



Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 12:24 am BST

PDB ID : 2N3O
Title : Structure of PTB RRM1(41-163) bound to an RNA stemloop containing a structured loop derived from viral internal ribosomal entry site RNA
Authors : Maris, C.; Jayne, S.F.; Damberger, F.F.; Ravindranathan, S.; Allain, F.H.-T.
Deposited on : 2015-06-08

This is a Full wwPDB NMR Structure Validation 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
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 : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

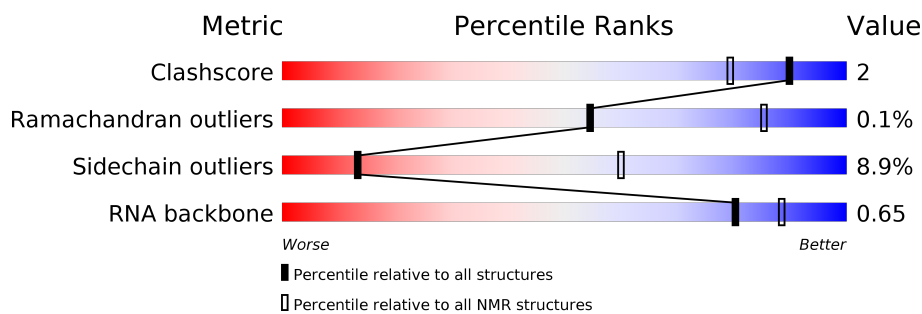
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 79%.

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	123	 62% 6% 33%
2	B	23	 74% 17% 9%

2 Ensemble composition and analysis i

This entry contains 20 models. Model 6 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:59-A:131, A:135-A:137, A:147-A:153 (83)	0.22	6

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 3 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2621 atoms, of which 1201 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Polypyrimidine tract-binding protein 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	123	1892	586	954	168	181	3	0

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

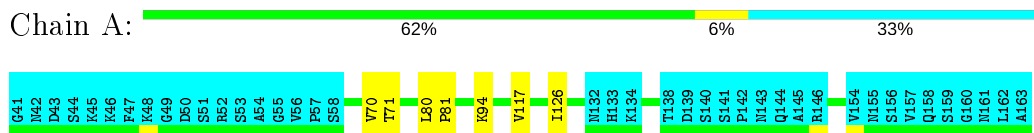
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	23	729	216	247	81	163	22	0

4 Residue-property plots i

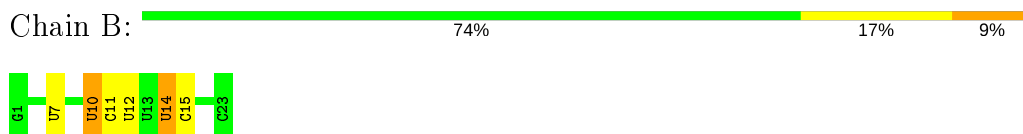
4.1 Average score per residue in the NMR ensemble

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: Polypyrimidine tract-binding protein 1



- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

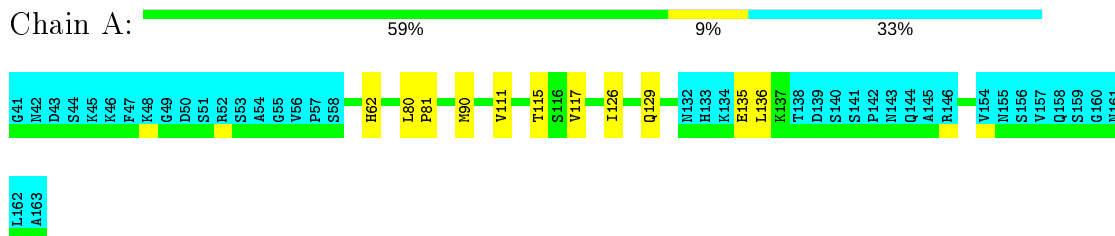


4.2 Scores per residue for each member of the ensemble

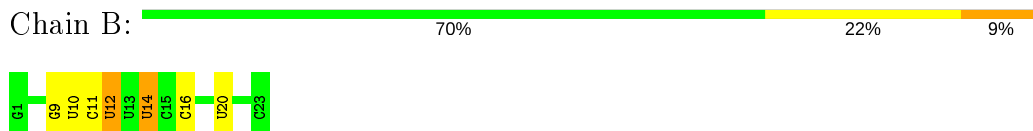
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Polypyrimidine tract-binding protein 1

