2.50	Depositor
% Data completeness (in resolution range)	95.0 (28.51-2.50)	Depositor
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.03 (at 2.51Å)	Xtrriage
Refinement program	PHENIX (1.15.2_3472: ???)	Depositor
R, $R_{free}$	0.263 , 0.305	Depositor
Wilson B-factor (Å <sup>2</sup> )	44.4	Xtrriage
Anisotropy	0.684	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.018 for k,h,-l	Xtrriage
Total number of atoms	2875	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.07% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical 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.

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

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

### 4.2 Too-close contacts [i](#)

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

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

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

#### 4.3.2 Protein sidechains [i](#)

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

#### 4.3.3 RNA [i](#)

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

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

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

### 4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 4.6 Ligand geometry [i](#)

11 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
2	NAG	A	505	1	14,14,15	0.80	1 (7%)	17,19,21	0.92	1 (5%)
2	NAG	A	508	1	14,14,15	0.46	0	17,19,21	0.64	1 (5%)
2	NAG	A	507	1	14,14,15	1.11	2 (14%)	17,19,21	0.97	1 (5%)
2	NAG	A	502	1	14,14,15	0.82	1 (7%)	17,19,21	0.53	0
2	NAG	A	503	1	14,14,15	0.26	0	17,19,21	0.61	1 (5%)
2	NAG	A	501	1	14,14,15	0.27	0	17,19,21	0.62	0
3	EPE	A	511	-	15,15,15	0.67	0	18,20,20	2.17	7 (38%)
2	NAG	A	504	1	14,14,15	0.68	0	17,19,21	0.64	0
2	NAG	A	510	1	14,14,15	0.30	0	17,19,21	1.00	1 (5%)
2	NAG	A	509	1	14,14,15	0.87	1 (7%)	17,19,21	0.66	0
2	NAG	A	506	1	14,14,15	0.46	0	17,19,21	0.49	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	A	505	1	-	1/6/23/26	0/1/1/1
2	NAG	A	508	1	-	2/6/23/26	0/1/1/1
2	NAG	A	507	1	-	0/6/23/26	0/1/1/1
2	NAG	A	502	1	-	0/6/23/26	0/1/1/1
2	NAG	A	503	1	-	2/6/23/26	0/1/1/1
2	NAG	A	501	1	-	0/6/23/26	0/1/1/1
3	EPE	A	511	-	-	6/9/19/19	0/1/1/1
2	NAG	A	504	1	-	0/6/23/26	0/1/1/1
2	NAG	A	510	1	-	0/6/23/26	0/1/1/1
2	NAG	A	509	1	-	2/6/23/26	0/1/1/1
2	NAG	A	506	1	-	2/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	507	NAG	O5-C1	-3.05	1.38	1.43
2	A	505	NAG	O5-C1	-2.66	1.39	1.43
2	A	509	NAG	O5-C1	-2.65	1.39	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	507	NAG	C1-C2	2.36	1.55	1.52
2	A	502	NAG	O5-C1	-2.25	1.40	1.43

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	511	EPE	C5-N4-C3	3.88	117.56	108.83
3	A	511	EPE	O1S-S-C10	3.69	111.36	106.92
2	A	510	NAG	C1-O5-C5	3.69	117.19	112.19
3	A	511	EPE	C7-N4-C5	3.53	120.27	111.23
3	A	511	EPE	C7-N4-C3	3.12	119.22	111.23
2	A	505	NAG	C1-O5-C5	-3.11	107.97	112.19
2	A	507	NAG	C4-C3-C2	2.80	115.12	111.02
3	A	511	EPE	O2S-S-C10	2.77	110.25	106.92
3	A	511	EPE	C9-N1-C6	-2.60	104.58	111.23
3	A	511	EPE	C9-N1-C2	-2.23	105.53	111.23
2	A	508	NAG	C1-O5-C5	2.20	115.18	112.19
2	A	503	NAG	C1-O5-C5	2.12	115.06	112.19

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	511	EPE	C8-C7-N4-C5
3	A	511	EPE	S-C10-C9-N1
3	A	511	EPE	C9-C10-S-O1S
2	A	506	NAG	O5-C5-C6-O6
2	A	509	NAG	O5-C5-C6-O6
2	A	509	NAG	C4-C5-C6-O6
2	A	506	NAG	C4-C5-C6-O6
3	A	511	EPE	C9-C10-S-O3S
2	A	508	NAG	O5-C5-C6-O6
2	A	505	NAG	O5-C5-C6-O6
3	A	511	EPE	C9-C10-S-O2S
3	A	511	EPE	C8-C7-N4-C3
2	A	503	NAG	C4-C5-C6-O6
2	A	503	NAG	O5-C5-C6-O6
2	A	508	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

#### 4.7 Other polymers [i](#)

There are no such residues in this entry.

#### 4.8 Polymer linkage issues [i](#)

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.