



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 09:12 PM BST

PDB ID : 2HGH
Title : Transcription Factor IIIA zinc fingers 4-6 bound to 5S rRNA 55mer (NMR structure)
Authors : Lee, B.M.
Deposited on : 2006-06-27

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

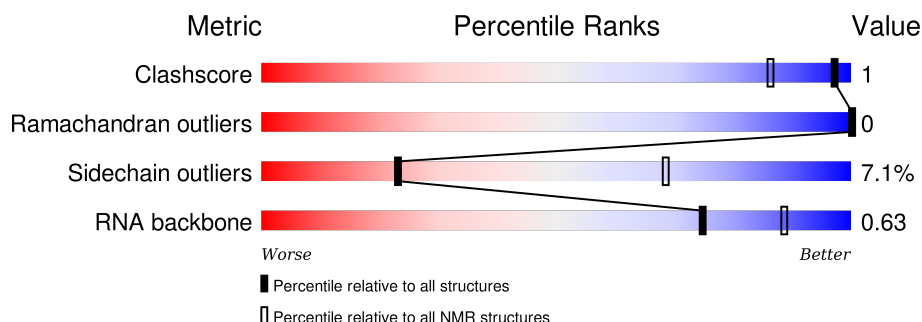
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR



The overall completeness of chemical shifts assignment is 43%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958
RNA backbone	3027	600

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	55	 69% 25% 5%
2	A	87	 84% 13% ..

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 3 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:104-A:188 (85)	0.21	3

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. No single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3166 atoms, of which 1276 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called 55-MER.

Mol	Chain	Residues	Atoms						Trace
1	B	55	Total	C	H	N	O	P	0
			1758	520	591	201	391	55	

- Molecule 2 is a protein called Transcription factor IIIA.

Mol	Chain	Residues	Atoms						Trace
2	A	87	Total	C	H	N	O	S	0
			1405	455	685	133	124	8	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	MET	-	INITIATING METHIONINE	UNP P03001

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

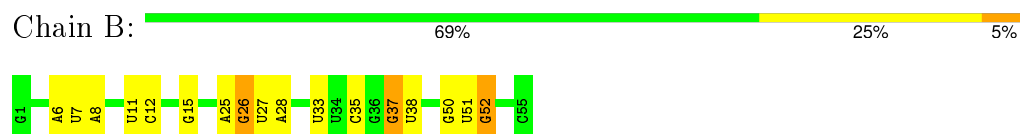
Mol	Chain	Residues	Atoms	
3	A	3	Total	Zn
			3	3

4 Residue-property plots [i](#)

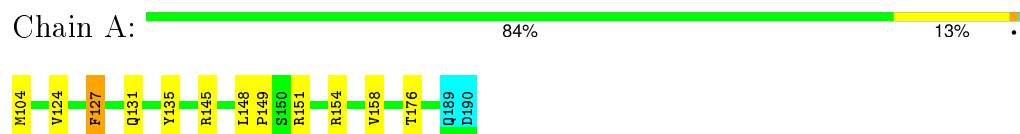
4.1 Average score per residue in the NMR ensemble

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: 55-MER



- Molecule 2: Transcription factor IIIA

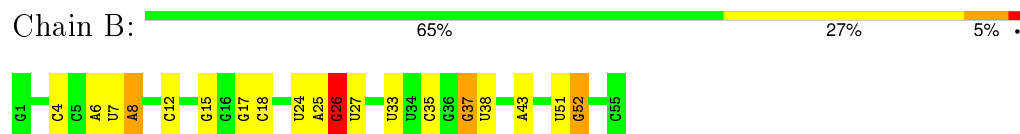


4.2 Scores per residue for each member of the ensemble

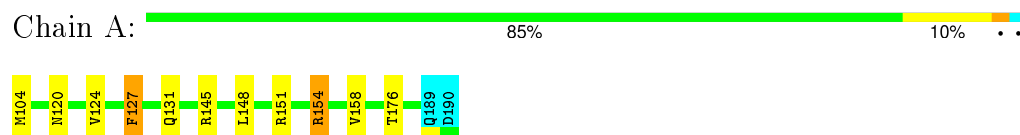
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: 55-MER

