



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 08:14 PM UTC

PDB ID : 2ADB / pdb_00002adb
Title : Solution structure of Polypyrimidine Tract Binding protein RBD2 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

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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

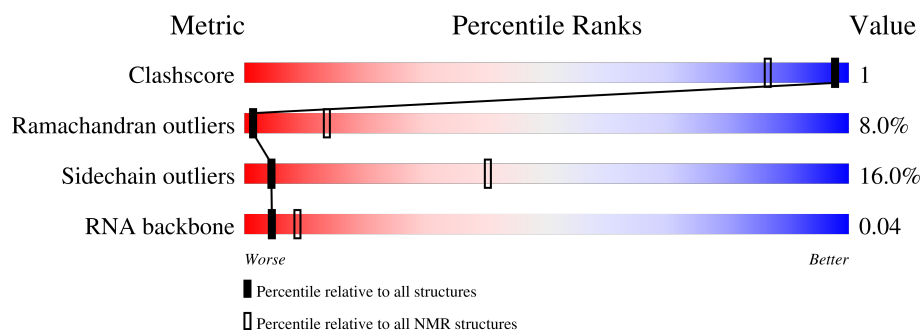
1 Overall quality at a glance

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	6	
2	A	148	

2 Ensemble composition and analysis

This entry contains 20 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: *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:180-A:282 (103)	0.87	2
2	A:287-A:297 (11)	0.36	1

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 2 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2154 atoms, of which 1048 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	

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

Mol	Chain	Residues	Atoms						Trace
2	A	127	Total	C	H	N	O	S	0
			1972	627	983	167	190	5	

There are 21 discrepancies between the modelled and reference sequences:

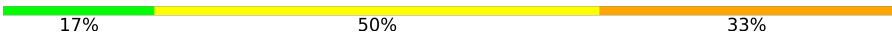
Chain	Residue	Modelled	Actual	Comment	Reference
A	151	MET	-	expression tag	UNP P26599
A	152	GLY	-	expression tag	UNP P26599
A	153	SER	-	expression tag	UNP P26599
A	154	SER	-	expression tag	UNP P26599
A	155	HIS	-	expression tag	UNP P26599
A	156	HIS	-	expression tag	UNP P26599
A	157	HIS	-	expression tag	UNP P26599
A	158	HIS	-	expression tag	UNP P26599
A	159	HIS	-	expression tag	UNP P26599
A	160	HIS	-	expression tag	UNP P26599
A	161	SER	-	expression tag	UNP P26599
A	162	SER	-	expression tag	UNP P26599
A	163	GLY	-	expression tag	UNP P26599
A	164	LEU	-	expression tag	UNP P26599
A	165	VAL	-	expression tag	UNP P26599
A	166	PRO	-	expression tag	UNP P26599
A	167	ARG	-	expression tag	UNP P26599
A	168	GLY	-	expression tag	UNP P26599
A	169	SER	-	expression tag	UNP P26599
A	170	HIS	-	expression tag	UNP P26599
A	171	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, 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.

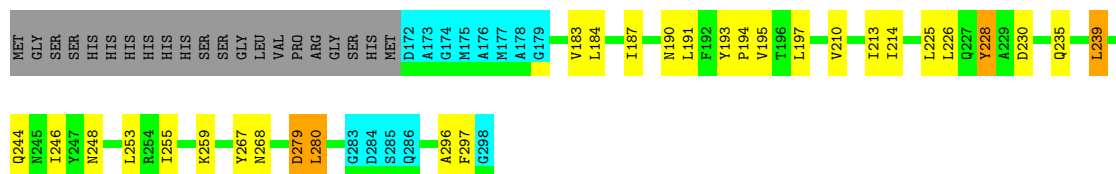
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B: 



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A: 

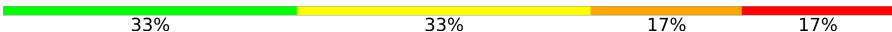


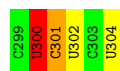
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

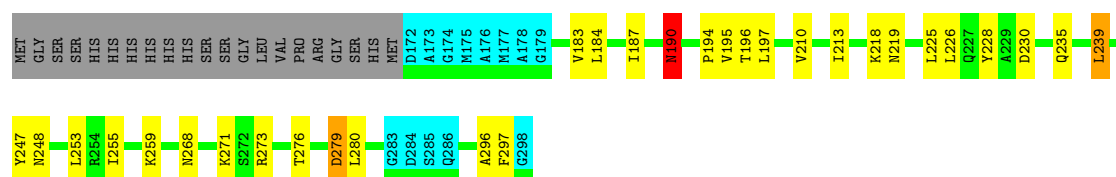
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B: 



