



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 09:02 pm GMT

PDB ID : 2ADC  
Title : Solution structure of Polypyrimidine Tract Binding protein RBD34 complexed with CUCUCU RNA  
Authors : Oberstrass, F.C.; Auweter, S.D.; Erat, M.; Hargous, Y.; Henning, A.; Wenter, P.; Reymond, L.; Pitsch, S.; Black, D.L.; Allain, F.H.T.  
Deposited on : 2005-07-20

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : trunk28760  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

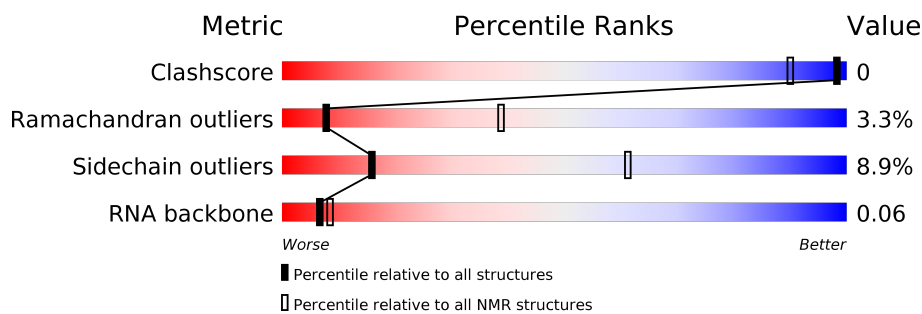
# 1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367
RNA backbone	3398	623

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  $\geq 3$ , 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	6	50% 50%
1	C	6	67% 17% 17%
2	A	229	72% 7% 12% 9%

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 11 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:336-A:417, A:426-A:438, A:446-A:531 (181)	0.69	11

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3623 atoms, of which 1771 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms						Trace
1	B	6	Total	C	H	N	O	P	0
			182	54	65	15	43	5	
1	C	6	Total	C	H	N	O	P	0
			182	54	65	15	43	5	

- Molecule 2 is a protein called Polypyrimidine tract-binding protein 1.

Mol	Chain	Residues	Atoms						Trace
2	A	208	Total	C	H	N	O	S	0
			3259	1023	1641	296	295	4	

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	303	MET	-	EXPRESSION TAG	UNP P26599
A	304	GLY	-	EXPRESSION TAG	UNP P26599
A	305	SER	-	EXPRESSION TAG	UNP P26599
A	306	SER	-	EXPRESSION TAG	UNP P26599
A	307	HIS	-	EXPRESSION TAG	UNP P26599
A	308	HIS	-	EXPRESSION TAG	UNP P26599
A	309	HIS	-	EXPRESSION TAG	UNP P26599
A	310	HIS	-	EXPRESSION TAG	UNP P26599
A	311	HIS	-	EXPRESSION TAG	UNP P26599
A	312	HIS	-	EXPRESSION TAG	UNP P26599
A	313	SER	-	EXPRESSION TAG	UNP P26599
A	314	SER	-	EXPRESSION TAG	UNP P26599
A	315	GLY	-	EXPRESSION TAG	UNP P26599
A	316	LEU	-	EXPRESSION TAG	UNP P26599
A	317	VAL	-	EXPRESSION TAG	UNP P26599
A	318	PRO	-	EXPRESSION TAG	UNP P26599
A	319	ARG	-	EXPRESSION TAG	UNP P26599
A	320	GLY	-	EXPRESSION TAG	UNP P26599
A	321	SER	-	EXPRESSION TAG	UNP P26599
A	322	HIS	-	EXPRESSION TAG	UNP P26599
A	323	MET	-	EXPRESSION TAG	UNP P26599

## 4 Residue-property plots [i](#)

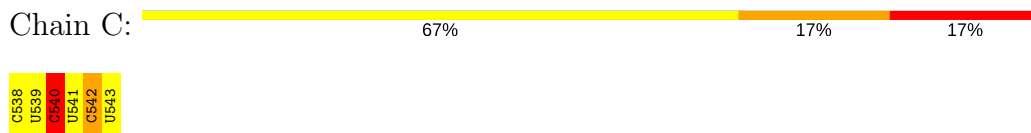
### 4.1 Average score per residue in the NMR ensemble

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.

