



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1K1G / pdb_00001k1g
Title : STRUCTURAL BASIS FOR RECOGNITION OF THE INTRON BRANCH
SITE RNA BY SPLICING FACTOR 1
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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	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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)	:	2.49

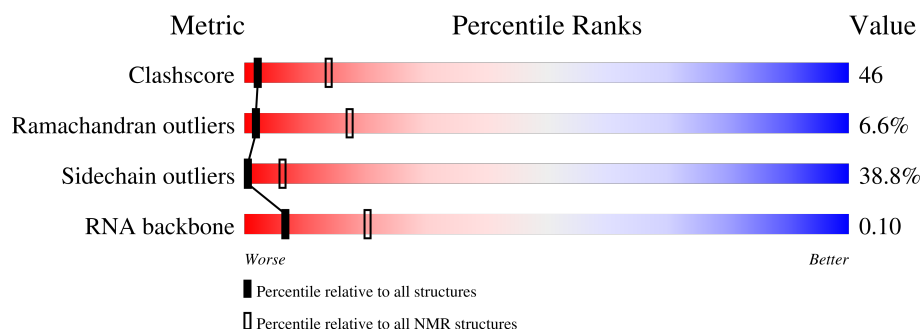
1 Overall quality at a glance

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	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823
RNA backbone	8273	777

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	B	11	
2	A	131	

2 Ensemble composition and analysis

This entry contains 10 models. Model 8 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:134-A:184, A:195-A:255 (112)	0.67	8

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 2 clusters and 4 single-model clusters were found.

Cluster number	Models
1	3, 4, 5, 8
2	1, 6
Single-model clusters	2; 7; 9; 10

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2308 atoms, of which 1122 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called 5'-R(*UP*AP*UP*AP*CP*UP*AP*AP*CP*AP*A)-3'.

Mol	Chain	Residues	Atoms						Trace
1	B	11	Total	C	H	N	O	P	0
			349	105	120	42	72	10	

- Molecule 2 is a protein called SF1-Bo isoform.

Mol	Chain	Residues	Atoms						Trace
2	A	122	Total	C	H	N	O	S	0
			1959	591	1002	178	182	6	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	130	GLY	LYS	cloning artifact	UNP Q15637
A	131	ALA	PRO	cloning artifact	UNP Q15637
A	132	MET	PRO	cloning artifact	UNP Q15637

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

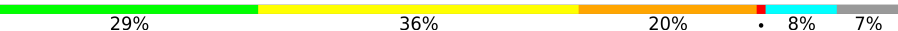
These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for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

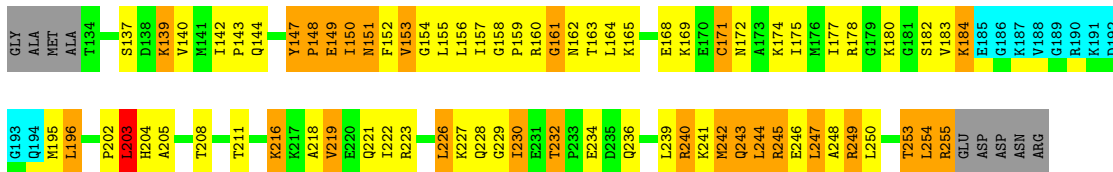
- Molecule 1: 5'-R(*UP*AP*UP*AP*CP*UP*AP*AP*CP*AP*A)-3'

Chain B: 



- Molecule 2: SF1-Bo isoform

Chain A: 



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

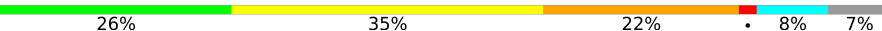
The representative model is number 8. Colouring as in section 4.1 above.

- Molecule 1: 5'-R(*UP*AP*UP*AP*CP*UP*AP*AP*CP*AP*A)-3'

Chain B: 



- Molecule 2: SF1-Bo isoform

Chain A: 



M195	L196	E199	L203	H204	A205	T208	T211	M212	E213	M214	V215	K216	K217	A218	V219	L222	R223	L226	K227	Q228	G229	I230	E231	T232	P233	E234	D235	Q236	L239	R240	K241	M242	Q243	L244	R245	F246	L247	R249	L250	N251	Q252	T253	L254	R255	GLU	ASP	ASP	ASN	ARG
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5 Refinement protocol and experimental data overview

The models were refined using the following method: *restrained molecular dynamics, simulated annealing*.

Of the 100 calculated structures, 10 were deposited, based on the following criterion: *10 lowest energy structures consistent with experimental distance and dihedral angle restraints*.

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

Software name	Classification	Version
ARIA/CNS	structure solution	1.0
ARIA/CNS	refinement	1.0

No chemical shift data was provided.

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	B	229	120	120	27±3
2	A	883	927	925	90±6
All	All	11120	10470	10450	1001

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 46.

5 of 281 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:507:A:C2	2:A:184:LYS:HG3	0.81	2.11	9	1
2:A:159:PRO:HD3	2:A:247:LEU:HB2	0.79	1.53	2	9
1:B:502:A:H2'	2:A:255:ARG:HA	0.75	1.58	8	7
2:A:151:ASN:HB2	2:A:155:LEU:HG	0.75	1.58	3	6
2:A:155:LEU:HD22	2:A:243:GLN:HB3	0.73	1.60	10	10

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	110/131 (84%)	80±2 (73±2%)	22±2 (20±2%)	7±1 (7±1%)	2	17
All	All	1100/1310 (84%)	803 (73%)	224 (20%)	73 (7%)	2	17

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	148	PRO	10
2	A	150	ILE	10
2	A	161	GLY	10
2	A	203	LEU	10
2	A	202	PRO	8

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	99/112 (88%)	61±2 (61±2%)	38±2 (39±2%)	0	6
All	All	990/1120 (88%)	606 (61%)	384 (39%)	0	6

5 of 76 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	139	LYS	10
2	A	149	GLU	10
2	A	153	VAL	10
2	A	196	LEU	10
2	A	203	LEU	10

6.3.3 RNA [i](#)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	11/11 (100%)	7±0 (64±0%)	2±1 (23±9%)	0.44±0.00
All	All	104/110 (95%)	70 (67%)	25 (24%)	0.44

The overall RNA backbone suiteness is 0.10.

5 of 7 unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	502	A	10
1	B	503	U	10
1	B	504	A	10
1	B	506	U	10
1	B	507	A	10

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	507	A	10
1	B	505	C	7
1	B	501	U	4
1	B	502	A	2
1	B	503	U	2

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 oligosaccharides 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 ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided