



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:22 PM UTC

PDB ID : 4F43 / pdb_00004f43
Title : Protelomerase TelA mutant R255A complexed with CAAG hairpin DNA
Authors : Shi, K.; Aihara, H.
Deposited on : 2012-05-10
Resolution : 2.35 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
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

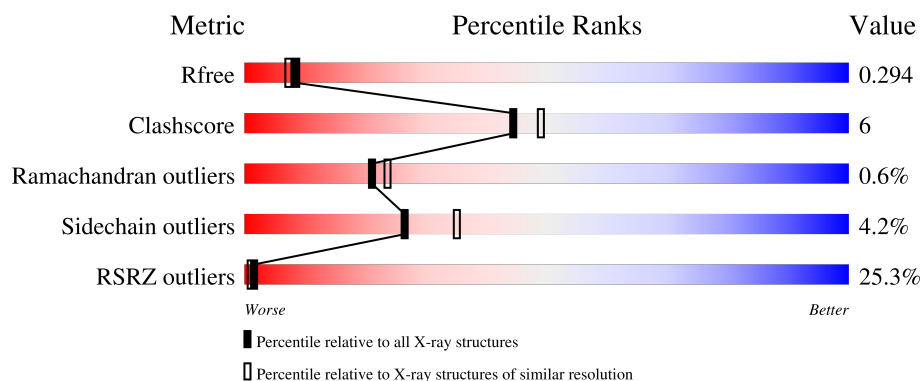
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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))
R_{free}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	320	24% 82% 17% .
2	C	32	38% 69% 31%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3467 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 Protelomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	6	7	0
			2569	1636	438	480	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	255	ALA	ARG	engineered mutation	UNP Q7CWV1

- Molecule 2 is a DNA chain called DNA hairpin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	32	Total	C	N	O	P	0	2	0
			694	337	128	197	32			

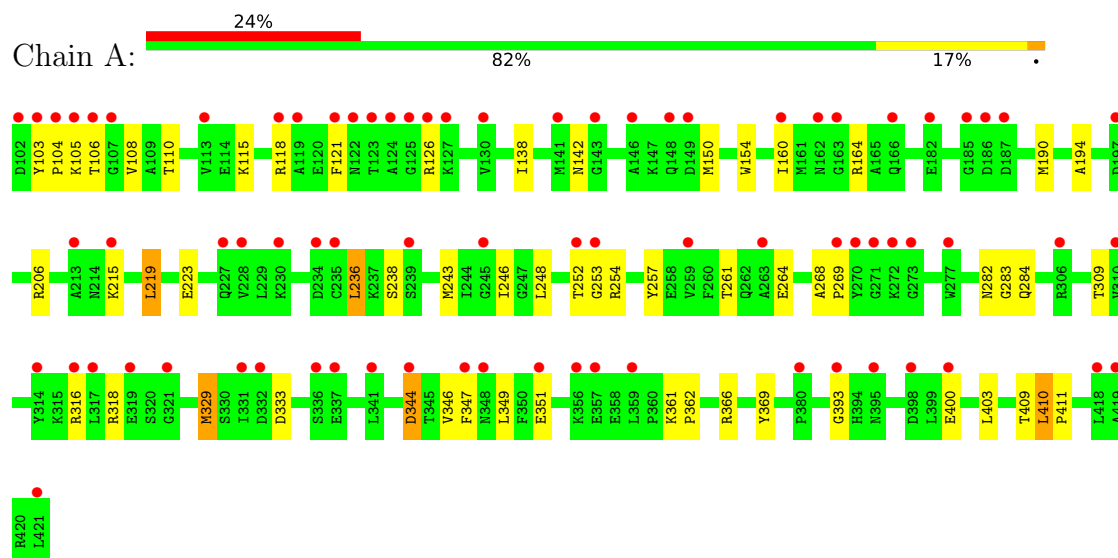
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	147	Total	O	0	0
			147	147		
3	C	57	Total	O	0	0
			57	57		