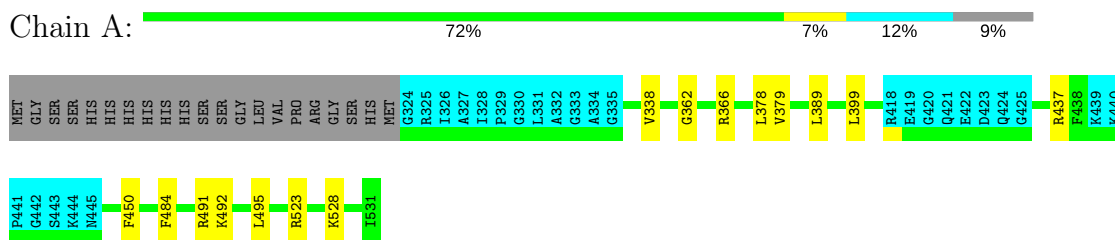
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 2: Polypyrimidine tract-binding protein 1



### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

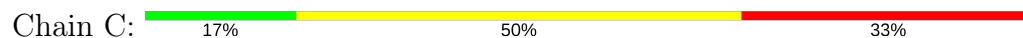
#### 4.2.1 Score per residue for model 1

- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

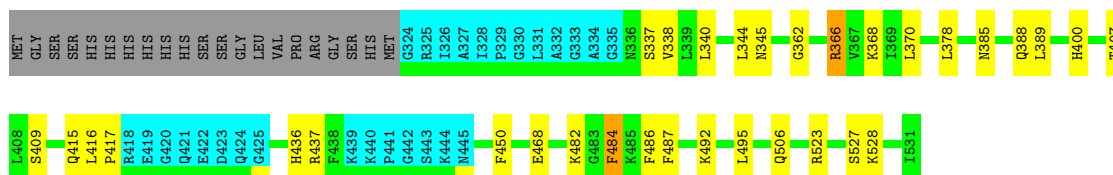




- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 2: Polypyrimidine tract-binding protein 1



#### 4.2.2 Score per residue for model 2

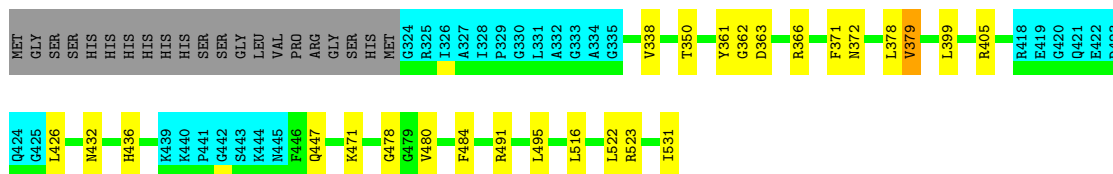
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 2: Polypyrimidine tract-binding protein 1



### 4.2.3 Score per residue for model 3

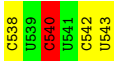
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain B: 



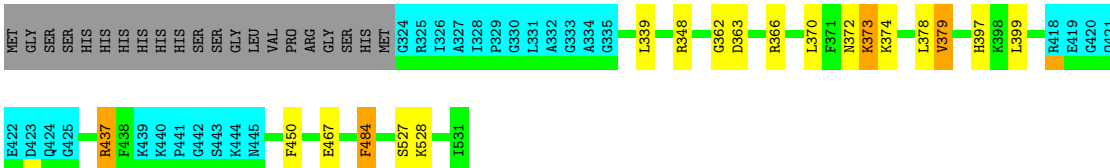
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain C: 



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A: 



### 4.2.4 Score per residue for model 4

- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain B: 



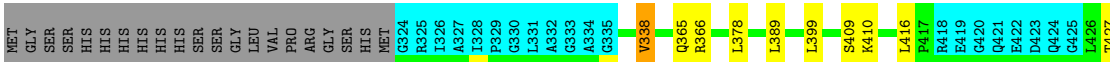
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain C: 



- Molecule 2: Polypyrimidine tract-binding protein 1

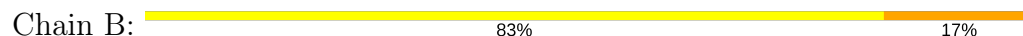
Chain A: 





#### 4.2.5 Score per residue for model 5

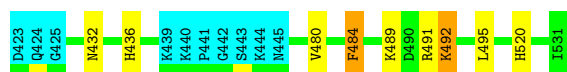
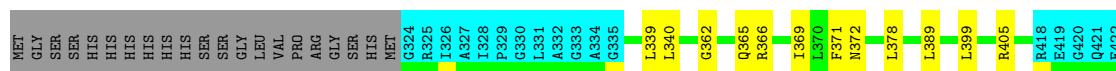
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

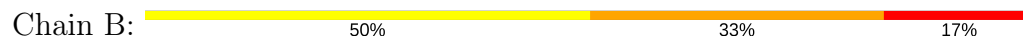


- Molecule 2: Polypyrimidine tract-binding protein 1

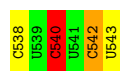


#### 4.2.6 Score per residue for model 6

- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



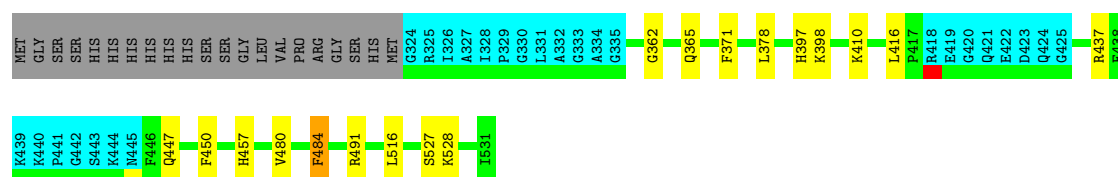
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 2: Polypyrimidine tract-binding protein 1

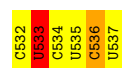




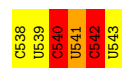


#### 4.2.7 Score per residue for model 7

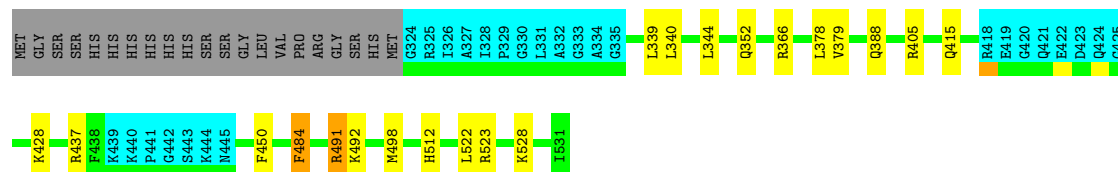
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 2: Polypyrimidine tract-binding protein 1

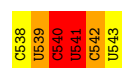


#### 4.2.8 Score per residue for model 8

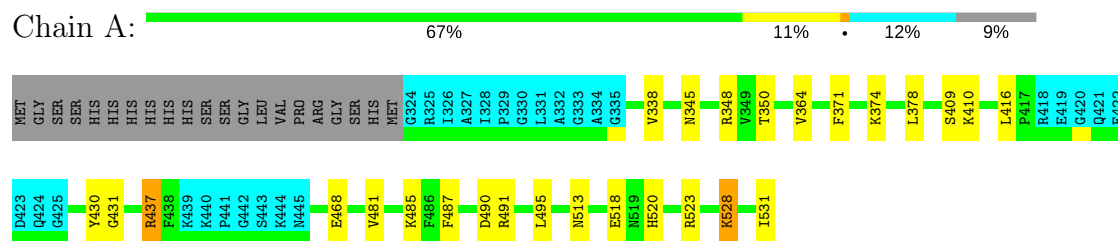
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

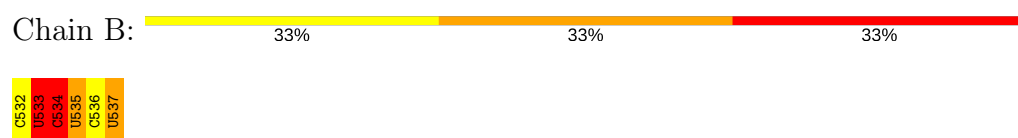


- Molecule 2: Polypyrimidine tract-binding protein 1



#### 4.2.9 Score per residue for model 9

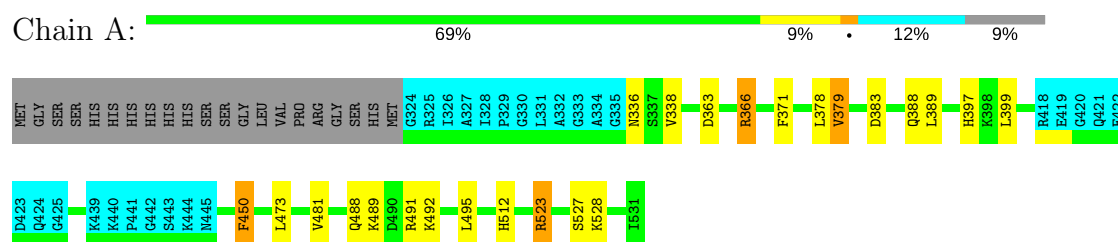
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

