



Full wwPDB NMR Structure Validation Report ⓘ

Apr 7, 2022 – 08:02 AM EDT

PDB ID : 7K4L
Title : DENV1 SLA bottom stem RNA (DenvBS)
Authors : Sun, Y.T.; Varani, G.; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2020-09-15

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 ⓘ symbol.

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

MolProbity	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	FAILED
PANAV	:	FAILED
ShiftChecker	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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.

There are no overall percentile quality scores available for this entry.

The sequence quality summary graphics cannot be shown.

2 Ensemble composition and analysis ⓘ

This entry contains 10 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 1147 atoms, of which 386 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called DenvSLA RNA.

Mol	Chain	Residues	Atoms						Trace
1	A	36	Total	C	H	N	O	P	0
			1147	341	386	130	255	35	

4 Residue-property plots

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: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

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: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.2 Score per residue for model 2

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.3 Score per residue for model 3

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.4 Score per residue for model 4

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.5 Score per residue for model 5

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.6 Score per residue for model 6

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.7 Score per residue for model 7

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.8 Score per residue for model 8

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.9 Score per residue for model 9

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

4.2.10 Score per residue for model 10

- Molecule 1: DenvSLA RNA

Chain A:  100%

There are no outlier residues in this chain.

5 Refinement protocol and experimental data overview ⓘ

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

Of the 400 calculated structures, 10 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
X-PLOR NIH	refinement	
X-PLOR NIH	structure calculation	

No chemical shift data was provided.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3.3 RNA [i](#)

MolProbity failed to run properly - this section will have to be empty.

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

MolProbity failed to run properly - this section will have to be empty.

6.5 Carbohydrates [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.6 Ligand geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.7 Other polymers [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided