Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2CD3
Title	:	Refinement of RNase P P4 stemloop structure using residual dipolar coupling data - C70U mutant
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Deposited on	:	2006-01-19

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 (i)) were used in the production of this report:

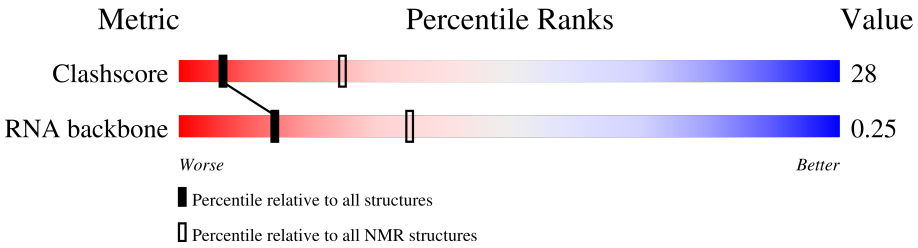
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	27	48% 30% 22%

2 Ensemble composition and analysis (i)

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 862 atoms, of which 292 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	27	862	255	292	98	191	26	0

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: 5'-R(*GP*GP*AP*AP*GP*UP*UP*CP*GP*GP *UP*CP*UP*UP*CP*GP*GP*AP*CP*CP*GP*GP*CP*UP*UP*CP*C)-3'

Chain A:

5 Refinement protocol and experimental data overview

The models were refined using the following method: *RESTRAINED MOLECULAR DYNAMICS*.

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

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

Software name	Classification	Version
Xplor-NIH	refinement	NIH
Xplor-NIH	structure solution	NIH

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

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	292	292	24
All	All	570	292	292	24

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 28.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:3:A:O2'	1:A:4:A:H5'	0.69	1.87
1:A:16:G:H2'	1:A:17:G:O4'	0.65	1.91
1:A:4:A:O2'	1:A:5:G:H5'	0.64	1.93
1:A:13:U:O2'	1:A:14:U:C6	0.63	2.51
1:A:14:U:O2'	1:A:15:C:H5'	0.56	2.00
1:A:7:U:O2'	1:A:8:C:C5	0.56	2.59
1:A:5:G:N7	1:A:6:U:C5	0.54	2.76
1:A:7:U:HO2'	1:A:8:C:H5	0.53	1.45
1:A:13:U:O2'	1:A:14:U:C5	0.53	2.61
1:A:6:U:C4	1:A:8:C:N4	0.52	2.78
1:A:14:U:O2'	1:A:15:C:C5'	0.51	2.58
1:A:1:G:HO2'	1:A:2:G:H8	0.51	1.42
1:A:1:G:O2'	1:A:2:G:C8	0.47	2.66
1:A:4:A:O2'	1:A:5:G:C5'	0.46	2.62
1:A:1:G:O2'	1:A:2:G:O4'	0.45	2.34

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:3:A:O2'	1:A:4:A:C5'	0.45	2.63
1:A:15:C:O4'	1:A:16:G:N2	0.45	2.49
1:A:16:G:O6	1:A:17:G:N2	0.44	2.50
1:A:17:G:C6	1:A:18:A:C6	0.43	3.06
1:A:5:G:N7	1:A:6:U:C4	0.43	2.87
1:A:7:U:O2'	1:A:8:C:H5	0.42	1.97
1:A:17:G:C8	1:A:17:G:OP2	0.42	2.72
1:A:16:G:C4'	1:A:16:G:OP1	0.42	2.68
1:A:5:G:C8	1:A:6:U:C5	0.41	3.09

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 (23%)	0 (0%)	0.25
All	All	26/27 (96%)	6 (23%)	0 (0%)	0.25

The overall RNA backbone suiteness is 0.25.

All RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	U
1	A	8	C
1	A	14	U
1	A	15	C
1	A	16	G
1	A	17	G

There are no RNA pucker outliers to report.

6.4 Non-standard residues in protein, DNA, RNA chains

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

6.5 Carbohydrates

There are no monosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

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