



wwPDB NMR Structure Validation Summary Report ⓘ

May 29, 2020 – 01:22 am BST

PDB ID : 2TPK
Title : AN INVESTIGATION OF THE STRUCTURE OF THE PSEUDOKNOT
WITHIN THE GENE 32 MESSENGER RNA OF BACTERIOPHAGE T2
USING HETERONUCLEAR NMR METHODS
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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 ⓘ 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 : 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 : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

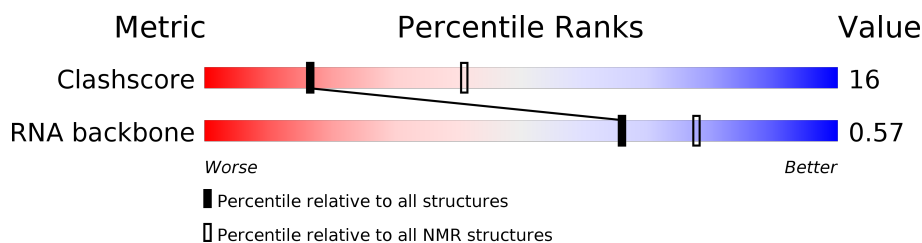
1 Overall quality at a glance

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	158937	12864
RNA backbone	4643	676

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	36	 19% 33% 25% 22%

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 is only 1 type of molecule in this entry. The entry contains 1155 atoms, of which 390 are hydrogens and 0 are deuteriums.

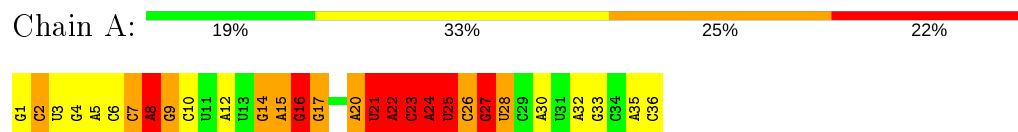
- Molecule 1 is a RNA chain called RNA (MRNA PSEUDOKNOT).

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	36	1155	342	390	136	251	36	0

4 Residue-property plots

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: RNA (MRNA PSEUDOKNOT)



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DISTANCE GEOMETRY-SIMULATED ANNEALING AND ENERGY MINIZATION PROTOCOLS*.

Of the 19 calculated structures, 1 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
FELIX	structure solution	
XPLOR	structure solution	3.1

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

COVALENT-GEOMETRY INFOmissingINFO

5.1 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	765	390	389	18
All	All	765	390	389	18

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 16.

5 of 18 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:25:U:H2'	1:A:26:C:O4'	0.76	1.81
1:A:23:C:H2'	1:A:24:A:O4'	0.68	1.88
1:A:17:G:H1'	1:A:27:G:O6	0.63	1.92
1:A:20:A:H2'	1:A:21:U:O4'	0.59	1.97
1:A:2:C:H2'	1:A:3:U:O4'	0.56	2.00

5.2 Torsion angles [i](#)

5.2.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.2.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.2.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	A	35/36 (97%)	12 (34%)	6 (17%)	0.57
All	All	35/36 (97%)	12 (34%)	6 (17%)	0.57

The overall RNA backbone suiteness is 0.57.

5 of 12 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	16	G
1	A	27	G
1	A	24	A
1	A	23	C
1	A	25	U

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	27	G
1	A	23	C
1	A	8	A
1	A	22	A
1	A	7	C

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

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

5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.5 Ligand geometry [i](#)

There are no ligands in this entry.

5.6 Other polymers [i](#)

There are no such molecules in this entry.

5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Chemical shift validation

No chemical shift data were provided