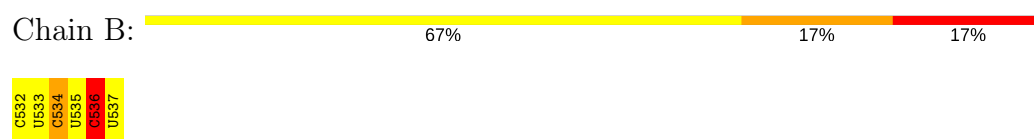


- Molecule 2: Polypyrimidine tract-binding protein 1



#### 4.2.10 Score per residue for model 10

- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

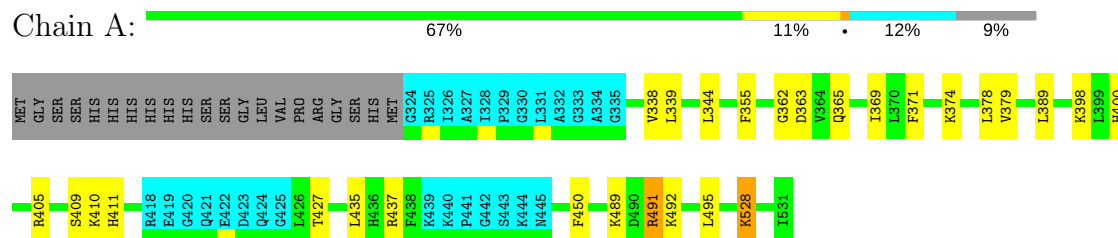


- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



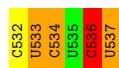


• Molecule 2: Polypyrimidine tract-binding protein 1



#### 4.2.11 Score per residue for model 11 (medoid)

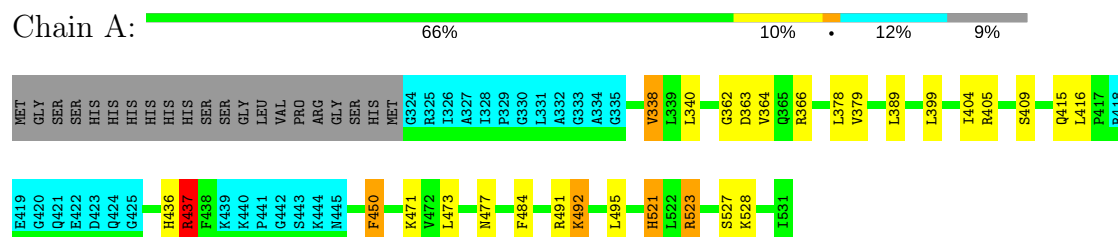
• Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



• Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



• Molecule 2: Polypyrimidine tract-binding protein 1




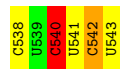
#### 4.2.12 Score per residue for model 12

• Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



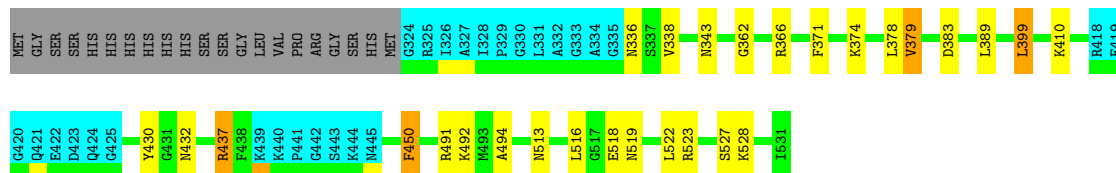
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain C: 



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A: 




#### 4.2.13 Score per residue for model 13

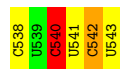
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain B: 



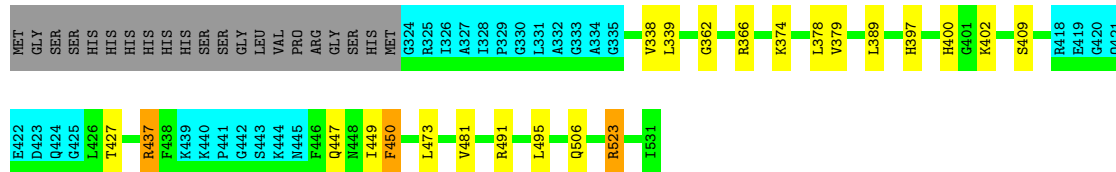
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain C: 



- Molecule 2: Polypyrimidine tract-binding protein 1

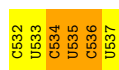
Chain A: 



#### 4.2.14 Score per residue for model 14

- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

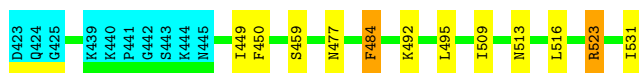
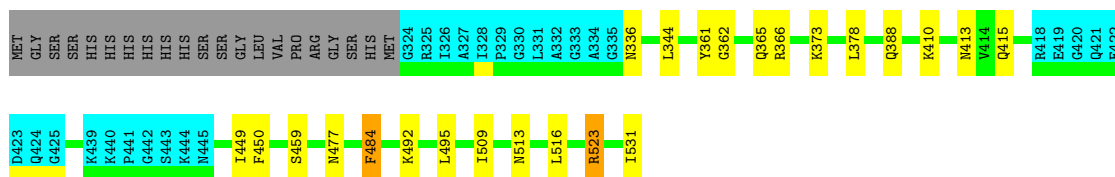
Chain B: 



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 2: Polypyrimidine tract-binding protein 1

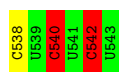


#### 4.2.15 Score per residue for model 15

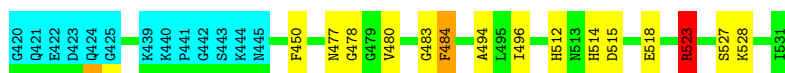
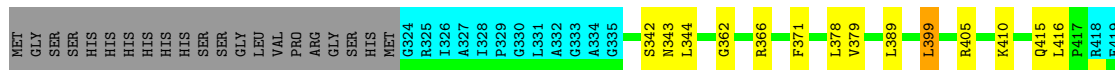
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



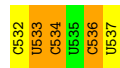
- Molecule 2: Polypyrimidine tract-binding protein 1



#### 4.2.16 Score per residue for model 16

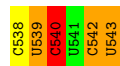
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain B:  17% 33% 50%



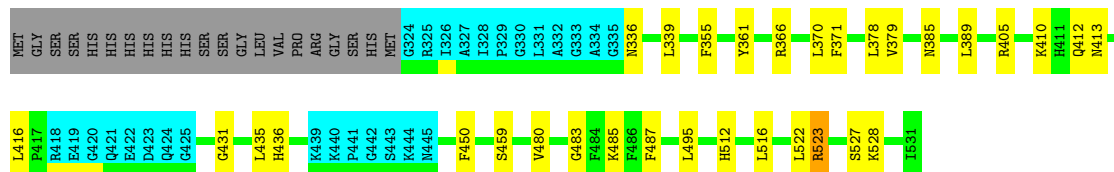
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain C:  17% 17% 50% 17%



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A:  65% 14% 12% 9%



#### 4.2.17 Score per residue for model 17

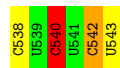
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain B:  17% 33% 33% 17%



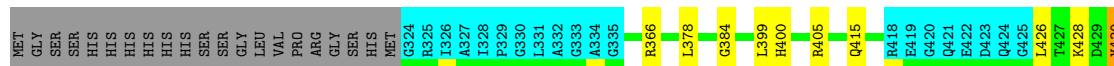
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain C:  33% 33% 17% 17%



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A:  69% 8% 12% 9%



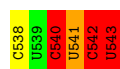
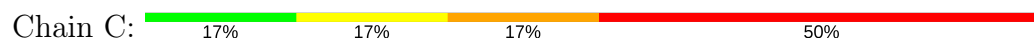


#### 4.2.18 Score per residue for model 18

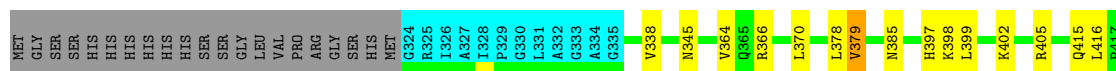
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

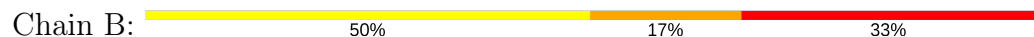


- Molecule 2: Polypyrimidine tract-binding protein 1



#### 4.2.19 Score per residue for model 19

- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

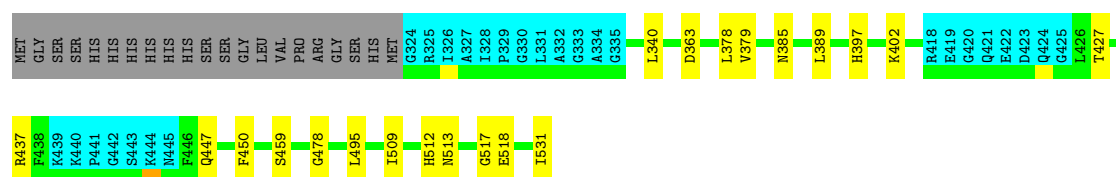


- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'



- Molecule 2: Polypyrimidine tract-binding protein 1





#### 4.2.20 Score per residue for model 20

- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain B: 33% 67%



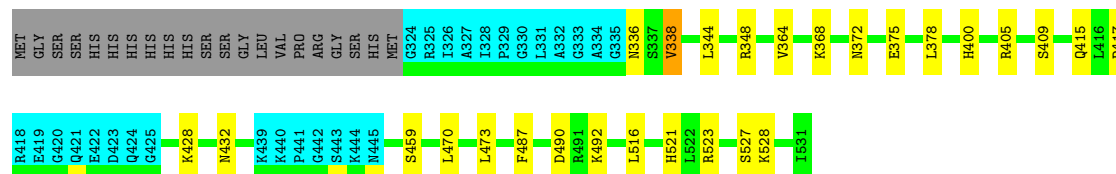
- Molecule 1: 5'-R(\*CP\*UP\*CP\*UP\*CP\*U)-3'

Chain C: 50% 17% 33%



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A: 67% 11% 12% 9%





## 5 Refinement protocol and experimental data overview ⓘ

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

Of the 40 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
DYANA	structure solution	3.02
AMBER	refinement	7

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	1.38±0.03	0±0/128 (0.0±0.0%)	2.16±0.06	7±1/196 (3.6±0.6%)
1	C	1.35±0.03	0±0/128 (0.0±0.0%)	2.21±0.08	8±2/196 (3.8±1.0%)
2	A	0.67±0.00	0±0/1461 (0.0±0.0%)	1.05±0.02	4±2/1972 (0.2±0.1%)
All	All	0.81	0/34340 (0.0%)	1.31	360/47280 (0.8%)

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	B	0.0±0.0	1.4±1.1
1	C	0.0±0.0	1.5±0.6
2	A	0.0±0.0	3.0±1.6
All	All	0	118

There are no bond-length outliers.

All 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(°)	Ideal(°)	Models	
								Worst	Total
1	B	533	U	O4'-C1'-N1	10.64	116.71	108.20	12	14
1	C	538	C	O4'-C1'-N1	8.64	115.11	108.20	11	8
2	A	491	ARG	NE-CZ-NH1	8.51	124.56	120.30	18	9
1	B	536	C	C3'-C2'-C1'	8.30	108.14	101.50	7	16
1	C	538	C	N3-C2-O2	-7.77	116.46	121.90	3	20
1	C	540	C	C3'-C2'-C1'	7.59	107.57	101.50	7	7
2	A	523	ARG	NE-CZ-NH1	7.42	124.01	120.30	9	11
1	C	542	C	N3-C2-O2	-7.35	116.75	121.90	3	20
1	B	532	C	N3-C2-O2	-7.29	116.80	121.90	13	20
1	C	541	U	O4'-C1'-N1	7.23	113.98	108.20	8	10
2	A	405	ARG	NE-CZ-NH1	7.14	123.87	120.30	5	10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	C	540	C	N3-C2-O2	-7.13	116.91	121.90	11	19
1	C	538	C	N1-C2-O2	7.04	123.12	118.90	11	15
1	B	534	C	N3-C2-O2	-6.96	117.03	121.90	10	20
1	B	532	C	O4'-C1'-N1	6.95	113.76	108.20	6	4
1	B	532	C	N1-C2-O2	6.87	123.02	118.90	13	15
1	C	540	C	C6-N1-C2	-6.86	117.56	120.30	7	9
1	B	533	U	N3-C2-O2	-6.85	117.40	122.20	12	10
2	A	366	ARG	NE-CZ-NH1	6.54	123.57	120.30	4	14
1	B	534	C	O4'-C1'-N1	6.50	113.40	108.20	2	7
2	A	437	ARG	NE-CZ-NH1	6.37	123.48	120.30	8	11
1	C	541	U	N1-C2-N3	6.21	118.62	114.90	14	2
1	B	536	C	N1-C1'-C2'	-6.13	105.26	112.00	11	3
1	C	543	U	N3-C2-O2	-6.12	117.92	122.20	18	3
1	B	536	C	N3-C2-O2	-6.09	117.64	121.90	13	15
1	C	543	U	O4'-C1'-N1	6.09	113.07	108.20	20	7
1	B	536	C	N1-C2-O2	6.06	122.54	118.90	19	4
2	A	487	PHE	CB-CG-CD2	-6.02	116.59	120.80	1	1
1	C	540	C	O4'-C1'-N1	5.98	112.98	108.20	19	3
1	B	536	C	P-O3'-C3'	5.93	126.82	119.70	4	3
2	A	348	ARG	NE-CZ-NH1	5.78	123.19	120.30	8	3
2	A	483	GLY	C-N-CA	5.76	136.11	121.70	15	1
2	A	484	PHE	CB-CG-CD2	-5.60	116.88	120.80	15	1
2	A	366	ARG	NE-CZ-NH2	-5.58	117.51	120.30	17	3
1	B	533	U	P-O3'-C3'	5.49	126.28	119.70	15	1
2	A	379	VAL	CA-CB-CG1	5.48	119.11	110.90	9	5
1	C	539	U	O4'-C4'-C3'	5.43	110.44	106.10	7	4
1	C	540	C	C5'-C4'-O4'	5.35	115.52	109.10	7	4
1	C	542	C	N1-C2-O2	5.33	122.10	118.90	9	14
2	A	487	PHE	CB-CG-CD1	5.33	124.53	120.80	1	1
1	B	535	U	N3-C2-O2	-5.31	118.48	122.20	7	3
1	B	537	U	O4'-C1'-N1	5.26	112.41	108.20	19	1
1	C	539	U	C5-C6-N1	-5.26	120.07	122.70	16	1
1	C	539	U	C5'-C4'-C3'	-5.22	107.65	116.00	19	1
1	B	537	U	N3-C2-O2	-5.22	118.55	122.20	15	1
1	C	540	C	N1-C2-O2	5.17	122.00	118.90	15	2
1	B	534	C	N1-C2-O2	5.16	122.00	118.90	2	3
1	C	538	C	N3-C4-C5	5.03	123.91	121.90	12	1

