



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1THT  
Title : STRUCTURE OF A MYRISTOYL-ACP-SPECIFIC THIOESTERASE  
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Deposited on : 1994-04-19  
Resolution : 2.10 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.

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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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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)	:	2.11

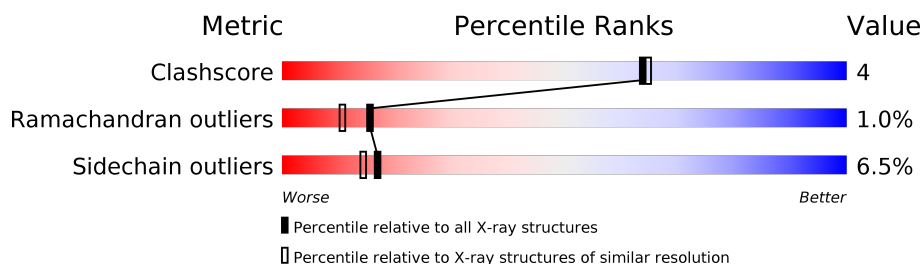
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	305	
1	B	305	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4647 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 THIOESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2294	1456	383	446	9			
1	B	293	Total	C	N	O	S	0	0	0
			2298	1460	388	441	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	THR	GLU	CONFLICT	UNP P05521
A	299	ASN	SER	CONFLICT	UNP P05521
B	60	THR	GLU	CONFLICT	UNP P05521
B	299	ASN	SER	CONFLICT	UNP P05521

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	26	Total	O	0	0
			26	26		
2	B	29	Total	O	0	0
			29	29		



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.50Å 83.80Å 47.40Å 90.00° 97.30° 90.00°	Depositor
Resolution (Å)	8.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.10)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, $R_{free}$	0.227 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4647	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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	0.84	0/2344	1.55	26/3190 (0.8%)
1	B	0.83	0/2347	1.52	29/3191 (0.9%)
All	All	0.84	0/4691	1.53	55/6381 (0.9%)

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	A	0	1

There are no bond length outliers.

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	ARG	NE-CZ-NH1	13.47	127.04	120.30
1	A	168	GLU	CA-C-N	-13.10	90.00	116.20
1	B	48	MET	CG-SD-CE	-10.44	83.50	100.20
1	B	237	LEU	CA-CB-CG	9.37	136.85	115.30
1	B	147	LYS	CA-CB-CG	-9.04	93.51	113.40
1	A	213	TRP	CD1-CG-CD2	8.99	113.49	106.30
1	B	99	TRP	CD1-CG-CD2	8.51	113.11	106.30
1	A	23	TRP	CD1-CG-CD2	8.26	112.91	106.30
1	B	142	ARG	NE-CZ-NH2	-8.15	116.22	120.30
1	B	23	TRP	CD1-CG-CD2	8.00	112.70	106.30
1	A	251	ARG	NE-CZ-NH2	-7.79	116.41	120.30
1	A	67	ARG	NE-CZ-NH2	-7.64	116.48	120.30
1	A	99	TRP	CD1-CG-CD2	7.60	112.38	106.30
1	B	5	CYS	CA-CB-SG	7.52	127.54	114.00
1	B	251	ARG	NE-CZ-NH1	7.45	124.03	120.30
1	B	99	TRP	CE2-CD2-CG	-7.05	101.66	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	67	ARG	NE-CZ-NH1	7.00	123.80	120.30
1	A	23	TRP	CE2-CD2-CG	-6.98	101.72	107.30
1	B	23	TRP	CE2-CD2-CG	-6.98	101.72	107.30
1	A	213	TRP	CE2-CD2-CG	-6.97	101.72	107.30
1	B	213	TRP	CD1-CG-CD2	6.86	111.79	106.30
1	B	213	TRP	CE2-CD2-CG	-6.84	101.83	107.30
1	A	99	TRP	CE2-CD2-CG	-6.81	101.85	107.30
1	A	169	GLY	N-CA-C	-6.51	96.81	113.10
1	B	99	TRP	CG-CD2-CE3	6.47	139.72	133.90
1	A	213	TRP	CG-CD1-NE1	-6.31	103.79	110.10
1	A	67	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	A	168	GLU	O-C-N	6.18	133.71	123.20
1	B	99	TRP	CG-CD1-NE1	-6.16	103.94	110.10
1	A	48	MET	CG-SD-CE	-6.12	90.41	100.20
1	B	292	ARG	NE-CZ-NH1	6.07	123.33	120.30
1	A	254	TYR	CB-CG-CD2	-6.04	117.38	121.00
1	B	141	LEU	CA-CB-CG	5.88	128.82	115.30
1	B	57	TYR	CB-CG-CD2	-5.74	117.56	121.00
1	B	227	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	B	238	GLY	N-CA-C	-5.63	99.02	113.10
1	B	99	TRP	CB-CG-CD1	-5.52	119.83	127.00
1	A	101	GLN	CA-CB-CG	-5.45	101.41	113.40
1	B	240	SER	N-CA-C	-5.45	96.30	111.00
1	A	124	ILE	CB-CA-C	-5.41	100.77	111.60
1	A	209	ASN	N-CA-CB	-5.41	100.87	110.60
1	B	67	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	B	147	LYS	CG-CD-CE	-5.31	95.98	111.90
1	A	183	GLU	CA-CB-CG	-5.29	101.77	113.40
1	B	124	ILE	CB-CA-C	-5.27	101.05	111.60
1	A	110	LEU	CA-CB-CG	5.27	127.42	115.30
1	A	288	VAL	CA-CB-CG2	-5.23	103.05	110.90
1	A	273	VAL	N-CA-CB	-5.22	100.03	111.50
1	A	99	TRP	CG-CD1-NE1	-5.13	104.97	110.10
1	A	23	TRP	CG-CD1-NE1	-5.10	105.00	110.10
1	B	20	LEU	CA-CB-CG	5.05	126.91	115.30
1	B	230	HIS	CA-CB-CG	5.04	122.17	113.60
1	A	181	CYS	CB-CA-C	-5.04	100.32	110.40
1	B	213	TRP	CG-CD2-CE3	5.01	138.41	133.90
1	B	227	ARG	NE-CZ-NH1	5.00	122.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	168	GLU	Mainchain

## 5.2 Too-close contacts

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	2294	0	2185	23	0
1	B	2298	0	2212	18	0
2	A	26	0	0	0	0
2	B	29	0	0	0	0
All	All	4647	0	4397	38	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 4.

All (38) 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:185:HIS:HE1	1:B:156:LEU:O	1.56	0.86
1:B:289:ASN:HA	1:B:292:ARG:HD3	1.57	0.84
1:A:156:LEU:O	1:B:185:HIS:HE1	1.66	0.78
1:A:185:HIS:CE1	1:B:156:LEU:O	2.45	0.65
1:A:9:ALA:HB1	1:A:297:ILE:HD12	1.83	0.60
1:B:237:LEU:HD12	1:B:238:GLY:H	1.67	0.59
1:B:237:LEU:HD12	1:B:238:GLY:N	2.22	0.55
1:A:20:LEU:HD21	1:A:96:VAL:HG22	1.87	0.55
1:B:228:THR:HB	1:B:230:HIS:CE1	2.43	0.54
1:A:196:VAL:HG13	1:A:226:ILE:HG12	1.90	0.53
1:B:118:ARG:HB2	1:B:138:VAL:HG22	1.90	0.53
1:A:7:THR:HA	1:A:24:GLU:O	2.10	0.52
1:A:161:LEU:HG	1:A:174:SER:HB3	1.94	0.50
1:A:124:ILE:HD12	1:A:199:THR:HG21	1.94	0.50
1:A:285:ILE:O	1:A:289:ASN:HB2	2.12	0.50
1:A:145:LEU:O	1:A:149:LEU:HG	2.11	0.49
1:A:147:LYS:HD3	1:A:212:ASP:O	2.12	0.49
1:A:36:ASN:OD1	1:A:107:ASN:HB3	2.14	0.48
1:A:10:HIS:HE1	1:A:24:GLU:OE1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:ILE:HD11	1:B:196:VAL:HG22	1.98	0.46
1:B:255:GLN:HG3	1:B:275:PHE:CZ	2.51	0.45
1:B:112:ALA:O	1:B:134:THR:HA	2.17	0.45
1:B:48:MET:CE	1:B:243:LEU:HB2	2.48	0.44
1:A:202:PRO:HG3	1:A:230:HIS:CE1	2.54	0.43
1:B:213:TRP:N	1:B:213:TRP:CD1	2.87	0.43
1:A:221:ASP:O	1:A:225:HIS:ND1	2.49	0.42
1:A:118:ARG:HB2	1:A:138:VAL:CG2	2.49	0.42
1:A:68:TYR:CG	1:A:96:VAL:HG21	2.55	0.42
1:A:161:LEU:HA	1:A:162:PRO:HD2	1.88	0.42
1:B:115:LEU:HD12	1:B:115:LEU:HA	1.82	0.41
1:A:209:ASN:HB2	1:A:236:LEU:O	2.21	0.41
1:B:28:LYS:O	1:B:31:VAL:HG22	2.19	0.41
1:A:206:PHE:HA	1:A:234:TYR:O	2.19	0.41
1:B:98:HIS:O	1:B:102:THR:HG23	2.20	0.41
1:B:56:GLU:O	1:B:60:THR:HB	2.21	0.41
1:B:203:LEU:O	1:B:231:CYS:HA	2.20	0.40
1:A:56:GLU:O	1:A:60:THR:HB	2.22	0.40
1:A:171:LYS:HB2	1:A:171:LYS:HE3	1.89	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	290/305 (95%)	273 (94%)	14 (5%)	3 (1%)	15	11
1	B	289/305 (95%)	276 (96%)	10 (4%)	3 (1%)	15	11
All	All	579/610 (95%)	549 (95%)	24 (4%)	6 (1%)	15	11

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	6	LYS
1	B	15	ASN
1	B	6	LYS
1	B	239	SER
1	A	238	GLY

### 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	248/266 (93%)	228 (92%)	20 (8%)	11	8
1	B	248/266 (93%)	236 (95%)	12 (5%)	25	24
All	All	496/532 (93%)	464 (94%)	32 (6%)	17	14

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	VAL
1	A	60	THR
1	A	73	HIS
1	A	74	VAL
1	A	110	LEU
1	A	126	ASP
1	A	141	LEU
1	A	161	LEU
1	A	163	ASN
1	A	210	ASN
1	A	223	LEU
1	A	251	ARG
1	A	255	GLN
1	A	269	LEU
1	A	273	VAL
1	A	289	ASN
1	A	298	GLU
1	A	300	ARG

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Mol	Chain	Res	Type
1	A	301	THR
1	A	304	MET
1	B	13	ARG
1	B	60	THR
1	B	110	LEU
1	B	126	ASP
1	B	161	LEU
1	B	163	ASN
1	B	174	SER
1	B	223	LEU
1	B	230	HIS
1	B	251	ARG
1	B	269	LEU
1	B	273	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	185	HIS
1	A	230	HIS
1	B	35	ASN
1	B	185	HIS
1	B	230	HIS
1	B	252	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 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

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.