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A: 

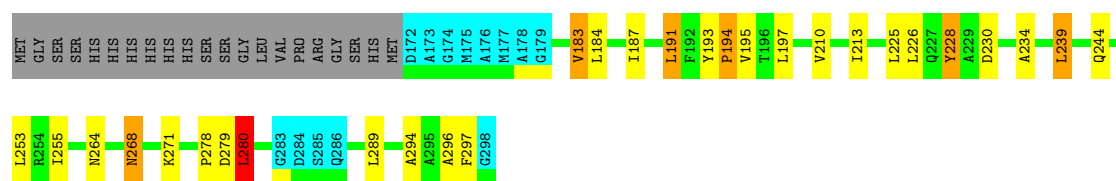


4.2.2 Score per residue for model 2 (medoid)

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



- Molecule 2: Polypyrimidine tract-binding protein 1

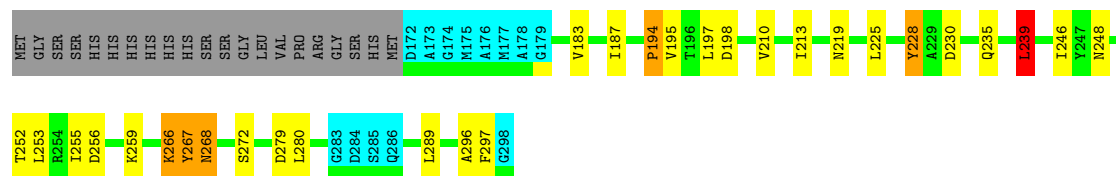


4.2.3 Score per residue for model 3

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

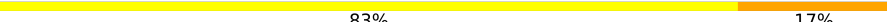


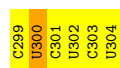
- Molecule 2: Polypyrimidine tract-binding protein 1



4.2.4 Score per residue for model 4

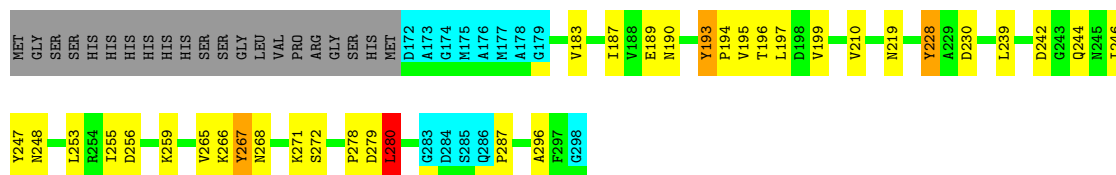
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B:  83% 17%



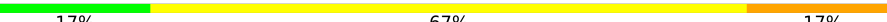
- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A:  53% 21% 9% 14%



4.2.5 Score per residue for model 5

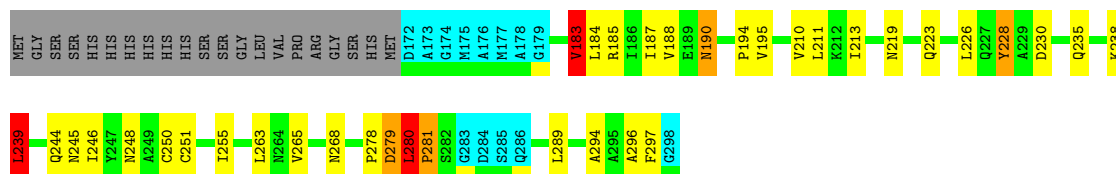
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B:  17% 67% 17%



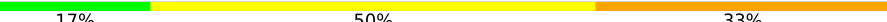
- Molecule 2: Polypyrimidine tract-binding protein 1

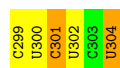
Chain A:  52% 20% 9% 14%



4.2.6 Score per residue for model 6

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

Chain B:  17% 50% 33%



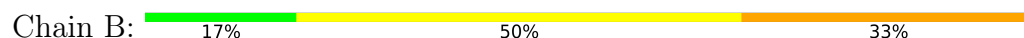
- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A:  51% 20% 5% 9% 14%

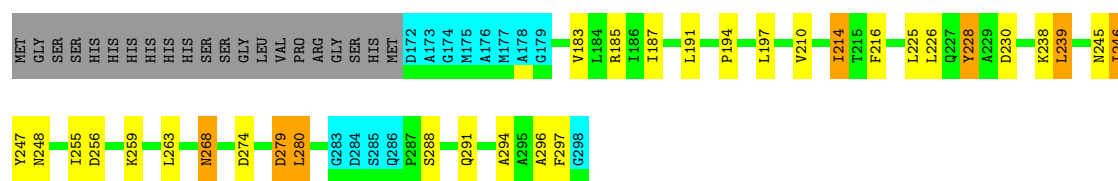


4.2.7 Score per residue for model 7

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



- Molecule 2: Polypyrimidine tract-binding protein 1

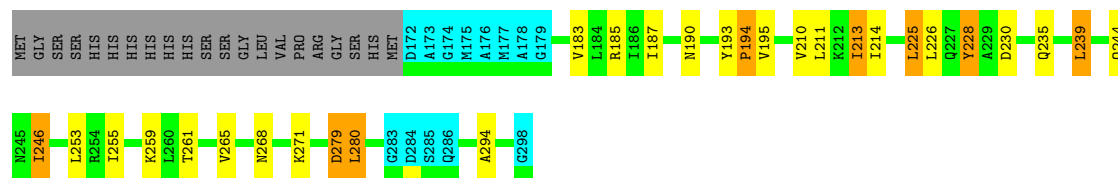


4.2.8 Score per residue for model 8

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

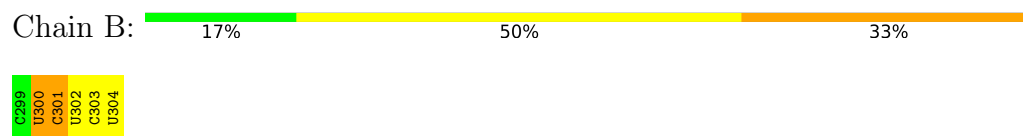


- Molecule 2: Polypyrimidine tract-binding protein 1

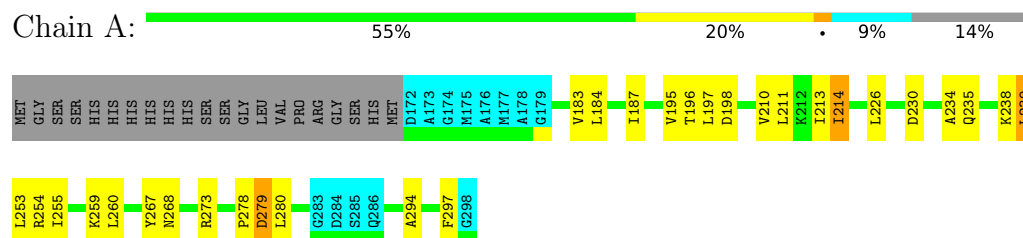


4.2.9 Score per residue for model 9

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

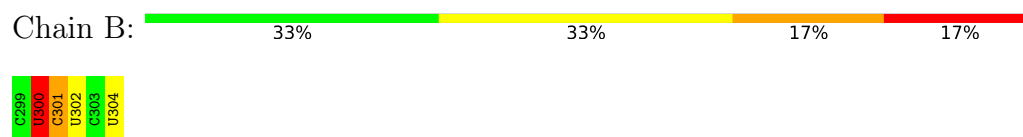


- Molecule 2: Polypyrimidine tract-binding protein 1

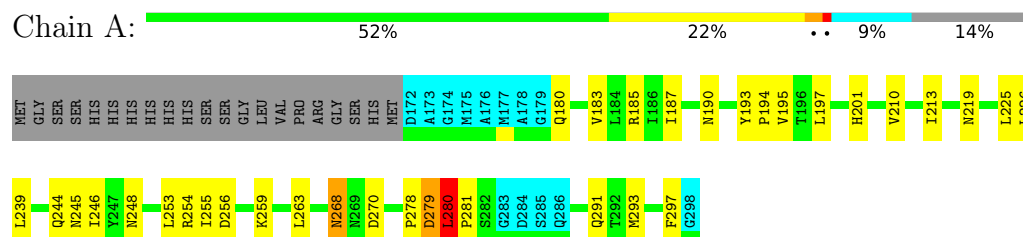


4.2.10 Score per residue for model 10

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

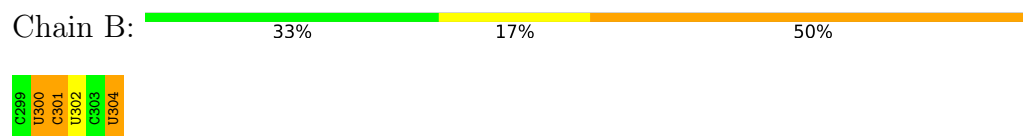


- Molecule 2: Polypyrimidine tract-binding protein 1



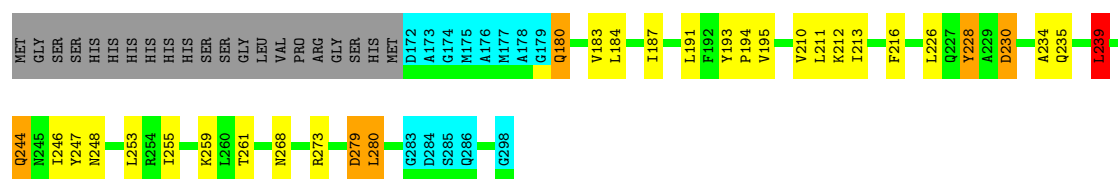
4.2.11 Score per residue for model 11

- 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 2: Polypyrimidine tract-binding protein 1