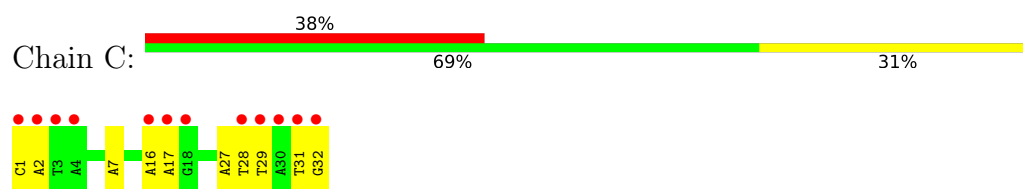
3 Residue-property plots

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: Protelomerase



• Molecule 2: DNA hairpin



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	118.12Å 121.26Å 58.12Å 90.00° 111.30° 90.00°	Depositor
Resolution (Å)	40.39 – 2.35 40.39 – 2.35	Depositor EDS
% Data completeness (in resolution range)	57.9 (40.39-2.35) 57.9 (40.39-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.84 (at 2.37Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.237 , 0.290 0.235 , 0.294	Depositor DCC
R_{free} test set	901 reflections (2.85%)	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3467	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.27% 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](#)

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	0.27	0/2640	0.73	2/3568 (0.1%)
2	C	0.14	0/779	0.61	0/1199
All	All	0.24	0/3419	0.70	2/4767 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	410	LEU	CA-C-N	5.09	125.12	119.32
1	A	410	LEU	C-N-CA	5.09	125.12	119.32

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	2569	0	2560	30	0
2	C	694	0	390	7	0
3	A	147	0	0	4	0
3	C	57	0	0	2	0
All	All	3467	0	2950	36	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 6.

All (36) 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:223:GLU:HA	1:A:411:PRO:HG3	1.76	0.68
2:C:16:DA:N3	3:C:147:HOH:O	2.27	0.66
1:A:164:ARG:NH1	3:A:527:HOH:O	2.37	0.57
1:A:238:SER:O	1:A:316:ARG:NH2	2.40	0.55
1:A:164:ARG:NH2	3:A:634:HOH:O	2.39	0.55
2:C:17[A]:DA:H5'	2:C:17[A]:DA:N3	2.22	0.55
1:A:138:ILE:O	1:A:142:ASN:ND2	2.40	0.54
1:A:400[A]:GLU:HA	1:A:403[A]:LEU:HD13	1.91	0.52
1:A:318:ARG:NH2	3:A:602:HOH:O	2.43	0.52
1:A:344:ASP:HA	1:A:347:PHE:HB2	1.92	0.51
1:A:236:LEU:HD23	1:A:309:THR:HG22	1.94	0.49
1:A:253:GLY:HA3	1:A:369:TYR:CD2	2.47	0.48
1:A:257:TYR:O	1:A:261:THR:OG1	2.30	0.48
2:C:1:DC:H2'	2:C:2:DA:C8	2.49	0.48
1:A:282:ASN:HA	1:A:283:GLY:HA2	1.60	0.47
1:A:154:TRP:CE2	1:A:194:ALA:HA	2.50	0.47
1:A:248:LEU:O	1:A:252:THR:HG22	2.14	0.47
1:A:268:ALA:HA	1:A:269:PRO:HD3	1.81	0.47
1:A:252:THR:HG23	1:A:254:ARG:HG2	1.96	0.46
1:A:284:GLN:NE2	1:A:393:GLY:O	2.49	0.46
1:A:103:TYR:HB2	1:A:104:PRO:HD3	1.97	0.46
1:A:115:LYS:HG2	1:A:118:ARG:HH21	1.79	0.45
2:C:28:DT:H2''	2:C:29:DT:O5'	2.16	0.45
2:C:31:DT:H2''	2:C:32:DG:C8	2.52	0.44
1:A:264:GLU:N	1:A:282:ASN:O	2.51	0.43
1:A:105:LYS:HG3	1:A:106:THR:HG23	2.01	0.43
1:A:346:VAL:HG21	1:A:362:PRO:HG3	2.00	0.43
1:A:219:LEU:HD23	1:A:409:THR:HB	2.01	0.42
1:A:346:VAL:HG23	3:A:603:HOH:O	2.19	0.42
2:C:7:DA:N7	3:C:150:HOH:O	2.37	0.42
1:A:329:MET:HE2	1:A:333:ASP:HB3	2.02	0.41
1:A:243:MET:HA	1:A:246:ILE:HD12	2.02	0.41
1:A:253:GLY:O	1:A:366:ARG:NH1	2.53	0.41
1:A:126:ARG:HH11	2:C:27:DA:H1'	1.86	0.41
1:A:150:MET:HB3	1:A:190:MET:SD	2.61	0.40
1:A:410:LEU:HA	1:A:411:PRO:HD3	1.90	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	325/320 (102%)	309 (95%)	14 (4%)	2 (1%)	21	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	349	LEU
1	A	160	ILE

