

Full wwPDB X-ray Structure Validation Report (i)

Feb 10, 2024 - 06:33 PM EST

PDB ID	:	2R4G
Title	:	The high resolution structure of the RNA-binding domain of telomerase
Authors	:	Rouda, S.; Skordalakes, E.
Deposited on		
Resolution	:	1.71 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 (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 (1)) were used in the production of this report:

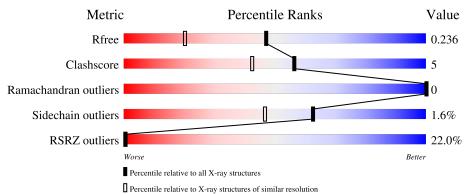
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 1.71 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	5722(1.74-1.70)
Clashscore	141614	6152(1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)
RSRZ outliers	127900	5629(1.74-1.70)

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% 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	
			21%	
1	А	267	84%	9% • 6%



2R4G

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2364 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 Telomerase reverse transcriptase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	250	Total 2145	C 1401	N 354	O 383	S 7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	253	MET	-	initiating methionine	UNP 077448

• Molecule 2 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	7	Total Br 7 7	0	0

• Molecule 3 is water.

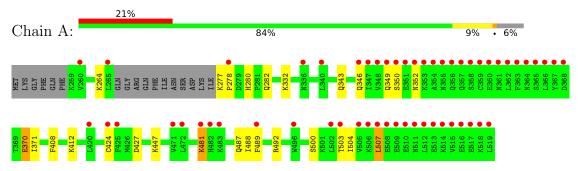
Mol	Chain	Residues	Ator	ns	ZeroOcc	AltConf
3	А	212	Total 212	O 212	0	0



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 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: Telomerase reverse transcriptase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	39.35Å 67.22Å 51.53Å	Denesiten
a, b, c, α , β , γ	90.00° 90.66° 90.00°	Depositor
Resolution (Å)	20.00 - 1.71	Depositor
Resolution (A)	28.49 - 1.71	EDS
% Data completeness	99.9(20.00-1.71)	Depositor
(in resolution range)	99.8(28.49-1.71)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.05	Depositor
$< I/\sigma(I) > 1$	$1.22 (at 1.71 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.200 , 0.239	Depositor
II, IIfree	0.199 , 0.236	DCC
R_{free} test set	1472 reflections (5.09%)	wwPDB-VP
Wilson B-factor $(Å^2)$	19.1	Xtriage
Anisotropy	0.401	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 56.0	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2364	wwPDB-VP
Average B, all atoms $(Å^2)$	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.58% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: BR

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	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.42	0/2187	0.44	0/2931

There are no bond length outliers.

There are no bond angle outliers.

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	А	2145	0	2210	22	0
2	А	7	0	0	2	0
3	А	212	0	0	3	0
All	All	2364	0	2210	22	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 5.

All (22) 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:280:HIS:HD2	1:A:282:GLN:H	1.20	0.88

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Atom-1	Atom-2	Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
1:A:481:LYS:HB3	1:A:489:PHE:CE2	2.12	0.84	
1:A:349:GLN:HA	1:A:350:SER:HB2	1.73	0.70	
1:A:424:CYS:HB3	3:A:718:HOH:O	1.94	0.68	
1:A:371:ILE:HD11	1:A:492:ARG:HG2	1.76	0.66	
1:A:280:HIS:CD2	1:A:282:GLN:H	2.12	0.58	
1:A:264:LYS:HE2	1:A:408:PHE:O	2.04	0.57	
1:A:481:LYS:HD2	1:A:489:PHE:CZ	2.40	0.56	
1:A:280:HIS:CD2	1:A:282:GLN:HG2	2.46	0.51	
1:A:481:LYS:HB3	1:A:489:PHE:CD2	2.45	0.50	
1:A:487:GLN:HB3	1:A:489:PHE:CE2	2.49	0.48	
1:A:487:GLN:HB3	1:A:489:PHE:HE2	1.78	0.47	
1:A:332:LYS:HE3	3:A:724:HOH:O	2.15	0.46	
1:A:412:LYS:HA	1:A:488:ILE:HG12	1.98	0.45	
1:A:343:GLN:O	1:A:346:GLN:HG3	2.17	0.45	
1:A:277:LYS:HD2	1:A:278:PRO:HD3	2.00	0.44	
1:A:370:GLU:HG3	1:A:489:PHE:CD1	2.54	0.42	
1:A:332:LYS:HD2	3:A:619:HOH:O	2.19	0.42	
1:A:500:SER:O	1:A:504:ILE:HG12	2.19	0.42	
1:A:447:LYS:HG3	2:A:4:BR:BR	2.75	0.41	
1:A:427:ASP:HA	2:A:3:BR:BR	2.75	0.41	
1:A:503:THR:O	1:A:507:LEU:HB2	2.21	0.40	

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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.

Μ	Iol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
	1	А	246/267~(92%)	240 (98%)	6(2%)	0	100 100

There are no Ramachandran outliers to report.



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	246/261~(94%)	242 (98%)	4 (2%)	62 47	

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	352	ASN
1	А	370	GLU
1	А	481	LYS
1	А	507	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	280	HIS
1	А	282	GLN
1	А	385	GLN
1	А	487	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)

Of 7 ligands modelled in this entry, 7 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 (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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95^{th} 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 $>$			$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9	
1	А	250/267~(93%)	1.44	55~(22%)	0 0		13, 20, 64, 85	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	511	ASN	15.2
1	А	519	LEU	11.9
1	А	516	GLU	11.7
1	А	507 LEU		11.7
1	А	515	VAL	11.5
1	А	518	LYS	10.7
1	А	517	GLU	10.5
1	А	512	LEU	9.8
1	А	514	LYS	9.7
1	А	354	ALA	8.7
1	А	505	VAL	6.9
1	А	359	CYS	6.9
1	А	510	GLU	6.9
1	А	350	SER	6.1
1	А	357	GLN	6.0
1	А	361	ASN	5.8
1	А	513	GLU	5.7
1	А	355	ASN	5.7
1	А	364	ASN	5.4
1	А	353	LYS	5.4
1	А	508	GLU	5.4
1	А	358	SER	5.3
1	А	352	ASN	5.1
1	А	367	TYR	5.0
1	А	356	GLN	4.7
1	А	482	HIS	4.7
1	A	496	TRP	4.5

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Mol	Chain	Res	Type	RSRZ
1	А	502	LEU	4.2
1	А	260	VAL	3.9
1	А	340	LEU	3.8
1	А	503	THR	3.5
1	А	348	VAL	3.5
1	А	509	GLU	3.4
1	А	360	GLU	3.4
1	А	336	ASN	3.3
1	А	265	LEU	3.3
1	А	362	LEU	3.3
1	А	489	PHE	3.3
1	А	425	PHE	3.1
1	А	506	LYS	2.9
1	А	424	CYS	2.8
1	А	363	PHE	2.8
1	А	472	LEU	2.7
1	А	351	GLU	2.5
1	А	368	ASP	2.4
1	А	347	ILE	2.3
1	А	483	LYS	2.3
1	А	420	LEU	2.2
1	А	471	VAL	2.2
1	А	481	LYS	2.2
1	А	366	LEU	2.1
1	А	346	GLN	2.1
1	А	365	SER	2.1
1	А	278	PRO	2.1
1	А	349	GLN	2.0

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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 monosaccharides 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,



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	BR	А	3	1/1	0.91	0.11	$59,\!59,\!59,\!59$	0
2	BR	А	4	1/1	0.96	0.05	49,49,49,49	0
2	BR	А	2	1/1	0.98	0.13	$45,\!45,\!45,\!45$	0
2	BR	А	5	1/1	0.98	0.10	46,46,46,46	0
2	BR	А	6	1/1	0.98	0.07	42,42,42,42	0
2	BR	А	1	1/1	0.99	0.05	28,28,28,28	0
2	BR	А	7	1/1	0.99	0.05	28,28,28,28	0

median, 95^{th} 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.

6.5 Other polymers (i)

There are no such residues in this entry.