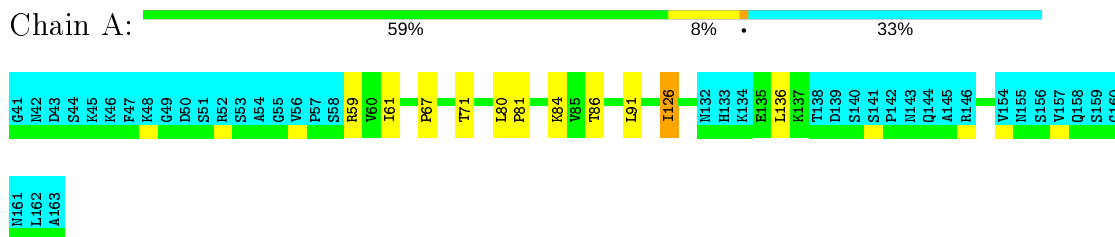


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

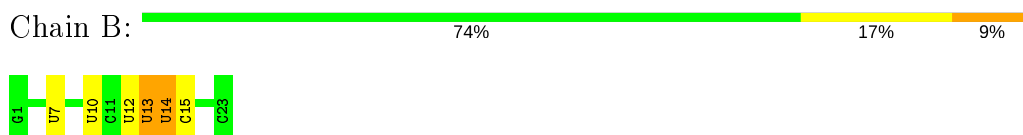


4.2.2 Score per residue for model 2

- Molecule 1: Polypyrimidine tract-binding protein 1

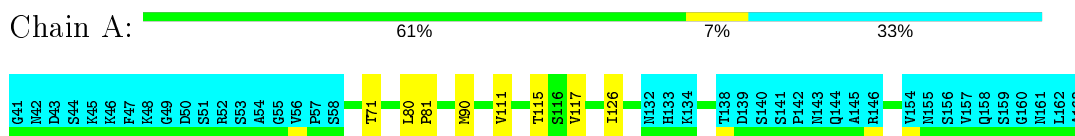


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

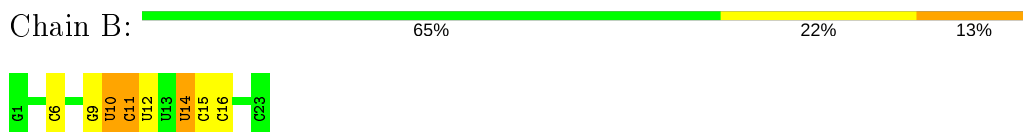


4.2.3 Score per residue for model 3

- Molecule 1: Polypyrimidine tract-binding protein 1

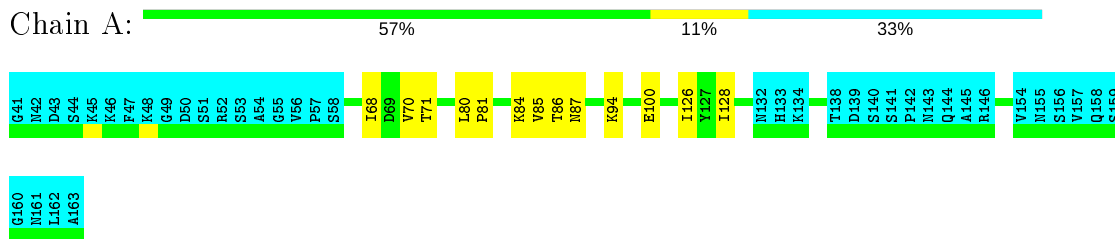


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

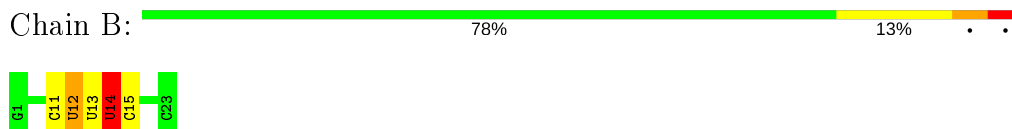


4.2.4 Score per residue for model 4

- Molecule 1: Polypyrimidine tract-binding protein 1

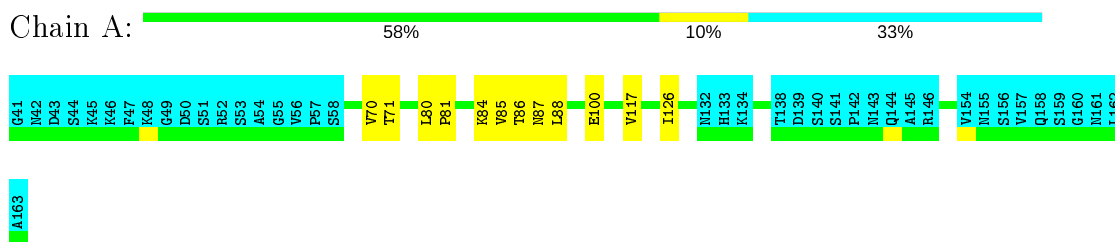