4.2.13 Score per residue for model 13

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

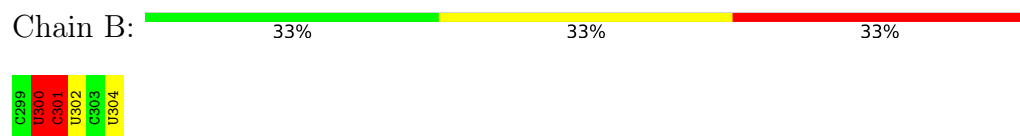


- Molecule 2: Polypyrimidine tract-binding protein 1

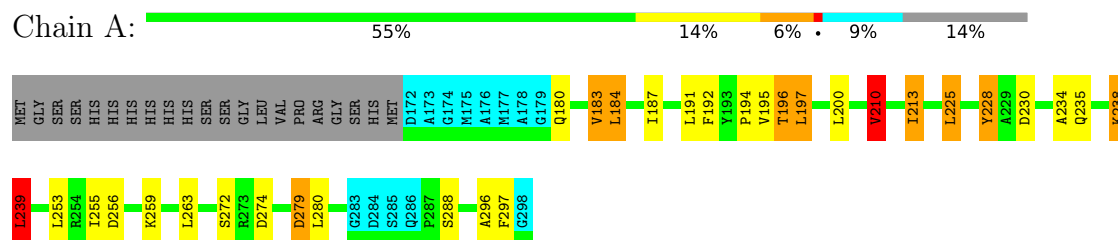


4.2.14 Score per residue for model 14

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

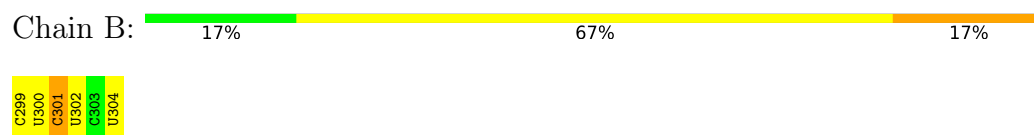


- Molecule 2: Polypyrimidine tract-binding protein 1

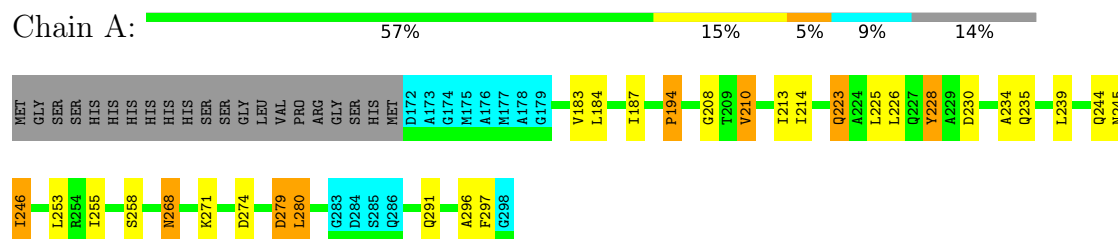


4.2.15 Score per residue for model 15

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

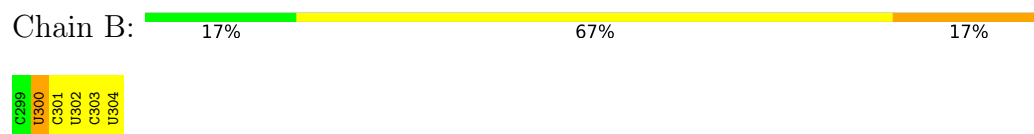


- Molecule 2: Polypyrimidine tract-binding protein 1



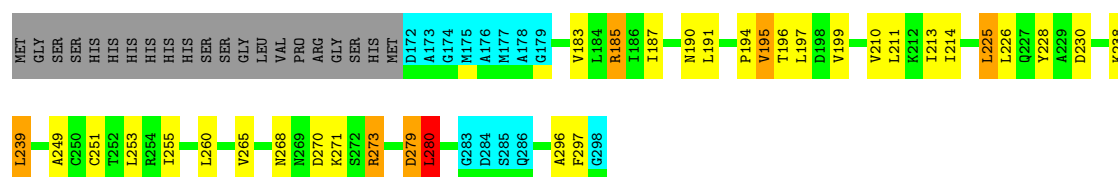
4.2.16 Score per residue for model 16

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



- Molecule 2: Polypyrimidine tract-binding protein 1

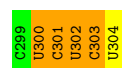




4.2.17 Score per residue for model 17

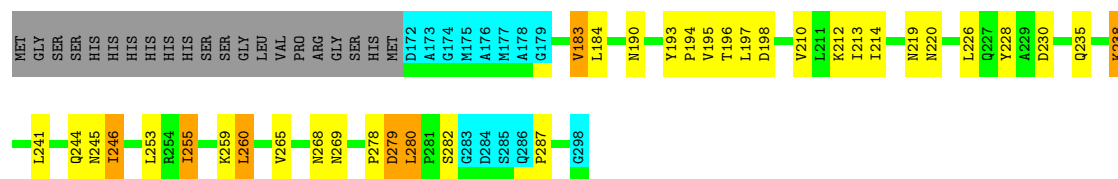
