



Full wwPDB NMR Structure Validation Report ⓘ

Mar 1, 2026 – 09:35 PM UTC

PDB ID : 2MKK / pdb_00002mkk
BMRB ID : 19778
Title : Structural model of tandem RRM domains of cytoplasmic polyadenylation element binding protein 1 (CPEB1) in complex with RNA
Authors : Afroz, T.; Skrisovska, L.; Belloc, E.; Boixet, J.G.; Mendez, R.; Allain, F.H.-T.
Deposited on : 2014-02-07

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

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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

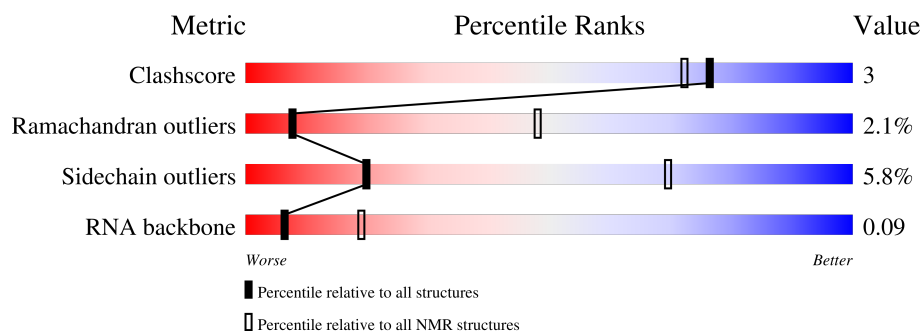
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 51%.

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	A	213	
2	B	5	

2 Ensemble composition and analysis

This entry contains 10 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: *closest to the average*.

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:218-A:267, A:279-A:301, A:310-A:385, A:393-A:430 (187)	2.32	2

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 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3532 atoms, of which 1746 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cytoplasmic polyadenylation element-binding protein 1.

Mol	Chain	Residues	Atoms						Trace
1	A	213	Total	C	H	N	O	S	0
			3380	1088	1693	290	301	8	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	218	MET	-	expression tag	UNP Q9BZB8

- Molecule 2 is a RNA chain called RNA (5'-R(*UP*UP*UP*UP*A)-3').

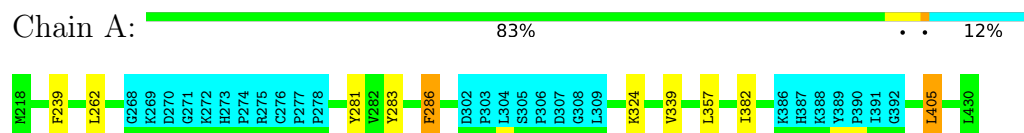
Mol	Chain	Residues	Atoms						Trace
2	B	5	Total	C	H	N	O	P	0
			152	46	53	13	36	4	

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: Cytoplasmic polyadenylation element-binding protein 1



- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')

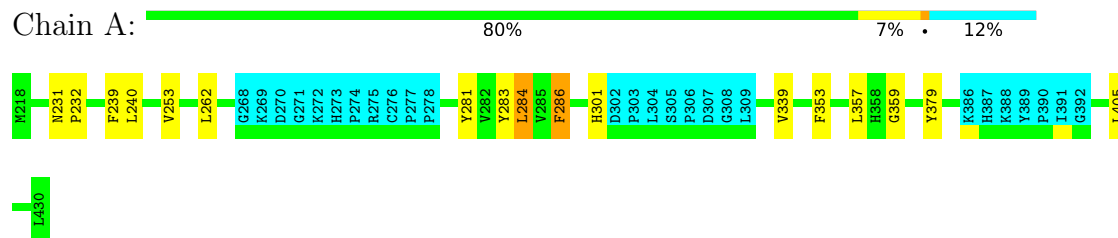


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1



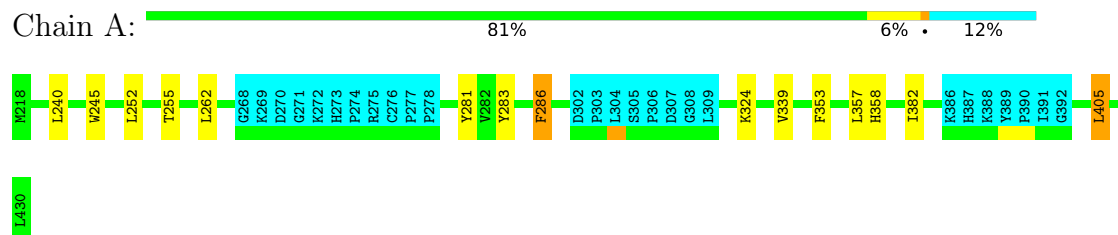
- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')



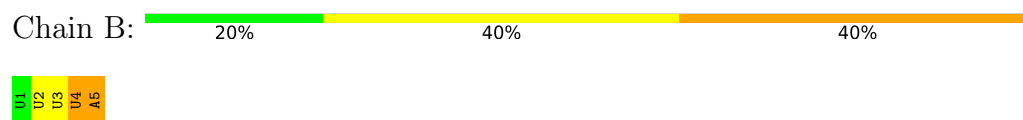


4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1

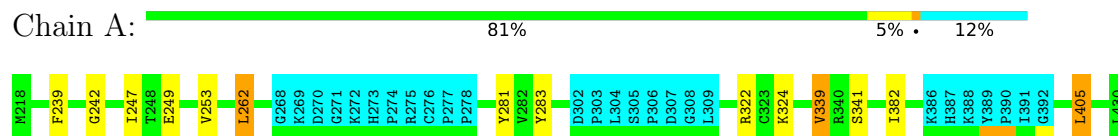


- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')



4.2.3 Score per residue for model 3

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1

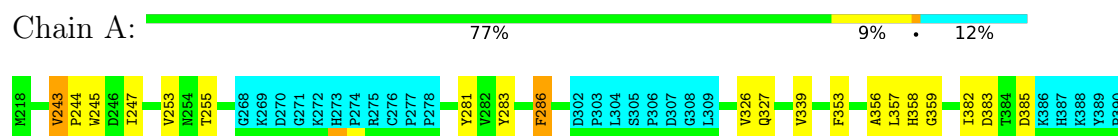


- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')



4.2.4 Score per residue for model 4

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1





- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')

Chain B: 20% 40% 40%



4.2.5 Score per residue for model 5

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1

Chain A: 78% 8% 12%



- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')

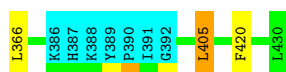
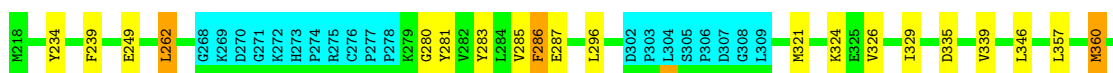
Chain B: 40% 60%



4.2.6 Score per residue for model 6

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1

Chain A: 77% 9% 12%



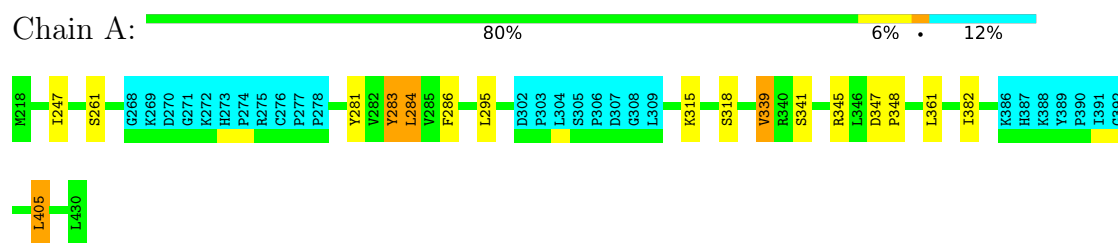
- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')

Chain B: 20% 40% 40%



4.2.7 Score per residue for model 7

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1

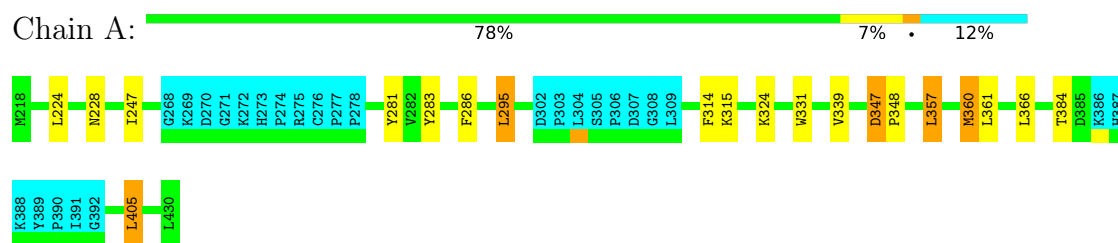


- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')

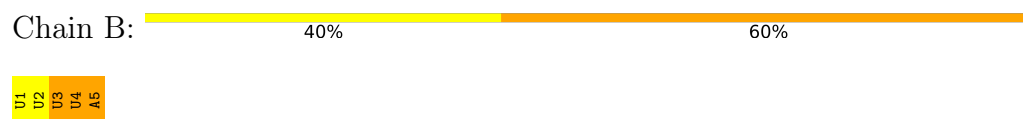


4.2.8 Score per residue for model 8

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1

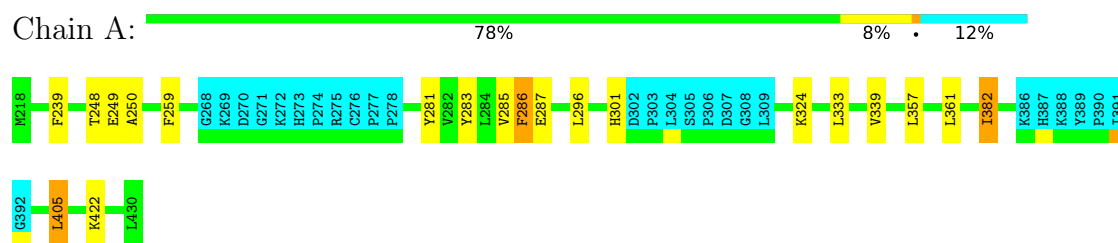


- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')



4.2.9 Score per residue for model 9

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1

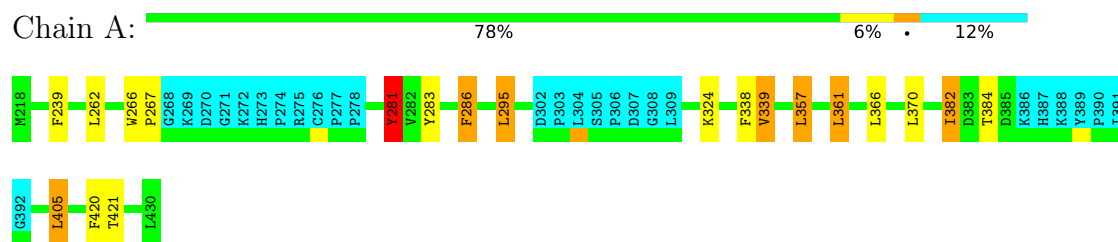


- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')



4.2.10 Score per residue for model 10

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 1



- Molecule 2: RNA (5'-R(*UP*UP*UP*UP*A)-3')



5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 10 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
Amber	refinement	
CYANA	structure solution	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1463
Number of shifts mapped to atoms	1463
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	51%

6 Model quality

6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.53±0.01	0±0/1528 (0.0± 0.0%)	0.97±0.02	0±0/2071 (0.0± 0.0%)
2	B	0.77±0.02	0±0/109 (0.0± 0.0%)	1.22±0.07	0±0/167 (0.0± 0.0%)
All	All	0.55	0/16370 (0.0%)	0.99	5/22380 (0.0%)

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
2	B	0.0±0.0	0.1±0.3
All	All	0	1

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	A	286	PHE	CA-CB-CG	6.22	120.02	113.80	2	4
1	A	358	HIS	CB-CG-CD2	-5.14	124.51	131.20	5	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
2	B	1	U	Sidechain	1

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1490	1496	1493	9±2
2	B	99	53	53	3±1
All	All	15890	15490	15460	95

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:295:LEU:H	1:A:295:LEU:HD13	0.66	1.50	8	2
1:A:405:LEU:HD22	1:A:405:LEU:C	0.65	2.17	9	9
1:A:324:LYS:CD	2:B:1:U:C6	0.60	2.84	5	1
1:A:239:PHE:CE2	2:B:3:U:C6	0.60	2.89	6	4
1:A:347:ASP:H	1:A:348:PRO:HD2	0.57	1.59	8	1
1:A:324:LYS:HE3	2:B:1:U:C6	0.55	2.37	9	1
1:A:357:LEU:HD12	1:A:359:GLY:H	0.55	1.62	1	1
1:A:382:ILE:HD13	1:A:382:ILE:N	0.55	2.17	9	1
1:A:285:VAL:HG12	1:A:286:PHE:H	0.53	1.62	9	1
1:A:283:TYR:CD1	2:B:4:U:C4	0.51	2.98	10	5
1:A:266:TRP:CG	1:A:267:PRO:HD2	0.50	2.42	10	1
2:B:5:A:C8	2:B:5:A:H5'	0.50	2.42	1	1
1:A:324:LYS:HE3	2:B:1:U:C1'	0.49	2.38	8	1
1:A:347:ASP:N	1:A:348:PRO:CD	0.49	2.75	5	2
1:A:324:LYS:HD2	2:B:1:U:C6	0.49	2.42	5	2
1:A:353:PHE:CE2	2:B:5:A:H1'	0.48	2.43	2	3
1:A:360:MET:HE3	2:B:3:U:C4	0.47	2.43	8	1
1:A:283:TYR:CD2	2:B:4:U:C2	0.47	3.02	8	1
1:A:262:LEU:HD13	1:A:262:LEU:C	0.47	2.35	6	3
1:A:361:LEU:CD1	1:A:361:LEU:H	0.47	2.22	10	1
1:A:283:TYR:CD2	2:B:4:U:C4	0.47	3.03	4	2
1:A:231:ASN:N	1:A:232:PRO:CD	0.47	2.78	1	1
1:A:324:LYS:HD3	2:B:1:U:C6	0.47	2.44	5	1
1:A:357:LEU:H	1:A:357:LEU:HD23	0.46	1.69	6	1
1:A:283:TYR:CD2	2:B:4:U:N3	0.46	2.84	8	1
1:A:324:LYS:CE	2:B:1:U:O4'	0.46	2.64	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:283:TYR:CE2	2:B:4:U:C2	0.46	3.04	9	1
1:A:285:VAL:HG12	1:A:286:PHE:N	0.46	2.25	9	1
1:A:283:TYR:CG	2:B:4:U:C4	0.45	3.05	7	1
1:A:361:LEU:H	1:A:361:LEU:HD13	0.45	1.72	10	1
1:A:339:VAL:HG13	1:A:341:SER:H	0.45	1.71	5	2
1:A:285:VAL:HG22	1:A:286:PHE:H	0.45	1.72	6	1
1:A:405:LEU:C	1:A:405:LEU:CD2	0.44	2.90	7	7
1:A:224:LEU:H	1:A:224:LEU:HD23	0.44	1.73	8	1
1:A:357:LEU:C	1:A:357:LEU:HD22	0.44	2.38	10	1
1:A:252:LEU:HA	1:A:255:THR:HG22	0.44	1.90	2	1
1:A:284:LEU:HD22	1:A:284:LEU:C	0.44	2.38	7	2
1:A:281:TYR:CD1	1:A:281:TYR:N	0.43	2.86	10	1
1:A:357:LEU:HD23	1:A:357:LEU:N	0.43	2.29	4	1
1:A:239:PHE:CZ	2:B:3:U:O4'	0.43	2.72	10	2
1:A:248:THR:C	1:A:250:ALA:H	0.43	2.22	9	1
1:A:239:PHE:CZ	1:A:241:GLY:CA	0.43	3.02	5	1
2:B:5:A:C8	2:B:5:A:H5''	0.42	2.49	8	1
1:A:240:LEU:HD23	1:A:240:LEU:C	0.42	2.39	2	1
1:A:360:MET:N	1:A:360:MET:SD	0.42	2.92	8	1
1:A:339:VAL:CG1	1:A:341:SER:H	0.42	2.27	7	1
1:A:331:TRP:CD2	1:A:384:THR:HG23	0.42	2.49	8	1
1:A:283:TYR:CG	2:B:4:U:N3	0.42	2.88	10	1
1:A:266:TRP:CD2	1:A:267:PRO:HD2	0.42	2.50	10	1
1:A:262:LEU:HD12	1:A:262:LEU:C	0.42	2.40	3	1
1:A:247:ILE:HD12	1:A:247:ILE:C	0.41	2.40	4	1
1:A:420:PHE:CD1	1:A:420:PHE:C	0.41	2.98	4	1
1:A:360:MET:SD	1:A:360:MET:N	0.41	2.94	6	1
1:A:338:PHE:CG	1:A:339:VAL:N	0.41	2.89	10	1
1:A:357:LEU:H	1:A:357:LEU:CD2	0.41	2.29	6	1
1:A:283:TYR:CD1	2:B:4:U:N3	0.41	2.89	3	2
1:A:347:ASP:H	1:A:348:PRO:CD	0.40	2.27	8	1
1:A:379:TYR:CD1	1:A:379:TYR:C	0.40	3.00	1	1
1:A:245:TRP:CZ2	1:A:324:LYS:HE3	0.40	2.51	2	1
1:A:314:PHE:CG	1:A:315:LYS:N	0.40	2.90	8	1
1:A:244:PRO:HA	1:A:245:TRP:CE3	0.40	2.52	4	1
1:A:382:ILE:C	1:A:384:THR:H	0.40	2.25	10	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	
1	A	185/213 (87%)	163±6 (88±3%)	19±6 (10±3%)	4±2 (2±1%)	8	48
All	All	1850/2130 (87%)	1626 (88%)	186 (10%)	38 (2%)	8	48

All 26 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	357	LEU	3
1	A	249	GLU	3
1	A	286	PHE	3
1	A	287	GLU	3
1	A	301	HIS	2
1	A	358	HIS	2
1	A	242	GLY	2
1	A	359	GLY	2
1	A	322	ARG	1
1	A	243	VAL	1
1	A	356	ALA	1
1	A	383	ASP	1
1	A	385	ASP	1
1	A	323	CYS	1
1	A	336	SER	1
1	A	374	PHE	1
1	A	280	GLY	1
1	A	335	ASP	1
1	A	261	SER	1
1	A	318	SER	1
1	A	345	ARG	1
1	A	347	ASP	1
1	A	259	PHE	1
1	A	333	LEU	1
1	A	281	TYR	1
1	A	421	THR	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
1	A	163/185 (88%)	154±3 (94±2%)	9±3 (6±2%)	20 69
All	All	1630/1850 (88%)	1536 (94%)	94 (6%)	20 69

All 35 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	281	TYR	10
1	A	339	VAL	10
1	A	405	LEU	10
1	A	286	PHE	7
1	A	382	ILE	6
1	A	361	LEU	4
1	A	253	VAL	3
1	A	247	ILE	3
1	A	262	LEU	3
1	A	296	LEU	3
1	A	366	LEU	3
1	A	295	LEU	3
1	A	284	LEU	2
1	A	326	VAL	2
1	A	324	LYS	2
1	A	360	MET	2
1	A	420	PHE	2
1	A	357	LEU	2
1	A	240	LEU	1
1	A	243	VAL	1
1	A	255	THR	1
1	A	327	GLN	1
1	A	419	LYS	1
1	A	224	LEU	1
1	A	358	HIS	1
1	A	373	LEU	1
1	A	234	TYR	1
1	A	321	MET	1
1	A	329	ILE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	346	LEU	1
1	A	283	TYR	1
1	A	315	LYS	1
1	A	228	ASN	1
1	A	422	LYS	1
1	A	370	LEU	1

6.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	4/5 (80%)	4±0 (100±0%)	0±0 (5±10%)	0.00±0.00
All	All	40/50 (80%)	40 (100%)	2 (5%)	0.00

The overall RNA backbone suiteness is 0.09.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	2	U	10
2	B	3	U	10
2	B	4	U	10
2	B	5	A	10

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	4	U	1
2	B	2	U	1

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 ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 51% for the well-defined parts and 48% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *CPEB1RRM12Complex*

7.1.1 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	1463
Number of shifts mapped to atoms	1463
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

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	110	2.70 ± 0.21	Should be applied
$^{13}\text{C}_\beta$	87	2.79 ± 0.14	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	183	-0.09 ± 0.19	None needed (< 0.5 ppm)

7.1.3 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 51%, i.e. 1361 atoms were assigned a chemical shift out of a possible 2683. 0 out of 37 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	538/929 (58%)	272/377 (72%)	101/374 (27%)	165/178 (93%)
Sidechain	668/1414 (47%)	469/925 (51%)	192/431 (45%)	7/58 (12%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	155/253 (61%)	95/123 (77%)	56/124 (45%)	4/6 (67%)
Sugar	0/55 (0%)	0/30 (0%)	0/25 (0%)	0/0 (—%)
Base	0/32 (0%)	0/17 (0%)	0/10 (0%)	0/5 (0%)
Overall	1361/2683 (51%)	836/1472 (57%)	349/964 (36%)	176/247 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 48%, i.e. 1463 atoms were assigned a chemical shift out of a possible 3018. 0 out of 39 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	594/1051 (57%)	301/427 (70%)	110/426 (26%)	183/198 (92%)
Sidechain	710/1604 (44%)	498/1047 (48%)	205/492 (42%)	7/65 (11%)
Aromatic	159/276 (58%)	97/135 (72%)	58/133 (44%)	4/8 (50%)
Sugar	0/55 (0%)	0/30 (0%)	0/25 (0%)	0/0 (—%)
Base	0/32 (0%)	0/17 (0%)	0/10 (0%)	0/5 (0%)
Overall	1463/3018 (48%)	896/1656 (54%)	373/1086 (34%)	194/276 (70%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

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

Random coil index (RCI) for chain A:

