Full wwPDB NMR Structure Validation Report (i)

May 29, 2020 – 11:27 am BST

PDB ID	:	6RSA
Title	:	NUCLEAR MAGNETIC RESONANCE AND NEUTRON DIFFRACTION STUDIES OF THE COMPLEX OF RIBONUCLEASE*A WITH URIDINE VANADATE, A TRANSITION-STATE ANALOGUE
Authors	:	Wlodawer, A.
Deposited on	:	1986-02-25

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 following versions of software and data (see references (1)) were used in the production of this report:

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
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

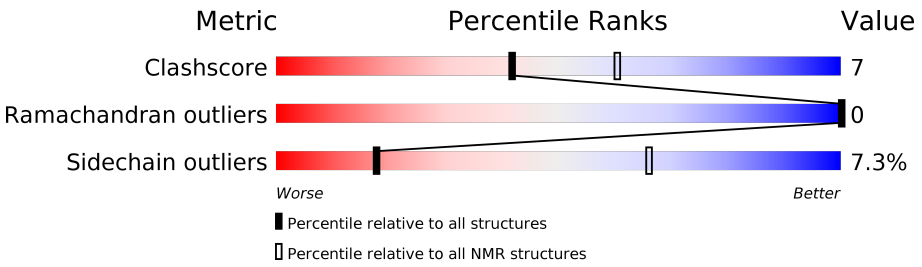
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
NEUTRON DIFFRACTION, SOLUTION NMR

The reported resolution of this entry is 2.00 Å.

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
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	124	56% 35% 6% •

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 are 3 unique types of molecules in this entry. The entry contains 2227 atoms, of which 692 are hydrogens and 451 are deuteriums.

- Molecule 1 is a protein called RIBONUCLEASE A.

Mol	Chain	Residues	Atoms							Trace
			Total	C	D	H	N	O	S	
1	A	124	1860	575	225	684	171	193	12	0

- Molecule 2 is a ligand with the chemical component id UVC but its atom names do not match the existing wwPDB Chemical Component Dictionary definition for UVC. ERROR THIS SHOULD NOT HAPPEN FOLLOWING ANNOTATION.

Mol	Chain	Residues	Atoms						
			Total	C	D	H	N	O	V
2	A	1	31	9	2	8	2	9	1

- Molecule 3 is water.

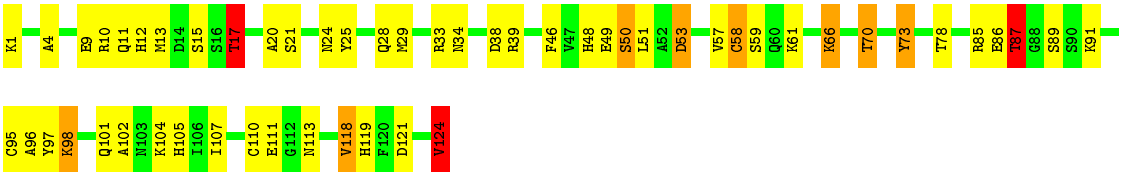
Mol	Chain	Residues	Atoms		
			Total	D	O
3	A	112	336	224	112

4 Residue-property plots (i)

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: RIBONUCLEASE A

Chain A:



5 Refinement protocol and experimental data overview (i)

Of the ? calculated structures, 1 were deposited, based on the following criterion: *?*.

The authors did not provide any information on software used for structure solution, optimization or refinement.

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 (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	1176	684	905	17
2	A	23	8	10	2
3	A	336	0	0	8
All	All	1535	692	915	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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:58:CYS:O	3:A:339:DOD:O	0.78	2.01
1:A:119:HIS:ND1	3:A:323:DOD:O	0.76	2.18
1:A:17:THR:HG22	1:A:48:HIS:ND1	0.70	2.00
1:A:53:ASP:OD2	3:A:184:DOD:O	0.70	2.10
2:A:125:UVC:O3'	3:A:323:DOD:O	0.63	2.17
1:A:113:ASN:ND2	3:A:140:DOD:O	0.60	2.34
1:A:87:THR:CG2	1:A:89:SER:HB2	0.53	2.34
1:A:17:THR:CG2	1:A:48:HIS:CE1	0.49	2.95
1:A:17:THR:HG22	1:A:48:HIS:CE1	0.46	2.45
1:A:66:LYS:NZ	3:A:327:DOD:O	0.46	2.49
1:A:61:LYS:O	1:A:73:TYR:HA	0.46	2.11
1:A:17:THR:CG2	1:A:48:HIS:ND1	0.45	2.78
1:A:101:GLN:HG2	3:A:235:DOD:O	0.45	2.10
1:A:105:HIS:N	1:A:124:VAL:OXT	0.43	2.47
1:A:119:HIS:CE1	3:A:323:DOD:O	0.43	2.67

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:11:GLN:NE2	2:A:125:UVC:O1V	0.41	2.53
1:A:104:LYS:HB3	1:A:124:VAL:OXT	0.41	2.15
1:A:25:TYR:CZ	1:A:29:MET:HG3	0.40	2.51

5.2 Torsion angles (i)

5.2.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	122/124 (98%)	117 (96%)	5 (4%)	0 (0%)	100	100
All	All	122/124 (98%)	117 (96%)	5 (4%)	0 (0%)	100	100

There are no Ramachandran outliers.

5.2.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	109/109 (100%)	101 (93%)	8 (7%)	18	66
All	All	109/109 (100%)	101 (93%)	8 (7%)	18	66

All 8 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	118	VAL
1	A	124	VAL
1	A	50	SER
1	A	70	THR
1	A	98	LYS
1	A	34	ASN

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Mol	Chain	Res	Type
1	A	17	THR
1	A	87	THR

5.2.3 RNA (i)

There are no RNA molecules in this entry.

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)

Of 1 ligands modelled in this entry, 1 could not be matched to an existing wwPDB Chemical Component Dictionary definition at this stage - leaving 0 for Mogul analysis.

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 (i)

No chemical shift data were provided