

# Full wwPDB NMR Structure Validation Report (i)

### Jun 5, 2023 – 02:55 PM JST

PDB ID	:	7EXY
BMRB ID	:	36422
Title	:	T-hairpin structure found in the RNA element involved in the piRNA biogen-
		esis
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Deposited on	:	2021-05-29

This is a Full wwPDB NMR Structure Validation 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) 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)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. $(2010)$
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

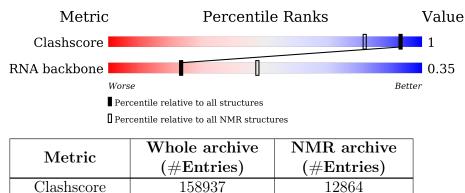
**RNA** backbone

# 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 is 23%.

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.



4643

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%

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Mol	Chain	Length	Quality of chain		
1	А	16	56%	44%	



# 2 Ensemble composition and analysis (i)

This entry contains 11 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 506 atoms, of which 171 are hydrogens and 0 are deuteriums.

• Molecule 1 is a RNA chain called RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\* UP\*CP\*CP\*AP\*AP\*G)-3').

Mol	Chain	Residues	Atoms			Trace			
1	Δ	16	Total	С	Η	Ν	0	Р	0
	A	10	506	151	171	55	114	15	0



# 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: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

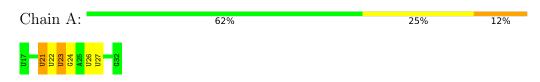
Chain A:	56%	44%
117 1221 1223 1238 1238 1226 1226 132 132 132		

### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

### 4.2.1 Score per residue for model 1

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')



#### 4.2.2 Score per residue for model 2

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Chain A:	62%	38%
U17 U21 U22 U23 024 U25 U25 U25 G32		



#### 4.2.3 Score per residue for model 3

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Chain A:	62%	38%
017 021 022 023 023 024 026 026 026 027 027 027		

#### 4.2.4 Score per residue for model 4

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Chain A:	56%	44%
U17 U21 U22 U23 G24 A26 U26 U27 G32		

### 4.2.5 Score per residue for model 5

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Chain A:	50%	50%
U17 U21 U22 U22 U22 U26 U26 U26 U26 U26 U26 U26		

#### 4.2.6 Score per residue for model 6

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Chain A:	56%	44%
117 121 122 122 122 122 122 122 122 122		

### 4.2.7 Score per residue for model 7

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')



38%

Chain A:

U17 U21 U22 U23 U26 U26 U26 U27 U27 U27 U27

### 4.2.8 Score per residue for model 8

62%

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Chain A:	62%	38%
<b>u1</b> 122 123 123 123 <b>12</b> 5 <b>12</b> 5 <b>12</b> 5 <b>12</b> 5 <b>12</b> 7 <b>12</b> 7 <b>12</b> 7 <b>12</b> 7		

#### 4.2.9 Score per residue for model 9

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Ch	nain A:	56%	44%
U17	U22 U23 A26 U27 U27 C28 C28 C32 C38		

### 4.2.10 Score per residue for model 10

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')

Chain A:	50%	31%	19%
U17 U21 U22 U22 028 U27 U27 C28 C28 C28 C28			

### 4.2.11 Score per residue for model 11

• Molecule 1: RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*UP\*UP\*GP\*AP\*UP\*UP\*CP\*CP\*AP\*AP\*G)-3')



# 5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 11 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	structure calculation	1.3

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	76
Number of shifts mapped to atoms	76
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	23%



# 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	А	335	171	171	1±1
All	All	3685	1881	1881	7

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.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
Atom-1	Atom-2	Clash(A)		Worst	Total
1:A:24:G:H2'	1:A:25:A:O4'	0.59	1.98	10	1
1:A:25:A:HO2'	1:A:28:C:H5	0.56	1.41	10	2
1:A:23:U:H3'	1:A:24:G:H5"	0.50	1.82	11	1
1:A:21:U:H3'	1:A:23:U:H3	0.42	1.74	1	1
1:A:23:U:H5"	1:A:23:U:C6	0.42	2.49	1	1
1:A:23:U:C5	1:A:24:G:C2	0.40	3.10	10	1

All unique clashes are listed below, sorted by their clash magnitude.

## 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	А	15/16~(94%)	$6\pm1~(42\pm6\%)$	$0\pm0~(1\pm2\%)$	$0.35 {\pm} 0.05$
All	All	165/176~(94%)	69 (42%)	1 (1%)	0.35

The overall RNA backbone suiteness is 0.35.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	А	24	G	11
1	А	26	U	11
1	А	27	U	11
1	А	21	U	10
1	А	22	U	10
1	А	23	U	10
1	А	25	А	4
1	А	28	С	1
1	А	32	G	1

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	А	23	U	1

### 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)

The completeness of assignment taking into account all chemical shift lists is 23% for the well-defined parts and 23% for the entire structure.

## 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: peak\_table\_17-32\_298\_210505\_bmrb.txt

### 7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	76
Number of shifts mapped to atoms	76
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

### 7.1.2 Chemical shift referencing (i)

No chemical shift referencing corrections were calculated (not enough data).

### 7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 23%, i.e. 69 atoms were assigned a chemical shift out of a possible 294. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}$ N
Sugar	47/176~(27%)	47/96~(49%)	0/80~(0%)	0/0 (%)
Base	22/118~(19%)	22/70~(31%)	0/28~(0%)	0/20~(0%)
Overall	69/294~(23%)	69/166~(42%)	0/108~(0%)	0/20~(0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 23%, i.e. 69 atoms were assigned a chemical shift out of a possible 294. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.



	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Sugar	47/176~(27%)	47/96~(49%)	0/80~(0%)	$0/0 \ (\%)$
Base	22/118~(19%)	22/70~(31%)	0/28~(0%)	0/20~(0%)
Overall	69/294~(23%)	69/166~(42%)	0/108~(0%)	0/20~(0%)

### 7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

### 7.1.5 Random Coil Index (RCI) plots (i)

No random coil index (RCI) plot could be generated from the current chemical shift list. RCI is only applicable to proteins

Restraints validation did not run

