



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 11:55 pm GMT

PDB ID : 2LD8
Title : Structure of Human Telomeric DNA in Crowded Solution
Authors : Heddi, B.; Phan, A.T.
Deposited on : 2011-05-17

This is a Full wwPDB NMR Structure Validation 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/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

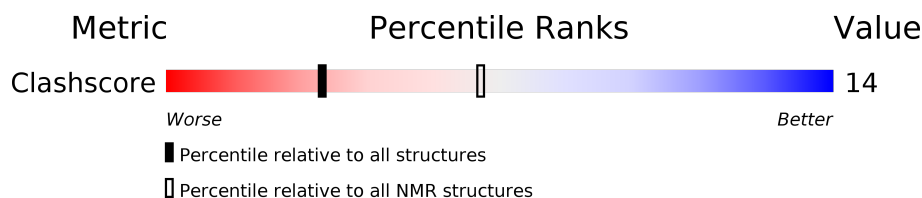
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 37%.

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)	NMR archive (#Entries)
Clashscore	125131	11601

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	23	

2 Ensemble composition and analysis ⓘ

This entry contains 10 models. This entry does not contain polypeptide chains, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 747 atoms, of which 262 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called Human Telomeric DNA.

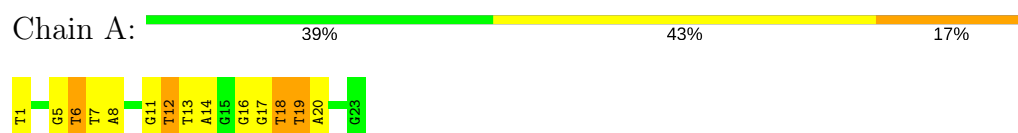
Mol	Chain	Residues	Atoms						Trace
1	A	23	Total	C	H	N	O	P	0
			747	230	262	94	139	22	

