

# wwPDB NMR Structure Validation Summary Report (i)

#### Feb 14, 2022 – 09:24 AM EST

PDB ID	:	1IV6
Title	:	Solution Structure of the DNA Complex of Human TRF1
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Deposited on	:	2002-03-14

This is a wwPDB NMR Structure Validation Summary 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/NMRValidationReportHelp with specific help available everywhere you see the (i) symbol.

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

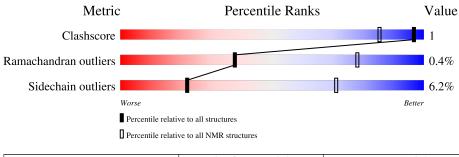
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. $(2010)$
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $SOLUTION\ NMR$ 

The overall completeness of chemical shifts assignment was not calculated.

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	NMR archive		
Metric	$(\# {\rm Entries})$	(# Entries)		
Clashscore	158937	12864		
Ramachandran outliers	154571	11451		
Sidechain outliers	154315	11428		

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 <=5%

Mol	Chain	Length		Quality of chain	1	
1	В	13	15%	77%		8%
2	С	13	31%	62%	)	8%
3	А	70		69%	• 11%	19%



## 2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 16 is the overall representative, medoid model (most similar to other models). The authors have identified model 2 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues							
Well-defined core Residue range (total) Backbone RMSD (Å) Medoid model							
1	A:381-A:429 (49)	0.35	16				

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models



## 3 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1846 atoms, of which 819 are hydrogens and 0 are deuteriums.

• Molecule 1 is a DNA chain called 5'-D(\*GP\*TP\*TP\*AP\*GP\*GP\*GP\*TP\*TP\*AP\*GP\*G P\*G)-3'.

Mol	Chain	Residues		Atoms				Trace	
1	D	19	Total	С	Η	Ν	0	Р	0
	D	10	422	130	149	53	78	12	0

• Molecule 2 is a DNA chain called 5'-D(\*CP\*CP\*CP\*TP\*AP\*AP\*CP\*CP\*CP\*CP\*TP\*AP\*AP \*C)-3'.

Mol	Chain	Residues		Atoms				Trace	
0	C	19	Total	С	Η	Ν	Ο	Р	0
	C	10	401	123	147	45	74	12	0

• Molecule 3 is a protein called TELOMERIC REPEAT BINDING FACTOR 1.

Mol	Chain	Residues	Atoms					Trace	
3	А	57	Total 1023	C 320	Н 523	N 98	O 80	$\frac{S}{2}$	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	370	MET	-	SEE REMARK 999	UNP P54274



# 4 Residue-property plots (i)

## 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: 5'-D(\*GP\*TP\*TP\*AP\*GP\*GP\*GP\*TP\*TP\*AP\*GP\*GP\*G)-3'

Chain B:	15%	77%		8%
G1 72 65 65 78 78	T9 A10 G12 G13 G13			
• Molecule	2: 5'-D(*CP*Cl	P*CP*TP*AP*AP	*CP*CP*CP*TP*.	AP*AP*C)-3'
Chain C:	31%	_	62%	8%
C14 T17 A18 A18 C20 C21 C21 C22	T23 A24 A25 C26			
• Molecule	3: TELOMERI	C REPEAT BINDI	NG FACTOR 1	
Chain A:		69%	• 11%	19%
MET THR PRO GLU GLU LYS HTS ARG ALA	R378 K379 R380 R385 L430 L430 L432 1433 S434 SER	ASP SER GLU ASP		

# 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 16. Colouring as in section 4.1 above.

• Molecule 1: 5'-D(\*GP\*TP\*TP\*AP\*GP\*GP\*GP\*TP\*TP\*AP\*GP\*GP\*G)-3'



• Molecule 2: 5'-D(\*CP\*CP\*CP\*TP\*AP\*AP\*CP\*CP\*CP\*TP\*AP\*AP\*C)-3'



Chain C:	23%		62%			15%		
C14 117 117 117 117 117 117 123 123 123 123 123 123 123 123								
• Molecule 3: TELOMERIC REPEAT BINDING FACTOR 1								
Chain A:		56%	139	% •	11%	19%		
MET THR PRO GLU LYS HIS ARG	R1A R378 R379 R380 R385 R380 R385 R380 R385 R380 R385 F412 F412	R4 15 L420 K421 B422 R423 W424 M427	L430 K431 L432 1433 S434 SER ASP SER	GLU ASP				



## 5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: distance geometry/simulated annealing.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: structures with the least restraint violations.