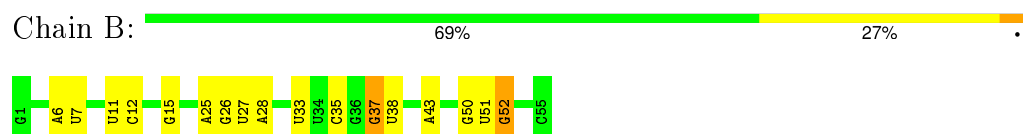


- Molecule 2: Transcription factor IIIA

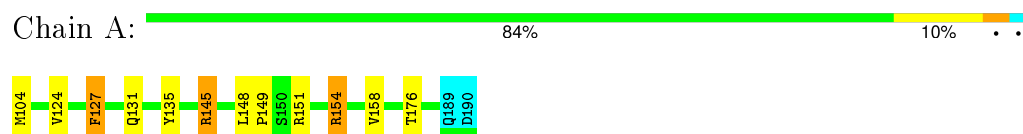


4.2.2 Score per residue for model 2

- Molecule 1: 55-MER

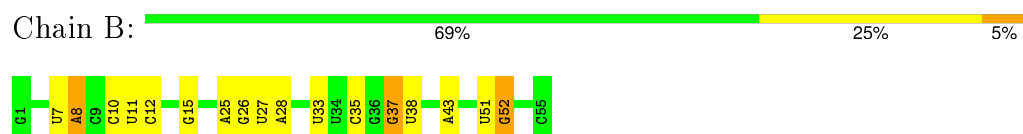


- Molecule 2: Transcription factor IIIA

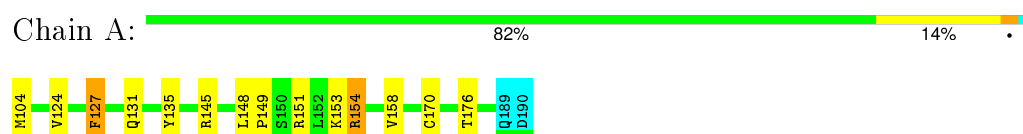


4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: 55-MER

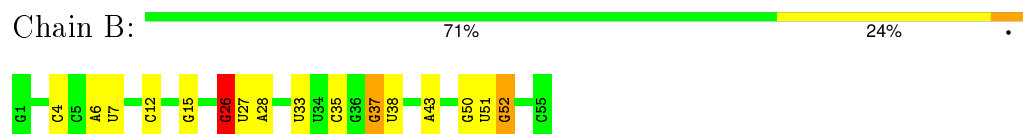


- Molecule 2: Transcription factor IIIA

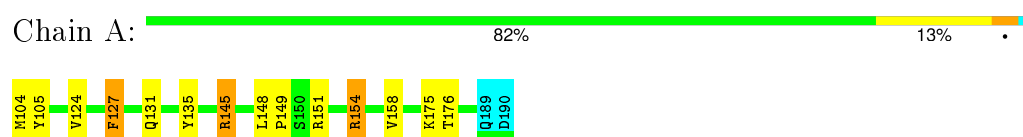


4.2.4 Score per residue for model 4

- Molecule 1: 55-MER

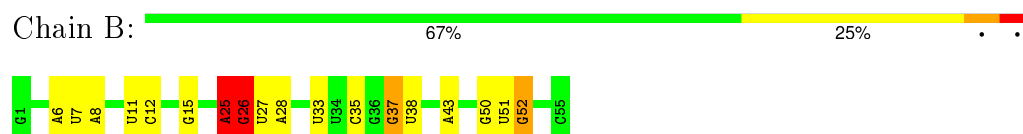


- Molecule 2: Transcription factor IIIA

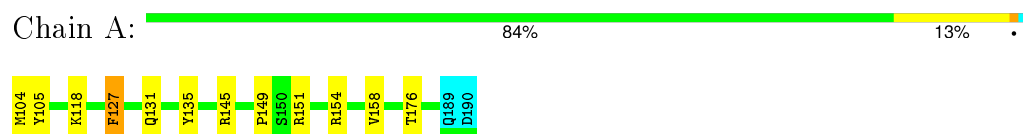


4.2.5 Score per residue for model 5

- Molecule 1: 55-MER

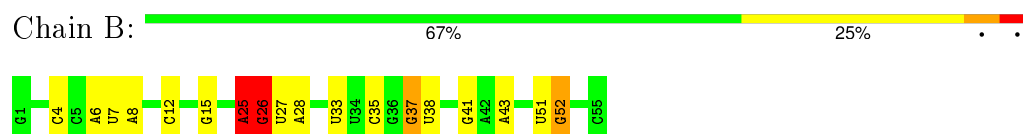


- Molecule 2: Transcription factor IIIA

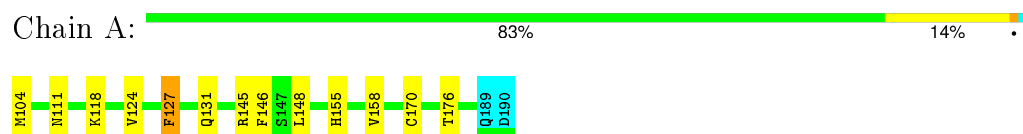


4.2.6 Score per residue for model 6

- Molecule 1: 55-MER

