wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2RQC
Title	:	Solution Structure of RNA-binding domain 3 of CUGBP1 in complex with RNA (UG)3
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Deposited on	:	2009-04-09

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
https://www.wwpdb.org/validation/2017/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:

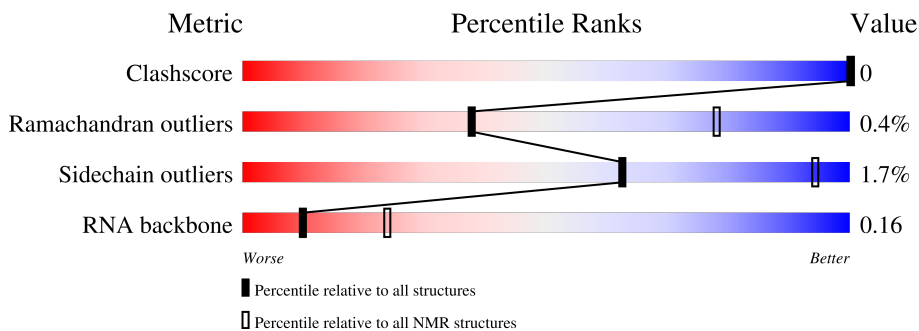|		
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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	Percentile Ranks	Value
Clashscore		0
Ramachandran outliers		0.4%
Sidechain outliers		1.7%
RNA backbone		0.16

Worse — *Better*

▮ Percentile relative to all structures

▯ Percentile relative to all NMR structures

Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428
RNA backbone	4643	676

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	115	71%		29%
2	B	6	17%	17%	67%

WORLDWIDE
wwPDB
PROTEIN DATA BANK

2 Ensemble composition and analysis ⓘ

This entry contains 20 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:390-A:434, A:441-A:477 (82)	0.23	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 5 clusters. No single-model clusters were found.

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

3 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 1899 atoms, of which 913 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CUG-BP- and ETR-3-like factor 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	115	1708	537	848	149	169	5	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	376	GLY	-	expression tag	UNP Q92879
A	377	SER	-	expression tag	UNP Q92879
A	378	SER	-	expression tag	UNP Q92879
A	379	GLY	-	expression tag	UNP Q92879
A	380	SER	-	expression tag	UNP Q92879
A	381	SER	-	expression tag	UNP Q92879
A	382	GLY	-	expression tag	UNP Q92879
A	485	SER	-	expression tag	UNP Q92879
A	486	GLY	-	expression tag	UNP Q92879
A	487	PRO	-	expression tag	UNP Q92879
A	488	SER	-	expression tag	UNP Q92879
A	489	SER	-	expression tag	UNP Q92879
A	490	GLY	-	expression tag	UNP Q92879

- Molecule 2 is a RNA chain called 5'-R(*UP*GP*UP*GP*UP*G)-3'.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	6	191	57	65	21	43	5	0

4 Residue-property plots ⓘ

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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.
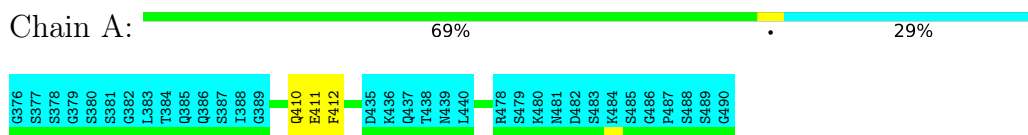
• Molecule 1: CUG-BP- and ETR-3-like factor 1

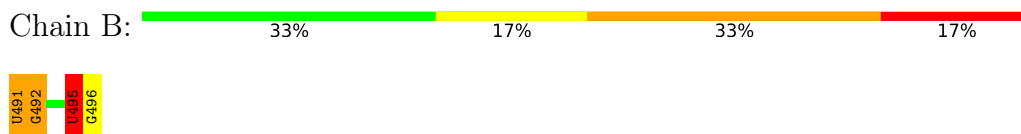Chain A:

• Molecule 2: 5'-R(*UP*GP*UP*GP*UP*G)-3'

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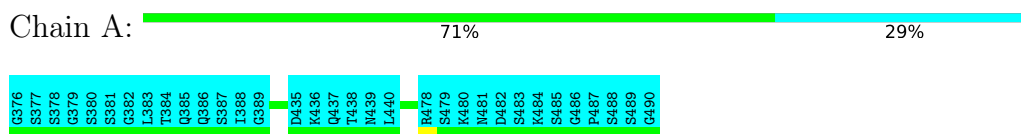
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

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

• Molecule 1: CUG-BP- and ETR-3-like factor 1

Chain A:

• Molecule 2: 5'-R(*UP*GP*UP*GP*UP*G)-3'

Chain B:

5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *DGSA-distance geometry simulated an-nealing, RESTRAINTED MOLECULAR DYNAMICS, SIMULATED ANNEALING, ENERGY MINIMIZATION.*

Of the 100 calculated structures, 20 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
Amber	refinement	9
CYANA	structure solution	2.1

No chemical shift data was provided.

6 Model quality ⓘ

6.1 Standard geometry ⓘ

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	0.70±0.00	0±0/648 (0.0± 0.0%)	0.86±0.01	0±0/871 (0.0± 0.0%)
2	B	1.35±0.02	0±0/140 (0.0± 0.0%)	2.06±0.04	4±1/217 (1.8± 0.3%)
All	All	0.85	0/15760 (0.0%)	1.20	77/21760 (0.4%)

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
2	B	0.0±0.0	2.2±0.9
All	All	0	45

There are no bond-length outliers.

5 of 11 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
2	B	495	U	O4'-C1'-N1	9.29	115.63	108.20	14	18
2	B	492	G	O4'-C1'-N9	8.47	114.98	108.20	11	20
2	B	496	G	O4'-C1'-N9	7.62	114.30	108.20	6	4
2	B	491	U	C5-C6-N1	-6.29	119.56	122.70	16	18
2	B	495	U	C3'-C2'-C1'	5.68	106.04	101.50	5	1

There are no chirality outliers.

5 of 6 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
2	B	491	U	Sidechain	14
2	B	496	G	Sidechain	13

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Mol	Chain	Res	Type	Group	Models (Total)
2	B	495	U	Sidechain	9
2	B	494	G	Sidechain	5
2	B	493	U	Sidechain	3

6.2   Too-close contacts ⓘ

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	15180	13860	13860	-

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 ⓘ

6.3.1   Protein backbone ⓘ

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	82/115 (71%)	79±1 (96±1%)	3±1 (4±1%)	0±1 (0±1%)	38	78
All	All	1640/2300 (71%)	1575 (96%)	59 (4%)	6 (0%)	38	78

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	469	MET	3
1	A	407	HIS	2
1	A	390	ALA	1

6.3.2 Protein sidechains ⓘ

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	67/94 (71%)	66±1 (98±1%)	1±1 (2±1%)	62	94
All	All	1340/1880 (71%)	1317 (98%)	23 (2%)	62	94

5 of 8 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	412	PHE	7
1	A	394	GLN	6
1	A	410	GLN	4
1	A	411	GLU	2
1	A	420	MET	1

6.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	5/6 (83%)	3±1 (55±15%)	0±0 (6±9%)	0.16±0.06
All	All	100/120 (83%)	55 (55%)	6 (6%)	0.15

The overall RNA backbone suiteness is 0.16.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	492	G	18
2	B	496	G	18
2	B	495	U	16
2	B	494	G	3

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	495	U	6

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation ⓘ

No chemical shift data were provided