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

Software name	Classification	Version
EMBOSS	refinement	5.0
EMBOSS	structure solution	5.0

No chemical shift data was provided.



# 6 Model quality (i)

## 6.1 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 (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol Chain		B	ond lengths	Bond angles		
		RMSZ $\#Z > 5$		RMSZ	#Z>5	
1	В	$1.24{\pm}0.02$	$0{\pm}0/307~(~0.0{\pm}~0.0\%)$	$2.33 \pm 0.03$	$21{\pm}1/475$ ( $4.4{\pm}$ $0.2\%$ )	
2	С	$1.26 {\pm} 0.01$	$0{\pm}0/283~(~0.0{\pm}~0.0\%)$	$1.93 \pm 0.04$	$11{\pm}2/432$ ( $2.5{\pm}$ $0.5\%$ )	
3	А	$0.62 {\pm} 0.01$	$0{\pm}0/442~(~0.0{\pm}~0.0\%)$	$0.95 {\pm} 0.04$	$0{\pm}1/592~(~0.1{\pm}~0.1\%)$	
All	All	1.03	0/20640~(~0.0%)	1.77	645/29980~(~2.2%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	В	$0.0{\pm}0.0$	$2.2{\pm}0.9$
2	С	$0.0{\pm}0.0$	$3.0{\pm}1.2$
3	А	$0.0{\pm}0.0$	$0.3 \pm 0.5$
All	All	0	110

There are no bond-length outliers.

5 of 63 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(°)	$Ideal(^{o})$	Moo Worst	dels Total
1	В	3	DT	C6-C5-C7	-12.79	115.22	122.90	8	20
1	В	4	DA	O4'-C1'-N9	12.64	116.85	108.00	3	20
1	В	9	DT	C6-C5-C7	-12.20	115.58	122.90	4	20
2	С	17	DT	C6-C5-C7	-11.97	115.72	122.90	20	20
1	В	8	DT	C6-C5-C7	-11.47	116.02	122.90	6	20

There are no chirality outliers.

5 of 21 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.



Mol	Chain	Res	Type	Group	Models (Total)
2	С	22	DC	Sidechain	14
1	В	4	DA	Sidechain	13
2	С	23	DT	Sidechain	13
2	С	21	DC	Sidechain	9
1	В	7	DG	Sidechain	6

#### 6.2 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 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	В	273	149	149	1±1
2	С	254	147	147	1±1
3	А	430	433	433	1±1
All	All	19140	14580	14580	25

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 1.

5 of 8 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom 2	Clash(Å)	Distance(Å)	Models	
Atom-1	Atom-2	Atom-2 $Clash(A)$ $Dist$		Worst	Total
3:A:385:TRP:CG	3:A:386:GLU:N	0.51	2.79	19	5
1:B:4:DA:C2	2:C:24:DA:C2	0.46	3.03	5	7
3:A:412:PHE:CE2	3:A:420:LEU:HD21	0.46	2.45	16	2
3:A:395:VAL:HG11	3:A:424:TRP:CZ2	0.43	2.49	11	2
3:A:385:TRP:CD1	3:A:386:GLU:N	0.43	2.87	15	1

#### 6.3 Torsion angles (i)

#### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	
3	А	49/70~(70%)	$46 \pm 1 (93 \pm 2\%)$	$3\pm1~(7\pm2\%)$	0±0 (0±1%)	38	78
All	All	980/1400~(70%)	910 (93%)	66 (7%)	4 (0%)	38	78

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
3	А	414	ASN	2
3	А	400	GLU	1
3	А	385	TRP	1

#### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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
3	А	45/65~(69%)	$42 \pm 1 (94 \pm 3\%)$	$3\pm1~(6\pm3\%)$	22 71
All	All	900/1300~(69%)	844 (94%)	56 (6%)	22 71

5 of 18 unique residues with a non-rotameric side chain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
3	А	385	TRP	8
3	А	423	ARG	7
3	А	421	LYS	7
3	А	427	MET	6
3	А	411	LYS	4

#### 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 monosaccharides 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 (i)

No chemical shift data were provided