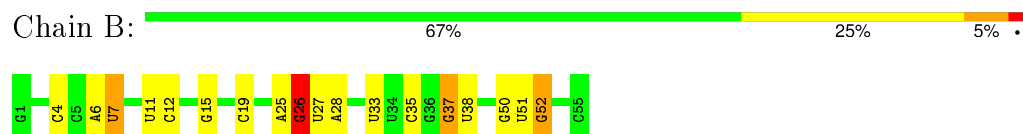


- Molecule 2: Transcription factor IIIA

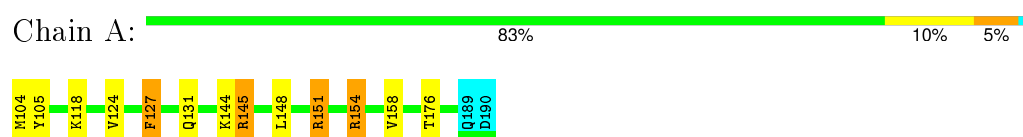


4.2.7 Score per residue for model 7

- Molecule 1: 55-MER



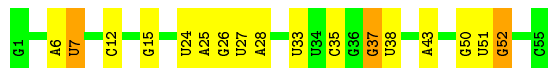
- Molecule 2: Transcription factor IIIA




4.2.8 Score per residue for model 8

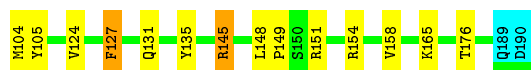
- Molecule 1: 55-MER

Chain B:  69% 25% 5%



- Molecule 2: Transcription factor IIIA

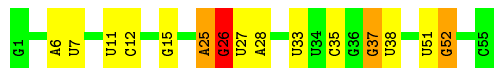
Chain A:  82% 14% ..




4.2.9 Score per residue for model 9

- Molecule 1: 55-MER

Chain B:  73% 20% 5% .



- Molecule 2: Transcription factor IIIA

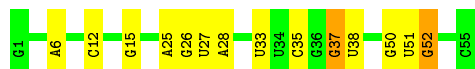
Chain A:  83% 13% ..




4.2.10 Score per residue for model 10

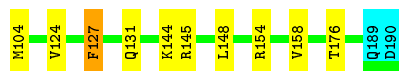
- Molecule 1: 55-MER

Chain B:  75% 22% .



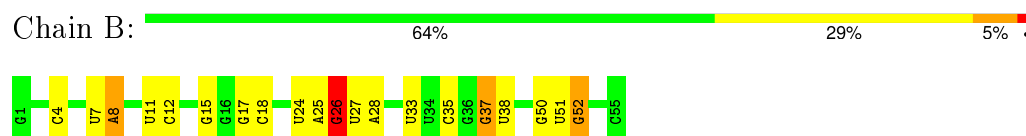
- Molecule 2: Transcription factor IIIA

Chain A:  86% 10% ..