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

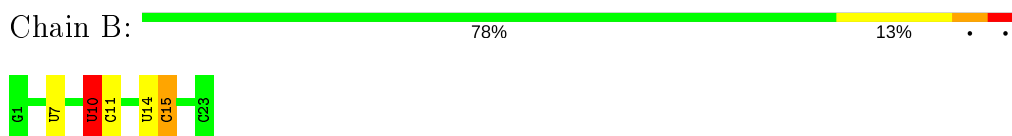


4.2.5 Score per residue for model 5

- Molecule 1: Polypyrimidine tract-binding protein 1

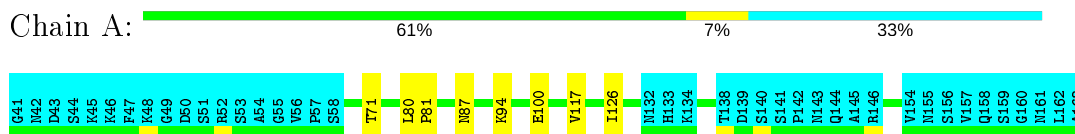


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

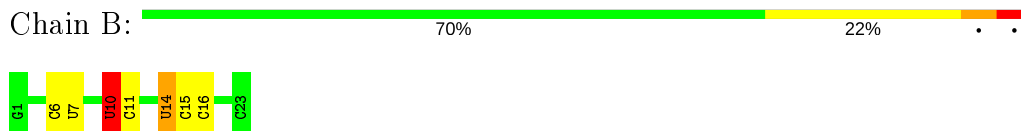


4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Polypyrimidine tract-binding protein 1

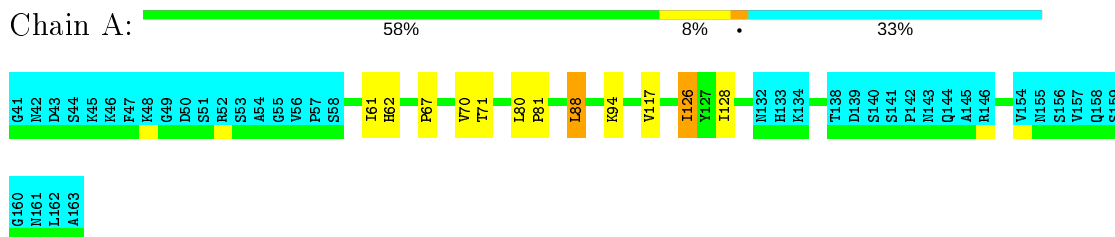


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

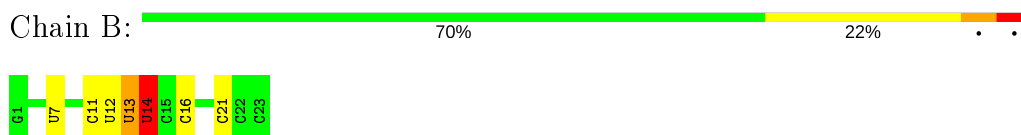


4.2.7 Score per residue for model 7

- Molecule 1: Polypyrimidine tract-binding protein 1

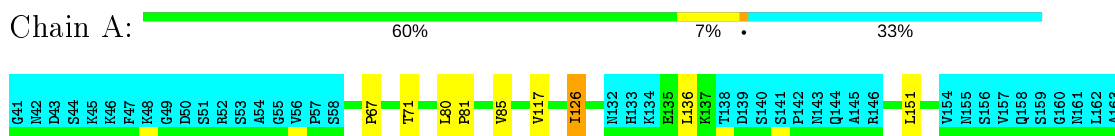


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')



4.2.8 Score per residue for model 8

- Molecule 1: Polypyrimidine tract-binding protein 1



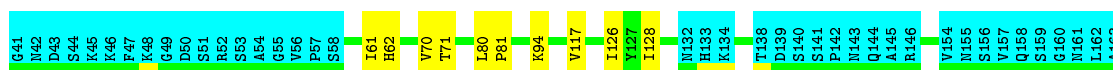
- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')



4.2.9 Score per residue for model 9

- Molecule 1: Polypyrimidine tract-binding protein 1

Chain A: 



- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

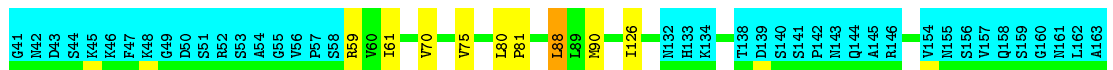
Chain B: 




4.2.10 Score per residue for model 10

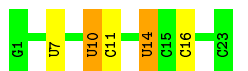
- Molecule 1: Polypyrimidine tract-binding protein 1

Chain A: 



- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

Chain B: 



4.2.11 Score per residue for model 11

- Molecule 1: Polypyrimidine tract-binding protein 1

Chain A: 



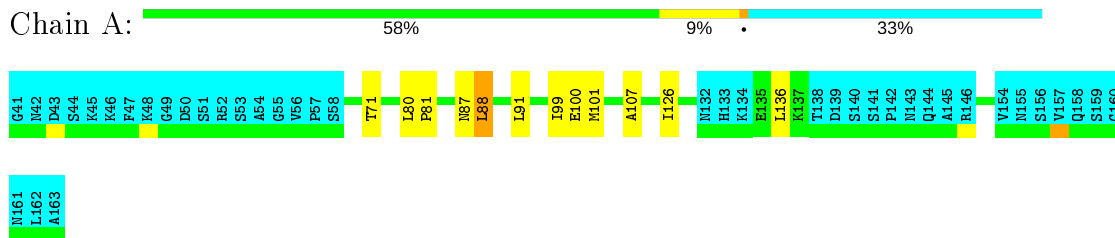
- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

Chain B: 

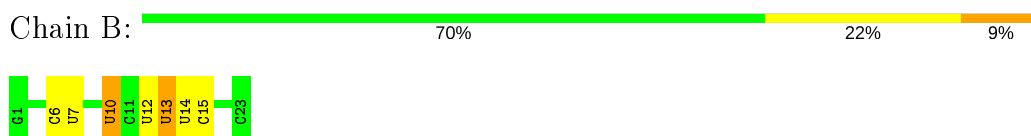


4.2.12 Score per residue for model 12

- Molecule 1: Polypyrimidine tract-binding protein 1

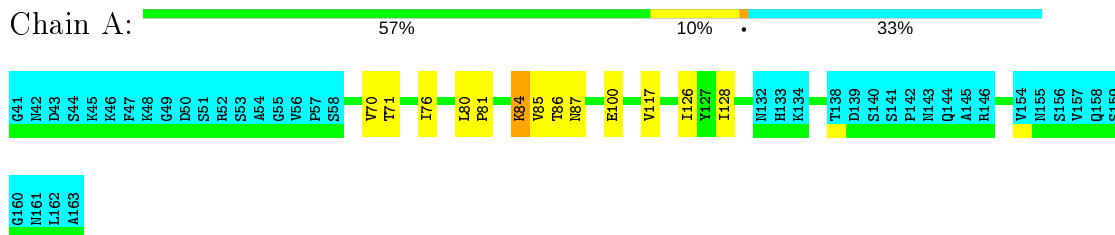


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

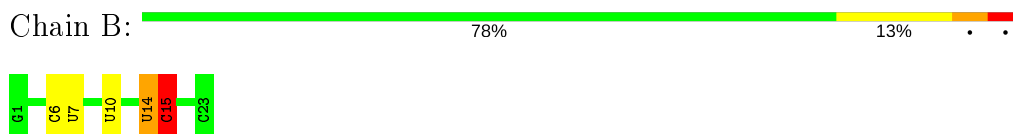


4.2.13 Score per residue for model 13

- Molecule 1: Polypyrimidine tract-binding protein 1

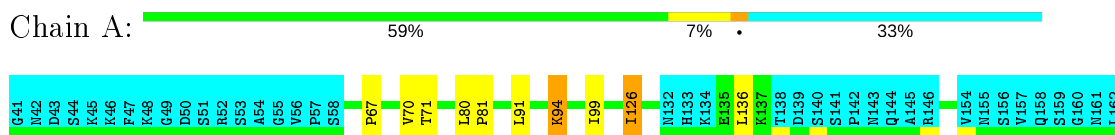


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')



4.2.14 Score per residue for model 14

- Molecule 1: Polypyrimidine tract-binding protein 1



A163

- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

Chain B:  70% 13% 17%

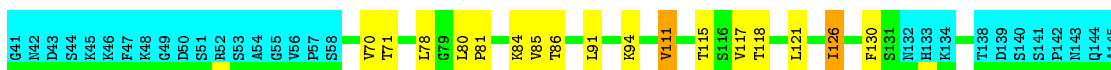


G1 C6 U7 U10 C11 U12 U13 U14 C15 C23

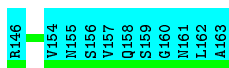
4.2.15 Score per residue for model 15

- Molecule 1: Polypyrimidine tract-binding protein 1

Chain A:  54% 12% 33%



G41 M42 D43 S44 K45 K46 F47 K48 G49 D50 S51 S52 S53 A54 G55 V56 P57 S58 V70 T71 L78 G79 L80 P81 K84 V85 T86 L91 K94 V111 T115 S116 V117 T118 L121 I126 F130 M132 H133 K134 T138 D139 S140 P142 M143 Q144 A145 I146 V154 M155 S156 V157 Q158 S159 G160 M161 L162 D138 S140 S141 P142 M143 Q144 A145



R146 V154 M155 S156 V157 Q158 S159 G160 M161 L162 A163

- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

Chain B:  65% 26% 9%



G1 C6 U7 U10 C11 U12 U13 U14 C15 C16 U20 C23

4.2.16 Score per residue for model 16

- Molecule 1: Polypyrimidine tract-binding protein 1

Chain A:  61% 7% 33%



G41 M42 D43 S44 K45 K46 F47 K48 G49 D50 S51 S52 S53 A54 G55 V56 P57 S58 I61 V70 T71 L80 P81 K94 V117 I126 M132 H133 K134 T138 D139 S140 P142 M143 Q144 A145 M146 V154 M155 S156 V157 Q158 S159 G160 M161 L162 A163

- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

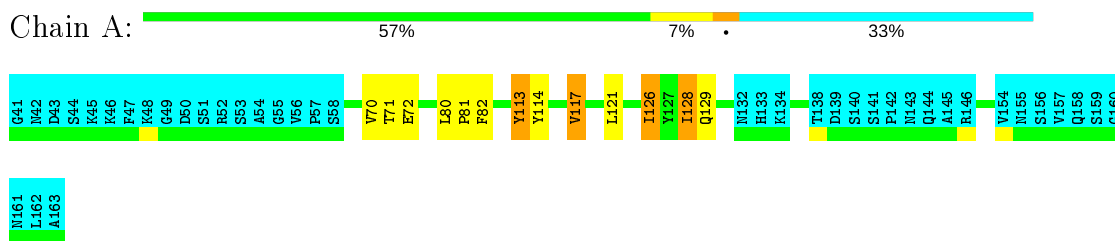
Chain B:  65% 17% 17%



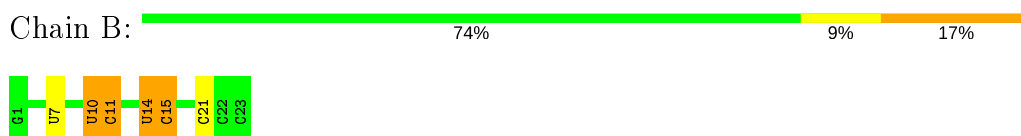
G1 C6 U7 U10 C11 U12 U13 U14 C15 C21 C22 C23

4.2.17 Score per residue for model 17

- Molecule 1: Polypyrimidine tract-binding protein 1

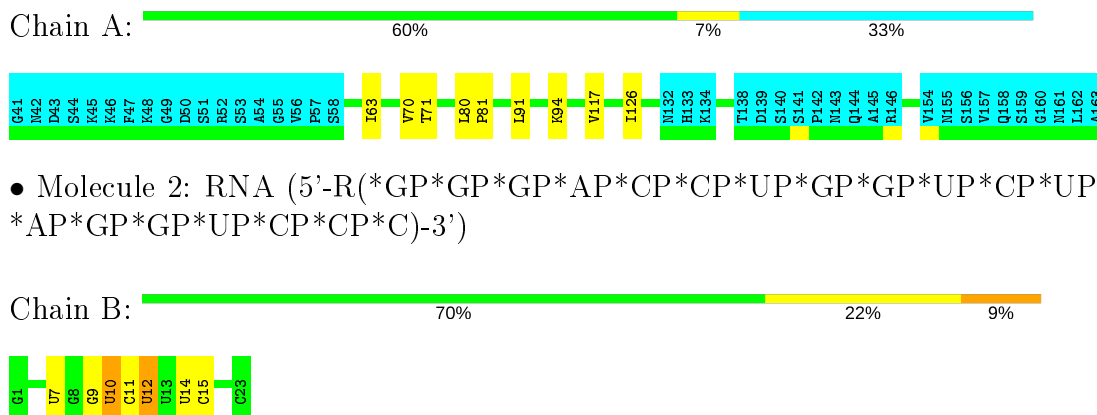


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

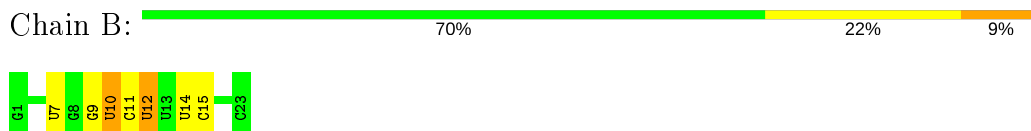


4.2.18 Score per residue for model 18

- Molecule 1: Polypyrimidine tract-binding protein 1

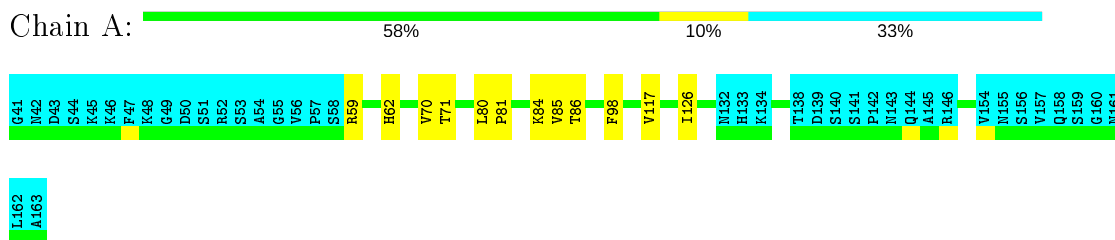


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

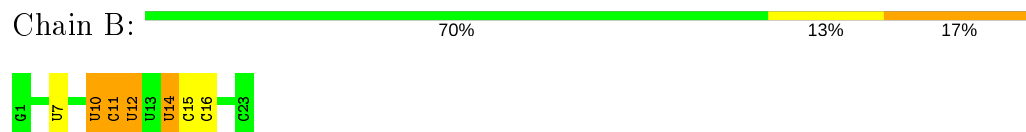


4.2.19 Score per residue for model 19

- Molecule 1: Polypyrimidine tract-binding protein 1

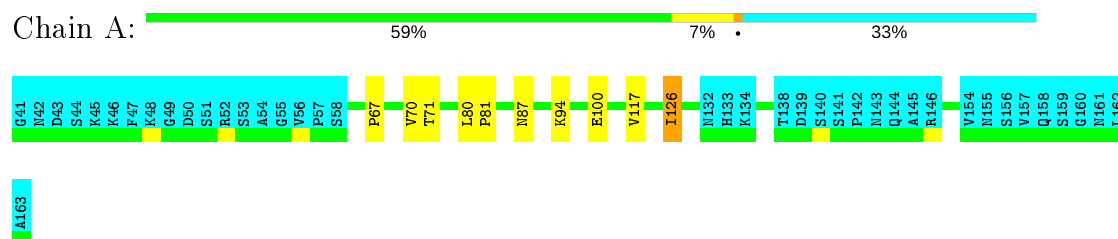


- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')

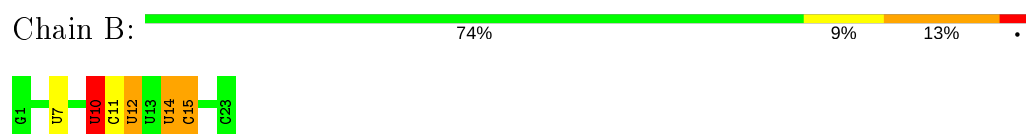


4.2.20 Score per residue for model 20

- Molecule 1: Polypyrimidine tract-binding protein 1



- Molecule 2: RNA (5'-R(*GP*GP*GP*AP*CP*CP*UP*GP*GP*UP*CP*UP*UP*UP*CP*CP*AP*GP*GP*UP*CP*CP*C)-3')



5 Refinement protocol and experimental data overview (i)

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

Of the 250 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 calculation	3.0
AMBER	refinement	12

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	2
Total number of shifts	1667
Number of shifts mapped to atoms	1667
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	79%

No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 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	648	676	676	3±1
2	B	482	247	249	1±1
All	All	22600	18460	18500	69

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 2.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:94:LYS:HE2	2:B:14:U:C6	0.55	2.37	9	3
1:A:94:LYS:HE3	2:B:13:U:C5'	0.53	2.33	4	1
2:B:14:U:C5	2:B:15:C:C5	0.53	2.97	17	5
1:A:82:PHE:CZ	1:A:113:TYR:CD2	0.52	2.96	17	1
1:A:113:TYR:CZ	1:A:117:VAL:HG21	0.52	2.38	17	1
1:A:113:TYR:CE1	1:A:117:VAL:HG21	0.52	2.39	17	1
1:A:80:LEU:N	1:A:81:PRO:HD2	0.52	2.20	11	20
1:A:121:LEU:HD13	1:A:126:ILE:CD1	0.52	2.34	15	2
1:A:111:VAL:HG21	1:A:130:PHE:CE2	0.50	2.41	15	1
1:A:94:LYS:HE2	2:B:14:U:C5	0.50	2.41	6	1
1:A:91:LEU:HD13	1:A:94:LYS:CE	0.46	2.41	18	1
1:A:91:LEU:CD2	1:A:94:LYS:HE2	0.46	2.40	15	1
1:A:101:MET:SD	1:A:107:ALA:HA	0.46	2.50	12	1
1:A:75:VAL:HG21	1:A:90:MET:SD	0.46	2.51	10	1
1:A:67:PRO:HD3	1:A:126:ILE:HG21	0.45	1.89	20	5
1:A:91:LEU:HD23	1:A:94:LYS:CE	0.45	2.41	14	1
1:A:94:LYS:HE2	2:B:14:U:C2	0.44	2.47	7	1
1:A:94:LYS:CB	2:B:14:U:C5	0.44	3.00	4	1
1:A:88:LEU:C	1:A:88:LEU:HD13	0.44	2.32	10	1
2:B:22:C:H2'	2:B:23:C:H5''	0.44	1.90	8	1
1:A:88:LEU:HD13	1:A:88:LEU:C	0.42	2.34	7	2
1:A:87:ASN:HB2	1:A:100:GLU:HB3	0.42	1.91	6	6
1:A:62:HIS:CD2	1:A:98:PHE:CZ	0.42	3.07	19	1
1:A:91:LEU:HD23	1:A:94:LYS:HE2	0.42	1.89	14	2
1:A:94:LYS:HD3	2:B:14:U:C6	0.42	2.50	16	1
1:A:111:VAL:O	1:A:115:THR:N	0.41	2.54	15	3
1:A:84:LYS:HA	1:A:84:LYS:HE3	0.41	1.92	13	1
1:A:114:TYR:HB3	1:A:128:ILE:CG2	0.41	2.46	17	1
1:A:80:LEU:N	1:A:81:PRO:CD	0.41	2.83	11	1
1:A:78:LEU:CD2	1:A:121:LEU:HD11	0.41	2.46	15	1

5.2 Torsion angles [i](#)

5.2.1 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	83/123 (67%)	80±1 (96±2%)	3±1 (4±2%)	0±0 (0±0%)	54 85
All	All	1660/2460 (67%)	1596 (96%)	63 (4%)	1 (0%)	54 85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	135	GLU	1

5.2.2 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	71/104 (68%)	65±2 (91±2%)	6±2 (9±2%)	13 60
All	All	1420/2080 (68%)	1293 (91%)	127 (9%)	13 60

All 26 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	126	ILE	20
1	A	71	THR	18
1	A	117	VAL	15
1	A	70	VAL	14
1	A	84	LYS	6
1	A	85	VAL	6
1	A	86	THR	6
1	A	128	ILE	5
1	A	61	ILE	5
1	A	136	LEU	5
1	A	88	LEU	4
1	A	62	HIS	3
1	A	59	ARG	3
1	A	90	MET	2
1	A	129	GLN	2
1	A	91	LEU	2
1	A	99	ILE	2
1	A	111	VAL	1

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Mol	Chain	Res	Type	Models (Total)
1	A	80	LEU	1
1	A	72	GLU	1
1	A	68	ILE	1
1	A	63	ILE	1
1	A	94	LYS	1
1	A	118	THR	1
1	A	76	ILE	1
1	A	151	LEU	1

5.2.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	22/23 (96%)	3±1 (16±4%)	1±1 (6±5%)	0.65±0.03
All	All	440/460 (96%)	69 (16%)	27 (6%)	0.65

The overall RNA backbone suiteness is 0.65.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	14	U	20
2	B	11	C	17
2	B	12	U	14
2	B	15	C	13
2	B	13	U	3
2	B	9	G	1
2	B	23	C	1

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	10	U	13
2	B	11	C	11
2	B	12	U	3

5.3 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.5 Ligand geometry [i](#)

There are no ligands in this entry.

5.6 Other polymers [i](#)

There are no such molecules in this entry.

5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 79% for the well-defined parts and 78% for the entire structure.

6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *RNA-chemical-shifts*

6.1.1 Bookkeeping [i](#)

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	327
Number of shifts mapped to atoms	327
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

6.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

6.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 22%, i.e. 317 atoms were assigned a chemical shift out of a possible 1461. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/407 (0%)	0/162 (0%)	0/166 (0%)	0/79 (0%)
Sidechain	0/564 (0%)	0/328 (0%)	0/212 (0%)	0/24 (0%)
Aromatic	0/58 (0%)	0/31 (0%)	0/26 (0%)	0/1 (0%)
Overall	317/1461 (22%)	170/769 (22%)	147/558 (26%)	0/134 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 17%, i.e. 317 atoms were assigned a chemical shift out of a possible 1913. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	0/603 (0%)	0/240 (0%)	0/246 (0%)	0/117 (0%)
Sidechain	0/804 (0%)	0/471 (0%)	0/292 (0%)	0/41 (0%)
Aromatic	0/74 (0%)	0/40 (0%)	0/32 (0%)	0/2 (0%)
Overall	317/1913 (17%)	170/999 (17%)	147/724 (20%)	0/190 (0%)

6.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

6.1.5 Random Coil Index (RCI) plots [i](#)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (RNA-chemical-shifts). RCI is only applicable to proteins.

6.2 Chemical shift list 2

File name: input_cs.cif

Chemical shift list name: *protein-chemical-shifts*

6.2.1 Bookkeeping [i](#)

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	1340
Number of shifts mapped to atoms	1340
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

6.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
¹³ C _{α}	112	-0.17 \pm 0.23	None needed (< 0.5 ppm)
¹³ C _{β}	110	-0.11 \pm 0.10	None needed (< 0.5 ppm)
¹³ C'	0	—	None (insufficient data)
¹⁵ N	109	0.53 \pm 0.45	None needed (imprecise)

6.2.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 57%, i.e. 838 atoms were assigned a chemical shift out of a possible 1461. 16 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	318/407 (78%)	161/162 (99%)	79/166 (48%)	78/79 (99%)
Sidechain	479/564 (85%)	292/328 (89%)	180/212 (85%)	7/24 (29%)
Aromatic	41/58 (71%)	28/31 (90%)	13/26 (50%)	0/1 (0%)
Overall	838/1461 (57%)	481/769 (63%)	272/558 (49%)	85/134 (63%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 61%, i.e. 1171 atoms were assigned a chemical shift out of a possible 1913. 19 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	455/603 (75%)	234/240 (98%)	112/246 (46%)	109/117 (93%)
Sidechain	664/804 (83%)	411/471 (87%)	243/292 (83%)	10/41 (24%)
Aromatic	52/74 (70%)	35/40 (88%)	17/32 (53%)	0/2 (0%)
Overall	1171/1913 (61%)	680/999 (68%)	372/724 (51%)	119/190 (63%)

6.2.4 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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	81	PRO	HB2	-0.00	3.82 – 0.32	-5.9

6.2.5 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.

Random coil index (RCI) for chain A:

