



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2NBJ
Title : DNA-archeal MC1 protein complex structure by NMR
Authors : Paquet, F.; Loth, K.; Landon, C.
Deposited on : 2016-02-25

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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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-20028442
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

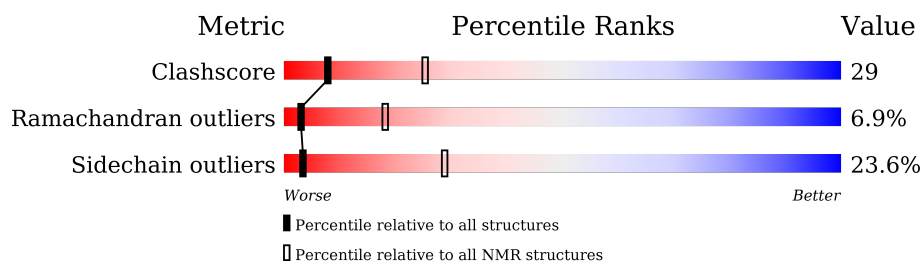
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR


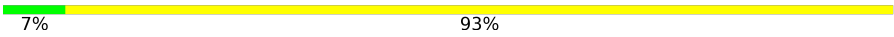
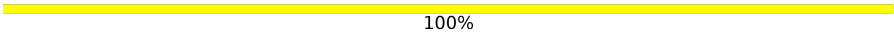
The overall completeness of chemical shifts assignment was not calculated.

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
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	93	 67% 20% 9% . .
2	B	15	 7% 93%
3	C	15	 100%

2 Ensemble composition and analysis

This entry contains 12 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:3-A:92 (90)	0.19	10

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 5, 7, 8, 9, 10, 12
2	3, 6, 11
Single-model clusters	4

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2487 atoms, of which 1122 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Chromosomal protein MC1.

Mol	Chain	Residues	Atoms						Trace
1	A	93	Total	C	H	N	O	S	0
			1534	472	781	147	133	1	

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*AP*AP*AP*AP*CP*AP*CP*AP*CP*AP*CP*CP*CP*A)-3').

Mol	Chain	Residues	Atoms						Trace
2	B	15	Total	C	H	N	O	P	0
			466	144	166	63	79	14	

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

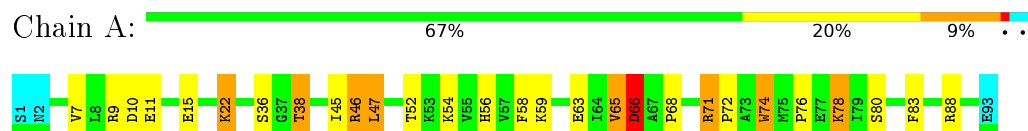
Mol	Chain	Residues	Atoms						Trace
3	C	15	Total	C	H	N	O	P	0
			487	150	175	48	99	15	

4 Residue-property plots

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.

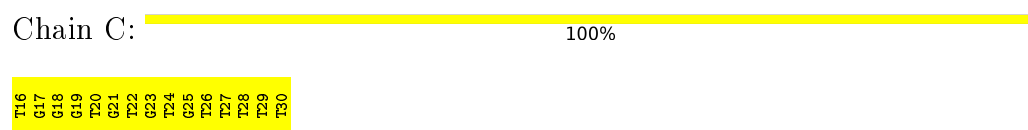
- Molecule 1: Chromosomal protein MC1



- Molecule 2: DNA (5'-D(*AP*AP*AP*AP*AP*CP*AP*CP*AP*CP*AP*CP*CP*CP*A)-3')



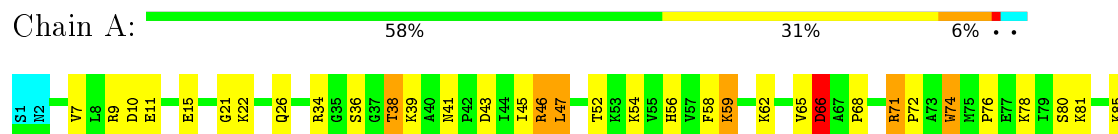
- Molecule 3: DNA (5'-D(P*TP*GP*GP*GP*TP*GP*TP*GP*TP*GP*TP*TP*TP*T)-3')



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

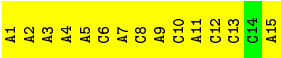
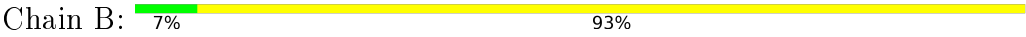
The representative model is number 10. Colouring as in section 4.1 above.

- Molecule 1: Chromosomal protein MC1

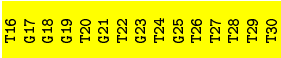
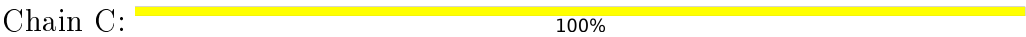




● Molecule 2: DNA (5'-D(*AP*AP*AP*AP*AP*CP*AP*CP*AP*CP*AP*CP*CP*CP*A)-3')



● Molecule 3: DNA (5'-D(P*TP*GP*GP*GP*TP*GP*TP*GP*TP*GP*TP*TP*TP*TP*T)-3')



5 Refinement protocol and experimental data overview

Of the 200 calculated structures, 12 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
HADDOCK	structure solution	
HADDOCK	refinement	
CNS	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)	2nbj_cs.cif
Number of chemical shift lists	1
Total number of shifts	714
Number of shifts mapped to atoms	0
Number of unparsed shifts	714
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	0%

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](#)

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

There are no bond-length outliers.

There are no bond-angle outliers.

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	729	762	760	16±3
2	B	300	166	167	34±4
3	C	312	175	175	33±3
All	All	16092	13236	13224	855

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 29.

5 of 198 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:C:24:DT:H2''	3:C:25:DG:H5''	1.03	1.30	9	12
2:B:10:DC:H2''	2:B:11:DA:H4'	0.98	1.32	5	10
2:B:4:DA:H2''	2:B:5:DA:C8	0.92	1.99	4	12
2:B:10:DC:C2'	2:B:11:DA:H4'	0.91	1.95	1	12
3:C:22:DT:H2''	3:C:23:DG:H5'	0.85	1.46	6	4

6.3 Torsion angles [i](#)

6.3.1 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	90/93 (97%)	67±1 (75±1%)	17±1 (18±1%)	6±1 (7±1%)	3	18
All	All	1080/1116 (97%)	807 (75%)	198 (18%)	75 (7%)	3	18

5 of 11 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	66	ASP	12
1	A	38	THR	12
1	A	76	PRO	12
1	A	68	PRO	11
1	A	10	ASP	10

6.3.2 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	76/79 (96%)	58±1 (76±2%)	18±1 (24±2%)	3	29
All	All	912/948 (96%)	697 (76%)	215 (24%)	3	29

5 of 27 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	74	TRP	12
1	A	7	VAL	12
1	A	47	LEU	12
1	A	46	ARG	12
1	A	38	THR	12

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

The completeness of assignment taking into account all chemical shift lists is 0% for the well-defined parts and 0% for the entire structure.

7.1 Chemical shift list 1

File name: 2nbj_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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	714
Number of shifts mapped to atoms	0
Number of unparsed shifts	714
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following errors were found when reading this chemical shift list.

- Entity instance (chain) must be specified. First 5 (of 714) occurrences are reported below.

Shift ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	.	2	ASN	HA	4.928	0.04	1
2	.	2	ASN	HB2	2.806	0.04	1
3	.	2	ASN	HB3	2.902	0.04	1
4	.	2	ASN	HD21	7.679	0.04	1
5	.	2	ASN	HD22	7.037	0.04	1

7.1.2 Chemical shift referencing

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

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 0%, i.e. 0 atoms were assigned a chemical

shift out of a possible 1794. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/438 (0%)	0/174 (0%)	0/180 (0%)	0/84 (0%)
Sidechain	0/692 (0%)	0/411 (0%)	0/234 (0%)	0/47 (0%)
Aromatic	0/76 (0%)	0/40 (0%)	0/30 (0%)	0/6 (0%)
Overall	0/1794 (0%)	0/973 (0%)	0/648 (0%)	0/173 (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.