



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:36 PM GMT

PDB ID : 1BMV
Title : PROTEIN-RNA INTERACTIONS IN AN ICOSAHERAL VIRUS AT 3.0
ANGSTROMS RESOLUTION
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Deposited on : 1989-10-09
Resolution : 3.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : **NOT EXECUTED**
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **FAILED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026919

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 3.00 Å.

There are no percentiles available for this entry.

MolProbity and EDS were not executed - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4613 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 RNA chain called RNA (5'-R(*GP*GP*UP*CP*AP*AP*AP*AP*UP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	M	11	Total	C	N	O	P	0	0	0
			238	106	45	76	11			

- Molecule 2 is a protein called PROTEIN (ICOSAHEDRAL VIRUS - A DOMAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1	185	Total	C	N	O	S	0	0	0
			1451	924	244	274	9			

- Molecule 3 is a protein called PROTEIN (ICOSAHEDRAL VIRUS - B AND C DOMAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2	374	Total	C	N	O	S	0	6	0
			2924	1867	487	542	28			

MolProbity and EDS were not executed - this section will therefore be empty.

3 Data and refinement statistics

Xtriage (Phenix) failed to run properly; EDS was not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	311.20Å 284.20Å 350.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	0.330 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4613	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity was not executed - this section will therefore be empty.

4.2 Too-close contacts [i](#)

MolProbity was not executed - this section will therefore be empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity was not executed - this section will therefore be empty.

4.3.2 Protein sidechains [i](#)

MolProbity was not executed - this section will therefore be empty.

4.3.3 RNA [i](#)

MolProbity was not executed - this section will therefore be empty.

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

validation-pack was not executed - this section will therefore be empty.

4.5 Carbohydrates [i](#)

validation-pack was not executed - this section will therefore be empty.

4.6 Ligand geometry [i](#)

validation-pack was not executed - this section will therefore be empty.

4.7 Other polymers [i](#)

validation-pack was not executed - this section will therefore be empty.

4.8 Polymer linkage issues

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

5.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

5.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

5.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.