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Human Telomeric DNA

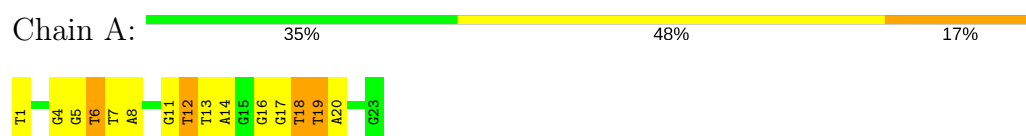


4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

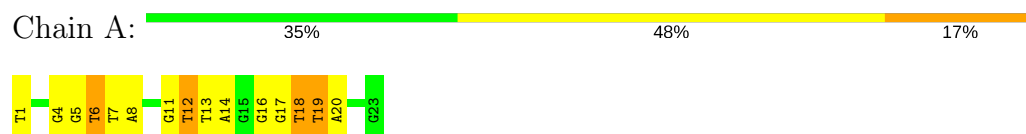
4.2.1 Score per residue for model 1

- Molecule 1: Human Telomeric DNA



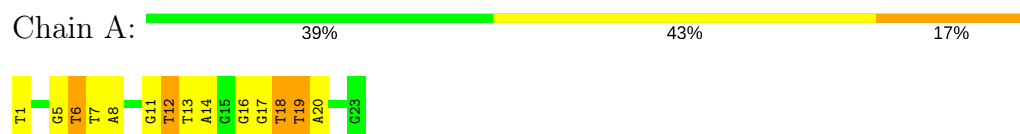
4.2.2 Score per residue for model 2

- Molecule 1: Human Telomeric DNA



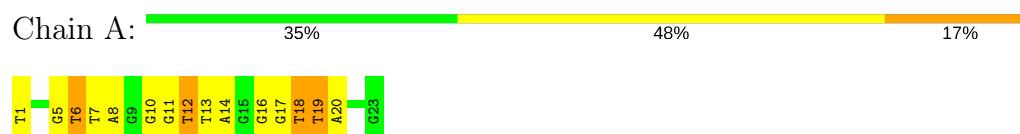
4.2.3 Score per residue for model 3

- Molecule 1: Human Telomeric DNA



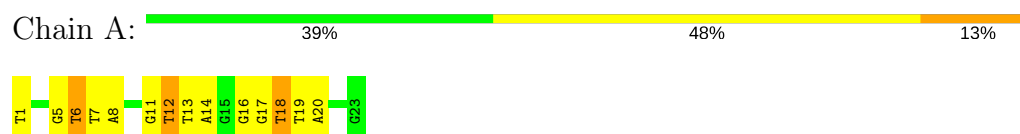
4.2.4 Score per residue for model 4

- Molecule 1: Human Telomeric DNA



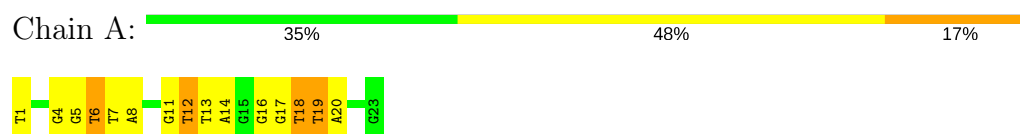
4.2.5 Score per residue for model 5

- Molecule 1: Human Telomeric DNA



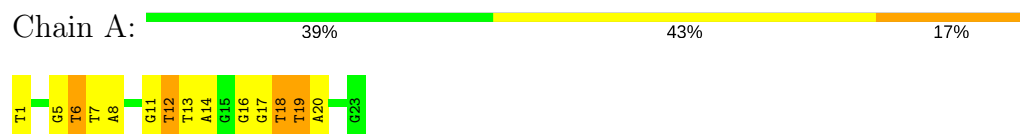
4.2.6 Score per residue for model 6

- Molecule 1: Human Telomeric DNA



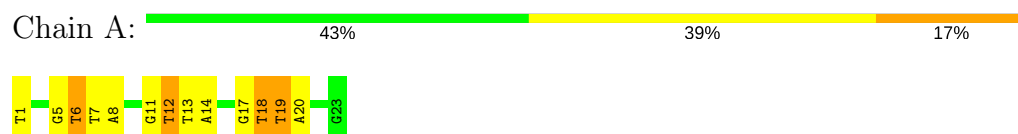
4.2.7 Score per residue for model 7

- Molecule 1: Human Telomeric DNA



4.2.8 Score per residue for model 8

- Molecule 1: Human Telomeric DNA



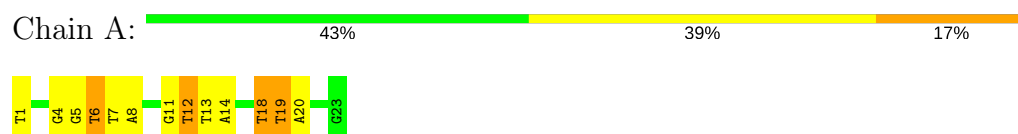
4.2.9 Score per residue for model 9

- Molecule 1: Human Telomeric DNA



4.2.10 Score per residue for model 10

- Molecule 1: Human Telomeric DNA



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing, simulated annealing, molecular dynamics*.

Of the 100 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR NIH	structure solution	2.26
AMBER	refinement	10.0
X-PLOR NIH	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	2ld8_cs.str
Number of chemical shift lists	1
Total number of shifts	175
Number of shifts mapped to atoms	175
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	37%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

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 (average) 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	1.14±0.01	7±0/546 (1.3±0.1%)	1.38±0.01	11±1/846 (1.3±0.1%)
All	All	1.14	69/5460 (1.3%)	1.38	110/8460 (1.3%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	6	DT	C5-C7	5.70	1.53	1.50	5	10
1	A	7	DT	C5-C7	5.63	1.53	1.50	6	10
1	A	18	DT	C5-C7	5.61	1.53	1.50	7	10
1	A	12	DT	C5-C7	5.55	1.53	1.50	8	9
1	A	13	DT	C5-C7	5.54	1.53	1.50	2	10
1	A	1	DT	C5-C7	5.52	1.53	1.50	9	10
1	A	19	DT	C5-C7	5.49	1.53	1.50	4	10

