Full wwPDB NMR Structure Validation Report (i)

Apr 27, 2016 – 12:51 AM BST

PDB ID	:	2LEE
Title	:	Unique structural features of interconverting monomeric and dimeric G-quadruplexes adopted by a sequence from intron of N-myc gene
Authors	:	Trajkovski, M.; Plavec, J.; Webba da Silva, M.
Deposited on	:	2011-06-15

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
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:

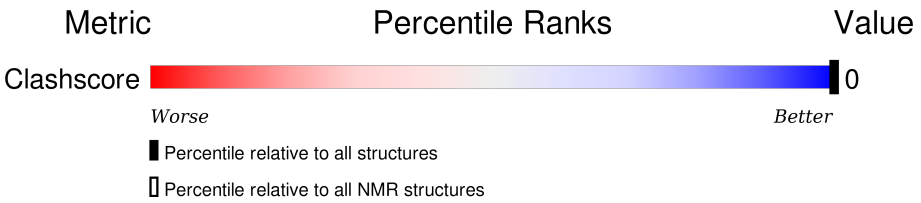
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 is 29%.

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	19	21% 74% 5%

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 617 atoms, of which 212 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	19	617	189	212	90	108	18	0

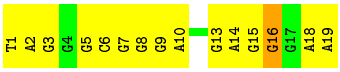
4 Residue-property plots (i)

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

Chain A: 21% 74% 5%



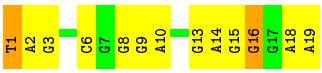
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

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

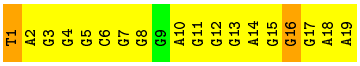
Chain A: 32% 58% 11%



4.2.2 Score per residue for model 2

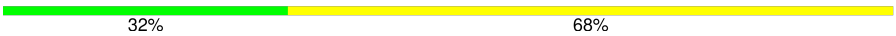
• Molecule 1: DNA (5'-D(*TP*AP*GP*GP*GP*CP*GP*GP*GP*AP*GP*GP*GP*AP*GP*GP*GP*AP*A)-3')

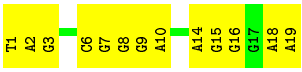
Chain A: 5% 84% 11%



4.2.3 Score per residue for model 3

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

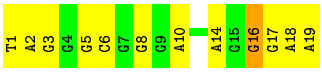
Chain A: 



4.2.4 Score per residue for model 4

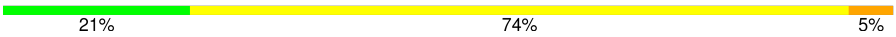
• Molecule 1: DNA (5'-D(*TP*AP*GP*GP*GP*CP*GP*GP*GP*AP*GP*GP*GP*AP*GP*GP*GP*AP*A)-3')

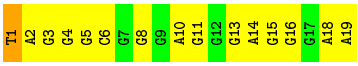
Chain A:



4.2.5 Score per residue for model 5

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

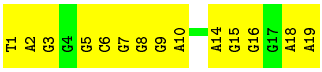
Chain A: 



4.2.6 Score per residue for model 6

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

Chain A:



4.2.7 Score per residue for model 7

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

Chain A: 26% 74%

T1 A2 G3 G4 G5 C6 G7 G8 G9 A10 G11 G12 G13 A14 G15 G16 G17 A18 A19

4.2.8 Score per residue for model 8

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

Chain A: 21% 68% 11%

T1 A2 G3 G4 G5 C6 G7 A10 G11 G12 G13 A14 G15 G16 G17 A18 A19

4.2.9 Score per residue for model 9

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

Chain A: 21% 68% 11%

T1 A2 G3 G4 G5 C6 G7 G8 G9 A10 G11 G12 G13 A14 G15 G16 G17 A18 A19

4.2.10 Score per residue for model 10

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

Chain A: 21% 74% 5%

T1 A2 G3 G4 G5 C6 G7 G8 G9 A10 G13 A14 G15 G16 G17 A18 A19

5 Refinement protocol and experimental data overview (i)

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

Of the 50 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
AMBER	structure solution	9
AMBER	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	2lee_cs.str
Number of chemical shift lists	1
Total number of shifts	115
Number of shifts mapped to atoms	115
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	29%

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	1.59±0.01	0±0/459 (0.0±0.0%)	2.41±0.02	29±1/711 (4.1±0.2%)
All	All	1.59	0/4590 (0.0%)	2.41	289/7110 (4.1%)

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	A	0.0±0.0	1.9±1.1
All	All	0	19

There are no bond-length outliers.