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B: 17% 17% 67%



- Molecule 2: Polypyrimidine tract-binding protein 1

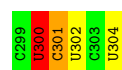
Chain A: 53% 20% 5% 9% 14%



4.2.18 Score per residue for model 18

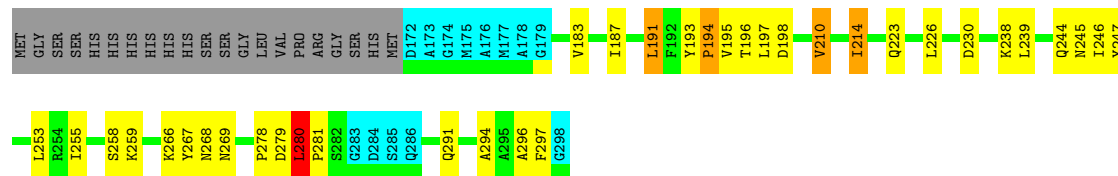
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B: 33% 33% 17% 17%



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A: 53% 21% 9% 14%



4.2.19 Score per residue for model 19

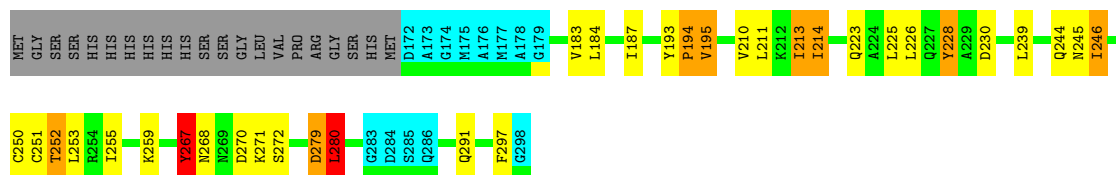
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B:  17% 17% 50% 17%



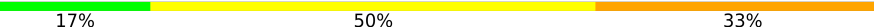
- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A:  54% 16% 5% 9% 14%



4.2.20 Score per residue for model 20

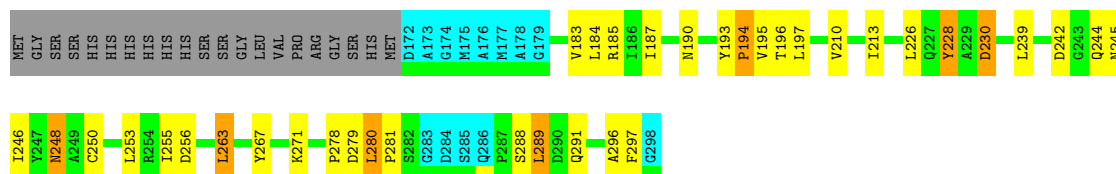
- Molecule 1: 5'-R(*CP*UP*CP*UP*CP*U)-3'

Chain B:  17% 50% 33%



- Molecule 2: Polypyrimidine tract-binding protein 1

Chain A:  52% 20% 5% 9% 14%



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.

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	0.87±0.03	0±0/128 (0.0± 0.0%)	1.41±0.09	1±1/196 (0.4± 0.5%)
2	A	0.86±0.01	0±0/930 (0.0± 0.0%)	1.71±0.04	14±4/1265 (1.1± 0.3%)
All	All	0.86	0/21160 (0.0%)	1.67	286/29220 (1.0%)

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	2.1±0.9
2	A	0.0±0.0	5.2±2.0
All	All	0	145

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
2	A	196	THR	CA-C-N	9.34	133.15	120.54	14	2
2	A	196	THR	C-N-CA	9.34	133.15	120.54	14	2
2	A	252	THR	CA-C-N	8.12	136.31	121.70	19	1
2	A	252	THR	C-N-CA	8.12	136.31	121.70	19	1
2	A	194	PRO	CA-C-N	7.69	135.81	121.97	19	15
2	A	194	PRO	C-N-CA	7.69	135.81	121.97	19	15
2	A	225	LEU	CB-CA-C	6.92	120.48	111.42	8	5
2	A	230	ASP	CA-CB-CG	6.81	119.41	112.60	20	5
2	A	280	LEU	CA-C-N	6.79	127.35	119.47	6	11
2	A	280	LEU	C-N-CA	6.79	127.35	119.47	6	11
2	A	272	SER	CA-C-N	6.76	134.45	121.54	14	1
2	A	272	SER	C-N-CA	6.76	134.45	121.54	14	1
2	A	288	SER	CA-C-N	6.64	134.23	121.54	7	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	288	SER	C-N-CA	6.64	134.23	121.54	7	3
1	B	300	U	C2'-C3'-O3'	6.57	119.36	109.50	1	4
2	A	258	SER	CA-C-N	6.52	133.44	121.70	18	2
2	A	258	SER	C-N-CA	6.52	133.44	121.70	18	2
2	A	268	ASN	CA-CB-CG	6.38	118.97	112.60	7	2
2	A	184	LEU	CA-C-N	6.36	132.18	122.77	20	4
2	A	184	LEU	C-N-CA	6.36	132.18	122.77	20	4
2	A	197	LEU	N-CA-CB	-6.36	100.47	109.94	14	2
2	A	267	TYR	CA-C-N	6.31	133.59	121.54	4	1
2	A	267	TYR	C-N-CA	6.31	133.59	121.54	4	1
2	A	193	TYR	CA-C-N	6.28	127.69	119.84	8	8
2	A	193	TYR	C-N-CA	6.28	127.69	119.84	8	8
2	A	296	ALA	CA-C-N	6.20	128.91	120.54	4	12
2	A	296	ALA	C-N-CA	6.20	128.91	120.54	4	12
2	A	268	ASN	CA-C-N	6.15	131.13	122.46	13	3
2	A	268	ASN	C-N-CA	6.15	131.13	122.46	13	3
2	A	244	GLN	N-CA-C	6.09	118.03	108.96	8	1
2	A	190	ASN	CA-CB-CG	-5.99	106.61	112.60	20	1
2	A	273	ARG	N-CA-C	5.83	117.82	109.14	9	5
2	A	213	ILE	CA-CB-CG1	5.82	120.30	110.40	14	3
1	B	300	U	O4'-C1'-C2'	-5.77	101.83	107.60	12	1
2	A	190	ASN	N-CA-CB	-5.77	102.97	111.51	17	4
2	A	195	VAL	CA-C-N	5.76	130.35	121.19	19	3
2	A	195	VAL	C-N-CA	5.76	130.35	121.19	19	3
2	A	278	PRO	CA-C-N	5.73	132.49	121.54	2	9
2	A	278	PRO	C-N-CA	5.73	132.49	121.54	2	9
