



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:06 PM UTC

PDB ID : 3ED7 / pdb_00003ed7
Title : Replacement of Val3 in Human Thymidylate Synthase Affects Its Kinetic Properties and Intracellular Stability
Authors : Huang, X.; Gibson, L.M.; Bell, B.J.; Lovelace, L.L.; Pena, M.M.; Berger, F.G.; Berger, S.H.
Deposited on : 2008-09-02
Resolution : 1.56 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

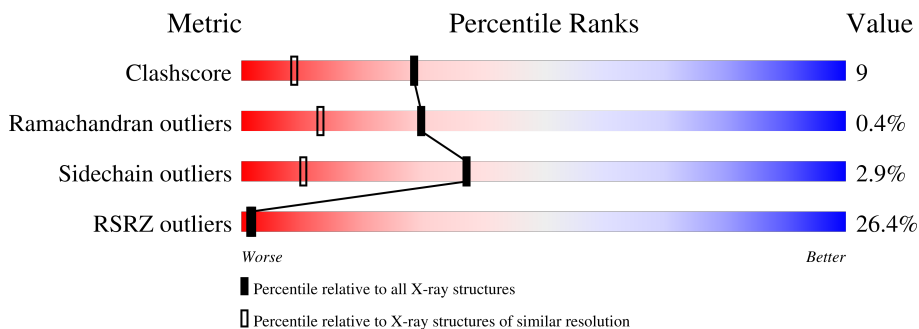
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.56 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	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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 $\leq 5\%$. 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	295	25% 78% 17% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2450 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.

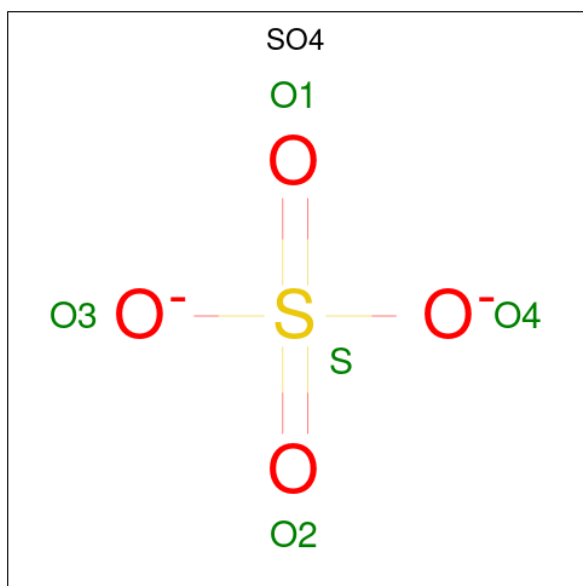
- Molecule 1 is a protein called Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	284	2286	1461	399	414	12	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	LEU	VAL	engineered mutation	UNP P04818

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

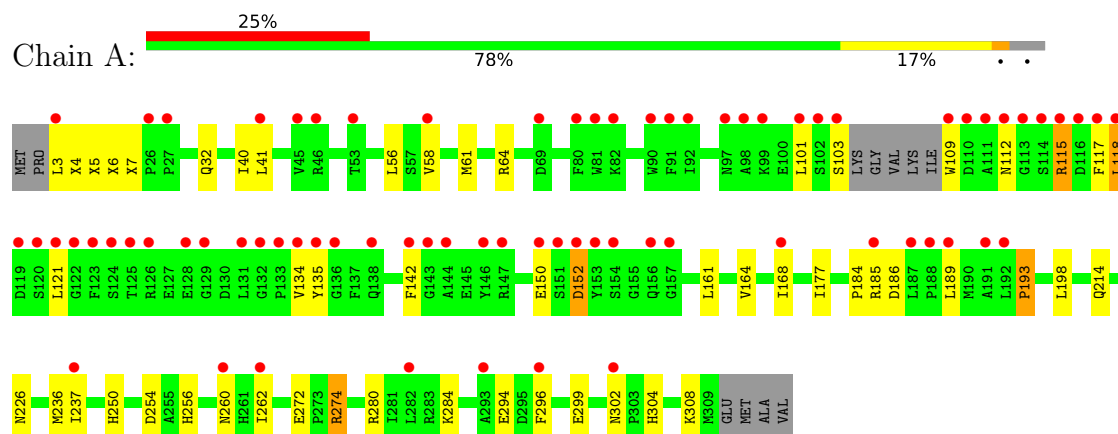
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	149	Total 149	O 149	0	0

3 Residue-property plots

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: Thymidylate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	95.55Å 95.55Å 80.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.56 50.00 – 1.56	Depositor EDS
% Data completeness (in resolution range)	86.8 (50.00-1.56) 79.3 (50.00-1.56)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.74 (at 1.56Å)	Xtriage
Refinement program	REFMAC 5.2.0019, CNS	Depositor
R, R_{free}	0.209 , 0.233 0.200 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.633	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2450	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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: SO4

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	0.92	1/2324 (0.0%)	0.94	2/3142 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	164	VAL	CA-CB	5.52	1.60	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	193	PRO	CA-C-N	-5.35	114.47	120.14
1	A	193	PRO	C-N-CA	-5.35	114.47	120.14

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	2286	0	2234	40	0
2	A	15	0	0	1	0
3	A	149	0	0	2	0
All	All	2450	0	2234	40	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.

All (40) 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:4:UNK:CB	1:A:5:UNK:HA	2.15	0.76
1:A:32:GLN:HE22	1:A:64:ARG:H	1.33	0.75
1:A:112:ASN:HB2	1:A:135:TYR:OH	1.85	0.75
1:A:280:ARG:HG3	1:A:299:GLU:OE2	1.90	0.72
1:A:3:LEU:HG	1:A:142:PHE:CZ	2.26	0.70
1:A:186:ASP:HA	1:A:189:LEU:HD12	1.77	0.67
1:A:58:VAL:HG21	1:A:61:MET:HE3	1.77	0.64
1:A:6:UNK:CB	3:A:350:HOH:O	2.48	0.61
1:A:115:ARG:HB3	1:A:118:LEU:CD2	2.31	0.60
1:A:185:ARG:NH1	2:A:316:SO4:O2	2.36	0.59
1:A:112:ASN:HB3	1:A:115:ARG:HG3	1.87	0.57
1:A:3:LEU:HG	1:A:142:PHE:HZ	1.70	0.56
1:A:274:ARG:HD3	1:A:302:ASN:O	2.07	0.55
1:A:40:ILE:HG12	1:A:58:VAL:HG22	1.91	0.53
1:A:214:GLN:OE1	1:A:250:HIS:HE1	1.96	0.49
1:A:112:ASN:HB2	1:A:135:TYR:HH	1.77	0.48
1:A:280:ARG:CG	1:A:299:GLU:OE2	2.61	0.48
1:A:4:UNK:CB	1:A:5:UNK:CA	2.91	0.47
1:A:32:GLN:NE2	1:A:64:ARG:H	2.07	0.47
1:A:152:ASP:N	1:A:152:ASP:OD1	2.49	0.46
1:A:142:PHE:C	1:A:142:PHE:CD2	2.94	0.45
1:A:41:LEU:CD2	1:A:262:ILE:CD1	2.95	0.45
1:A:134:VAL:HB	1:A:184:PRO:HB3	1.98	0.45
1:A:260:ASN:HB2	3:A:440:HOH:O	2.18	0.44
1:A:41:LEU:CD2	1:A:262:ILE:HD12	2.48	0.43
1:A:56:LEU:HD23	1:A:56:LEU:HA	1.87	0.43
1:A:272:GLU:O	1:A:304:HIS:HE1	2.02	0.43
1:A:254:ASP:O	1:A:256:HIS:HD2	2.02	0.42
1:A:117:PHE:HB3	1:A:185:ARG:HA	2.01	0.42
1:A:308:LYS:HD3	1:A:308:LYS:HA	1.80	0.42
1:A:3:LEU:HD13	1:A:193:PRO:HD2	2.01	0.42
1:A:6:UNK:HA	1:A:7:UNK:HA	1.84	0.41
1:A:214:GLN:HE22	1:A:226:ASN:ND2	2.18	0.41
1:A:5:UNK:CB	1:A:226:ASN:OD1	2.68	0.41
1:A:168:ILE:HD13	1:A:177:ILE:HD13	2.02	0.41
1:A:161:LEU:HD11	1:A:237:ILE:HD11	2.03	0.41
1:A:198:LEU:C	1:A:198:LEU:HD23	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:MET:HE2	1:A:296:PHE:CZ	2.55	0.41
1:A:103:SER:C	1:A:109:TRP:HB2	2.46	0.40
1:A:294:GLU:CD	1:A:294:GLU:H	2.28	0.40

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	275/295 (93%)	266 (97%)	8 (3%)	1 (0%)	30 13

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	115	ARG

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	A	245/254 (96%)	238 (97%)	7 (3%)	37 10

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LEU
1	A	118	LEU
1	A	121	LEU
1	A	150	GLU
1	A	152	ASP
1	A	274	ARG
1	A	284	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	156	GLN
1	A	214	GLN
1	A	250	HIS
1	A	256	HIS
1	A	304	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	316	-	4,4,4	0.32	0	6,6,6	0.66	0
2	SO4	A	317	-	4,4,4	0.34	0	6,6,6	0.46	0
2	SO4	A	315	-	4,4,4	0.37	0	6,6,6	0.34	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	316	SO4	1	0

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	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	7:UNK	C	26:PRO	N	35.64
1	A	3:LEU	C	4:UNK	N	21.80

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	280/295 (94%)	1.62	74 (26%) ⓘ ⓘ	26, 33, 72, 115	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	LEU	12.1
1	A	109	TRP	8.8
1	A	117	PHE	7.1
1	A	111	ALA	6.9
1	A	121	LEU	6.4
1	A	142	PHE	5.9
1	A	118	LEU	5.2
1	A	123	PHE	5.0
1	A	120	SER	4.7
1	A	113	GLY	4.6
1	A	26	PRO	4.4
1	A	134	VAL	4.3
1	A	116	ASP	4.2
1	A	82	LYS	3.9
1	A	112	ASN	3.9
1	A	98	ALA	3.9
1	A	110	ASP	3.9
1	A	131	LEU	3.8
1	A	114	SER	3.8
1	A	135	TYR	3.8
1	A	133	PRO	3.7
1	A	146	TYR	3.7
1	A	189	LEU	3.6
1	A	101	LEU	3.5
1	A	150	GLU	3.4
1	A	293	ALA	3.4
1	A	81	TRP	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	138	GLN	3.2
1	A	124	SER	3.2
1	A	191	ALA	3.1
1	A	152	ASP	3.1
1	A	91	PHE	3.1
1	A	129	GLY	3.1
1	A	125	THR	3.0
1	A	115	ARG	2.9
1	A	103	SER	2.9
1	A	119	ASP	2.9
1	A	102	SER	2.9
1	A	302	ASN	2.9
1	A	99	LYS	2.8
1	A	143	GLY	2.8
1	A	153	TYR	2.8
1	A	128	GLU	2.8
1	A	260	ASN	2.8
1	A	168	ILE	2.7
1	A	237	ILE	2.6
1	A	187	LEU	2.5
1	A	122	GLY	2.5
1	A	262	ILE	2.5
1	A	45	VAL	2.5
1	A	126	ARG	2.4
1	A	144	ALA	2.4
1	A	92	ILE	2.4
1	A	136	GLY	2.4
1	A	58	VAL	2.4
1	A	27	PRO	2.4
1	A	41	LEU	2.4
1	A	185	ARG	2.3
1	A	53	THR	2.3
1	A	132	GLY	2.3
1	A	154	SER	2.3
1	A	46	ARG	2.2
1	A	151	SER	2.2
1	A	188	PRO	2.2
1	A	80	PHE	2.2
1	A	296	PHE	2.2
1	A	147	ARG	2.1
1	A	157	GLY	2.1
1	A	282	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	90	TRP	2.1
1	A	69	ASP	2.1
1	A	192	LEU	2.0
1	A	156	GLN	2.0
1	A	97	ASN	2.0

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	SO4	A	315	5/5	0.82	0.12	58,59,61,61	0
2	SO4	A	317	5/5	0.91	0.13	40,43,47,48	0
2	SO4	A	316	5/5	0.93	0.12	38,38,41,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.