

wwPDB X-ray Structure Validation Summary Report (i)

Oct 3, 2023 – 12:23 AM EDT

PDB ID : 6UCT

Title : Crystal structure of Mal de Rio Cuarto virus P9-1 viroplasm protein (C-arm

deletion mutant)

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Deposited on : 2019-09-17

Resolution : 3.47 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 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 3.47 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 is only 1 type of molecule in this entry. The entry contains 2013 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 p9-1.

\mathbf{Mol}	Chain	Residues		Ato	oms			ZeroOcc	AltConf	Trace
1	A	243	Total 2013	C 1299	N 327	O 383	S 4	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference	
A	-5	MET	-	initiating methionine	UNP D9U542	
A	-4	HIS	-	expression tag	UNP D9U542	
A	-3	HIS	-	expression tag	UNP D9U542	
A	-2	HIS	-	expression tag	UNP D9U542	
A	-1	HIS	-	expression tag	UNP D9U542	
A	0	HIS	-	expression tag	UNP D9U542	
A	1	HIS	-	expression tag	UNP D9U542	

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 43 21 2	Depositor	
Cell constants	86.56Å 86.56Å 95.60Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°		
Resolution (Å)	43.28 - 3.47	Depositor	
% Data completeness	99.0 (43.28-3.47)	Depositor	
(in resolution range)	33.0 (43.20-3.41)	-	
R_{merge}	0.13	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.22 (at 3.48Å)	Xtriage	
Refinement program	BUSTER 2.10.3	Depositor	
R, R_{free}	0.220 , 0.277	Depositor	
Wilson B-factor (\mathring{A}^2)	161.0	Xtriage	
Anisotropy	0.119	Xtriage	
L-test for twinning ²	$ < L > = 0.47, < L^2> = 0.30$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2013	wwPDB-VP	
Average B, all atoms (Å ²)	185.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.61% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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)

There are no ligands in this entry.

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.