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	7	DT	C6-C5-C7	-6.29	119.13	122.90	9	10
1	A	19	DT	C6-C5-C7	-6.22	119.17	122.90	2	10
1	A	13	DT	C6-C5-C7	-5.98	119.31	122.90	10	10
1	A	1	DT	C6-C5-C7	-5.85	119.39	122.90	4	10
1	A	18	DT	C6-C5-C7	-5.61	119.53	122.90	1	10
1	A	6	DT	C6-C5-C7	-5.54	119.58	122.90	4	10
1	A	12	DT	C6-C5-C7	-5.43	119.64	122.90	1	10
1	A	6	DT	C4-C5-C6	5.23	121.14	118.00	10	8
1	A	18	DT	C4-C5-C6	5.22	121.13	118.00	6	7
1	A	1	DT	C4-C5-C6	5.21	121.13	118.00	9	7
1	A	12	DT	C4-C5-C6	5.19	121.11	118.00	9	3
1	A	13	DT	C4-C5-C6	5.11	121.06	118.00	7	6

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	7	DT	C4-C5-C6	5.10	121.06	118.00	2	5
1	A	19	DT	C4-C5-C6	5.07	121.04	118.00	9	4

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	485	262	262	10±1
All	All	4850	2620	2620	104

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 14.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:DT:H2''	1:A:14:DA:N7	0.78	1.93	3	2
1:A:12:DT:H2''	1:A:14:DA:C8	0.76	2.14	3	8
1:A:18:DT:H1'	1:A:19:DT:OP1	0.63	1.92	10	7
1:A:6:DT:C2	1:A:8:DA:N6	0.63	2.66	10	10
1:A:18:DT:C2	1:A:20:DA:N6	0.58	2.72	7	7
1:A:4:DG:H4'	1:A:6:DT:O4	0.56	2.01	6	4
1:A:12:DT:C2	1:A:14:DA:N6	0.54	2.77	8	2
1:A:5:DG:H5''	1:A:6:DT:O5'	0.53	2.04	4	2
1:A:5:DG:H4'	1:A:6:DT:H5''	0.53	1.81	5	2
1:A:18:DT:C1'	1:A:19:DT:OP1	0.51	2.59	7	9
1:A:16:DG:H1'	1:A:18:DT:O4	0.49	2.07	1	2
1:A:11:DG:N2	1:A:16:DG:C8	0.48	2.80	3	6
1:A:5:DG:H4'	1:A:6:DT:H5'	0.48	1.86	10	6
1:A:12:DT:C2'	1:A:14:DA:N7	0.47	2.73	3	1
1:A:18:DT:O2	1:A:20:DA:N6	0.45	2.50	1	3
1:A:12:DT:O2	1:A:14:DA:N6	0.45	2.50	4	7
1:A:11:DG:H5''	1:A:12:DT:O4'	0.44	2.12	10	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:DG:H5'	1:A:18:DT:C5	0.44	2.47	5	2
1:A:18:DT:C2'	1:A:20:DA:C8	0.44	3.01	10	1
1:A:11:DG:C4'	1:A:12:DT:H5'	0.44	2.43	5	2
1:A:16:DG:H2'	1:A:17:DG:C8	0.43	2.49	1	1
1:A:5:DG:H5'	1:A:6:DT:C6	0.43	2.49	5	2
1:A:5:DG:C4'	1:A:6:DT:H5'	0.43	2.44	9	6
1:A:5:DG:H4'	1:A:6:DT:C5'	0.42	2.43	6	1
1:A:17:DG:C4'	1:A:18:DT:H5'	0.41	2.45	6	5
1:A:6:DT:N3	1:A:8:DA:N6	0.41	2.69	2	1
1:A:10:DG:H2''	1:A:11:DG:OP2	0.40	2.15	4	1
1:A:17:DG:H4'	1:A:18:DT:H5'	0.40	1.93	3	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

6.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 37% for the well-defined parts and 37% for the entire structure.

7.1 Chemical shift list 1

File name: 2ld8_cs.str

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	175
Number of shifts mapped to atoms	175
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 37%, i.e. 168 atoms were assigned a chemical shift out of a possible 458. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Sidechain	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	168/458 (37%)	168/274 (61%)	0/149 (0%)	0/35 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 37%, i.e. 168 atoms were assigned a chemical shift out of a possible 458. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Sidechain	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	168/458 (37%)	168/274 (61%)	0/149 (0%)	0/35 (0%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_1). RCI is only applicable to proteins.