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)
1	C	540	C	Sidechain	20
2	A	450	PHE	Sidechain	12
2	A	527	SER	Peptide	10
2	A	492	LYS	Peptide	9
1	B	536	C	Sidechain	8
1	B	537	U	Sidechain	6
1	B	534	C	Sidechain	5
1	B	535	U	Sidechain	5
1	C	542	C	Sidechain	4
1	B	533	U	Sidechain	4
2	A	361	TYR	Sidechain	3
2	A	449	ILE	Peptide	3
2	A	478	GLY	Peptide	3
1	C	541	U	Sidechain	2
1	C	539	U	Sidechain	2
1	C	543	U	Sidechain	2
2	A	494	ALA	Peptide	2
2	A	521	HIS	Sidechain,Peptide	2
2	A	523	ARG	Sidechain	2
2	A	370	LEU	Peptide	1
2	A	415	GLN	Peptide	1
2	A	437	ARG	Sidechain	1
2	A	525	SER	Peptide	1
2	A	428	LYS	Peptide	1
2	A	434	PRO	Peptide	1
2	A	485	LYS	Peptide	1
2	A	430	TYR	Sidechain	1
2	A	399	LEU	Peptide	1
2	A	520	HIS	Peptide	1
2	A	483	GLY	Peptide	1
2	A	489	LYS	Peptide	1
2	A	369	ILE	Peptide	1
2	A	522	LEU	Peptide	1

## 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	117	65	65	0±0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	C	117	65	65	0±1
2	A	1430	1450	1450	1±1
All	All	33280	31600	31600	17

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:540:C:C5	2:A:340:LEU:HD22	0.74	2.18	7	2
2:A:338:VAL:HG23	2:A:409:SER:HB2	0.53	1.79	10	4
1:B:536:C:H2'	2:A:528:LYS:HE3	0.48	1.85	10	1
1:C:540:C:C4	2:A:340:LEU:HD22	0.46	2.46	19	1
1:B:536:C:N4	2:A:450:PHE:CE1	0.45	2.84	13	2
2:A:338:VAL:HG23	2:A:409:SER:HB3	0.44	1.88	8	3
2:A:338:VAL:HG21	2:A:411:HIS:HB2	0.44	1.88	10	1
1:C:540:C:N1	2:A:340:LEU:HD13	0.42	2.29	19	1
1:B:536:C:C6	2:A:528:LYS:HE3	0.42	2.49	8	1
1:B:536:C:C2	2:A:457:HIS:CD2	0.40	3.10	6	1

## 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	
2	A	180/229 (79%)	152±4 (84±2%)	22±3 (12±2%)	6±1 (3±1%)	8	39
All	All	3600/4580 (79%)	3039 (84%)	441 (12%)	120 (3%)	8	39

All 42 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	528	LYS	13
2	A	362	GLY	11