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	DC	O4'-C1'-N1	14.82	118.37	108.00	6	10
1	A	10	DA	N1-C6-N6	-11.40	111.76	118.60	7	10
1	A	19	DA	N1-C6-N6	-10.33	112.40	118.60	8	10
1	A	6	DC	N3-C2-O2	-9.83	115.02	121.90	6	10
1	A	14	DA	N1-C6-N6	-9.57	112.86	118.60	4	10
1	A	3	DG	O4'-C1'-N9	9.55	114.69	108.00	7	10
1	A	6	DC	N1-C2-O2	9.14	124.38	118.90	6	10
1	A	2	DA	N1-C6-N6	-9.08	113.15	118.60	4	10
1	A	18	DA	N1-C6-N6	-9.06	113.17	118.60	1	10
1	A	12	DG	O4'-C1'-N9	8.78	114.15	108.00	9	1
1	A	10	DA	O4'-C1'-N9	8.35	113.84	108.00	8	3
1	A	10	DA	C5-C6-N1	7.85	121.63	117.70	7	10
1	A	14	DA	C5-C6-N1	7.84	121.62	117.70	4	10
1	A	1	DT	C6-C5-C7	-7.76	118.24	122.90	10	10
1	A	18	DA	C5-C6-N1	7.76	121.58	117.70	6	10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	19	DA	C5-C6-N1	7.71	121.55	117.70	8	10
1	A	18	DA	C4-C5-C6	-7.60	113.20	117.00	2	10
1	A	13	DG	O4'-C1'-N9	7.55	113.28	108.00	9	7
1	A	9	DG	O4'-C1'-N9	7.28	113.09	108.00	6	5
1	A	8	DG	O4'-C1'-N9	7.19	113.03	108.00	1	4
1	A	1	DT	N3-C2-O2	-7.12	118.03	122.30	8	10
1	A	19	DA	C4-C5-C6	-7.03	113.48	117.00	5	10
1	A	2	DA	C5-C6-N1	6.94	121.17	117.70	6	10
1	A	14	DA	C4-C5-C6	-6.81	113.59	117.00	2	10
1	A	10	DA	C4-C5-C6	-6.76	113.62	117.00	4	10
1	A	5	DG	O4'-C1'-N9	6.68	112.68	108.00	8	8
1	A	15	DG	O4'-C1'-N9	6.64	112.65	108.00	2	7
1	A	16	DG	N3-C2-N2	-6.52	115.34	119.90	10	10
1	A	2	DA	C4-C5-C6	-6.33	113.84	117.00	4	10
1	A	18	DA	O4'-C1'-N9	6.21	112.35	108.00	4	3
1	A	3	DG	N3-C2-N2	-6.16	115.59	119.90	7	10
1	A	8	DG	N3-C2-N2	-5.83	115.82	119.90	9	1
1	A	7	DG	O4'-C1'-N9	5.69	111.98	108.00	7	2
1	A	11	DG	O4'-C1'-N9	5.57	111.90	108.00	7	3
1	A	7	DG	N3-C2-N2	-5.57	116.00	119.90	8	2
1	A	1	DT	O4'-C1'-C2'	-5.51	101.49	105.90	5	3
1	A	17	DG	O4'-C1'-N9	5.41	111.79	108.00	4	3
1	A	16	DG	C5-C6-N1	5.18	114.09	111.50	1	4
1	A	11	DG	C5-C6-N1	5.05	114.03	111.50	5	1
1	A	4	DG	N3-C2-N2	-5.05	116.36	119.90	5	1
1	A	7	DG	N3-C4-C5	-5.03	126.08	128.60	9	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	16	DG	Sidechain	5
1	A	8	DG	Sidechain	5
1	A	1	DT	Sidechain	4
1	A	7	DG	Sidechain	3
1	A	4	DG	Sidechain	1
1	A	12	DG	Sidechain	1

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	4050	2120	2120	-

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)

The completeness of assignment taking into account all chemical shift lists is 29% for the well-defined parts and 29% for the entire structure.

7.1 Chemical shift list 1

File name: 2lee_cs.str

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	115
Number of shifts mapped to atoms	115
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing (i)

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 29%, i.e. 112 atoms were assigned a chemical shift out of a possible 390. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}**H**	^{13}**C**	^{15}**N**
Backbone	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Sidechain	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	112/390 (29%)	112/238 (47%)	0/121 (0%)	0/31 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 29%, i.e. 112 atoms were assigned a chemical shift out of a possible 390. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Sidechain	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	112/390 (29%)	112/238 (47%)	0/121 (0%)	0/31 (0%)

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (i)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_1). RCI is only applicable to proteins.