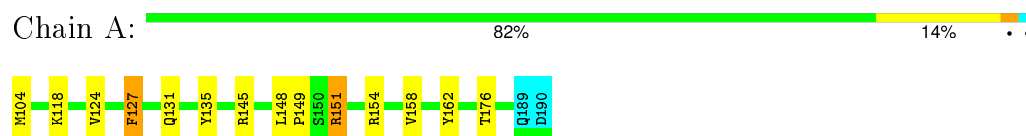


4.2.11 Score per residue for model 11

- Molecule 1: 55-MER

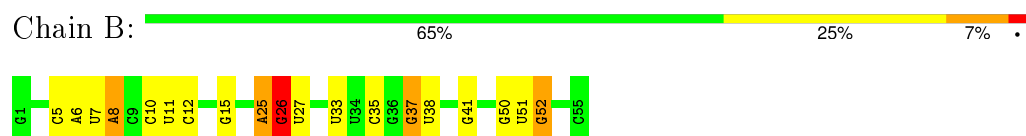


- Molecule 2: Transcription factor IIIA

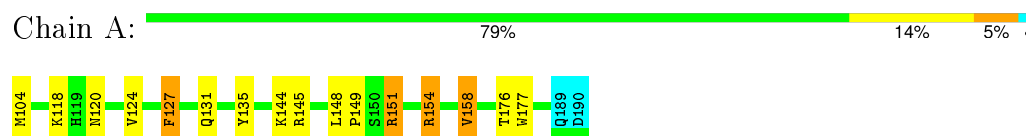


4.2.12 Score per residue for model 12

- Molecule 1: 55-MER

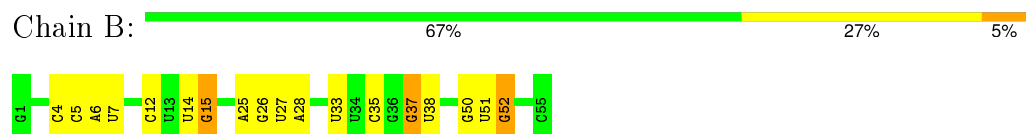


- Molecule 2: Transcription factor IIIA

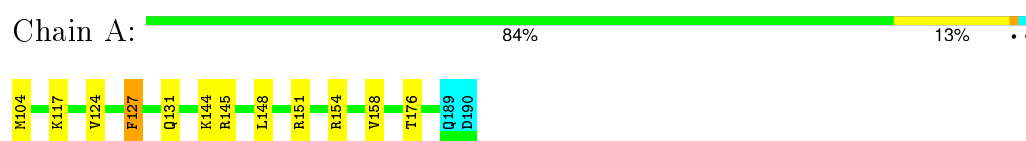


4.2.13 Score per residue for model 13

- Molecule 1: 55-MER



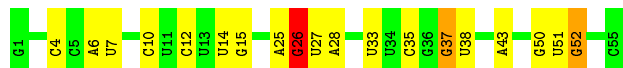
- Molecule 2: Transcription factor IIIA




4.2.14 Score per residue for model 14

- Molecule 1: 55-MER

Chain B:  65% 29% . .



- Molecule 2: Transcription factor IIIA

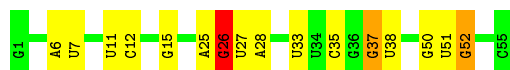
Chain A:  83% 14% . .




4.2.15 Score per residue for model 15

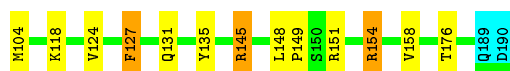
- Molecule 1: 55-MER

Chain B:  71% 24% . .



- Molecule 2: Transcription factor IIIA

Chain A:  83% 11% . .




4.2.16 Score per residue for model 16

- Molecule 1: 55-MER

Chain B:  64% 29% 5% .



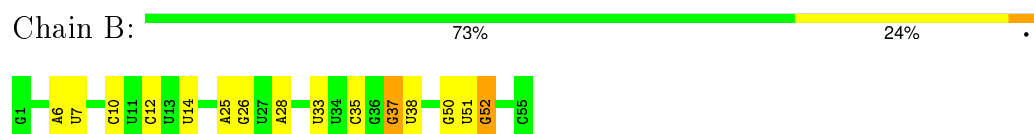
- Molecule 2: Transcription factor IIIA

Chain A:  84% 11% . .

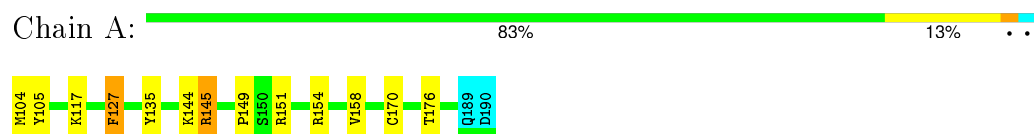


4.2.17 Score per residue for model 17

- Molecule 1: 55-MER

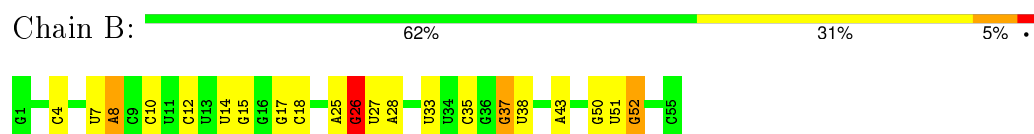


- Molecule 2: Transcription factor IIIA

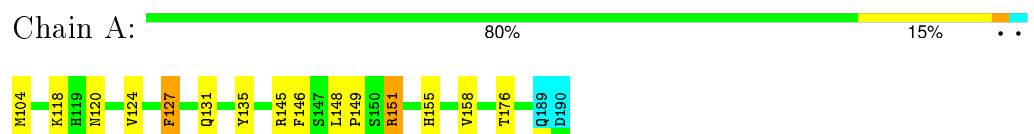


4.2.18 Score per residue for model 18

- Molecule 1: 55-MER

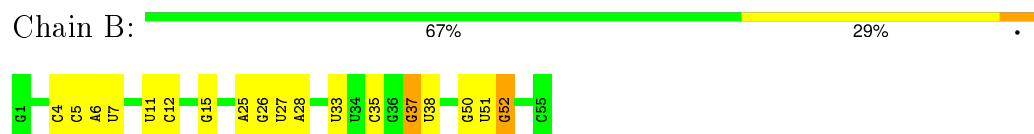


- Molecule 2: Transcription factor IIIA

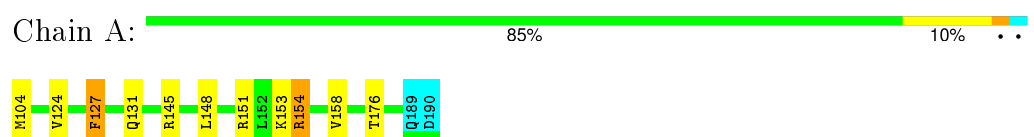


4.2.19 Score per residue for model 19

- Molecule 1: 55-MER

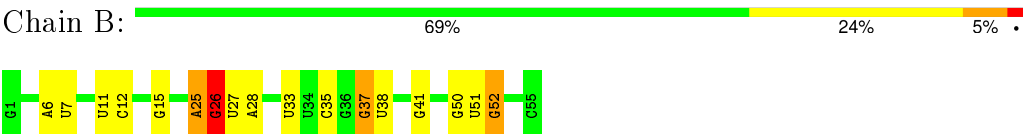


- Molecule 2: Transcription factor IIIA

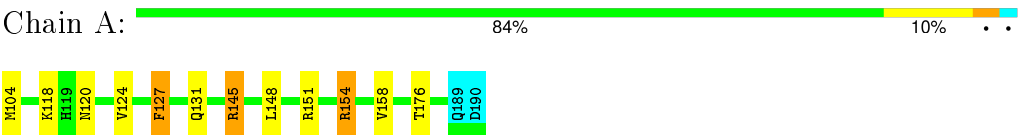


4.2.20 Score per residue for model 20

- Molecule 1: 55-MER



- Molecule 2: Transcription factor IIIA



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics, molecular dynamics, generalized Born solvation model*.

Of the 200 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	1.5
AMBER	refinement	8

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)	BMRB entry 7194
Number of chemical shift lists	1
Total number of shifts	977
Number of shifts mapped to atoms	977
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	43%

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

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	1.31±0.00	0±0/1301 (0.0±0.0%)	1.31±0.01	6±1/2025 (0.3±0.1%)
2	A	0.79±0.00	0±0/727 (0.0±0.0%)	1.00±0.02	6±1/977 (0.6±0.1%)
All	All	1.15	0/40560 (0.0%)	1.21	231/60040 (0.4%)

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	11.4±1.6
2	A	0.0±0.0	0.8±0.8
All	All	0	246

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	154	ARG	NE-CZ-NH1	8.07	124.34	120.30	12	18
2	A	151	ARG	NE-CZ-NH1	8.00	124.30	120.30	7	15
1	B	25	A	C3'-C2'-C1'	-7.96	95.13	101.50	8	16
1	B	6	A	O4'-C4'-C3'	6.72	111.48	106.10	2	16
2	A	151	ARG	NE-CZ-NH2	-6.66	116.97	120.30	20	7
2	A	145	ARG	NE-CZ-NH1	6.64	123.62	120.30	5	17
1	B	26	G	C5'-C4'-O4'	6.59	117.01	109.10	15	5
2	A	158	VAL	CG1-CB-CG2	-6.30	100.82	110.90	15	20
2	A	154	ARG	NE-CZ-NH2	-6.04	117.28	120.30	9	6
1	B	26	G	O4'-C1'-C2'	-5.94	99.86	105.80	4	7

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	8	A	C3'-C2'-C1'	-5.86	96.81	101.50	11	8
1	B	15	G	C5'-C4'-O4'	5.82	116.09	109.10	13	1
2	A	105	TYR	CB-CG-CD2	-5.80	117.52	121.00	9	6
1	B	37	G	C4'-C3'-C2'	-5.73	96.87	102.60	15	20
2	A	127	PHE	CB-CG-CD2	-5.67	116.83	120.80	18	19
2	A	162	TYR	CB-CG-CD1	-5.42	117.75	121.00	11	1
1	B	15	G	C5'-C4'-C3'	-5.40	107.36	116.00	14	2
1	B	19	C	C5'-C4'-O4'	5.40	115.58	109.10	7	1
1	B	7	U	O4'-C4'-C3'	5.36	110.38	106.10	7	2
1	B	38	U	C5'-C4'-O4'	5.28	115.44	109.10	16	20
1	B	26	G	C5'-C4'-C3'	-5.27	107.57	116.00	16	3
1	B	11	U	C5'-C4'-O4'	5.25	115.40	109.10	5	11
1	B	26	G	C3'-C2'-C1'	-5.23	97.32	101.50	6	3
2	A	127	PHE	CB-CG-CD1	5.13	124.39	120.80	20	4
1	B	24	U	C5'-C4'-O4'	5.04	115.15	109.10	11	1
2	A	145	ARG	NE-CZ-NH2	-5.04	117.78	120.30	11	1
1	B	25	A	C1'-O4'-C4'	-5.01	105.89	109.90	8	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	B	51	U	Sidechain	20
1	B	33	U	Sidechain	20
1	B	35	C	Sidechain	20
1	B	52	G	Sidechain	20
1	B	37	G	Sidechain	20
1	B	27	U	Sidechain	19
1	B	7	U	Sidechain	19
1	B	28	A	Sidechain	18
1	B	50	G	Sidechain	16
1	B	26	G	Sidechain	13
1	B	4	C	Sidechain	10
2	A	145	ARG	Sidechain	10
1	B	43	A	Sidechain	10
1	B	8	A	Sidechain	6
2	A	154	ARG	Sidechain	6
1	B	10	C	Sidechain	5
1	B	25	A	Sidechain	4
1	B	41	G	Sidechain	3

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Mol	Chain	Res	Type	Group	Models (Total)
1	B	5	C	Sidechain	3
1	B	24	U	Sidechain	2
2	A	105	TYR	Sidechain	1
1	B	14	U	Sidechain	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	1167	591	592	1±1
2	A	703	673	671	3±1
All	All	37460	25280	25260	58

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
1:B:25:A:N3	2:A:118:LYS:HE2	0.55	2.16	5	5
2:A:124:VAL:HG21	2:A:148:LEU:HD23	0.55	1.78	4	8
2:A:124:VAL:HG21	2:A:148:LEU:HD13	0.53	1.79	19	10
1:B:26:G:O4'	2:A:118:LYS:HE3	0.52	2.04	9	7
2:A:124:VAL:HG21	2:A:148:LEU:CD2	0.49	2.38	18	8
2:A:127:PHE:CD1	2:A:127:PHE:C	0.45	2.89	17	1
2:A:135:TYR:CZ	2:A:149:PRO:HD3	0.45	2.46	5	12
1:B:17:G:C5	1:B:18:C:C5	0.41	3.09	18	3
2:A:146:PHE:CZ	2:A:155:HIS:CG	0.40	3.10	6	2
1:B:6:A:C8	2:A:177:TRP:CE2	0.40	3.10	12	1
1:B:5:C:H2'	2:A:158:VAL:HG22	0.40	1.93	12	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	84/87 (97%)	80±1 (95±1%)	4±1 (5±1%)	0±0 (0±0%)	100	100
All	All	1680/1740 (97%)	1595 (95%)	85 (5%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	78/80 (98%)	73±1 (93±1%)	6±1 (7±1%)	23	68
All	All	1560/1600 (98%)	1450 (93%)	110 (7%)	23	68

All 14 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	104	MET	20
2	A	127	PHE	20
2	A	176	THR	20
2	A	131	GLN	19
2	A	144	LYS	6
2	A	151	ARG	5
2	A	120	ASN	4
2	A	154	ARG	4
2	A	170	CYS	3
2	A	165	LYS	2
2	A	153	LYS	2
2	A	175	LYS	2
2	A	117	LYS	2
2	A	111	ASN	1

6.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	B	54/55 (98%)	4±0 (8±0%)	0±0 (0±0%)	0.63±0.01
All	All	1080/1100 (98%)	81 (8%)	1 (0%)	0.63

The overall RNA backbone suiteness is 0.63.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	12	C	20
1	B	26	G	20
1	B	52	G	20
1	B	15	G	17
1	B	14	U	4

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	B	14	U	1

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 carbohydrates in this entry.

6.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 43% for the well-defined parts and 43% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 7194

Chemical shift list name: *assigned_chem_shift_list_1*

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	977
Number of shifts mapped to atoms	977
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
$^{13}\text{C}_\alpha$	87	-0.08 ± 0.25	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	80	0.41 ± 0.30	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	82	-0.32 ± 0.44	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 43%, i.e. 921 atoms were assigned a chemical shift out of a possible 2141. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	330/417 (79%)	165/166 (99%)	85/170 (50%)	80/81 (99%)
Sidechain	458/537 (85%)	291/324 (90%)	158/187 (84%)	9/26 (35%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	133/153 (87%)	69/83 (83%)	59/59 (100%)	5/11 (45%)
Overall	921/2141 (43%)	525/1167 (45%)	302/784 (39%)	94/190 (49%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 43%, i.e. 941 atoms were assigned a chemical shift out of a possible 2165. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	338/427 (79%)	169/170 (99%)	87/174 (50%)	82/83 (99%)
Sidechain	470/551 (85%)	299/332 (90%)	161/192 (84%)	10/27 (37%)
Aromatic	133/153 (87%)	69/83 (83%)	59/59 (100%)	5/11 (45%)
Overall	941/2165 (43%)	537/1179 (46%)	307/793 (39%)	97/193 (50%)

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.

Random coil index (RCI) for chain A:

