wwPDB NMR Structure Validation Summary Report (i)

Apr 20, 2024 – 02:27 PM EDT

PDB ID	:	2I7Z
Title	:	GAAA tetraloop receptor complex with associated manganese ions.
Authors	:	Davis, J.H.; Butcher, S.E.
Deposited on	:	2006-08-31

This is a wwPDB NMR Structure Validation Summary 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:

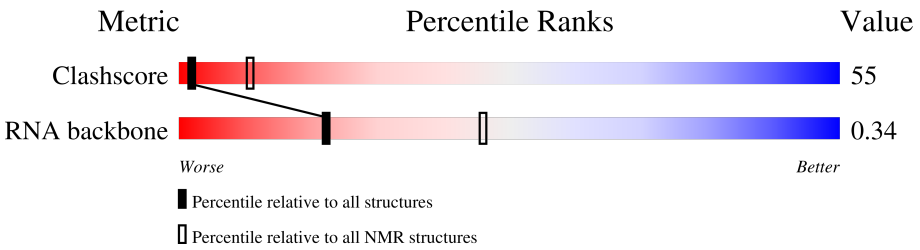
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson 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	43	9% 72% 19%
1	B	43	16% 67% 16%

2 Ensemble composition and analysis (i)

This entry contains 20 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 are 3 unique types of molecules in this entry. The entry contains 2954 atoms, of which 1048 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called 43-MER.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	43	1382	411	464	166	299	42	0
1	B	43	1382	411	464	166	299	42	0

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	
			Total	Mn
2	A	5	5	5
2	B	5	5	5

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		
			Total	H	O
3	A	30	90	60	30
3	B	30	90	60	30

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: 43-MER

Chain A: 9% 72% 19%

• Molecule 1: 43-MER

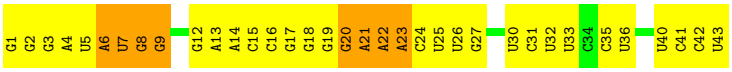
Chain B: 16% 67% 16%

4.2 Residue scores for the representative (author defined) model from the NMR ensemble

The representative model is number 1. Colouring as in section 4.1 above.

• Molecule 1: 43-MER

Chain A: 19% 63% 19%



• Molecule 1: 43-MER

Chain B: 30% 49% 21%

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *Structures were refined by cooling from 3000 K to 100 K in 58 cycles of restrained Cartesian coordinate space corresponding to a total of 28 ps. The force constant for RDCs was increased from 0.001 to 0.2 kcal mol-1 Hz-2. Five hundred steps of energy minimization using the Powell algorithm followed simulated annealing..*

Of the 100 calculated structures, 20 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	refinement	1.0
X-PLOR	refinement	2.11

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MN

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

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	B	0.1±0.2	0.0±0.0
All	All	1	0

There are no bond-length outliers.

There are no bond-angle outliers.

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	B	80	A	C4'	1

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	918	464	464	89±10
1	B	918	464	464	76±12
3	A	30	60	0	3±1
3	B	30	60	0	2±2
All	All	38120	20960	18560	3136

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 55.

5 of 691 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:50:U:O2'	1:B:51:G:H5'	1.05	1.49	2	12
1:A:18:G:O2'	1:A:19:G:H5'	1.03	1.54	7	20
1:A:25:U:O2'	1:A:26:U:H5'	1.01	1.55	12	20
1:B:61:G:O2'	1:B:62:G:H5'	1.01	1.54	17	20
1:A:5:U:O2'	1:A:6:A:H5"	0.98	1.56	5	1

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	42/43 (98%)	11±1 (25±4%)	2±1 (5±2%)	0.32±0.02
1	B	42/43 (98%)	11±1 (25±3%)	2±1 (4±3%)	0.36±0.03
All	All	1680/1720 (98%)	425 (25%)	74 (4%)	0.34

The overall RNA backbone suiteness is 0.34.

5 of 30 unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	8	G	20
1	A	20	G	20
1	A	23	A	20
1	B	49	A	20
1	B	66	A	20

5 of 23 unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	7	U	9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	5	U	7
1	A	6	A	6
1	B	49	A	6
1	B	48	U	5

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)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

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)

No chemical shift data were provided