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Mol	Chain	Res	Type	Models (Total)
2	A	371	PHE	7
2	A	484	PHE	7
2	A	450	PHE	5
2	A	480	VAL	5
2	A	416	LEU	4
2	A	363	ASP	4
2	A	513	ASN	4
2	A	436	HIS	4
2	A	481	VAL	4
2	A	491	ARG	3
2	A	364	VAL	3
2	A	400	HIS	3
2	A	490	ASP	3
2	A	512	HIS	3
2	A	336	ASN	3
2	A	430	TYR	2
2	A	417	PRO	2
2	A	426	LEU	2
2	A	399	LEU	2
2	A	372	ASN	2
2	A	518	GLU	2
2	A	517	GLY	2
2	A	374	LYS	2
2	A	431	GLY	2
2	A	493	MET	1
2	A	454	ALA	1
2	A	452	PRO	1
2	A	432	ASN	1
2	A	375	GLU	1
2	A	384	GLY	1
2	A	373	LYS	1
2	A	461	ILE	1
2	A	489	LYS	1
2	A	514	HIS	1
2	A	413	ASN	1
2	A	398	LYS	1
2	A	515	ASP	1
2	A	437	ARG	1
2	A	404	ILE	1
2	A	337	SER	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	
2	A	162/197 (82%)	148±3 (91±2%)	14±3 (9±2%)	16	61
All	All	3240/3940 (82%)	2952 (91%)	288 (9%)	16	61

All 81 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	378	LEU	20
2	A	495	LEU	13
2	A	379	VAL	12
2	A	389	LEU	11
2	A	523	ARG	10
2	A	399	LEU	9
2	A	410	LYS	8
2	A	484	PHE	8
2	A	338	VAL	7
2	A	415	GLN	7
2	A	437	ARG	7
2	A	516	LEU	6
2	A	522	LEU	6
2	A	397	HIS	6
2	A	344	LEU	6
2	A	339	LEU	6
2	A	491	ARG	5
2	A	365	GLN	5
2	A	531	ILE	5
2	A	416	LEU	4
2	A	473	LEU	4
2	A	432	ASN	4
2	A	388	GLN	4
2	A	427	THR	4
2	A	385	ASN	4
2	A	447	GLN	4
2	A	459	SER	4
2	A	487	PHE	3
2	A	340	LEU	3

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Mol	Chain	Res	Type	Models (Total)
2	A	492	LYS	3
2	A	477	ASN	3
2	A	345	ASN	3
2	A	370	LEU	3
2	A	436	HIS	3
2	A	509	ILE	3
2	A	402	LYS	3
2	A	374	LYS	3
2	A	518	GLU	3
2	A	521	HIS	2
2	A	366	ARG	2
2	A	371	PHE	2
2	A	471	LYS	2
2	A	398	LYS	2
2	A	355	PHE	2
2	A	488	GLN	2
2	A	350	THR	2
2	A	512	HIS	2
2	A	383	ASP	2
2	A	373	LYS	2
2	A	486	PHE	2
2	A	343	ASN	2
2	A	363	ASP	2
2	A	506	GLN	2
2	A	428	LYS	2
2	A	372	ASN	2
2	A	435	LEU	2
2	A	468	GLU	2
2	A	336	ASN	2
2	A	368	LYS	2
2	A	400	HIS	2
2	A	519	ASN	2
2	A	482	LYS	1
2	A	430	TYR	1
2	A	412	GLN	1
2	A	369	ILE	1
2	A	528	LYS	1
2	A	364	VAL	1
2	A	489	LYS	1
2	A	514	HIS	1
2	A	513	ASN	1
2	A	520	HIS	1

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Mol	Chain	Res	Type	Models (Total)
2	A	498	MET	1
2	A	413	ASN	1
2	A	485	LYS	1
2	A	470	LEU	1
2	A	407	THR	1
2	A	352	GLN	1
2	A	342	SER	1
2	A	525	SER	1
2	A	496	ILE	1
2	A	467	GLU	1

### 6.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	5/6 (83%)	4±1 (73±16%)	0±0 (0±0%)	0.08±0.06
1	C	5/6 (83%)	4±1 (75±24%)	0±0 (0±0%)	0.04±0.06
All	All	200/240 (83%)	148 (74%)	0 (0%)	0.06

The overall RNA backbone suiteness is 0.06.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	C	540	C	20
1	B	537	U	19
1	C	542	C	18
1	B	534	C	16
1	B	536	C	15
1	C	541	U	13
1	C	543	U	13
1	B	533	U	13
1	C	539	U	11
1	B	535	U	10

There are no RNA pucker outliers to report.

## 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 [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

No chemical shift data were provided