



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 6, 2024 – 03:55 PM EST

PDB ID : 2F7T  
Title : Crystal structure of the catalytic domain of Mos1 mariner transposase  
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Deposited on : 2005-12-01  
Resolution : 2.25 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 : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

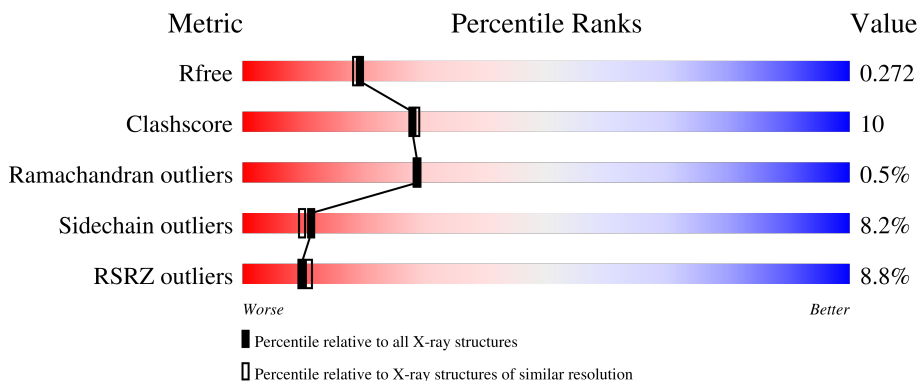
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	227	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1858 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 Mos1 transposase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	204	1742	1117	314	305	6	0	0	0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

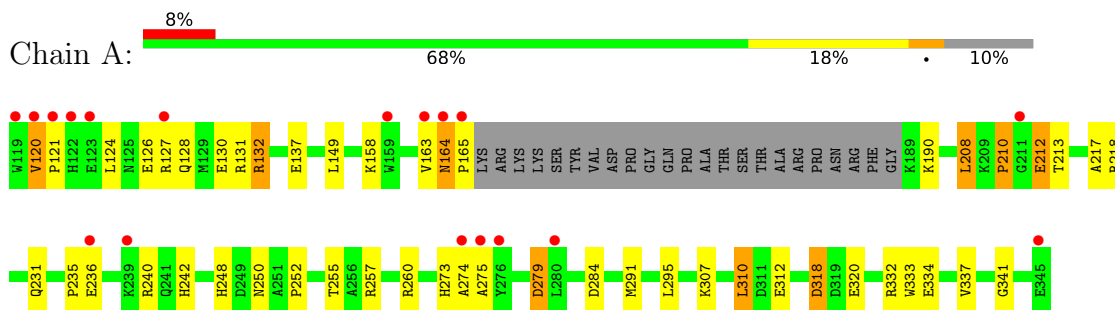
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	115	Total	O	0	0
			115	115		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Mos1 transposase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.24Å 44.24Å 206.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.25 19.49 – 2.25	Depositor EDS
% Data completeness (in resolution range)	97.7 (20.00-2.25) 97.7 (19.49-2.25)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.74 (at 2.26Å)	Xtrriage
Refinement program	REFMAC 5.2.0003	Depositor
R, $R_{free}$	0.189 , 0.277 0.189 , 0.272	Depositor DCC
$R_{free}$ test set	490 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.2	Xtrriage
Anisotropy	0.027	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 56.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	1858	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.65% 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.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	1.19	4/1795 (0.2%)	1.16	7/2427 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	GLU	CG-CD	6.95	1.62	1.51
1	A	320	GLU	CD-OE1	6.45	1.32	1.25
1	A	217	ALA	CA-CB	5.94	1.65	1.52
1	A	137	GLU	CD-OE2	5.44	1.31	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	ARG	NE-CZ-NH2	-19.62	110.49	120.30
1	A	132	ARG	NE-CZ-NH1	12.49	126.55	120.30
1	A	284	ASP	CB-CG-OD2	8.15	125.63	118.30
1	A	279	ASP	CB-CG-OD2	6.26	123.94	118.30
1	A	132	ARG	CD-NE-CZ	5.73	131.63	123.60
1	A	332	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	310	LEU	CA-CB-CG	5.25	127.38	115.30

There are no chirality outliers.

There are no planarity outliers.

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

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1742	0	1686	34	0
2	A	1	0	0	0	0
3	A	115	0	0	13	0
All	All	1858	0	1686	34	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (34) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:PRO:HD2	3:A:1113:HOH:O	1.82	0.80
1:A:240:ARG:NH2	3:A:1111:HOH:O	2.02	0.77
1:A:291:MET:HE3	1:A:295:LEU:HD11	1.68	0.75
1:A:236:GLU:OE1	1:A:242:HIS:HD2	1.72	0.72
1:A:291:MET:CE	1:A:295:LEU:HD11	2.22	0.70
1:A:275:ALA:HB3	3:A:1114:HOH:O	1.91	0.70
1:A:132:ARG:NH2	1:A:279:ASP:OD2	2.24	0.69
1:A:318:ASP:HB2	3:A:1021:HOH:O	1.93	0.69
1:A:334:GLU:HG2	3:A:1025:HOH:O	1.95	0.67
1:A:274:ALA:O	3:A:1001:HOH:O	2.13	0.66
1:A:158:LYS:HD3	1:A:291:MET:HE1	1.79	0.64
1:A:132:ARG:HD3	1:A:341:GLY:O	1.98	0.63
1:A:236:GLU:OE1	1:A:242:HIS:CD2	2.53	0.60
1:A:242:HIS:CD2	3:A:1094:HOH:O	2.55	0.60
1:A:273:HIS:HB3	3:A:1090:HOH:O	2.05	0.57
1:A:131:ARG:HH12	1:A:250:ASN:HD21	1.57	0.53
1:A:218:ARG:HG3	3:A:1075:HOH:O	2.09	0.53
1:A:242:HIS:CG	3:A:1094:HOH:O	2.62	0.52
1:A:235:PRO:CA	3:A:1109:HOH:O	2.59	0.51
1:A:208:LEU:HB3	1:A:212:GLU:HG2	1.94	0.49
1:A:164:ASN:HB2	1:A:165:PRO:HD2	1.95	0.48
1:A:124:LEU:HD22	1:A:128:GLN:HB3	1.96	0.47
1:A:158:LYS:HD3	1:A:291:MET:CE	2.46	0.46
1:A:131:ARG:HH12	1:A:250:ASN:ND2	2.15	0.45
1:A:333:TRP:O	1:A:337:VAL:HG23	2.17	0.45
1:A:128:GLN:O	1:A:132:ARG:HG3	2.15	0.45
1:A:235:PRO:N	3:A:1109:HOH:O	2.50	0.44
1:A:126:GLU:O	1:A:130:GLU:HB2	2.18	0.42
1:A:132:ARG:HH22	1:A:279:ASP:CG	2.16	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:ASN:H	1:A:164:ASN:HD22	1.68	0.42
1:A:120:VAL:HB	1:A:121:PRO:CD	2.50	0.41
1:A:190:LYS:O	1:A:210:PRO:HA	2.21	0.41
1:A:212:GLU:HB2	3:A:1047:HOH:O	2.20	0.41
1:A:255:THR:HB	1:A:260:ARG:HH21	1.85	0.40

There are no symmetry-related clashes.

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

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

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	200/227 (88%)	191 (96%)	8 (4%)	1 (0%)	29 29

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	PRO

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

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	183/202 (91%)	168 (92%)	15 (8%)	11 10

All (15) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	120	VAL
1	A	127	ARG
1	A	149	LEU
1	A	163	VAL
1	A	164	ASN
1	A	208	LEU
1	A	212	GLU
1	A	213	THR
1	A	231	GLN
1	A	248	HIS
1	A	257	ARG
1	A	307	LYS
1	A	310	LEU
1	A	312	GLU
1	A	318	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	ASN
1	A	242	HIS
1	A	250	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

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

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	204/227 (89%)	0.27	18 (8%) <b>10</b> <b>11</b>	16, 30, 57, 96	1 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120	VAL	8.6
1	A	121	PRO	8.6
1	A	119	TRP	6.6
1	A	165	PRO	6.3
1	A	345	GLU	6.0
1	A	164	ASN	5.2
1	A	276	TYR	4.5
1	A	163	VAL	4.1
1	A	211	GLY	3.8
1	A	275	ALA	3.6
1	A	239	LYS	3.1
1	A	159	TRP	3.0
1	A	122	HIS	2.9
1	A	127	ARG	2.4
1	A	274	ALA	2.4
1	A	123	GLU	2.1
1	A	236	GLU	2.1
1	A	280	LEU	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	A	1745	1/1	0.90	0.07	31,31,31,31	0

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

There are no such residues in this entry.