

wwPDB X-ray Structure Validation Summary Report (i)

Feb 5, 2024 – 03:02 AM EST

PDB ID	:	1TDA
Title	:	STRUCTURES OF THYMIDYLATE SYNTHASE WITH A C-TERMINAL
		DELETION: ROLE OF THE C-TERMINUS IN ALIGNMENT OF D/UMP
		AND CH2H4FOLATE
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Deposited on		
Resolution	:	3.09 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 (i)) were used in the production of this report:

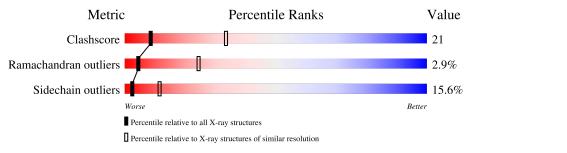
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as 541 be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.09 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)

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 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%

Note EDS was not executed.

Mol	Chain	Length		Quality of chain		
1	А	315	38%	39%	19%	•

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	PO4	А	317	-	Х	-	-



1TDA

2 Entry composition (i)

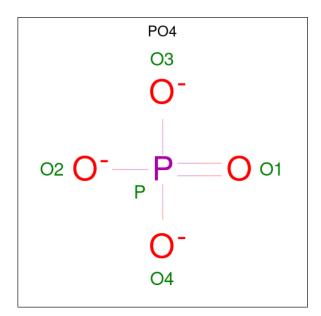
There are 3 unique types of molecules in this entry. The entry contains 2641 atoms, of which 0 are hydrogens and 16 are deuteriums.

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 THYMIDYLATE SYNTHASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	А	315	Total 2599	C 1672	D 16	N 437	0 466	S 8	0	0	0

• Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 5	0 4	Р 1	0	0

• Molecule 3 is water.

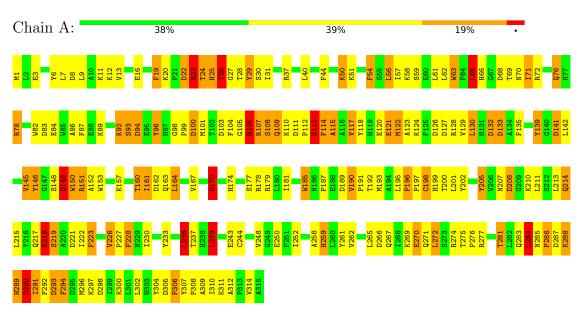
[Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	3	А	37	Total O 37 37	0	0



Residue-property plots (i) 3

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 was not executed.



• Molecule 1: THYMIDYLATE SYNTHASE



4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 61 2 2	Depositor	
Cell constants	78.80Å 78.80 Å 243.20 Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	(Not available) - 3.09	Depositor	
% Data completeness	(Not available) ((Not available)-3.09)	Depositor	
(in resolution range)		Depositor	
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	X-PLOR	Depositor	
R, R_{free}	0.160 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2641	wwPDB-VP	
Average B, all atoms $(Å^2)$	13.0	wwPDB-VP	



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: PO4

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	Chain	Bo	nd lengths	Bond angles		
Mol	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.77	25/2667~(0.9%)	2.38	154/3624~(4.2%)	

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	4

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	26	THR	C-N	33.18	1.92	1.33
1	А	114	PHE	C-N	25.76	1.93	1.34
1	А	108	SER	C-N	25.24	1.92	1.34
1	А	219	SER	CA-CB	-9.64	1.38	1.52
1	А	19	PHE	C-N	-8.92	1.13	1.34

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	26	THR	O-C-N	-16.03	95.95	123.20
1	А	178	ARG	NE-CZ-NH1	14.19	127.39	120.30
1	А	108	SER	O-C-N	-14.11	100.13	122.70
1	А	108	SER	CA-C-N	13.21	146.26	117.20
1	А	108	SER	C-N-CA	12.71	153.49	121.70

There are no chirality outliers.

All (4) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	А	111	ASP	Peptide
1	А	233	TYR	Sidechain
1	А	239	LEU	Mainchain
1	А	98	GLY	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	А	2599	0	2483	105	0
2	А	5	0	0	0	0
3	А	37	0	0	4	0
All	All	2641	0	2483	105	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 21.

The worst 5 of 105 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:108:SER:C	1:A:109:GLN:N	1.92	1.23
1:A:26:THR:C	1:A:27:GLY:N	1.92	1.22
1:A:114:PHE:C	1:A:115:ALA:N	1.93	1.21
1:A:114:PHE:O	1:A:117:VAL:HG22	1.59	1.03
1:A:107:ARG:HB3	1:A:114:PHE:CE2	1.97	0.99

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	${\rm the}$	total	number	of residues.
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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	А	313/315~(99%)	264 (84%)	40 (13%)	9~(3%)	4 24	

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	100	ASP
1	А	112	PRO
1	А	25	HIS
1	А	94	ASP
1	А	106	HIS

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	276/277~(100%)	233~(84%)	43 (16%)	2 11	

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	248	VAL
1	А	289	HIS
1	А	270	GLU
1	А	283	GLN
1	А	293	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	170	GLN
1	А	214	GLN
1	А	289	HIS
1	А	106	HIS
1	А	76	GLN



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)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	B	ond leng	gths	В	ond ang	gles
WIOI	туре	Ullalli	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	PO4	А	317	-	4,4,4	2.24	2 (50%)	$6,\!6,\!6$	3.21	4 (66%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	317	PO4	P-01	3.47	1.59	1.50
2	А	317	PO4	P-O4	-2.19	1.48	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	317	PO4	04-P-02	5.36	125.17	107.97
2	А	317	PO4	04-P-01	-3.40	98.47	110.89
2	А	317	PO4	03-P-01	-3.17	99.30	110.89
2	А	317	PO4	02-P-01	-2.55	101.58	110.89



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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks		
1	А	4		

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	114:PHE	С	115:ALA	Ν	1.93
1	А	26:THR	С	27:GLY	Ν	1.92
1	А	108:SER	С	109:GLN	Ν	1.92
1	А	19:PHE	С	20:LYS	Ν	1.13



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

