# wwPDB NMR Structure Validation Summary Report (i)

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| PDB ID | : | 2ARG |
| Title | : | FORMATION OF AN AMINO ACID BINDING POCKET THROUGH ADAPTIVE ZIPPERING-UP OF A LARGE DNA HAIRPIN LOOP, NMR, 9 STRUCTURES |
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| Deposited on | : | 1998-08-19 |

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
http://wwpdb.org/validation/2016/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

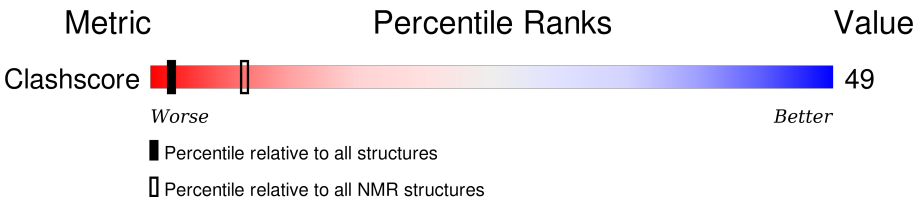
| | | |
|---|---|---|
| Cyrange | : | Kirchner and Güntert (2011) |
| NmrClust | : | Kelley et al. (1996) |
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.7.1 (RC1), CSD as537be (2016) |
| Percentile statistics | : | 20151230.v01 (using entries in the PDB archive December 30th 2015) |
| RCI | : | v_1n_11_5_13_A (Berjanski et al., 2005) |
| PANAV | : | Wang et al. (2010) |
| ShiftChecker | : | rb-20027457 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | rb-20027457 |

# 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 | 114402 | 11133 |

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 | 30 | 10% 90% |

## 2 Ensemble composition and analysis (i)

This entry contains 9 models. This entry does not contain protein, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.

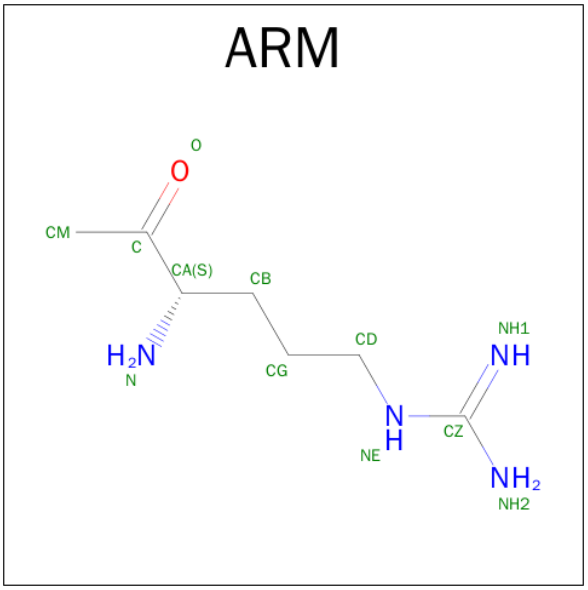
# 3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 989 atoms, of which 353 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called DNA APTAMER [5'-D (*TP*GP*AP*CP*CP*AP*GP*GP*GP*CP*AP*AP*AP*CP*GP*GP*TP*AP* GP*GP*TP*GP*AP*GP*TP*GP*GP*TP*CP*A)-3'].

| Mol | Chain | Residues | Atoms | | | | | | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | P | |
| 1 | A | 30 | 961 | 295 | 337 | 125 | 175 | 29 | 0 |

- Molecule 2 is DEOXY-METHYL-ARGININE (three-letter code: ARM) (formula: $C_7H_{16}N_4O$).




| Mol | Chain | Residues | Atoms | | | | |
|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O |
| 2 | A | 1 | 28 | 7 | 16 | 4 | 1 |

# 4 Residue-property plots (i)

## 4.1 Average score per residue in the NMR ensemble

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: DNA APTAMER [5'-D (*TP*GP*AP*CP*CP*AP*GP*GP*GP*CP*AP*AP*AP *CP*GP*GP*TP*AP* GP*GP*TP*GP*AP*GP*TP*GP*GP*TP*CP*A)-3']

Chain A: 10% 90%

## 4.2 Residue scores for the first model from the NMR ensemble

No representative models were identified. Colouring as in section 4.1 above.

• Molecule 1: DNA APTAMER [5'-D (*TP*GP*AP*CP*CP*AP*GP*GP*GP*CP*AP*AP*AP *CP*GP*GP*TP*AP* GP*GP*TP*GP*AP*GP*TP*GP*GP*TP*CP*A)-3']

Chain A: 7% 93%

# 5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DISTANCE GEOMETRY, MOLECULAR DYNAMIC*.

Of the 20 calculated structures, 9 were deposited, based on the following criterion: *LEAST NOE, VDW, AND BOND ANGLE VIOLATION, LEAST TOTAL ENERGY*.

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

| Software name | Classification | Version |
|---|---|---|
| X-PLOR | refinement | 3.1 |
| X-PLOR | structure solution | |

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

# 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: ARM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #Z>5 | RMSZ | #Z>5 |
| 1 | A | 2.27±0.04 | 41±4/703 (5.8±0.5%) | 3.05±0.06 | 80±3/1086 (7.4±0.3%) |
| All | All | 2.27 | 367/6327 (5.8%) | 3.05 | 724/9774 (7.4%) |

5 of 61 unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) | Models | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Worst | Total |
| 1 | A | 20 | DG | C8-N7 | 10.27 | 1.37 | 1.30 | 6 | 9 |
| 1 | A | 16 | DG | N9-C8 | -9.97 | 1.30 | 1.37 | 9 | 8 |
| 1 | A | 7 | DG | C8-N7 | 8.61 | 1.36 | 1.30 | 9 | 9 |
| 1 | A | 2 | DG | C8-N7 | 8.49 | 1.36 | 1.30 | 9 | 9 |
| 1 | A | 16 | DG | C8-N7 | 8.09 | 1.35 | 1.30 | 1 | 9 |

5 of 135 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) | Models | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Worst | Total |
| 1 | A | 16 | DG | O4'-C1'-N9 | 20.98 | 122.68 | 108.00 | 1 | 9 |
| 1 | A | 17 | DT | C6-C5-C7 | -18.82 | 111.61 | 122.90 | 6 | 9 |
| 1 | A | 18 | DA | O4'-C1'-N9 | 18.74 | 121.12 | 108.00 | 5 | 7 |
| 1 | A | 24 | DG | O4'-C1'-N9 | 18.61 | 121.03 | 108.00 | 6 | 9 |
| 1 | A | 10 | DC | O4'-C1'-N1 | 18.59 | 121.02 | 108.00 | 5 | 9 |

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 | A | 624 | 337 | 337 | 48±4 |
| All | All | 5724 | 3177 | 3168 | 435 |

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 49.

5 of 118 unique clashes are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) | Models | |
|---|---|---|---|---|---|
| | | | | Worst | Total |
| 1:A:1:DT:HO5' | 1:A:1:DT:H6 | 0.97 | 0.98 | 7 | 3 |
| 1:A:1:DT:H6 | 1:A:1:DT:HO5' | 0.96 | 0.96 | 1 | 6 |
| 1:A:18:DA:H2" | 1:A:19:DG:O4' | 0.73 | 1.83 | 6 | 7 |
| 1:A:11:DA:OP1 | 1:A:11:DA:H3' | 0.72 | 1.84 | 8 | 4 |
| 1:A:12:DA:N6 | 1:A:22:DG:H1' | 0.70 | 2.01 | 1 | 9 |

## 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)

There are no RNA molecules in this entry.

## 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 carbohydrates in this entry.

## 6.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

| Mol | Type | Chain | Res | Link | Bond lengths | | |
|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | #Z>2 |
| 2 | ARM | A | 31 | - | 9,11,11 | 2.31±0.02 | 1±0 (11±0%) |

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

| Mol | Type | Chain | Res | Link | Bond angles | | |
|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | #Z>2 |
| 2 | ARM | A | 31 | - | 11,13,13 | 1.42±0.09 | 0±0 (0±0%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 2 | ARM | A | 31 | - | - | 0±0,10,11,11 | 0±0,0,0,0 |

All unique bond outliers are listed below.

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) | Models | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Worst | Total |
| 2 | A | 31 | ARM | CM-C | 6.38 | 1.33 | 1.49 | 5 | 9 |

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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