wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	1UDM
Title	:	Solution structure of Coactosin-like protein (Cofilin family) from Mus Musculus
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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:

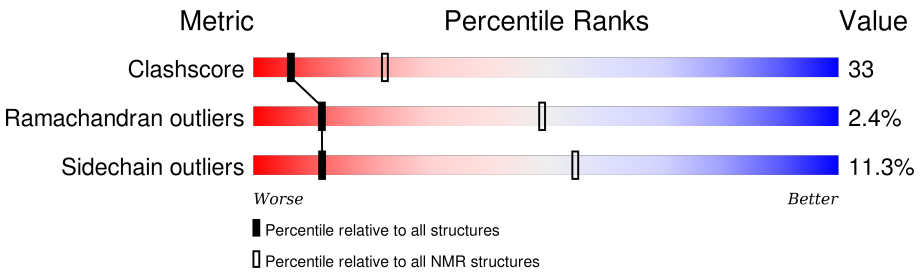
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal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

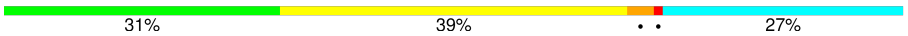
The overall completeness of chemical shifts assignment was not calculated.

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	149	

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 20 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 target function*.

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:11-A:26, A:31-A:70, A:83-A:135 (109)	0.15	20

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 3 clusters and 2 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2294 atoms, of which 1132 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Coactosin-like protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	149	2294	727	1132	201	230	4	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	UNP Q9CQI6
A	2	SER	-	CLONING ARTIFACT	UNP Q9CQI6
A	3	GLU	-	CLONING ARTIFACT	UNP Q9CQI6
A	4	GLY	-	CLONING ARTIFACT	UNP Q9CQI6
A	5	ALA	-	CLONING ARTIFACT	UNP Q9CQI6
A	6	ALA	-	CLONING ARTIFACT	UNP Q9CQI6
A	7	THR	-	CLONING ARTIFACT	UNP Q9CQI6

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: Coactosin-like protein

Chain A: 31% 39% • • 27%

G1 S2 E3 G4 A5 A6 T7 M8 A9 T10 K11 I12 D13 K14 E15 A16 C17 R18 A19 A20 Y21 N22 L23 V24 R25 D26 D27 G28 S29 A30 V31 I32 W33 V34 Y38 D39 G40 I43 Q48 D51 Y52 Q53 H54 F55 C59 V63 R64 L65 F66 A67 F68 V69 R70 F71

T72 T73 G74 D75 A76 W77 S78 K79 R80 S81 K82 F83 T87 W88 I89 G90 V93 S94 G95 L96 Q97 R98 A99 K100 D104 K105 T106 L107 V108 K109 V112 Q113 N114 F115 A116 K117 E118 F119 V120 I121 S122 E126 L127 E128 E129 D130 F131 I132 R133 L136 K137 K138 A139 G140

G141 A142 N143 Y144 D145 A146 Q147 S148 E149

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

The representative model is number 20. Colouring as in section 4.1 above.

- Molecule 1: Coactosin-like protein

Chain A: 30% 38% • • 27%

G1 S2 E3 G4 A5 A6 T7 M8 A9 T10 K11 I12 D13 K14 E15 A16 C17 A20 Y21 V24 D27 G28 S29 A30 W33 V34 T35 Y38 D39 G40 A41 T42 I43 G46 D47 D51 Y52 F55 Q58 C59 T60 V63 R64 L65 F66 A67 F68 V69 R70 F71

T72 T73 G74 D75 A76 W77 S78 K79 R80 S81 K82 F83 T87 W88 I89 G90 V93 S94 G95 L96 Q97 R98 A99 K100 D104 K105 T106 L107 V108 K109 V112 Q113 N114 F115 A116 K117 E118 F119 V120 I121 S122 E126 L127 E128 E129 D130 F131 I132 R133 S134 E135 L136 K137 K138 A139

G140 G141 A142 N143 Y144 D145 A146 Q147 S148 E149

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	refinement	2.0.13

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	887	871	870	58±6
All	All	17740	17420	17400	1154

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 33.

5 of 270 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:ALA:HB1	1:A:34:VAL:HG21	1.09	1.22	20	8
1:A:90:GLY:O	1:A:93:VAL:HG22	0.86	1.69	17	13
1:A:121:ILE:HG21	1:A:127:LEU:HD22	0.82	1.47	2	20
1:A:21:TYR:CD1	1:A:112:VAL:HG12	0.81	2.10	4	1
1:A:34:VAL:HG12	1:A:48:GLN:HG2	0.81	1.52	16	3

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	109/149 (73%)	90±2 (82±2%)	17±2 (15±2%)	3±1 (2±1%)	12 49
All	All	2180/2980 (73%)	1790 (82%)	337 (15%)	53 (2%)	12 49

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	14	LYS	20
1	A	115	PHE	19
1	A	46	GLY	3
1	A	95	GLY	2
1	A	40	GLY	2

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	94/120 (78%)	83±3 (89±3%)	11±3 (11±3%)	12 55
All	All	1880/2400 (78%)	1668 (89%)	212 (11%)	12 55

5 of 35 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	115	PHE	20
1	A	64	ARG	20
1	A	55	PHE	20
1	A	65	LEU	20
1	A	133	ARG	16

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