2	A	239	LEU	N-CA-CB	-5.72	100.82	110.49	3	12
2	A	288	SER	N-CA-C	5.70	122.65	114.39	20	1
2	A	267	TYR	N-CA-C	5.64	116.62	107.32	3	2
2	A	280	LEU	N-CA-C	5.62	122.24	109.81	6	5
2	A	204	PHE	CA-CB-CG	5.59	119.39	113.80	6	1
2	A	230	ASP	CA-C-N	5.58	125.19	119.56	2	7
2	A	230	ASP	C-N-CA	5.58	125.19	119.56	2	7
1	B	302	U	C5'-C4'-C3'	-5.54	107.69	116.00	3	1
1	B	301	C	C4'-C3'-O3'	-5.45	104.83	113.00	20	1
2	A	234	ALA	CA-C-N	5.44	127.83	120.65	15	6
2	A	234	ALA	C-N-CA	5.44	127.83	120.65	15	6
2	A	264	ASN	CA-C-N	5.44	127.91	120.35	2	1
2	A	264	ASN	C-N-CA	5.44	127.91	120.35	2	1
2	A	214	ILE	CA-CB-CG1	5.43	119.63	110.40	18	10
1	B	304	U	O4'-C1'-N1	5.42	116.62	108.50	19	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	300	U	C4'-C3'-O3'	5.41	117.51	109.40	18	1
1	B	301	C	O4'-C4'-C3'	5.38	109.38	104.00	3	2
2	A	252	THR	O-C-N	-5.36	115.46	122.59	19	1
1	B	301	C	C5'-C4'-O4'	5.29	117.73	109.80	20	1
2	A	216	PHE	N-CA-C	5.28	117.71	109.52	11	3
2	A	197	LEU	CA-C-N	5.28	128.33	120.31	16	1
2	A	197	LEU	C-N-CA	5.28	128.33	120.31	16	1
2	A	242	ASP	CA-C-N	5.26	125.94	119.99	4	2
2	A	242	ASP	C-N-CA	5.26	125.94	119.99	4	2
2	A	251	CYS	CA-C-N	5.26	131.59	121.54	19	1
2	A	251	CYS	C-N-CA	5.26	131.59	121.54	19	1
2	A	219	ASN	CA-C-N	5.25	131.57	121.54	6	1
2	A	219	ASN	C-N-CA	5.25	131.57	121.54	6	1
2	A	289	LEU	CA-C-N	5.24	128.28	120.31	5	3
2	A	289	LEU	C-N-CA	5.24	128.28	120.31	5	3
2	A	274	ASP	CA-CB-CG	5.23	117.83	112.60	14	2
1	B	302	U	O5'-C5'-C4'	5.18	119.28	111.50	13	1
2	A	280	LEU	CB-CA-C	5.17	120.35	110.17	4	1
2	A	279	ASP	CA-C-N	5.08	134.18	121.80	5	2
2	A	279	ASP	C-N-CA	5.08	134.18	121.80	5	2
2	A	187	ILE	CA-CB-CG1	5.08	119.03	110.40	6	1
2	A	281	PRO	CA-C-N	5.03	131.15	121.54	5	1
2	A	281	PRO	C-N-CA	5.03	131.15	121.54	5	1
2	A	272	SER	N-CA-C	5.03	116.24	107.49	6	1
2	A	180	GLN	N-CA-CB	-5.02	108.44	114.17	11	1
1	B	304	U	O4'-C1'-C2'	-5.02	102.58	107.60	8	1
1	B	300	U	N1-C1'-C2'	-5.02	106.47	114.00	3	1
2	A	250	CYS	CA-C-N	5.01	127.31	120.54	19	1
2	A	250	CYS	C-N-CA	5.01	127.31	120.54	19	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)
2	A	228	TYR	Sidechain	18
1	B	300	U	Sidechain	15
1	B	301	C	Sidechain	13
2	A	279	ASP	Peptide	13
2	A	253	LEU	Peptide	12
2	A	195	VAL	Peptide	10

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Mol	Chain	Res	Type	Group	Models (Total)
1	B	303	C	Sidechain	9
2	A	238	LYS	Peptide	6
2	A	184	LEU	Peptide	5
2	A	272	SER	Peptide	4
2	A	223	GLN	Peptide	4
2	A	180	GLN	Peptide	4
2	A	191	LEU	Peptide	3
2	A	194	PRO	Peptide	3
2	A	190	ASN	Peptide	3
2	A	185	ARG	Sidechain	3
2	A	270	ASP	Peptide	3
2	A	266	LYS	Peptide	2
1	B	304	U	Sidechain	2
2	A	271	LYS	Peptide	2
1	B	302	U	Sidechain	2
2	A	276	THR	Peptide	1
1	B	299	C	Sidechain	1
2	A	183	VAL	Peptide	1
2	A	188	VAL	Peptide	1
2	A	265	VAL	Peptide	1
2	A	209	THR	Peptide	1
2	A	267	TYR	Peptide	1
2	A	241	LEU	Peptide	1
2	A	255	ILE	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
2	A	910	917	917	1±1
All	All	20540	19640	19640	21

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:280:LEU:HD22	2:A:281:PRO:HD2	0.59	1.74	18	4
2:A:238:LYS:HB3	2:A:255:ILE:HD13	0.53	1.80	17	1
2:A:210:VAL:HG21	2:A:213:ILE:HD11	0.49	1.83	14	1
2:A:266:LYS:HE3	2:A:267:TYR:CE2	0.48	2.44	3	1
2:A:183:VAL:C	2:A:184:LEU:HD22	0.47	2.34	17	4
2:A:273:ARG:HA	2:A:280:LEU:HD12	0.47	1.87	16	1
2:A:190:ASN:ND2	2:A:190:ASN:H	0.45	2.07	1	1
2:A:185:ARG:HD2	2:A:187:ILE:HD11	0.44	1.90	6	1
1:B:301:C:H1'	2:A:225:LEU:HD11	0.44	1.90	14	1
2:A:260:LEU:HD13	2:A:260:LEU:H	0.42	1.75	17	1
1:B:302:U:H5'	2:A:216:PHE:CZ	0.41	2.50	13	1
2:A:263:LEU:CD1	2:A:263:LEU:H	0.41	2.29	20	1
2:A:289:LEU:C	2:A:291:GLN:H	0.41	2.23	20	1
1:B:303:C:H5''	1:B:303:C:C6	0.40	2.50	8	1
2:A:267:TYR:HA	2:A:280:LEU:HD13	0.40	1.92	19	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	114/148 (77%)	83±3 (73±3%)	22±3 (19±3%)	9±2 (8±2%)	1	13
All	All	2280/2960 (77%)	1657 (73%)	441 (19%)	182 (8%)	1	13

All 30 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	279	ASP	20
2	A	239	LEU	19
2	A	280	LEU	19
2	A	268	ASN	15
2	A	297	PHE	15
2	A	245	ASN	10
2	A	194	PRO	9
2	A	195	VAL	9

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Mol	Chain	Res	Type	Models (Total)
2	A	294	ALA	9
2	A	219	ASN	7
2	A	246	ILE	6
2	A	196	THR	5
2	A	267	TYR	5
2	A	210	VAL	5
2	A	247	TYR	4
2	A	248	ASN	3
2	A	265	VAL	2
2	A	287	PRO	2
2	A	250	CYS	2
2	A	251	CYS	2
2	A	208	GLY	2
2	A	220	ASN	2
2	A	249	ALA	2
2	A	244	GLN	2
2	A	190	ASN	1
2	A	272	SER	1
2	A	192	PHE	1
2	A	269	ASN	1
2	A	252	THR	1
2	A	289	LEU	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	104/128 (81%)	87±2 (84±2%)	17±2 (16±2%)	4	40
All	All	2080/2560 (81%)	1748 (84%)	332 (16%)	4	40

All 54 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	183	VAL	20
2	A	210	VAL	20
2	A	187	ILE	19

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Mol	Chain	Res	Type	Models (Total)
2	A	255	ILE	19
2	A	226	LEU	16
2	A	213	ILE	15
2	A	259	LYS	15
2	A	246	ILE	15
2	A	244	GLN	14
2	A	235	GLN	13
2	A	228	TYR	13
2	A	197	LEU	11
2	A	230	ASP	10
2	A	248	ASN	8
2	A	191	LEU	8
2	A	225	LEU	7
2	A	256	ASP	7
2	A	271	LYS	6
2	A	253	LEU	6
2	A	185	ARG	6
2	A	211	LEU	6
2	A	263	LEU	6
2	A	214	ILE	6
2	A	291	GLN	6
2	A	280	LEU	4
2	A	198	ASP	4
2	A	239	LEU	4
2	A	268	ASN	4
2	A	223	GLN	4
2	A	193	TYR	3
2	A	199	VAL	3
2	A	261	THR	3
2	A	265	VAL	3
2	A	260	LEU	3
2	A	190	ASN	2
2	A	238	LYS	2
2	A	254	ARG	2
2	A	212	LYS	2
2	A	196	THR	2
2	A	218	LYS	1
2	A	247	TYR	1
2	A	252	THR	1
2	A	266	LYS	1
2	A	189	GLU	1
2	A	264	ASN	1

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Mol	Chain	Res	Type	Models (Total)
2	A	180	GLN	1
2	A	201	HIS	1
2	A	293	MET	1
2	A	288	SER	1
2	A	200	LEU	1
2	A	274	ASP	1
2	A	282	SER	1
2	A	269	ASN	1
2	A	267	TYR	1

6.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	6/6 (100%)	4±0 (67±0%)	2±1 (27±15%)	0.33±0.00
All	All	104/120 (87%)	80 (77%)	32 (31%)	0.33

The overall RNA backbone suiteness is 0.04.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	300	U	20
1	B	301	C	20
1	B	302	U	20
1	B	304	U	20

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	300	U	15
1	B	301	C	7
1	B	303	C	6
1	B	299	C	4

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 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 [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided