



# wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1BBX / pdb\_00001bbx  
Title : NON-SPECIFIC PROTEIN-DNA INTERACTIONS IN THE SSO7D-DNA COMPLEX, NMR, 1 STRUCTURE  
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Deposited on : 1998-04-24

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

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
wwPDB-RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
wwPDB-ShiftChecker : v1.2  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

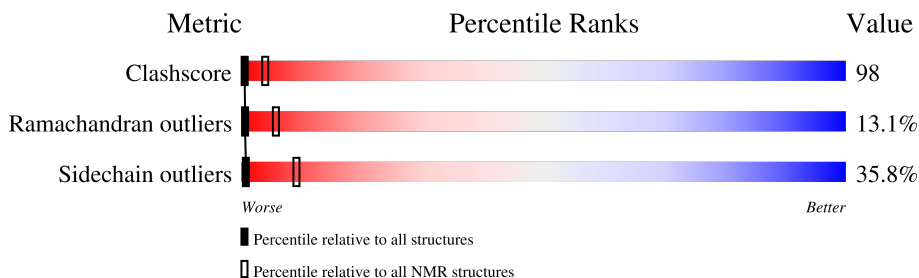
# 1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	A	12	8% 92%
1	B	12	8% 92%
2	C	63	13% 51% 35% .
2	D	63	13% 52% 33% .

## 2 Ensemble composition and analysis

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

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

There are 2 unique types of molecules in this entry. The entry contains 2834 atoms, of which 1344 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		P
1	A	12	379	116	136	46	70	11	0
1	B	12	379	116	136	46	70	11	0

- Molecule 2 is a protein called DNA-BINDING PROTEIN 7D.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
2	C	63	1038	320	536	87	93	2	0
2	D	63	1038	320	536	87	93	2	0

There are 2 discrepancies between the modelled and reference sequences:

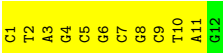
Chain	Residue	Modelled	Actual	Comment	Reference
C	13	GLN	GLU	conflict	UNP P39476
D	13	GLN	GLU	conflict	UNP P39476

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

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.

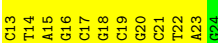
- Molecule 1: DNA (5'-D(\*CP\*TP\*AP\*GP\*CP\*GP\*CP\*GP\*CP\*TP\*AP\*G)-3')

Chain A: 


  
C1  
T2  
A3  
G4  
C5  
G6  
C7  
G8  
C9  
T10  
A11  
G12


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


Chain B: 

  
C13  
T14  
A15  
G16  
C17  
G18  
C19  
G20  
C21  
T22  
A23  
G24


- Molecule 2: DNA-BINDING PROTEIN 7D


Chain C: 


  
A1  
T2  
V3  
K4  
F5  
K6  
Y7  
K8  
G9  
E10  
E11  
K12  
Q13  
V14  
D15  
I16  
S17  
K18  
I19  
K20  
K21  
V22  
W23  
R24  
V25  
G26  
K27  
M28  
I29  
S30  
F31  
T32  
Y33  
D34  
E35  
G36  
G37  
G38  
K39  
T40  
G41  
R42  
G43  
A44  
V45  
S46  
E47  
K48  
D49  
A50  
F51  
K52  
E53  
L54  
L55  
Q56  
M57  
L58  
E59  
K60

  
G61  
K62  
K63

- Molecule 2: DNA-BINDING PROTEIN 7D

Chain D: 

  
A1  
T2  
V3  
K4  
F5  
K6  
Y7  
K8  
G9  
E10  
E11  
K12  
Q13  
V14  
D15  
I16  
S17  
K18  
I19  
K20  
K21  
V22  
W23  
R24  
V25  
G26  
K27  
M28  
I29  
S30  
F31  
T32  
Y33  
D34  
E35  
G36  
G37  
G38  
K39  
T40  
G41  
R42  
G43  
A44  
V45  
S46  
E47  
K48  
D49  
A50  
F51  
K52  
E53  
L54  
L55  
Q56  
M57  
L58  
E59  
K60

  
G61  
K62  
K63

## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 50 calculated structures, 1 were deposited, based on the following criterion: *LOWEST RESTRAINT ENERGY*.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
VNMR	structure solution	
ANSIG	structure solution	
XPLOR	structure solution	

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	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.63	0/272 ( 0.0%)	1.19	0/418 ( 0.0%)
1	B	0.63	0/272 ( 0.0%)	1.19	0/418 ( 0.0%)
2	C	1.40	0/508 ( 0.0%)	1.59	3/669 ( 0.4%)
2	D	1.40	0/508 ( 0.0%)	1.59	2/669 ( 0.3%)
All	All	1.19	0/1560 ( 0.0%)	1.45	5/2174 ( 0.2%)

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
2	C	0	2
2	D	0	2
All	All	0	4

There are no bond-length outliers.

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	22	VAL	N-CA-CB	-6.15	104.35	112.34
2	C	22	VAL	N-CA-CB	-6.11	104.39	112.34
2	C	52	LYS	N-CA-CB	-5.08	105.00	112.78
2	D	52	LYS	N-CA-CB	-5.07	105.02	112.78
2	C	45	VAL	N-CA-CB	-5.01	105.36	111.67

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
2	C	24	ARG	Sidechain
2	C	42	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	D	24	ARG	Sidechain
2	D	42	ARG	Sidechain

## 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	A	243	136	136	37
1	B	243	136	136	37
2	C	502	536	536	116
2	D	502	536	536	117
All	All	1490	1344	1344	278

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 98.

5 of 278 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
2:D:14:VAL:HG11	2:D:33:TYR:CB	0.97	1.89
2:C:14:VAL:HG11	2:C:33:TYR:CB	0.97	1.89
1:A:10:DT:H5''	1:A:11:DA:OP2	0.97	1.60
1:B:22:DT:H5''	1:B:23:DA:OP2	0.96	1.60
2:D:28:MET:O	2:D:29:ILE:HD13	0.95	1.62

## 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
2	C	61/63 (97%)	36 (59%)	17 (28%)	8 (13%)	<b>0</b> <b>6</b>
2	D	61/63 (97%)	36 (59%)	17 (28%)	8 (13%)	<b>0</b> <b>6</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	122/126 (97%)	72 (59%)	34 (28%)	16 (13%)	0 6

5 of 16 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
2	C	5	PHE
2	C	9	GLY
2	C	20	LYS
2	C	28	MET
2	C	30	SER

### 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
2	C	53/53 (100%)	34 (64%)	19 (36%)	1 9
2	D	53/53 (100%)	34 (64%)	19 (36%)	1 9
All	All	106/106 (100%)	68 (64%)	38 (36%)	1 9

5 of 38 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
2	C	2	THR
2	C	4	LYS
2	C	11	GLU
2	C	14	VAL
2	C	16	ILE

### 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 oligosaccharides 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

No chemical shift data were provided