wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2CPI
Title	:	Solution structure of the RNA recognition motif of CNOT4
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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:

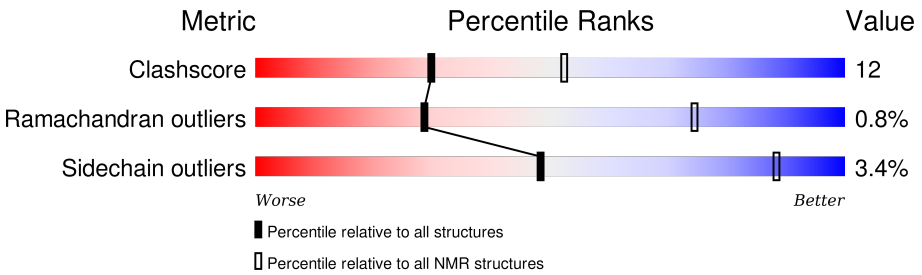
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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
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 <=5%

Mol	Chain	Length	Quality of chain
1	A	111	55% 10% 35%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:110-A:145, A:156-A:191 (72)	0.29	12

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 6 clusters and 3 single-model clusters were found.

Cluster number	Models
1	11, 12, 13, 17, 18
2	8, 14, 15
3	1, 16, 20
4	5, 10
5	4, 6
6	2, 9
Single-model clusters	3; 7; 19

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1652 atoms, of which 830 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CCR4-NOT transcription complex subunit 4.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	111	1652	513	830	147	160	2	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	GLY	-	CLONING ARTIFACT	UNP Q8BT14
A	95	SER	-	CLONING ARTIFACT	UNP Q8BT14
A	96	SER	-	CLONING ARTIFACT	UNP Q8BT14
A	97	GLY	-	CLONING ARTIFACT	UNP Q8BT14
A	98	SER	-	CLONING ARTIFACT	UNP Q8BT14
A	99	SER	-	CLONING ARTIFACT	UNP Q8BT14
A	100	GLY	-	CLONING ARTIFACT	UNP Q8BT14
A	199	SER	-	CLONING ARTIFACT	UNP Q8BT14
A	200	GLY	-	CLONING ARTIFACT	UNP Q8BT14
A	201	PRO	-	CLONING ARTIFACT	UNP Q8BT14
A	202	SER	-	CLONING ARTIFACT	UNP Q8BT14
A	203	SER	-	CLONING ARTIFACT	UNP Q8BT14
A	204	GLY	-	CLONING ARTIFACT	UNP Q8BT14

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: CCR4-NOT transcription complex subunit 4

Chain A: 55% 10% 35%

G94 S95 S96 G97 S98 S99 G100 A101 S102 V103 R104 V105 V106 Q107 K108 N109 F112 Q118 V125 Y131 K134 I138 V141 S146 T147 S148 Y149 A150 G151 S152 Q153 G154 P155 Y160 A172 V176 L190 G191 T192 T193 K194 Y195 C196 S197 Y198 S199 G200 P201

S202 S203 G204

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

The representative model is number 12. Colouring as in section 4.1 above.

- Molecule 1: CCR4-NOT transcription complex subunit 4

Chain A: 43% 20% • 35%

G94 S95 S96 G97 S98 S99 G100 A101 S102 V103 R104 V105 V106 Q107 K108 N109 F112 S117 Q118 R119 L120 A121 D122 V125 L126 K127 Y131 K134 I138 V141 S146 T147 S148 Y149 A150 G151 S152 Q153 G154 P155 S158 A159 Y160 Y163 A169 A172 I173

V176 V181 L186 K187 A188 S189 L190 G191 T192 T193 K194 Y195 C196 S197 Y198 S199 G200 P201 S202 S203 G204

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dyanamics, simulated annealing.*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function,structures with the lowest energy,structures with the least restraint violations.*

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

Software name	Classification	Version
Cyana	structure solution	2.0.17
Cyana	refinement	2.0.17

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)

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	559	584	584	14±4
All	All	11180	11680	11680	275

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 12.

5 of 104 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:VAL:HG22	1:A:173:ILE:HD11	0.93	1.39	18	6
1:A:114:VAL:HG12	1:A:158:SER:HB3	0.79	1.55	13	1
1:A:190:LEU:HD23	1:A:191:GLY:N	0.77	1.95	2	1
1:A:190:LEU:HD12	1:A:190:LEU:O	0.77	1.80	5	2
1:A:120:LEU:HD21	1:A:182:ASP:OD2	0.76	1.79	4	1

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	72/111 (65%)	65±2 (90±2%)	7±2 (9±2%)	1±1 (1±1%)	29 74
All	All	1440/2220 (65%)	1297 (90%)	131 (9%)	12 (1%)	29 74

All 3 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	121	ALA	5
1	A	133	GLY	4
1	A	118	GLN	3

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	61/91 (67%)	59±2 (97±3%)	2±2 (3±3%)	48 88
All	All	1220/1820 (67%)	1179 (97%)	41 (3%)	48 88

5 of 15 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	134	LYS	8
1	A	177	ASN	5
1	A	122	ASP	5
1	A	140	LYS	4
1	A	187	LYS	4

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