

# wwPDB X-ray Structure Validation Summary Report (i)

#### Oct 1, 2023 – 10:33 PM EDT

PDB ID : 6MEA

Title : Crystal structure of a Tylonycteris bat coronavirus HKU4 macrodomain in

complex with adenosine diphosphate ribose (ADP-ribose)

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Deposited on : 2018-09-06

Resolution : 1.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (1)) were used in the production of this report:

MolProbity : FAILED

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : FAILED

buster-report : 1.1.7 (2018)

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 1.35 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 3 unique types of molecules in this entry. The entry contains 2884 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.

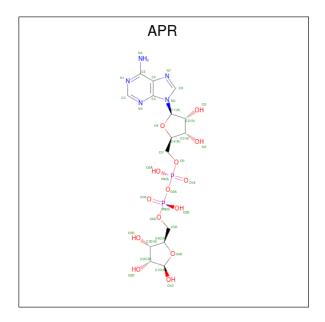
• Molecule 1 is a protein called Replicase polyprotein 1ab.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	162	Total 1230	_		O 238	S 2	0	2	0
1	В	161	Total 1210		N 210	O 232	S 2	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	SER	-	expression tag	UNP P0C6W3
A	306	HIS	-	expression tag	UNP P0C6W3
A	307	MET	-	expression tag	UNP P0C6W3
В	305	SER	-	expression tag	UNP P0C6W3
В	306	HIS	-	expression tag	UNP P0C6W3
В	307	MET	-	expression tag	UNP P0C6W3

• Molecule 2 is ADENOSINE-5-DIPHOSPHORIBOSE (three-letter code: APR) (formula:  $C_{15}H_{23}N_5O_{14}P_2$ ).





	$\mathbf{Mol}$	Chain	Residues	Atoms				ZeroOcc	AltConf	
	9	Λ	1	Total	С	N	О	Р	0	0
	2	A	1	36	15	5	14	2	U	
ĺ	2	D	1	Total	С	N	О	Р	0	0
	<i>Z</i>	В	1	36	15	5	14	2	U	0

## • Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	201	Total O 201 201	0	0
3	В	171	Total O 171 171	0	0

Mol Probity 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 1	Depositor
Cell constants	33.61Å $41.64$ Å $59.78$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$73.16^{\circ}$ $88.29^{\circ}$ $88.25^{\circ}$	Depositor
Resolution (Å)	33.59 - 1.35	Depositor
% Data completeness	92.9 (33.59-1.35)	Depositor
(in resolution range)	,	-
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.12  (at  1.35Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
$R, R_{free}$	0.142 , $0.162$	Depositor
Wilson B-factor $(Å^2)$	10.0	Xtriage
Anisotropy	0.171	Xtriage
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-l	Xtriage
Total number of atoms	2884	wwPDB-VP
Average B, all atoms $(\mathring{A}^2)$	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.18% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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)

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	Bo	$ ag{ths}$	Bond angles			
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	APR	A	500	-	34,39,39	0.94	2 (5%)	40,60,60	1.00	4 (10%)
2	APR	В	500	-	34,39,39	0.91	3 (8%)	40,60,60	1.19	4 (10%)

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	APR	A	500	-	-	2/18/54/54	0/4/4/4
2	APR	В	500	-	-	4/18/54/54	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
2	В	500	APR	PB-O2B	-2.95	1.41	1.55
2	A	500	APR	PB-O2B	-2.73	1.42	1.55
2	A	500	APR	PA-O2A	-2.64	1.42	1.55
2	В	500	APR	PA-O2A	-2.61	1.43	1.55
2	В	500	APR	PA-O1A	-2.03	1.43	1.50

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
2	В	500	APR	O2B-PB-O1B	3.80	131.03	112.24
2	В	500	APR	O2A-PA-O1A	3.74	130.74	112.24
2	A	500	APR	O2A-PA-O1A	3.01	127.10	112.24
2	В	500	APR	O5'-PA-O1A	-2.84	97.95	109.07
2	A	500	APR	O2B-PB-O1B	2.76	125.86	112.24

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	500	APR	C5D-O5D-PB-O1B
2	В	500	APR	O4'-C4'-C5'-O5'
2	A	500	APR	O4'-C4'-C5'-O5'

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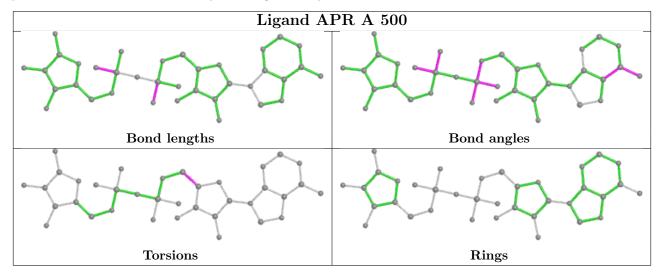
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Mol	Chain	Res	Type	Atoms
2	В	500	APR	C3'-C4'-C5'-O5'
2	A	500	APR	C3'-C4'-C5'-O5'

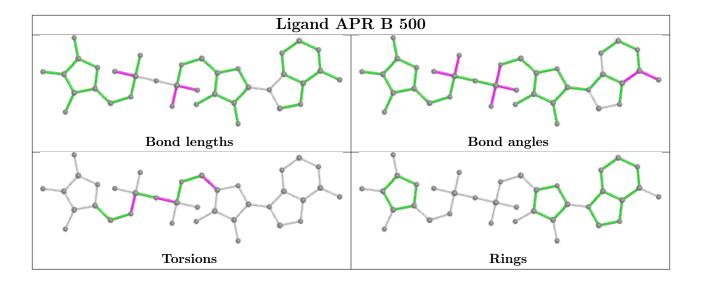
There are no ring outliers.

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 then 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.







# 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 (i)

### 5.1 Protein, DNA and RNA chains (i)

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

### 5.2 Non-standard residues in protein, DNA, RNA chains (i)

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

# 5.3 Carbohydrates (i)

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

### 5.4 Ligands (i)

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

## 5.5 Other polymers (i)

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

