



# wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1F7F  
Title : SOLUTION STRUCTURE OF THE RNASE P RNA (M1 RNA) P4 STEM OLIGORIBONUCLEOTIDE, NMR, ENSEMBLE OF 9 STRUCTURES  
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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](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
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

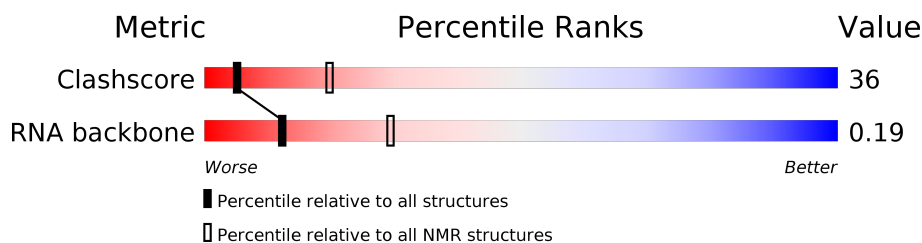
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment 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	125131	11601
RNA backbone	3398	623

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	27	 <div> <span>33%</span> <span>48%</span> <span>19%</span> </div>

## 2 Ensemble composition and analysis ⓘ

This entry contains 9 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 863 atoms, of which 293 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called RNASE P RNA RIBOZYME, P4 DOMAIN.

Mol	Chain	Residues	Atoms						Trace
1	A	27	Total	C	H	N	O	P	0
			863	255	293	99	190	26	



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *restrained molecular dynamics; simulated annealing*.

Of the 50 calculated structures, 9 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
X-PLOR	structure solution	3.841
X-PLOR	refinement	3.841

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](#)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

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	A	570	293	293	31±4
All	All	5130	2637	2637	277

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 36.

5 of 112 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:5:G:HO2'	1:A:7:C:H5	0.94	1.05	4	4
1:A:16:G:H2'	1:A:17:G:O4'	0.80	1.77	7	4
1:A:3:A:O2'	1:A:4:A:H5'	0.77	1.79	3	5
1:A:5:G:O2'	1:A:6:U:H2'	0.76	1.79	1	6
1:A:5:G:O3'	1:A:6:U:H2'	0.71	1.85	2	3

### 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](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	A	26/27 (96%)	6±1 (24±4%)	0±0 (0±0%)	0.19±0.06
All	All	234/243 (96%)	57 (24%)	0 (0%)	0.19

The overall RNA backbone suiteness is 0.19.

5 of 13 unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	17	G	9
1	A	7	C	9
1	A	6	U	9
1	A	15	C	9
1	A	14	U	9

There are no RNA pucker outliers to report.

## 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

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided