

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

#### Nov 18, 2024 – 06:42 PM JST

PDB ID	:	8X6K
Title	:	The X-ray structure of N-terminal catalytic domain of Thermoplasma aci-
		dophilum tRNA methyltransferase Trm56 (Ta0931).
Authors	:	Fukumoto, S.; Hasegawa, T.; Ototake, M.; Moriguchi, S.; Namba, M.; Yam-
		agami, R.; Kawamura, T.; Hirata, A.; Hori, H.
Deposited on	:	2023-11-21
Resolution	:	1.80 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:

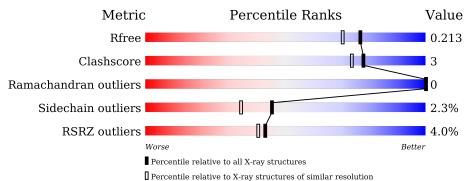
MolProbity		
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	164625	7108 (1.80-1.80)
Clashscore	180529	8162 (1.80-1.80)
Ramachandran outliers	177936	8077 (1.80-1.80)
Sidechain outliers	177891	8076 (1.80-1.80)
RSRZ outliers	164620	7108 (1.80-1.80)

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 >=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 <=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	А	151	2% <b>9</b> 4%	5% ••
1	В	151	<mark>6%</mark> 85%	12% ••



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# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2541 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 tRNA (cytidine(56)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	151	Total	С	Ν	0	S	0	0	0
		101	1218	774	214	226	4	0	0	0
1	р	149	Total	С	Ν	0	S	0	0	0
	I B	149	1198	760	212	222	4	0	0	U

• Molecule 2 is water.

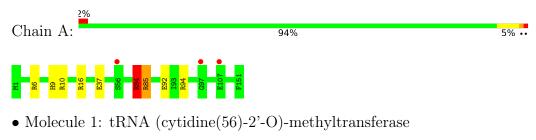
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	76	Total         O           76         76	0	0
2	В	49	Total         O           49         49	0	0

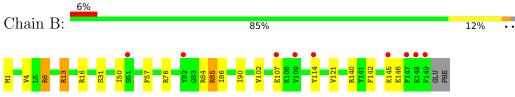


# 3 Residue-property plots (i)

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: tRNA (cytidine(56)-2'-O)-methyltransferase







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	110.07Å 110.07Å 57.73Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	36.03 - 1.80	Depositor
Resolution (A)	36.03 - 1.80	EDS
% Data completeness	98.7 (36.03-1.80)	Depositor
(in resolution range)	98.6(36.03-1.80)	EDS
R <sub>merge</sub>	0.05	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.85 (at 1.81Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
P. P.	0.170 , $0.203$	Depositor
R, $R_{free}$	0.181 , $0.213$	DCC
$R_{free}$ test set	1847 reflections $(5.00\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	29.4	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.39, $31.9$	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2541	wwPDB-VP
Average B, all atoms $(Å^2)$	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.82% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



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

# 5 Model quality (i)

## 5.1 Standard geometry (i)

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).

Mal	Mol Chain	Bond	lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.60	0/1241	0.92	6/1675~(0.4%)	
1	В	0.57	0/1220	0.85	1/1647~(0.1%)	
All	All	0.58	0/2461	0.88	7/3322~(0.2%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	1
1	В	0	5
All	All	0	6

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	10	ARG	NE-CZ-NH2	-7.36	116.62	120.30
1	А	92	GLU	CB-CA-C	-6.76	96.88	110.40
1	В	140	ARG	NE-CZ-NH2	-6.31	117.15	120.30
1	А	84	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	А	10	ARG	NE-CZ-NH1	5.39	123.00	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	84	ARG	Sidechain
1	В	13	ARG	Sidechain
1	В	16	ARG	Sidechain
1	В	6	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	В	84	ARG	Sidechain

## 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	А	1218	0	1210	5	1
1	В	1198	0	1195	11	2
2	А	76	0	0	1	0
2	В	49	0	0	1	0
All	All	2541	0	2405	13	2

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 3.

The worst 5 of 13 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:85:ARG:HH12	1:B:146:GLU:CD	1.78	0.85
1:A:85:ARG:NH1	1:B:146:GLU:OE1	2.16	0.77
1:B:86:ILE:HD11	1:B:90:ILE:HD13	1.65	0.77
1:A:16:ARG:HD3	2:A:455:HOH:O	1.95	0.66
1:B:4:VAL:HG22	1:B:102:VAL:HG13	1.91	0.53

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:GLU:OE1	1:B:107:GLU:OE1[5_555]	2.12	0.08
1:A:84:ARG:NH1	1:B:13:ARG:NH1[3_665]	2.18	0.02



## 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	Perce	ntiles
1	А	149/151~(99%)	148 (99%)	1 (1%)	0	100	100
1	В	147/151~(97%)	143~(97%)	4(3%)	0	100	100
All	All	296/302~(98%)	291~(98%)	5(2%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	А	132/132~(100%)	130~(98%)	2(2%)	60 53
1	В	130/132~(98%)	126~(97%)	4 (3%)	35 22
All	All	262/264~(99%)	256~(98%)	6(2%)	45 34

5 of 6 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	В	76	ARG
1	В	85	ARG
1	В	114	TYR
1	А	85	ARG
1	А	6	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such side chains are listed below:



Mol	Chain	Res	Type
1	В	52	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 oligosaccharides in this entry.

### 5.6 Ligand geometry (i)

There are no ligands in this entry.

### 5.7 Other polymers (i)

There are no such residues in this entry.

### 5.8 Polymer linkage issues (i)

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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	151/151~(100%)	-0.15	3 (1%) 64 63	20, 29, 42, 62	0
1	В	149/151~(98%)	0.27	9 (6%) 29 26	22, 32, 52, 87	0
All	All	300/302~(99%)	0.06	12 (4%) 43 40	20, 30, 50, 87	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	149	PHE	3.9
1	В	107	GLU	2.8
1	В	148	GLU	2.8
1	В	147	PHE	2.8
1	В	109	VAL	2.7

## 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)

There are no ligands in this entry.

### 6.5 Other polymers (i)

There are no such residues in this entry.

