wwPDB NMR Structure Validation Summary Report

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PDB ID	:	2KG1
BMRB ID	:	16194
Title	:	Structure of the third qRRM domain of hnRNP F in complex with a AGGGAU G-tract RNA
Authors	:	Allain, F.H.T.; Dominguez, C.
Deposited on	:	2009-03-02

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 ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

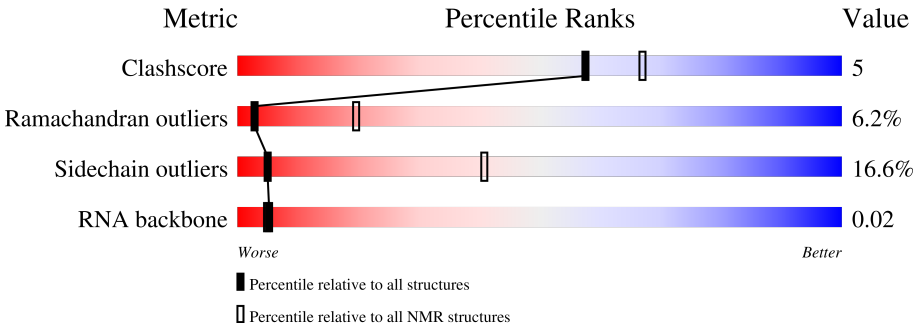
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 is 76%.

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	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	139	34% 11% • 29% 24%
2	B	6	17% 50% 33%

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: *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:289-A:296, A:300-A:320, A:331-A:365 (64)	0.63	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 and 3 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1755 atoms, of which 819 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Heterogeneous nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	105	1558	496	752	142	162	6	0

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	243	MET	-	expression tag	UNP P52597
A	244	GLY	-	expression tag	UNP P52597
A	245	SER	-	expression tag	UNP P52597
A	246	SER	-	expression tag	UNP P52597
A	247	HIS	-	expression tag	UNP P52597
A	248	HIS	-	expression tag	UNP P52597
A	249	HIS	-	expression tag	UNP P52597
A	250	HIS	-	expression tag	UNP P52597
A	251	HIS	-	expression tag	UNP P52597
A	252	HIS	-	expression tag	UNP P52597
A	253	SER	-	expression tag	UNP P52597
A	254	SER	-	expression tag	UNP P52597
A	255	GLY	-	expression tag	UNP P52597
A	256	LEU	-	expression tag	UNP P52597
A	257	VAL	-	expression tag	UNP P52597
A	258	PRO	-	expression tag	UNP P52597
A	259	ARG	-	expression tag	UNP P52597
A	260	GLY	-	expression tag	UNP P52597
A	261	SER	-	expression tag	UNP P52597
A	262	HIS	-	expression tag	UNP P52597
A	263	MET	-	expression tag	UNP P52597
A	264	ALA	-	expression tag	UNP P52597
A	265	SER	-	expression tag	UNP P52597
A	266	MET	-	expression tag	UNP P52597
A	267	THR	-	expression tag	UNP P52597
A	268	GLY	-	expression tag	UNP P52597
A	269	GLY	-	expression tag	UNP P52597
A	270	GLN	-	expression tag	UNP P52597
A	271	GLN	-	expression tag	UNP P52597
A	272	MET	-	expression tag	UNP P52597
A	273	GLY	-	expression tag	UNP P52597

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Chain	Residue	Modelled	Actual	Comment	Reference
A	274	ARG	-	expression tag	UNP P52597
A	275	GLY	-	expression tag	UNP P52597
A	276	SER	-	expression tag	UNP P52597

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

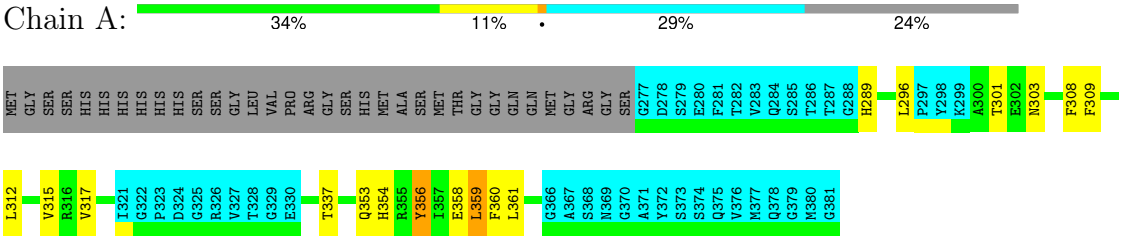
Mol	Chain	Residues	Atoms						Trace
2	B	6	Total	C	H	N	O	P	0
			197	59	67	27	39	5	

4 Residue-property plots

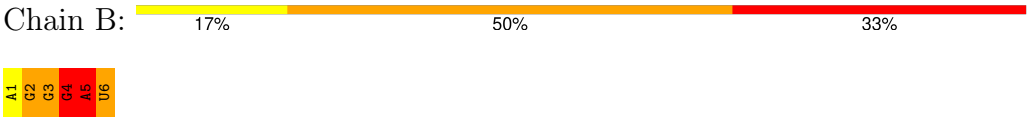
4.1 Average score per residue in the NMR ensemble

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: Heterogeneous nuclear ribonucleoprotein F



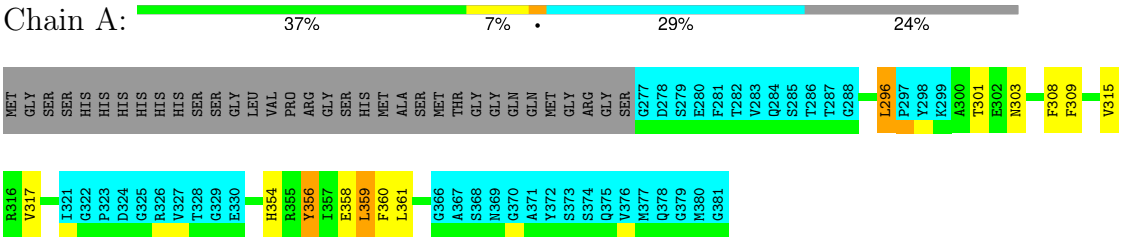
• Molecule 2: 5'-R(*AP*GP*GP*GP*AP*U)-3'



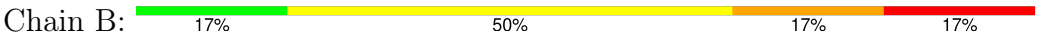
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

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

• Molecule 1: Heterogeneous nuclear ribonucleoprotein F



• Molecule 2: 5'-R(*AP*GP*GP*GP*AP*U)-3'




A1
G2
G3
G4
A5
U6

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 50 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
CYANA	structure solution	2.1
Amber	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1097
Number of shifts mapped to atoms	1097
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	76%

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	A	0.49±0.00	0±0/531 (0.0± 0.0%)	0.87±0.02	0±0/722 (0.1± 0.1%)
2	B	1.12±0.01	0±0/146 (0.0± 0.0%)	1.81±0.11	5±1/227 (2.3± 0.6%)
All	All	0.68	0/13540 (0.0%)	1.16	111/18980 (0.6%)

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
1	A	0.0±0.0	0.1±0.3
2	B	0.0±0.0	0.5±0.7
All	All	0	11

There are no bond-length outliers.

5 of 13 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	4	G	O4'-C1'-N9	12.31	118.05	108.20	20	15
2	B	4	G	C1'-O4'-C4'	-11.09	101.03	109.90	18	20
2	B	1	A	O4'-C1'-N9	8.88	115.30	108.20	11	12
2	B	2	G	O4'-C1'-N9	8.03	114.62	108.20	19	13
2	B	5	A	O4'-C1'-N9	7.55	114.24	108.20	16	3

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	B	2	G	Sidechain	3

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Mol	Chain	Res	Type	Group	Models (Total)
2	B	5	A	Sidechain	3
1	A	296	LEU	Peptide	2
2	B	4	G	Sidechain	2
2	B	3	G	Sidechain	1

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
1	A	518	489	489	4±3
2	B	130	67	67	4±2
All	All	12960	11120	11120	120

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 5.

5 of 47 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:3:G:H1'	2:B:4:G:C8	0.60	2.32	13	12
1:A:356:TYR:CD2	2:B:3:G:C6	0.60	2.90	14	6
1:A:289:HIS:CE1	1:A:341:ALA:HB2	0.55	2.35	18	1
1:A:356:TYR:CD2	2:B:3:G:C2	0.55	2.94	19	1
1:A:360:PHE:CD2	2:B:5:A:C6	0.54	2.96	20	5

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	64/139 (46%)	48±2 (74±3%)	12±2 (19±3%)	4±2 (6±2%)	3 19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1280/2780 (46%)	953 (74%)	248 (19%)	79 (6%)	3 19

5 of 15 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	315	VAL	18
1	A	350	ALA	10
1	A	353	GLN	10
1	A	348	ASP	7
1	A	354	HIS	7

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	56/112 (50%)	47±2 (83±3%)	9±2 (17±3%)	5 41
All	All	1120/2240 (50%)	934 (83%)	186 (17%)	5 41

5 of 20 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	303	ASN	20
1	A	359	LEU	20
1	A	360	PHE	20
1	A	361	LEU	20
1	A	308	PHE	18

6.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	5/6 (83%)	5±0 (96±8%)	4±1 (74±19%)	0.02±0.04
All	All	113/120 (94%)	96 (85%)	74 (65%)	0.02

The overall RNA backbone suiteness is 0.02.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	4	G	20
2	B	5	A	20
2	B	6	U	20
2	B	2	G	18
2	B	3	G	18

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	5	A	20
2	B	4	G	17
2	B	2	G	15
2	B	1	A	13
2	B	3	G	9

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 monosaccharides 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 76% for the well-defined parts and 75% for the entire structure.

7.1 Chemical shift list 1

File name: working_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	1097
Number of shifts mapped to atoms	1097
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	89	-0.15 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	88	-0.01 ± 0.25	None needed (< 0.5 ppm)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	101	0.00 ± 0.57	None needed (< 0.5 ppm)

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 76%, i.e. 760 atoms were assigned a chemical shift out of a possible 995. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	246/317 (78%)	127/127 (100%)	57/128 (45%)	62/62 (100%)
Sidechain	412/470 (88%)	282/306 (92%)	120/145 (83%)	10/19 (53%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	55/93 (59%)	35/48 (73%)	20/40 (50%)	0/5 (0%)
Sugar	36/66 (55%)	36/36 (100%)	0/30 (0%)	0/0 (—%)
Base	11/49 (22%)	11/31 (35%)	0/9 (0%)	0/9 (0%)
Overall	760/995 (76%)	491/548 (90%)	197/352 (56%)	72/95 (76%)

7.1.4 Statistically unusual chemical shifts (i)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	B	3	G	H5”	2.95	2.98 – 5.38	-5.1

7.1.5 Random Coil Index (RCI) plots (i)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A: