



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 14, 2020 – 01:44 AM BST

PDB ID : 3LMT
Title : Crystal structure of DTD from Plasmodium falciparum
Authors : Manickam, Y.; Bhatt, T.K.; Khan, S.; Sharma, A.
Deposited on : 2010-02-01
Resolution : 2.75 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
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) : 2.14.4.dev1

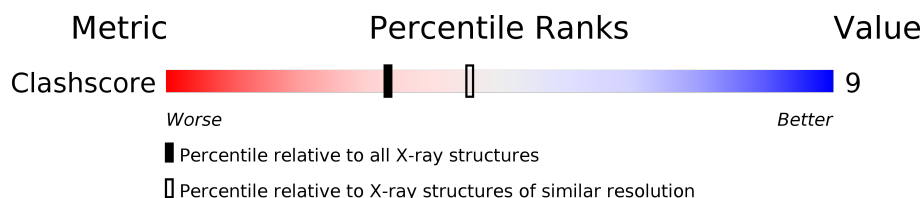
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1277 (2.78-2.74)

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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	164	84% 15% .
1	B	164	72% 20% . 7%
1	C	164	77% 21% .
1	D	164	74% 18% 8%
1	E	164	75% 16% 9%
1	F	164	77% 15% 7%

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	IOD	B	167	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IOD	B	169	-	-	X	-
2	IOD	E	167	-	-	X	-
2	IOD	E	170	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7593 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 D-tyrosyl-tRNA(Tyr) deacylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	0	2	0
			1310	846	221	240	3			
1	B	152	Total	C	N	O	S	0	0	0
			1233	796	205	229	3			
1	C	161	Total	C	N	O	S	0	1	0
			1263	817	215	228	3			
1	D	151	Total	C	N	O	S	2	1	0
			1203	776	204	220	3			
1	E	150	Total	C	N	O	S	0	0	0
			1194	774	203	214	3			
1	F	152	Total	C	N	O	S	0	1	0
			1184	767	199	215	3			

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	3	Total	I	0	0
			3	3		
2	E	6	Total	I	0	0
			6	6		
2	B	5	Total	I	0	0
			5	5		
2	C	5	Total	I	0	0
			5	5		
2	A	5	Total	I	0	0
			5	5		
2	F	5	Total	I	0	0
			5	5		

- Molecule 3 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	35	Total 35	O 35	0	0
3	B	42	Total 42	O 42	0	0
3	C	22	Total 22	O 22	0	0
3	D	21	Total 21	O 21	0	0
3	E	28	Total 28	O 28	0	0
3	F	29	Total 29	O 29	0	0

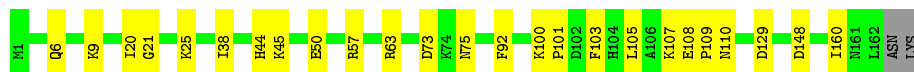
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS failed to run properly.

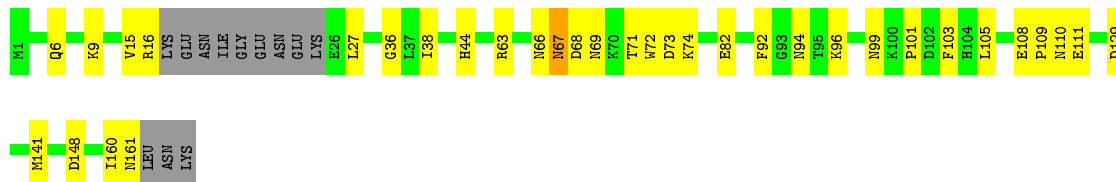
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain A: 



- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain B: 



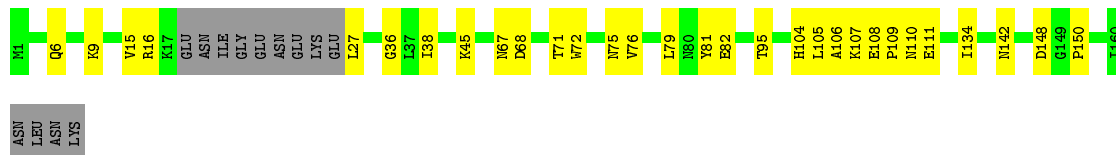
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain C: 



- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain D: 



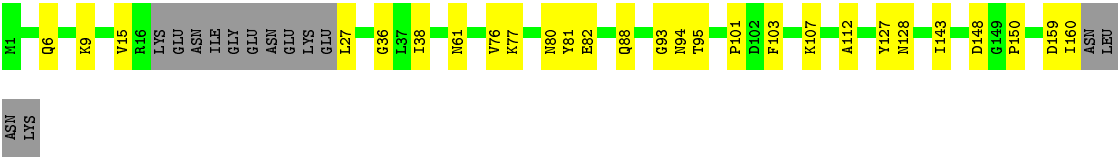
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain E:

75%

16%

9%



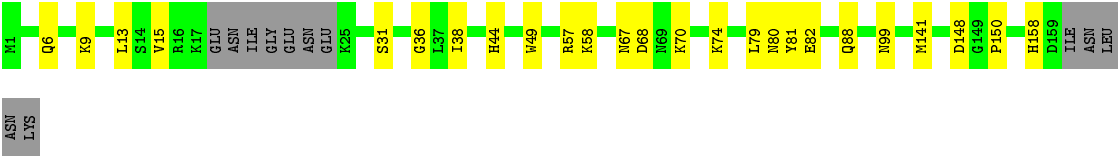
- Molecule 1: D-tyrosyl-tRNA(Tyr) deacylase

Chain F:

77%

15%

7%



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.34Å 57.88Å 91.63Å 102.80° 105.90° 99.60°	Depositor
Resolution (Å)	29.67 – 2.75	Depositor
% Data completeness (in resolution range)	95.8 (29.67-2.75)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.25 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.5_2	Depositor
R, R_{free}	0.181 , 0.235	Depositor
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.307	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.012 for k,h,-h-k-l	Xtriage
Total number of atoms	7593	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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

5.1 Standard geometry

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

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	0.41	0/1340	0.57	0/1813
1	B	0.43	0/1256	0.55	0/1699
1	C	11.79	4/1292 (0.3%)	7.20	6/1750 (0.3%)
1	D	0.41	0/1229	0.54	0/1666
1	E	0.40	0/1216	0.53	0/1646
1	F	0.42	0/1209	0.54	0/1642
All	All	4.89	4/7542 (0.1%)	3.02	6/10216 (0.1%)

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	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	57[A]	ARG	CZ-NH1	221.75	4.21	1.33
1	C	57[B]	ARG	CZ-NH1	221.75	4.21	1.33
1	C	57[A]	ARG	CZ-NH2	201.10	3.94	1.33
1	C	57[B]	ARG	CZ-NH2	201.10	3.94	1.33

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	57[A]	ARG	NE-CZ-NH1	-147.90	46.35	120.30
1	C	57[B]	ARG	NE-CZ-NH1	-147.90	46.35	120.30
1	C	57[A]	ARG	NE-CZ-NH2	-130.40	55.10	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	57[B]	ARG	NE-CZ-NH2	-130.40	55.10	120.30
1	C	57[A]	ARG	NH1-CZ-NH2	-79.20	32.28	119.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	67	ASN	Peptide

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	1310	0	1287	19	0
1	B	1233	0	1214	24	0
1	C	1263	0	1220	27	0
1	D	1203	0	1156	23	0
1	E	1194	0	1182	19	0
1	F	1184	0	1138	19	0
2	A	5	0	0	1	0
2	B	5	0	0	7	0
2	C	5	0	0	1	0
2	D	3	0	0	1	0
2	E	6	0	0	5	0
2	F	5	0	0	1	0
3	A	35	0	0	1	0
3	B	42	0	0	3	0
3	C	22	0	0	0	0
3	D	21	0	0	3	0
3	E	28	0	0	0	0
3	F	29	0	0	1	0
All	All	7593	0	7197	125	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 9.

The worst 5 of 125 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:B:99:ASN:OD1	2:B:167:IOD:I	2.31	1.18
2:B:169:IOD:I	3:B:195:HOH:O	2.66	0.82
1:C:21:GLY:O	1:C:22:GLU:CB	2.30	0.78
1:D:108:GLU:O	1:D:111:GLU:N	2.13	0.75
1:E:159:ASP:O	1:E:160:ILE:C	2.26	0.74

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 29 ligands modelled in this entry, 29 are 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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section is therefore empty.