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	272/266 (102%)	261 (96%)	11 (4%)	28	37

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	VAL
1	A	110	THR
1	A	121	PHE
1	A	206	ARG
1	A	215	LYS
1	A	219	LEU
1	A	236	LEU
1	A	329	MET
1	A	344	ASP

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Mol	Chain	Res	Type
1	A	351	GLU
1	A	361	LYS

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

Mol	Chain	Res	Type
1	A	214	ASN
1	A	224	ASN

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](#)

There are no ligands in this entry.

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

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	320/320 (100%)	1.32	77 (24%) 2 1	8, 41, 78, 128	7 (2%)
2	C	32/32 (100%)	1.36	12 (37%) 1 0	23, 52, 107, 124	2 (6%)
All	All	352/352 (100%)	1.33	89 (25%) 1 1	8, 42, 84, 128	9 (2%)

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	103	TYR	8.9
1	A	421	LEU	5.9
1	A	102	ASP	5.8
2	C	32	DG	5.3
2	C	1	DC	4.7
1	A	419	ALA	4.5
2	C	2	DA	4.5
1	A	163	GLY	4.4
1	A	121	PHE	4.3
1	A	124	ALA	4.3
1	A	336	SER	4.0
1	A	393	GLY	3.9
2	C	18[A]	DG	3.8
1	A	104	PRO	3.8
1	A	122	ASN	3.6
1	A	270	TYR	3.6
1	A	331	ILE	3.5
1	A	332	ASP	3.5
1	A	316	ARG	3.4
1	A	123	THR	3.3
1	A	106	THR	3.3
1	A	105	LYS	3.2
1	A	160	ILE	3.2
1	A	310	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
2	C	31	DT	3.2
1	A	125	GLY	3.2
1	A	263	ALA	3.2
1	A	149	ASP	3.1
1	A	186	ASP	3.1
1	A	113	VAL	3.1
1	A	259	VAL	3.0
1	A	347	PHE	3.0
1	A	230	LYS	2.9
1	A	314	TYR	2.9
1	A	227	GLN	2.9
2	C	3	DT	2.9
1	A	107	GLY	2.8
1	A	143	GLY	2.7
2	C	28	DT	2.7
1	A	213	ALA	2.7
1	A	400[A]	GLU	2.7
1	A	271	GLY	2.6
1	A	395	ASN	2.6
1	A	119	ALA	2.6
1	A	341	LEU	2.5
1	A	162	ASN	2.5
1	A	380	PRO	2.5
1	A	187	ASP	2.5
1	A	127	LYS	2.5
1	A	118	ARG	2.5
1	A	273	GLY	2.5
1	A	148	GLN	2.5
1	A	215	LYS	2.4
2	C	16	DA	2.4
1	A	253	GLY	2.4
1	A	197	ASP	2.4
1	A	306	ARG	2.4
2	C	29	DT	2.4
1	A	359	LEU	2.4
1	A	277	TRP	2.4
1	A	321	GLY	2.4
2	C	17[A]	DA	2.3
1	A	141	MET	2.3
1	A	239[A]	SER	2.3
1	A	130	VAL	2.3
1	A	418	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	234	ASP	2.3
1	A	348	ASN	2.3
1	A	252	THR	2.2
1	A	235[A]	CYS	2.2
1	A	272	LYS	2.2
1	A	351	GLU	2.2
2	C	30	DA	2.1
1	A	185	GLY	2.1
1	A	319	GLU	2.1
1	A	337	GLU	2.1
1	A	357	GLU	2.1
1	A	146	ALA	2.1
2	C	4	DA	2.1
1	A	398	ASP	2.1
1	A	269	PRO	2.1
1	A	245	GLY	2.1
1	A	166	GLN	2.1
1	A	317	LEU	2.1
1	A	228	VAL	2.1
1	A	182	GLU	2.0
1	A	344	ASP	2.0
1	A	126	ARG	2.0
1	A	356	LYS	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.