



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 03:57 PM UTC

PDB ID : 2ERR / pdb_00002err
Title : NMR Structure of the RNA Binding Domain of Human Fox-1 in Complex with UGCAUGU
Authors : Allain, F.H.; Auweter, S.D.
Deposited on : 2005-10-25

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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

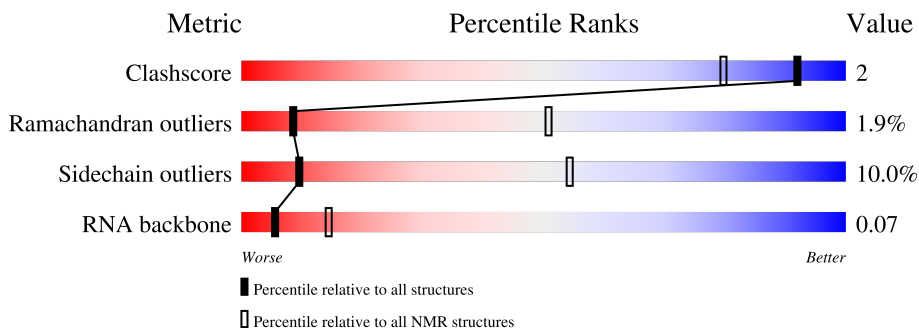
1 Overall quality at a glance i

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	7	
2	A	109	

2 Ensemble composition and analysis

This entry contains 30 models. Model 7 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:116-A:192 (77)	0.47	7

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 4 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 7, 11, 13, 14, 15, 16, 17, 18, 19, 21, 22, 24, 25, 28
2	6, 8, 10, 20, 30
3	5, 9, 12
4	23, 26
Single-model clusters	27; 29

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1636 atoms, of which 780 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called UGCAUGU.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		P
1	B	7	221	66	76	24	49	6	0

- Molecule 2 is a protein called Ataxin-2-binding protein 1.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
2	A	88	1415	443	704	135	131	2	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	MET	-	expression tag	UNP Q9NWB1
A	89	GLY	-	expression tag	UNP Q9NWB1
A	90	SER	-	expression tag	UNP Q9NWB1
A	91	SER	-	expression tag	UNP Q9NWB1
A	92	HIS	-	expression tag	UNP Q9NWB1
A	93	HIS	-	expression tag	UNP Q9NWB1
A	94	HIS	-	expression tag	UNP Q9NWB1
A	95	HIS	-	expression tag	UNP Q9NWB1
A	96	HIS	-	expression tag	UNP Q9NWB1
A	97	HIS	-	expression tag	UNP Q9NWB1
A	98	SER	-	expression tag	UNP Q9NWB1
A	99	SER	-	expression tag	UNP Q9NWB1
A	100	GLY	-	expression tag	UNP Q9NWB1
A	101	LEU	-	expression tag	UNP Q9NWB1
A	102	VAL	-	expression tag	UNP Q9NWB1
A	103	PRO	-	expression tag	UNP Q9NWB1
A	104	ARG	-	expression tag	UNP Q9NWB1
A	105	GLY	-	expression tag	UNP Q9NWB1
A	106	SER	-	expression tag	UNP Q9NWB1
A	107	HIS	-	expression tag	UNP Q9NWB1
A	108	MET	-	expression tag	UNP Q9NWB1

4 Residue-property plots

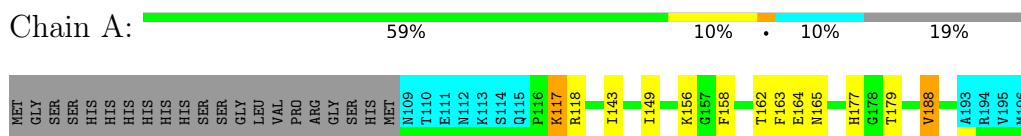
4.1 Average score per residue in the NMR ensemble

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: UGCAUGU



- Molecule 2: Ataxin-2-binding protein 1

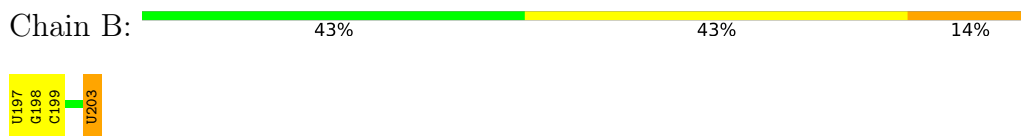


4.2 Scores per residue for each member of the ensemble

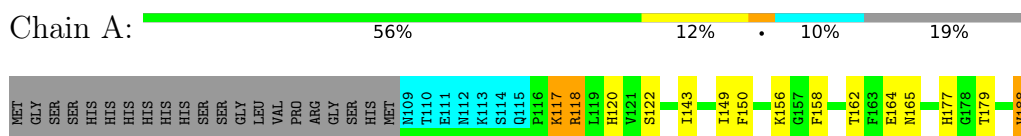
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: UGCAUGU



- Molecule 2: Ataxin-2-binding protein 1



V195
M196

4.2.2 Score per residue for model 2

- Molecule 1: UGCAUGU

Chain B:  43% 57%

U197
G198
C199
U203

- Molecule 2: Ataxin-2-binding protein 1


Chain A:  53% 17% 10% 19%

MET MET N109 T110 E111 M112 K113 S114 Q115 P116 K117 R118 V121 F137 V146 I149 K156 G157 F158 V161 T162 F163 E164 M165 L176 H177 G178 T179 E182 V188 T192

A193
R194
V195
M196

4.2.3 Score per residue for model 3

- Molecule 1: UGCAUGU

Chain B:  29% 57% 14%

U197
G198
C199
G202
U203

- Molecule 2: Ataxin-2-binding protein 1

Chain A:  55% 13% 10% 19%

MET MET N109 T110 E111 M112 K113 S114 Q115 P116 K117 R118 L119 H120 V121 S122 N123 I124 P125 R129 I148 I149 F150 F158 G159 F160 V161 T162 F163 E164 H177 G178 T179 V188 A193

R194
V195
M196

4.2.4 Score per residue for model 4

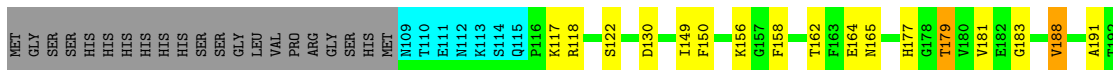
- Molecule 1: UGCAUGU

Chain B:  29% 43% 14% 14%



- Molecule 2: Ataxin-2-binding protein 1

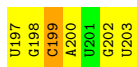
Chain A: 55% 14% 10% 19%



4.2.5 Score per residue for model 5

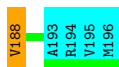
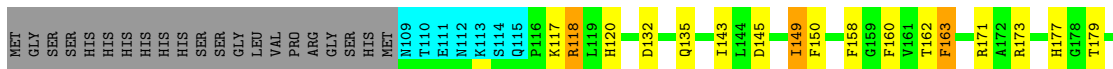
- Molecule 1: UGCAUGU

Chain B: 14% 71% 14%



- Molecule 2: Ataxin-2-binding protein 1

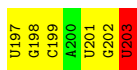
Chain A: 54% 13% 10% 19%



4.2.6 Score per residue for model 6

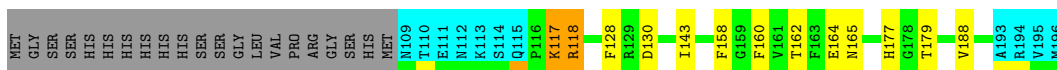
- Molecule 1: UGCAUGU

Chain B: 14% 71% 14%




- Molecule 2: Ataxin-2-binding protein 1

Chain A: 59% 10% 10% 19%



4.2.7 Score per residue for model 7 (medoid)

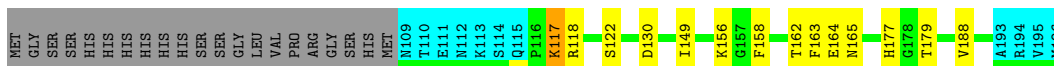
- Molecule 1: UGCAUGU

Chain B:  14% 57% 14% 14%



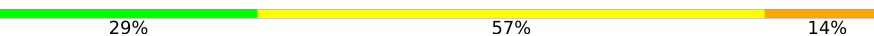
- Molecule 2: Ataxin-2-binding protein 1

Chain A:  58% 12% 10% 19%



4.2.8 Score per residue for model 8

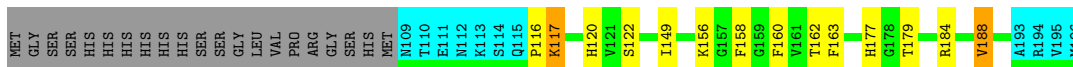
- Molecule 1: UGCAUGU

Chain B:  29% 57% 14%



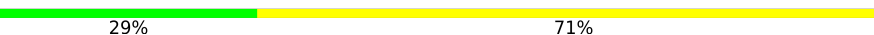
- Molecule 2: Ataxin-2-binding protein 1

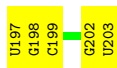
Chain A:  58% 11% 10% 19%



4.2.9 Score per residue for model 9

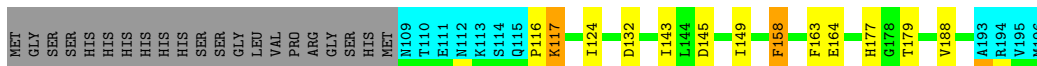
- Molecule 1: UGCAUGU

Chain B:  29% 71%



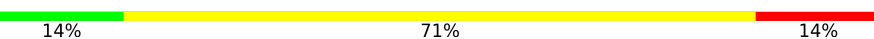
- Molecule 2: Ataxin-2-binding protein 1

Chain A:  59% 10% 10% 19%



4.2.10 Score per residue for model 10

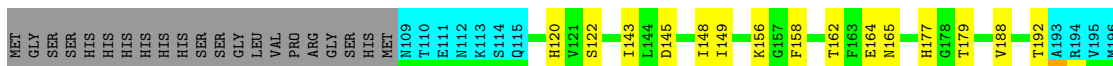
- Molecule 1: UGCAUGU

Chain B:  14% 71% 14%



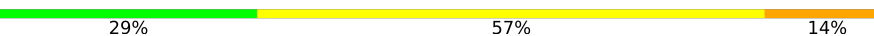
- Molecule 2: Ataxin-2-binding protein 1

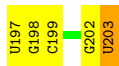
Chain A:  57% 14% 10% 19%



4.2.11 Score per residue for model 11

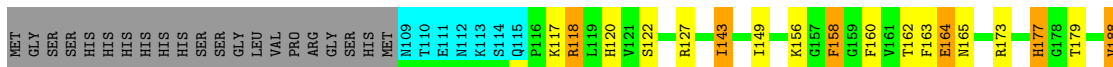
- Molecule 1: UGCAUGU

Chain B:  29% 57% 14%



- Molecule 2: Ataxin-2-binding protein 1

Chain A:  52% 13% 6% 10% 19%



4.2.12 Score per residue for model 12

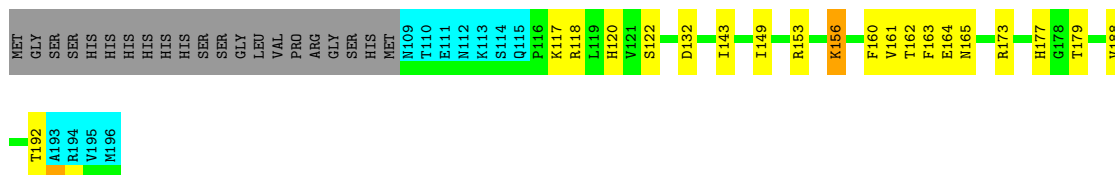
- Molecule 1: UGCAUGU

Chain B:  57% 29% 14%



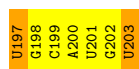
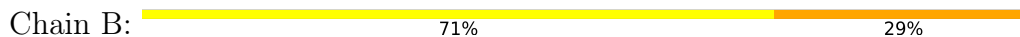
- Molecule 2: Ataxin-2-binding protein 1

Chain A:  52% 17% 10% 19%



4.2.13 Score per residue for model 13

- Molecule 1: UGCAUGU

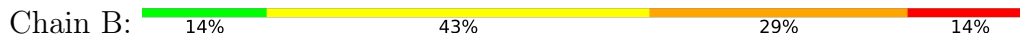


- Molecule 2: Ataxin-2-binding protein 1



4.2.14 Score per residue for model 14

- Molecule 1: UGCAUGU



- Molecule 2: Ataxin-2-binding protein 1



4.2.15 Score per residue for model 15

- Molecule 1: UGCAUGU



U197
G198
C199

G202
U203

- Molecule 2: Ataxin-2-binding protein 1

Chain A: 55% 12% 10% 19%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER SER GLY LEU VAL PRO ARG ARG GLY SER HIS MET M109 T110 E111 M112 K113 S114 Q115 P116 K117 D130 R134 I143 I149 K156 G157 F158 G159 F160 V161 T162 F163 E164 M165 R173 H177 G178 T179 V188 A193 R194

V195
M196

4.2.16 Score per residue for model 16

- Molecule 1: UGCAUGU

Chain B: 43% 43% 14%

U197
G198
C199
A200
U201
G202
U203

- Molecule 2: Ataxin-2-binding protein 1

Chain A: 54% 15% 10% 19%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER SER GLY LEU VAL PRO ARG ARG GLY SER HIS MET M109 T110 E111 M112 K113 S114 Q115 P116 R118 Q135 I143 I149 K156 F160 V161 T162 F163 E164 M165 R173 H177 G178 T179 E182 V188 A191 T192 A193

R194
V195
M196

4.2.17 Score per residue for model 17

- Molecule 1: UGCAUGU

Chain B: 43% 57%

U197
G198
C199

U203

- Molecule 2: Ataxin-2-binding protein 1

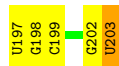
Chain A: 53% 16% 10% 19%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER SER GLY LEU VAL PRO ARG ARG GLY SER HIS MET M109 T110 E111 M112 K113 S114 Q115 P116 K117 R118 L119 H120 V121 S122 M123 I124 I143 I149 F150 M151 K156 G157 F158 G159 F160 V161 T162 F163 H177 G178 T179 R184 V188



4.2.18 Score per residue for model 18

- Molecule 1: UGCAUGU

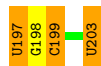


- Molecule 2: Ataxin-2-binding protein 1

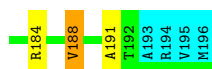


4.2.19 Score per residue for model 19

- Molecule 1: UGCAUGU



- Molecule 2: Ataxin-2-binding protein 1



4.2.20 Score per residue for model 20

- Molecule 1: UGCAUGU





- Molecule 2: Ataxin-2-binding protein 1

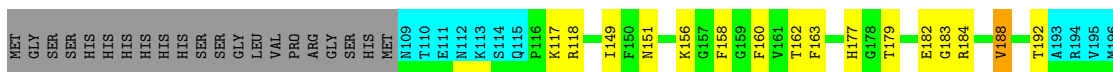


4.2.21 Score per residue for model 21

- Molecule 1: UGCAUGU

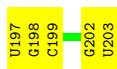


- Molecule 2: Ataxin-2-binding protein 1



4.2.22 Score per residue for model 22

- Molecule 1: UGCAUGU

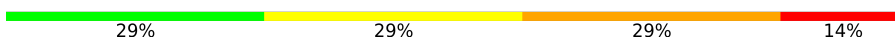


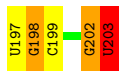
- Molecule 2: Ataxin-2-binding protein 1



4.2.23 Score per residue for model 23

- Molecule 1: UGCAUGU

Chain B:  29% 29% 29% 14%



- Molecule 2: Ataxin-2-binding protein 1

Chain A:  50% 17% 10% 19%



4.2.24 Score per residue for model 24

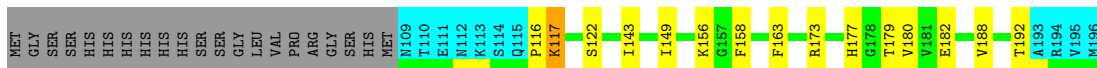
- Molecule 1: UGCAUGU

Chain B:  14% 71% 14%



- Molecule 2: Ataxin-2-binding protein 1

Chain A:  57% 13% 10% 19%



4.2.25 Score per residue for model 25

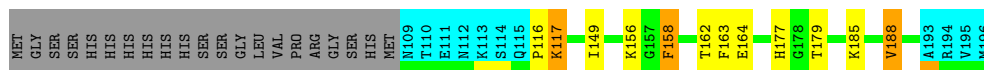
- Molecule 1: UGCAUGU

Chain B:  43% 14% 43%



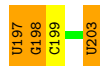
- Molecule 2: Ataxin-2-binding protein 1

Chain A:  60% 8% 10% 19%



4.2.26 Score per residue for model 26

- Molecule 1: UGCAUGU

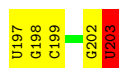
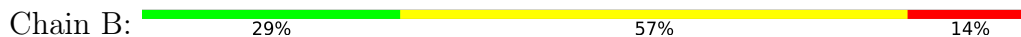


- Molecule 2: Ataxin-2-binding protein 1

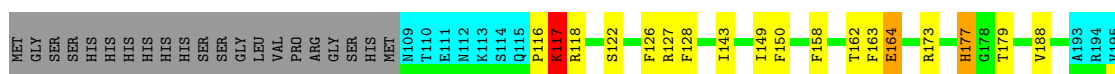


4.2.27 Score per residue for model 27

- Molecule 1: UGCAUGU

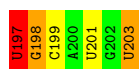
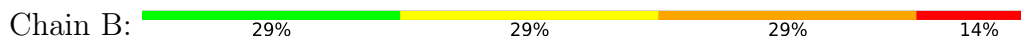


- Molecule 2: Ataxin-2-binding protein 1



4.2.28 Score per residue for model 28

- Molecule 1: UGCAUGU



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 30 calculated structures, 30 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CYANA	structure solution	2.0
Amber	refinement	7.0

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	0.90±0.02	0±0/161 (0.0± 0.0%)	1.31±0.07	2±1/249 (0.7± 0.5%)
2	A	0.86±0.01	0±0/636 (0.0± 0.0%)	1.64±0.03	6±3/852 (0.7± 0.3%)
All	All	0.87	0/23910 (0.0%)	1.57	241/33030 (0.7%)

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	1.8±1.0
2	A	0.0±0.0	4.0±1.4
All	All	0	173

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	177	HIS	CB-CG-CD2	-7.83	121.02	131.20	27	30
2	A	149	ILE	CA-C-N	7.63	136.12	121.54	18	3
2	A	149	ILE	C-N-CA	7.63	136.12	121.54	18	3
1	B	203	U	C5'-C4'-C3'	7.24	126.06	115.20	4	7
2	A	158	PHE	CA-CB-CG	7.18	120.98	113.80	27	26
2	A	117	LYS	CA-C-N	6.97	134.24	121.70	9	11
2	A	117	LYS	C-N-CA	6.97	134.24	121.70	9	11
1	B	202	G	C2'-C3'-O3'	6.92	119.87	109.50	6	16
1	B	197	U	O4'-C1'-C2'	-6.85	100.75	107.60	18	4
2	A	116	PRO	CA-C-N	6.58	134.12	121.54	15	9
2	A	116	PRO	C-N-CA	6.58	134.12	121.54	15	9
1	B	197	U	N1-C1'-C2'	6.28	121.42	112.00	3	8
2	A	118	ARG	CB-CA-C	6.16	119.96	109.80	1	7

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	200	A	C2'-C3'-O3'	5.90	118.34	109.50	16	3
2	A	149	ILE	N-CA-CB	-5.88	106.40	112.28	16	3
1	B	202	G	C4'-C3'-C2'	-5.86	96.75	102.60	7	10
2	A	127	ARG	CA-C-N	5.80	129.34	121.05	29	1
2	A	127	ARG	C-N-CA	5.80	129.34	121.05	29	1
2	A	154	GLY	CA-C-N	5.78	132.58	121.54	23	2
2	A	154	GLY	C-N-CA	5.78	132.58	121.54	23	2
2	A	188	VAL	CA-CB-CG2	5.70	120.09	110.40	5	16
2	A	161	VAL	CA-CB-CG1	5.61	119.93	110.40	17	3
2	A	188	VAL	N-CA-C	5.59	112.20	106.21	19	3
2	A	163	PHE	CA-C-N	5.52	129.43	120.60	5	3
2	A	163	PHE	C-N-CA	5.52	129.43	120.60	5	3
1	B	200	A	P-O3'-C3'	5.47	128.41	120.20	16	1
2	A	130	ASP	CA-C-N	5.47	124.93	119.24	19	3
2	A	130	ASP	C-N-CA	5.47	124.93	119.24	19	3
2	A	149	ILE	CB-CA-C	5.43	119.31	113.22	16	1
2	A	124	ILE	CA-C-N	5.42	126.62	119.84	30	2
2	A	124	ILE	C-N-CA	5.42	126.62	119.84	30	2
2	A	121	VAL	CA-CB-CG1	5.36	119.52	110.40	2	1
2	A	183	GLY	CA-C-N	5.32	130.59	121.87	4	1
2	A	183	GLY	C-N-CA	5.32	130.59	121.87	4	1
2	A	120	HIS	CB-CG-CD2	-5.29	124.32	131.20	3	15
2	A	142	LYS	CA-C-N	5.29	128.42	120.69	19	2
2	A	142	LYS	C-N-CA	5.29	128.42	120.69	19	2
2	A	126	PHE	CA-C-N	5.25	131.58	121.54	29	1
2	A	126	PHE	C-N-CA	5.25	131.58	121.54	29	1
2	A	118	ARG	N-CA-C	5.21	121.89	110.80	6	3
2	A	179	THR	CA-CB-CG2	5.20	119.34	110.50	4	1
2	A	173	ARG	CD-NE-CZ	5.07	131.49	124.40	30	1
2	A	168	ASP	CA-CB-CG	5.06	117.66	112.60	28	1
2	A	129	ARG	CA-C-N	5.05	127.03	120.26	23	2
2	A	129	ARG	C-N-CA	5.05	127.03	120.26	23	2
1	B	197	U	C2'-C3'-O3'	5.03	117.04	109.50	9	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	162	THR	Peptide	27
2	A	117	LYS	Peptide	20

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Mol	Chain	Res	Type	Group	Models (Total)
2	A	164	GLU	Peptide	20
2	A	163	PHE	Peptide	20
2	A	118	ARG	Peptide	19
1	B	203	U	Sidechain	16
1	B	197	U	Sidechain	15
2	A	191	ALA	Peptide	8
1	B	201	U	Sidechain	8
1	B	199	C	Sidechain	6
1	B	198	G	Sidechain	5
1	B	200	A	Sidechain	2
2	A	177	HIS	Sidechain	2
1	B	202	G	Sidechain	2
2	A	192	THR	Peptide	1
2	A	150	PHE	Sidechain	1
2	A	125	PRO	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	145	76	76	0±1
2	A	623	617	617	2±1
All	All	23040	20790	20788	66

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
2:A:149:ILE:HG22	2:A:156:LYS:CE	0.72	2.15	10	9
2:A:149:ILE:HG22	2:A:156:LYS:HE2	0.69	1.63	10	1
2:A:149:ILE:HG22	2:A:156:LYS:HE3	0.66	1.67	14	16
2:A:143:ILE:HD12	2:A:143:ILE:H	0.64	1.53	11	16
1:B:202:G:H1'	2:A:149:ILE:HD12	0.47	1.87	21	2
2:A:137:PHE:CE2	2:A:176:LEU:HD12	0.45	2.47	18	1
1:B:203:U:H5'	1:B:203:U:C6	0.44	2.48	23	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:177:HIS:HB2	2:A:188:VAL:HG22	0.44	1.88	11	1
2:A:148:ILE:CG2	2:A:150:PHE:CD1	0.44	3.01	3	1
2:A:149:ILE:HG13	2:A:158:PHE:CE2	0.43	2.49	25	7
2:A:143:ILE:H	2:A:143:ILE:HD12	0.41	1.75	28	1
2:A:137:PHE:CE1	2:A:176:LEU:HD12	0.41	2.51	2	2
1:B:203:U:C6	1:B:203:U:H5'	0.40	2.52	4	1
1:B:201:U:H4'	1:B:202:G:H5'	0.40	1.92	14	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	77/109 (71%)	67±2 (88±3%)	8±2 (10±2%)	1±1 (2±2%)	8	51
All	All	2310/3270 (71%)	2024 (88%)	242 (10%)	44 (2%)	8	51

All 16 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	117	LYS	11
2	A	182	GLU	5
2	A	150	PHE	3
2	A	125	PRO	3
2	A	127	ARG	3
2	A	126	PHE	3
2	A	156	LYS	2
2	A	164	GLU	2
2	A	192	THR	2
2	A	118	ARG	2
2	A	149	ILE	2
2	A	155	SER	2
2	A	116	PRO	1
2	A	183	GLY	1
2	A	128	PHE	1

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Mol	Chain	Res	Type	Models (Total)
2	A	166	SER	1

6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	66/94 (70%)	59±2 (90±2%)	7±2 (10±2%)	9	54
All	All	1980/2820 (70%)	1782 (90%)	198 (10%)	9	54

All 32 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	179	THR	30
2	A	188	VAL	30
2	A	165	ASN	18
2	A	122	SER	15
2	A	160	PHE	15
2	A	192	THR	11
2	A	173	ARG	11
2	A	184	ARG	8
2	A	117	LYS	6
2	A	150	PHE	6
2	A	127	ARG	5
2	A	143	ILE	5
2	A	132	ASP	4
2	A	128	PHE	4
2	A	146	VAL	3
2	A	148	ILE	3
2	A	130	ASP	3
2	A	145	ASP	3
2	A	124	ILE	3
2	A	135	GLN	2
2	A	151	ASN	2
2	A	161	VAL	1
2	A	181	VAL	1
2	A	171	ARG	1

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Mol	Chain	Res	Type	Models (Total)
2	A	164	GLU	1
2	A	153	ARG	1
2	A	134	ARG	1
2	A	142	LYS	1
2	A	175	LYS	1
2	A	180	VAL	1
2	A	185	LYS	1
2	A	118	ARG	1

6.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	7/7 (100%)	3±0 (43±0%)	1±1 (19±14%)	0.04±0.00
All	All	192/210 (91%)	90 (47%)	39 (20%)	0.04

The overall RNA backbone suiteness is 0.07.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	198	G	30
1	B	199	C	30
1	B	203	U	30

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	199	C	14
1	B	197	U	12
1	B	198	G	11
1	B	200	A	2

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided