



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 06:59 PM GMT

PDB ID : 4LMO
Title : Structure of a vertebrate RNA binding domain of telomerase (TRBD)
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Deposited on : 2013-07-10
Resolution : 2.37 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

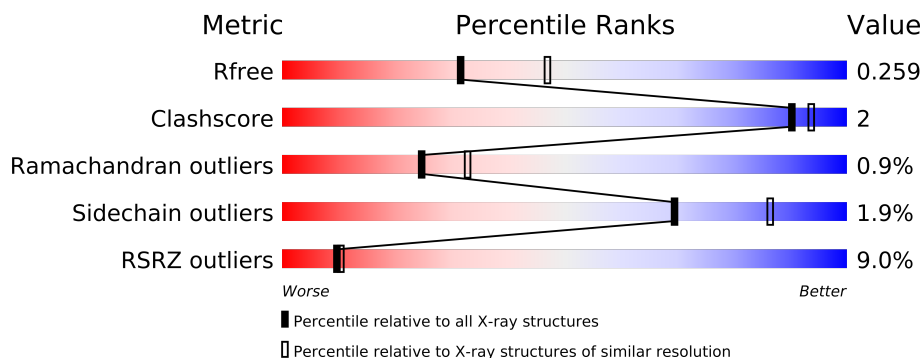
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	FAILED
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.37 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}	66092	2963 (2.40-2.36)
Clashscore	79885	3668 (2.40-2.36)
Ramachandran outliers	78287	3600 (2.40-2.36)
Sidechain outliers	78261	3602 (2.40-2.36)
RSRZ outliers	66119	2966 (2.40-2.36)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	254	
1	B	254	
1	C	254	
1	D	254	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8456 atoms, of which 0 are hydrogen and 0 are deuterium.

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	A	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			
1	B	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			
1	C	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			
1	D	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	291	SER	-	EXPRESSION TAG	UNP Q4KTA7
A	292	ASN	-	EXPRESSION TAG	UNP Q4KTA7
A	293	ALA	-	EXPRESSION TAG	UNP Q4KTA7
B	291	SER	-	EXPRESSION TAG	UNP Q4KTA7
B	292	ASN	-	EXPRESSION TAG	UNP Q4KTA7
B	293	ALA	-	EXPRESSION TAG	UNP Q4KTA7
C	291	SER	-	EXPRESSION TAG	UNP Q4KTA7
C	292	ASN	-	EXPRESSION TAG	UNP Q4KTA7
C	293	ALA	-	EXPRESSION TAG	UNP Q4KTA7
D	291	SER	-	EXPRESSION TAG	UNP Q4KTA7
D	292	ASN	-	EXPRESSION TAG	UNP Q4KTA7
D	293	ALA	-	EXPRESSION TAG	UNP Q4KTA7

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	30	Total	O	0	0
			30	30		
2	B	37	Total	O	0	0
			37	37		

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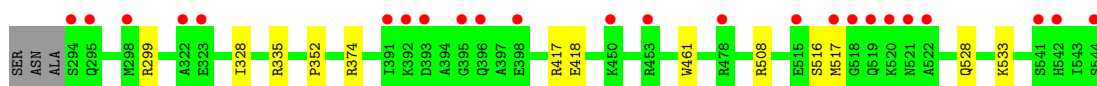
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	38	Total	O	0	0
			38	38		
2	D	39	Total	O	0	0
			39	39		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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

Chain A: 



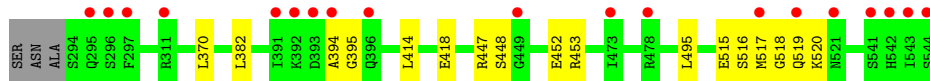
- Molecule 1: Telomerase reverse transcriptase

Chain B: 



- Molecule 1: Telomerase reverse transcriptase

Chain C: 



- Molecule 1: Telomerase reverse transcriptase

Chain D: 



4 Data and refinement statistics

Xtriage (Phenix) failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.63Å 84.51Å 137.17Å 90.00° 94.31° 90.00°	Depositor
Resolution (Å)	20.00 – 2.37 44.66 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-2.37) 78.9 (44.66-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.220 , 0.259 0.221 , 0.259	Depositor DCC
R_{free} test set	2163 reflections (5.10%)	DCC
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 34.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8456	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

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	0.46	1/2129 (0.0%)	0.50	0/2858
1	B	0.46	1/2129 (0.0%)	0.51	0/2858
1	C	0.46	0/2129	0.53	0/2858
1	D	0.46	1/2129 (0.0%)	0.50	0/2858
All	All	0.46	3/8516 (0.0%)	0.51	0/11432

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	461	TRP	CD2-CE2	5.06	1.47	1.41
1	D	461	TRP	CD2-CE2	5.03	1.47	1.41
1	B	461	TRP	CD2-CE2	5.01	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2078	0	0	5	0
1	B	2078	0	0	8	0
1	C	2078	0	0	3	0
1	D	2078	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	30	0	0	0	0
2	B	37	0	0	0	0
2	C	38	0	0	0	0
2	D	39	0	0	0	0
All	All	8456	0	0	17	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

The worst 5 of 17 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:394:ALA:CB	1:B:395:GLY:CA	2.55	0.83
1:A:516:SER:CB	1:A:517:MET:CA	2.58	0.82
1:C:394:ALA:N	1:C:395:GLY:CA	2.52	0.73
1:C:515:GLU:O	1:C:517:MET:N	2.40	0.54
1:B:432:GLU:OE2	1:B:435:ARG:NH1	2.41	0.53

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	249/254 (98%)	237 (95%)	12 (5%)	0	100	100
1	B	249/254 (98%)	233 (94%)	14 (6%)	2 (1%)	27	37
1	C	249/254 (98%)	231 (93%)	13 (5%)	5 (2%)	11	12
1	D	249/254 (98%)	239 (96%)	8 (3%)	2 (1%)	27	37
All	All	996/1016 (98%)	940 (94%)	47 (5%)	9 (1%)	25	33

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	448	SER

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Mol	Chain	Res	Type
1	C	516	SER
1	C	520	LYS
1	B	518	GLY
1	C	518	GLY

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	221/223 (99%)	218 (99%)	3 (1%)	78	91
1	B	221/223 (99%)	216 (98%)	5 (2%)	63	81
1	C	221/223 (99%)	215 (97%)	6 (3%)	57	77
1	D	221/223 (99%)	218 (99%)	3 (1%)	78	91
All	All	884/892 (99%)	867 (98%)	17 (2%)	69	86

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	506	LEU
1	C	370	LEU
1	C	495	LEU
1	B	447	ARG
1	D	447	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

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	251/254 (98%)	0.27	24 (9%) 8 9	25, 40, 87, 107	0
1	B	251/254 (98%)	0.36	25 (9%) 8 8	27, 39, 90, 119	0
1	C	251/254 (98%)	0.31	19 (7%) 14 15	27, 43, 93, 112	0
1	D	251/254 (98%)	0.39	22 (8%) 10 11	25, 42, 87, 111	0
All	All	1004/1016 (98%)	0.33	90 (8%) 10 10	25, 41, 90, 119	0

The worst 5 of 90 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	518	GLY	11.1
1	B	543	ILE	9.7
1	A	520	LYS	8.4
1	C	542	HIS	7.5
1	C	541	SER	7.2

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.