



wwPDB X-ray Structure Validation Summary Report ⓘ

May 30, 2020 – 03:35 am BST

PDB ID : 1VK8
Title : CRYSTAL STRUCTURE OF A PUTATIVE THIAMINE BIOSYNTHESIS/SALVAGE PROTEIN (TM0486) FROM THERMOTOGA MARITIMA AT 1.80 Å RESOLUTION
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2004-05-05
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 ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

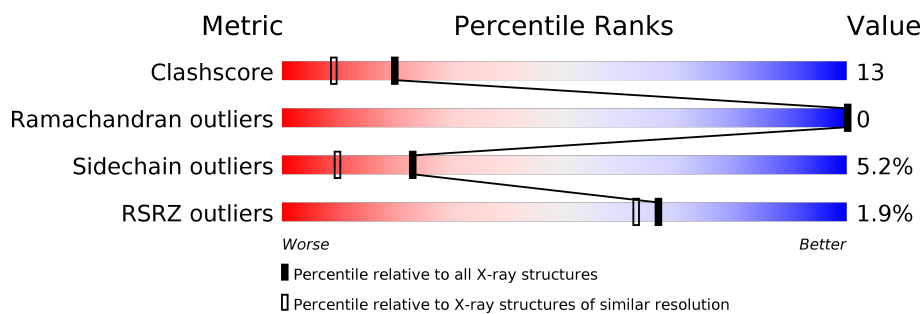
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (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 on 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 $\leq 5\%$. 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	106	<div> <div>%</div> <div> <div></div> <div>74%</div> <div>13%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	106	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>12%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	106	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>16%</div> <div>•</div> <div>11%</div> </div> </div>
1	D	106	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>13%</div> <div></div> <div>12%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNL	A	400	-	-	X	-
2	UNL	B	400	-	-	X	-
2	UNL	C	400	-	-	X	-
2	UNL	D	400	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3440 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 hypothetical protein TM0486.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	93	Total	C	N	O	Se	0	1	0
			758	483	129	144	2			
1	B	93	Total	C	N	O	Se	0	1	0
			756	482	126	146	2			
1	C	94	Total	C	N	O	Se	0	1	0
			765	488	130	145	2			
1	D	93	Total	C	N	O	Se	0	1	0
			757	483	128	144	2			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	LEADER SEQUENCE	UNP Q9WYV6
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYV6
A	-9	SER	-	LEADER SEQUENCE	UNP Q9WYV6
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYV6
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYV6
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYV6
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
A	0	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
A	35	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
A	54	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
B	-11	MET	-	LEADER SEQUENCE	UNP Q9WYV6
B	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYV6
B	-9	SER	-	LEADER SEQUENCE	UNP Q9WYV6
B	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYV6
B	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYV6
B	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYV6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
B	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
B	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
B	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
B	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
B	0	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
B	35	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
B	54	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
C	-11	MET	-	LEADER SEQUENCE	UNP Q9WYV6
C	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYV6
C	-9	SER	-	LEADER SEQUENCE	UNP Q9WYV6
C	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYV6
C	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYV6
C	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYV6
C	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
C	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
C	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
C	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
C	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
C	0	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
C	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
C	35	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
C	54	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
D	-11	MET	-	LEADER SEQUENCE	UNP Q9WYV6
D	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYV6
D	-9	SER	-	LEADER SEQUENCE	UNP Q9WYV6
D	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYV6
D	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYV6
D	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYV6
D	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
D	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
D	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
D	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
D	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
D	0	HIS	-	LEADER SEQUENCE	UNP Q9WYV6
D	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
D	35	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6
D	54	MSE	MET	MODIFIED RESIDUE	UNP Q9WYV6

- Molecule 2 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).

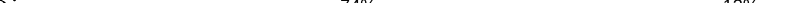
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O 12 12	0	0
2	A	1	Total O 12 12	0	0
2	D	1	Total O 12 12	0	0
2	C	1	Total O 12 12	0	0

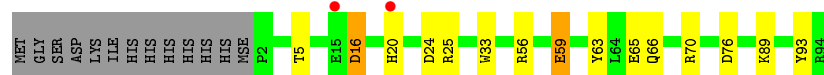
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	92	Total O 92 92	0	0
3	B	86	Total O 87 87	0	1
3	C	86	Total O 86 86	0	0
3	D	89	Total O 91 91	0	2

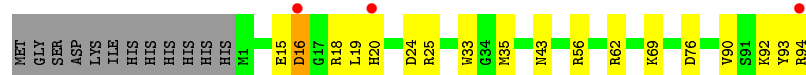
- Molecule 1: hypothetical protein TM0486

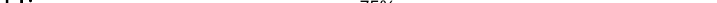


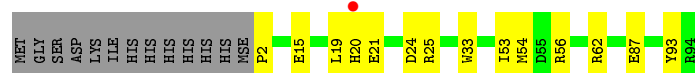
- Chain B:  2% 74% 12% 12%



- Chain C:  3% 72% 16% 11%



- Chain D:  %



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	47.65Å 47.65Å 49.61Å 73.80° 62.90° 73.62°	Depositor
Resolution (Å)	41.71 – 1.80 41.71 – 1.80	Depositor EDS
% Data completeness (in resolution range)	76.1 (41.71-1.80) 76.1 (41.71-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.142 , 0.190 (Not available) , (Not available)	Depositor DCC
R_{free} test set	1336 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	14.9	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 55.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3440	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: UNL

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	0.68	0/773	0.82	1/1033 (0.1%)
1	B	0.71	0/771	0.82	2/1031 (0.2%)
1	C	0.64	0/779	0.84	1/1042 (0.1%)
1	D	0.66	0/773	0.83	0/1034
All	All	0.67	0/3096	0.83	4/4140 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	16	ASP	CB-CG-OD2	7.58	125.12	118.30
1	B	76	ASP	CB-CG-OD2	6.04	123.74	118.30
1	C	76	ASP	CB-CG-OD2	5.91	123.61	118.30
1	B	16	ASP	CB-CG-OD2	5.27	123.04	118.30

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	758	0	775	12	0
1	B	756	0	768	9	0
1	C	765	0	781	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	757	0	769	10	0
2	A	12	0	0	13	0
2	B	12	0	0	9	0
2	C	12	0	0	10	0
2	D	12	0	0	12	0
3	A	92	0	0	3	0
3	B	87	0	0	3	0
3	C	86	0	0	3	0
3	D	91	0	0	4	0
All	All	3440	0	3093	78	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 13.

The worst 5 of 78 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)
2:D:400:UNL:O6	2:D:400:UNL:O5	1.52	1.27
2:A:400:UNL:O10	2:A:400:UNL:O11	1.53	1.21
2:C:400:UNL:O5	2:C:400:UNL:O6	1.56	1.21
2:A:400:UNL:O7	2:A:400:UNL:O8	1.56	1.21
2:A:400:UNL:O8	2:A:400:UNL:O10	1.60	1.17

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	92/106 (87%)	92 (100%)	0	0	100	100
1	B	92/106 (87%)	92 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	93/106 (88%)	92 (99%)	1 (1%)	0	100	100
1	D	92/106 (87%)	91 (99%)	1 (1%)	0	100	100
All	All	369/424 (87%)	367 (100%)	2 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	83/91 (91%)	82 (99%)	1 (1%)	71	65
1	B	83/91 (91%)	79 (95%)	4 (5%)	25	11
1	C	83/91 (91%)	73 (88%)	10 (12%)	5	1
1	D	83/91 (91%)	79 (95%)	4 (5%)	25	11
All	All	332/364 (91%)	313 (94%)	19 (6%)	23	8

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	18[B]	ARG
1	C	20	HIS
1	D	15	GLU
1	C	18[A]	ARG
1	D	19	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	B	20	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are unknown - 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 [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, 95th 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 ²)	Q<0.9
1	A	91/106 (85%)	-0.47	1 (1%) 80 78	6, 10, 25, 36	0
1	B	91/106 (85%)	-0.31	2 (2%) 62 57	6, 11, 33, 38	0
1	C	91/106 (85%)	-0.22	3 (3%) 46 40	6, 11, 35, 46	0
1	D	91/106 (85%)	-0.41	1 (1%) 80 78	7, 11, 35, 46	0
All	All	364/424 (85%)	-0.35	7 (1%) 66 63	6, 11, 33, 46	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	20[A]	HIS	3.7
1	B	20	HIS	2.9
1	C	20	HIS	2.5
1	C	16	ASP	2.3
1	C	94	ARG	2.2

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 carbohydrates 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, 95th 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(\AA^2)	Q<0.9
2	UNL	B	400	12/-	0.93	0.14	18,36,50,50	0
2	UNL	A	400	12/-	0.93	0.13	17,32,47,48	0
2	UNL	D	400	12/-	0.93	0.18	18,36,45,58	0
2	UNL	C	400	12/-	0.94	0.11	19,39,51,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.