



# wwPDB NMR Structure Validation Summary Report ⓘ

Apr 27, 2016 – 06:43 AM BST

PDB ID : 7GAT  
Title : SOLUTION NMR STRUCTURE OF THE L22V MUTANT DNA BINDING  
DOMAIN OF AREA COMPLEXED TO A 13 BP DNA CONTAINING A  
TGATA SITE, 34 STRUCTURES  
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Deposited on : 1997-11-07

This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

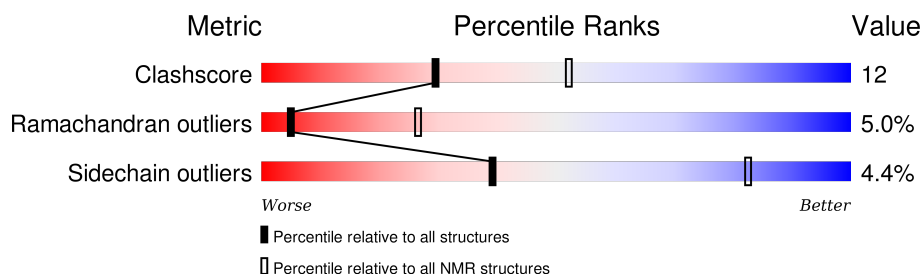
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment 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 (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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  $\geq 3$ , 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	B	13	<div> <div>62%</div> <div>38%</div> </div>
2	C	13	<div> <div>54%</div> <div>46%</div> </div>
3	A	66	<div> <div>53%</div> <div>21%</div> <div>•</div> <div>24%</div> </div>

## 2 Ensemble composition and analysis

This entry contains 34 models. Model 32 is the overall representative, medoid model (most similar to other models).

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:11-A:60 (50)	0.23	32

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

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

The models can be grouped into 6 clusters and 6 single-model clusters were found.

Cluster number	Models
1	2, 3, 5, 9, 15, 22, 26, 28, 29, 30, 32
2	6, 10, 14, 17, 24
3	1, 4, 7, 13, 25
4	18, 19, 23
5	11, 33
6	8, 21
Single-model clusters	12; 16; 20; 27; 31; 34

### 3 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1854 atoms, of which 814 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms						Trace
1	B	13	Total	C	H	N	O	P	0
			415	128	147	55	73	12	

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

Mol	Chain	Residues	Atoms						Trace
2	C	13	Total	C	H	N	O	P	0
			409	126	150	42	79	12	

- Molecule 3 is a protein called NITROGEN REGULATORY PROTEIN AREA.

Mol	Chain	Residues	Atoms						Trace
3	A	66	Total	C	H	N	O	S	0
			1029	313	517	100	94	5	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	THR	CONFLICT	UNP P17429
A	22	VAL	LEU	ENGINEERED	UNP P17429

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
4	A	1	Total	Zn
			1	1

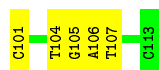
## 4 Residue-property plots [i](#)

### 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: DNA (5'-D(\*CP\*AP\*GP\*TP\*GP\*AP\*TP\*AP\*GP\*AP\*GP\*AP\*C)-3')

Chain B: 



- Molecule 2: DNA (5'-D(\*GP\*TP\*CP\*TP\*CP\*TP\*AP\*TP\*CP\*AP\*CP\*TP\*G)-3')

Chain C: 



- Molecule 3: NITROGEN REGULATORY PROTEIN AREA

Chain A: 

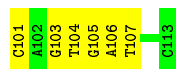


### 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 32. Colouring as in section 4.1 above.

- Molecule 1: DNA (5'-D(\*CP\*AP\*GP\*TP\*GP\*AP\*TP\*AP\*GP\*AP\*GP\*AP\*C)-3')

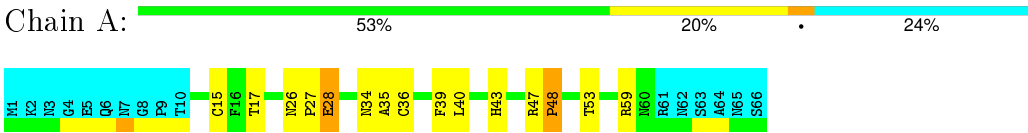
Chain B: 



- Molecule 2: DNA (5'-D(\*GP\*TP\*CP\*TP\*CP\*TP\*AP\*TP\*CP\*AP\*CP\*TP\*G)-3')



● Molecule 3: NITROGEN REGULATORY PROTEIN AREA



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING*.

Of the 34 calculated structures, 34 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
X-PLOR MODIFIED	structure solution	MODIFIED

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality i

### 6.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	B	1.14±0.02	2±0/302 (0.6±0.1%)	1.88±0.01	4±1/465 (0.8±0.3%)
2	C	1.32±0.02	5±0/288 (1.7±0.1%)	1.91±0.01	3±2/442 (0.8±0.4%)
3	A	1.00±0.01	0±0/403 (0.0±0.0%)	0.88±0.01	0±0/548 (0.0±0.0%)
All	All	1.14	235/33762 (0.7%)	1.59	243/49470 (0.5%)

5 of 7 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
2	C	121	DT	C5-C7	6.97	1.54	1.50	33	34
2	C	125	DT	C5-C7	6.91	1.54	1.50	34	34
2	C	115	DT	C5-C7	6.78	1.54	1.50	5	34
2	C	119	DT	C5-C7	6.63	1.54	1.50	5	33
2	C	117	DT	C5-C7	6.58	1.53	1.50	34	34

5 of 30 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	B	103	DG	O4'-C1'-N9	6.11	112.28	108.00	31	16
2	C	121	DT	O4'-C1'-N1	6.01	112.21	108.00	34	20
1	B	107	DT	O4'-C1'-N1	5.99	112.19	108.00	5	28
1	B	105	DG	O4'-C1'-N9	5.85	112.10	108.00	19	28
2	C	119	DT	C6-C5-C7	-5.76	119.44	122.90	4	20

There are no chirality outliers.

There are no planarity outliers.



## 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	B	268	147	147	2±1
2	C	259	150	150	3±2
3	A	394	407	407	17±4
All	All	31348	23936	23936	668

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 12.

5 of 143 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:101:DC:H6	1:B:101:DC:HO5'	0.91	0.94	32	11
3:A:22:VAL:H	3:A:34:ASN:ND2	0.68	1.86	15	4
3:A:39:PHE:CE2	3:A:43:HIS:CE1	0.68	2.82	34	34
3:A:26:ASN:HD22	3:A:28:GLU:H	0.68	1.31	20	6
1:B:101:DC:HO5'	1:B:101:DC:H6	0.67	1.31	28	7

## 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	A	50/66 (76%)	43±1 (87±2%)	4±1 (8±3%)	3±1 (5±2%)	5	26
All	All	1700/2244 (76%)	1472 (87%)	143 (8%)	85 (5%)	5	26

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

Mol	Chain	Res	Type	Models (Total)
3	A	27	PRO	34

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Mol	Chain	Res	Type	Models (Total)
3	A	48	PRO	30
3	A	52	LYS	12
3	A	16	PHE	8
3	A	46	VAL	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	A	46/59 (78%)	44±1 (96±3%)	2±1 (4±3%)	39 82
All	All	1564/2006 (78%)	1495 (96%)	69 (4%)	39 82

5 of 12 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
3	A	53	THR	23
3	A	34	ASN	12
3	A	20	THR	9
3	A	47	ARG	9
3	A	52	LYS	5

### 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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

## 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

No chemical shift data were provided