Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	1Y8D
Title	:	Dimeric parallel-stranded tetraplex with 3+1 5' G-tetrad interface, single-residue chain reversal loops and GAG triad in the context of A(GGGG) pentad
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Deposited on	:	2004-12-11

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
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:

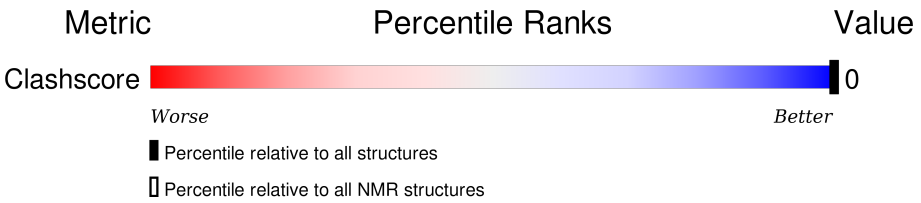
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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	16	94% 6%
1	B	16	94% 6%

2 Ensemble composition and analysis (i)

This entry contains 10 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 is only 1 type of molecule in this entry. The entry contains 1046 atoms, of which 360 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	16	523	160	180	74	94	15	0
1	B	16	523	160	180	74	94	15	0

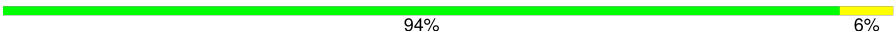
4 Residue-property plots (i)

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.

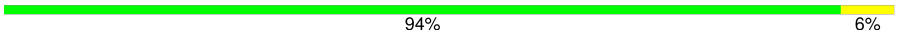
• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A:



• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B:



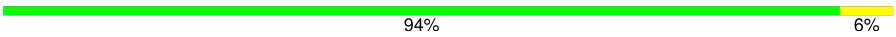
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

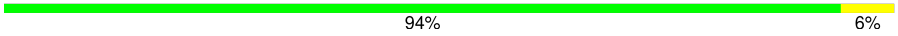
• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A:



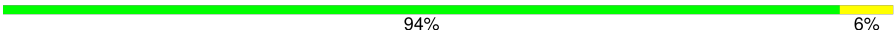
• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B:

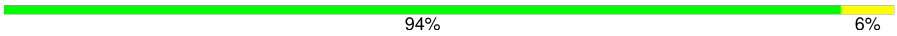


4.2.2 Score per residue for model 2

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A: 

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B: 

4.2.3 Score per residue for model 3

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A:

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B:

4.2.4 Score per residue for model 4

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A:

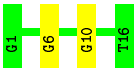
• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B:

4.2.5 Score per residue for model 5

• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A:



• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

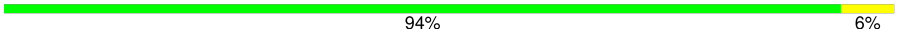
Chain B:

4.2.6 Score per residue for model 6

• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A:

• Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B: 

4.2.7 Score per residue for model 7

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A: 100%

There are no outlier residues in this chain.

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B: 100%

There are no outlier residues in this chain.

4.2.8 Score per residue for model 8

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A: 94% 6%

G1 G6 T16

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B: 94% 6%

G1 G6 T16

4.2.9 Score per residue for model 9

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A: 88% 13%

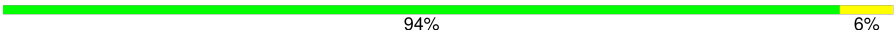
G1 G6 G10 T16

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

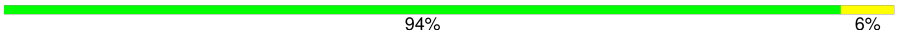
Chain B: 88% 13%

4.2.10 Score per residue for model 10

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain A: 

- Molecule 1: 5'-D(*GP*GP*GP*GP*TP*GP*GP*GP*AP*GP*GP*AP*GP*GP*GP*T)-3'

Chain B: 

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *distance geometry; simulated annealing; molecular dynamics; matrix relaxation.*

Of the 100 calculated structures, 10 were deposited, based on the following criterion: *all calculated structures submitted,back calculated data agree with experimental NOESY spectrum,structures with acceptable covalent geometry,structures with favorable non-bond energy.*

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

Software name	Classification	Version
X-PLOR	refinement	3.851

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)

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	1.32±0.01	0±0/388 (0.0±0.1%)	1.33±0.03	1±1/602 (0.2±0.1%)
1	B	1.32±0.01	0±0/388 (0.0±0.0%)	1.33±0.03	1±1/602 (0.2±0.1%)
All	All	1.32	1/7760 (0.0%)	1.33	27/12040 (0.2%)

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	10	DG	C5'-C4'	5.01	1.56	1.51	9	1

All 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	6	DG	O4'-C1'-N9	8.03	113.62	108.00	3	9
1	B	6	DG	O4'-C1'-N9	7.94	113.56	108.00	3	9
1	A	10	DG	O4'-C1'-C2'	-5.97	101.13	105.90	9	3
1	B	10	DG	O4'-C1'-C2'	-5.94	101.15	105.90	9	3
1	A	8	DG	P-O3'-C3'	5.67	126.51	119.70	4	2
1	B	8	DG	P-O3'-C3'	5.63	126.46	119.70	4	1

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
All	All	6860	3600	3600	-

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 -.

There are no clashes.

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)

There are no ligands in this entry.

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