wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2FY1
Title	:	A dual mode of RNA recognition by the RBMY protein
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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:

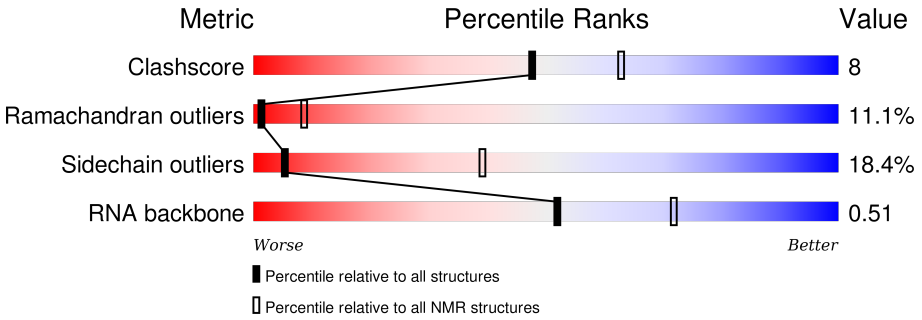
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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
RNA backbone	3027	600

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	B	21	38% 29% 33%
2	A	116	39% 23% • • 26% 7%

2 Ensemble composition and analysis (i)

This entry contains 17 models. Model 2 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:9-A:86 (78)	0.25	2

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 4 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2343 atoms, of which 1076 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called S1A stem-loop RNA.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	B	21	674	200	230	82	142	20	0

- Molecule 2 is a protein called RNA-binding motif protein, Y chromosome, family 1 member A1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	A	108	1669	511	846	159	150	3	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	GLU	-	EXPRESSION TAG	UNP Q15414
A	111	HIS	-	EXPRESSION TAG	UNP Q15414
A	112	HIS	-	EXPRESSION TAG	UNP Q15414
A	113	HIS	-	EXPRESSION TAG	UNP Q15414
A	114	HIS	-	EXPRESSION TAG	UNP Q15414
A	115	HIS	-	EXPRESSION TAG	UNP Q15414
A	116	HIS	-	EXPRESSION TAG	UNP Q15414

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

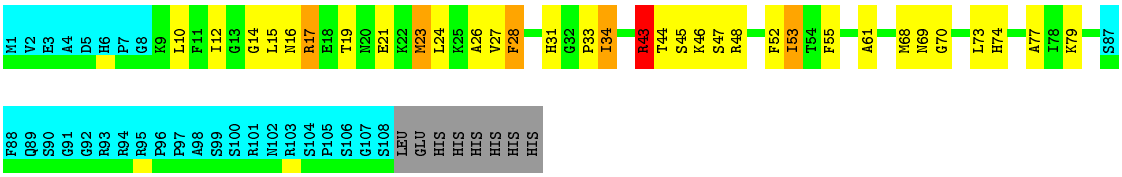
These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain 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: S1A stem-loop RNA

Chain B: 38% 29% 33%

- Molecule 2: RNA-binding motif protein, Y chromosome, family 1 member A1

Chain A: 39% 23% • • 26% 7%



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

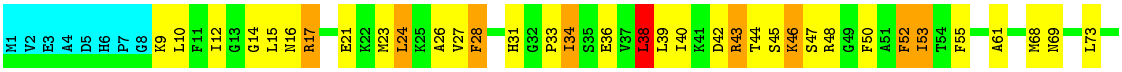
The representative model is number 2. Colouring as in section 4.1 above.

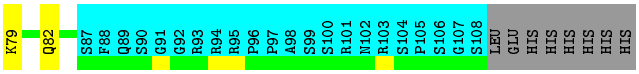
- Molecule 1: S1A stem-loop RNA

Chain B: 33% 38% 24% 5%

- Molecule 2: RNA-binding motif protein, Y chromosome, family 1 member A1

Chain A: 35% 24% 7% • 26% 7%




K79
Q82
S87
F88
Q89
S90
G91
G92
R93
R94
R95
P96
P97
A98
S99
S100
R101
N102
R103
S104
P105
S106
G107
S108
LEU
GLU
HIS
HIS
HIS
HIS
HIS
HIS

5 Refinement protocol and experimental data overview (i)

Of the 30 calculated structures, 17 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	7.0

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)

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	B	1.16±0.01	0±0/496 (0.0±0.0%)	1.81±0.05	17±3/771 (2.3±0.4%)
2	A	0.75±0.01	0±0/612 (0.0±0.0%)	1.47±0.03	7±2/815 (0.9±0.2%)
All	All	0.95	0/18836 (0.0%)	1.64	420/26962 (1.6%)

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	A	0.0±0.0	1.5±0.5
All	All	0	25

There are no bond-length outliers.

5 of 60 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	B	123	A	O4'-C1'-N9	12.34	118.07	108.20	7	17
1	B	122	G	C5'-C4'-O4'	11.16	122.49	109.10	8	17
2	A	48	ARG	NE-CZ-NH1	9.92	125.26	120.30	11	12
2	A	43	ARG	NE-CZ-NH1	9.78	125.19	120.30	5	16
1	B	118	A	O4'-C1'-N9	9.59	115.87	108.20	13	14

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)
2	A	28	PHE	Sidechain	17
2	A	74	HIS	Sidechain	4

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Mol	Chain	Res	Type	Group	Models (Total)
2	A	43	ARG	Sidechain	2
2	A	17	ARG	Sidechain	2

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	B	444	230	230	5±1
2	A	602	636	636	12±2
All	All	17782	14722	14722	250

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 8.

5 of 53 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:15:LEU:HD22	2:A:15:LEU:H	0.86	1.31	8	1
2:A:15:LEU:H	2:A:15:LEU:HD22	0.85	1.30	13	1
2:A:15:LEU:H	2:A:15:LEU:CD2	0.74	1.96	13	1
2:A:15:LEU:CD2	2:A:15:LEU:H	0.73	1.97	8	1
2:A:12:ILE:HD13	2:A:28:PHE:CE2	0.66	2.25	8	16

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
2	A	78/116 (67%)	53±2 (68±2%)	17±2 (21±2%)	9±1 (11±2%)	1 9
All	All	1326/1972 (67%)	898 (68%)	281 (21%)	147 (11%)	1 9

5 of 17 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	A	47	SER	17
2	A	45	SER	16
2	A	34	ILE	15
2	A	43	ARG	15
2	A	26	ALA	15

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
2	A	63/95 (66%)	51±2 (82±3%)	12±2 (18±3%)	5 39
All	All	1071/1615 (66%)	874 (82%)	197 (18%)	5 39

5 of 29 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)
2	A	31	HIS	17
2	A	73	LEU	17
2	A	53	ILE	17
2	A	17	ARG	16
2	A	79	LYS	15

6.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	20/21 (95%)	4±0 (18±2%)	2±1 (9±4%)	0.51±0.02
All	All	340/357 (95%)	61 (18%)	32 (9%)	0.51

The overall RNA backbone suiteness is 0.51.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	121	A	17

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Mol	Chain	Res	Type	Models (Total)
1	B	122	G	17
1	B	120	A	17
1	B	119	C	10

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	120	A	17
1	B	122	G	10
1	B	121	A	5

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