



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 11:58 pm BST

PDB ID : 2MS1  
Title : Solution NMR structure of tRNA<sup>pro</sup>:MLV Nucleocapsid Protein (1:1) Complex  
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Deposited on : 2014-07-19

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

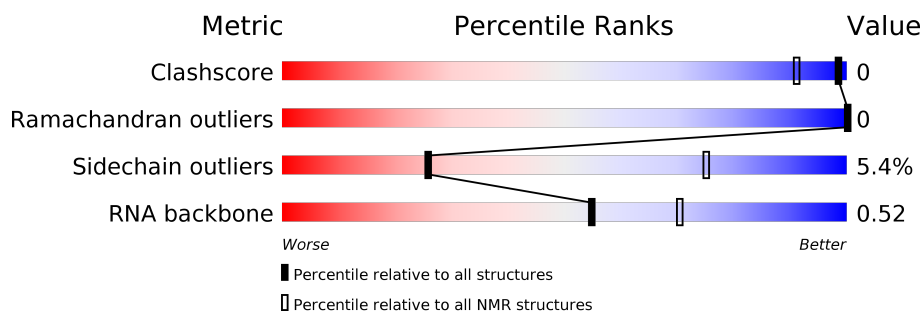
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 15%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428
RNA backbone	4643	676

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	56	 27% 70%
2	B	71	 24% 54% 20%

## 2 Ensemble composition and analysis

This entry contains 10 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:25-A:40 (16)	0.10	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 and 3 single-model clusters were found.

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

### 3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3155 atoms, of which 1201 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Nucleocapsid protein p10.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	55	871	260	435	94	79	3	0

- Molecule 2 is a RNA chain called tRNApro.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	71	2283	676	766	270	501	70	0

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

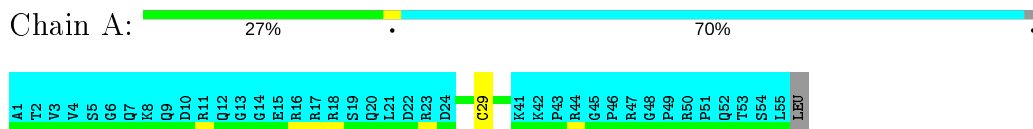
Mol	Chain	Residues	Atoms	
			Total	Zn
3	A	1	1	1

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

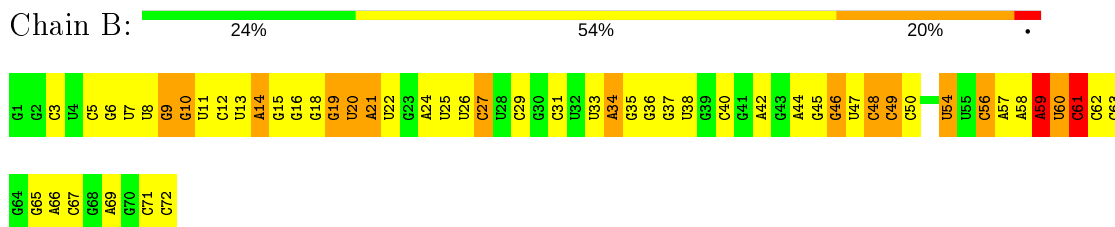
### 4.1 Average score per residue in the NMR ensemble

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: Nucleocapsid protein p10



- Molecule 2: tRNApro

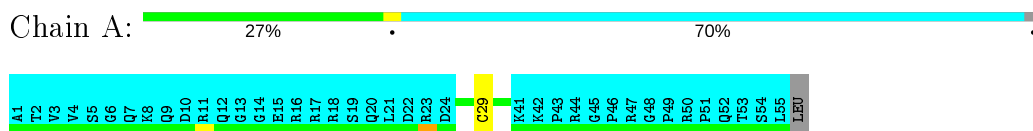


### 4.2 Scores per residue for each member of the ensemble

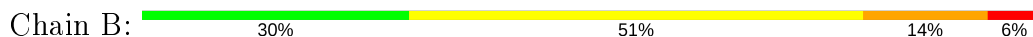
Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

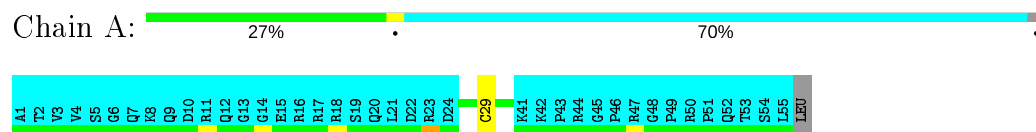
- Molecule 1: Nucleocapsid protein p10



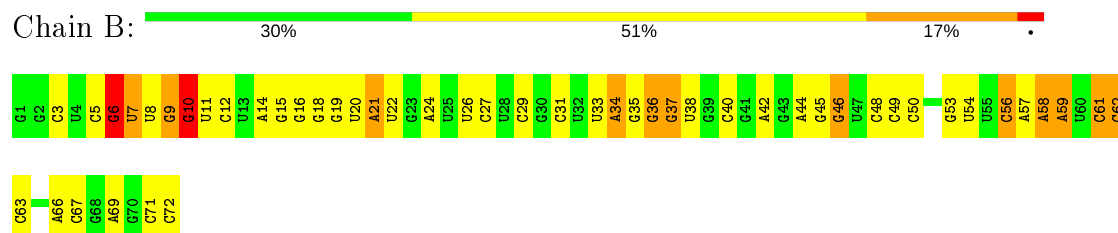
- Molecule 2: tRNApro





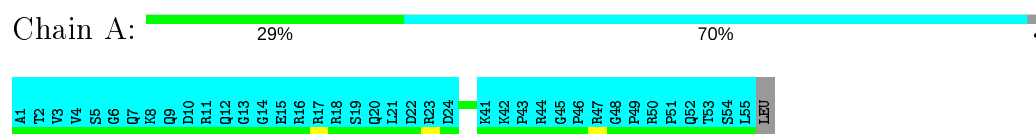


- Molecule 2: tRNA<sub>Pro</sub>

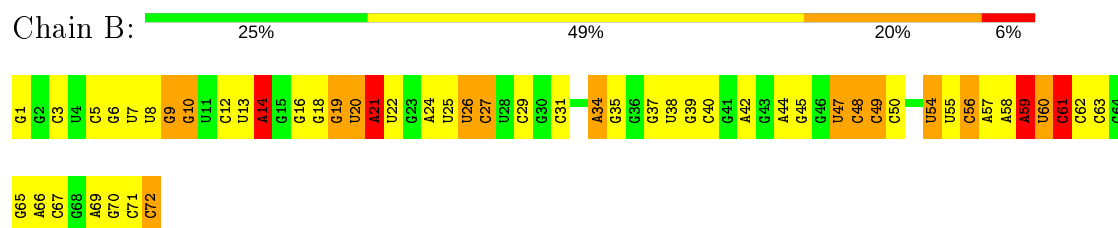


#### 4.2.5 Score per residue for model 5

- Molecule 1: Nucleocapsid protein p10

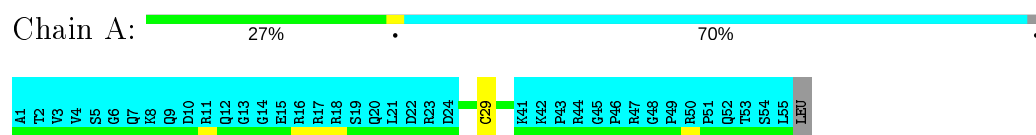


- Molecule 2: tRNA<sub>Pro</sub>

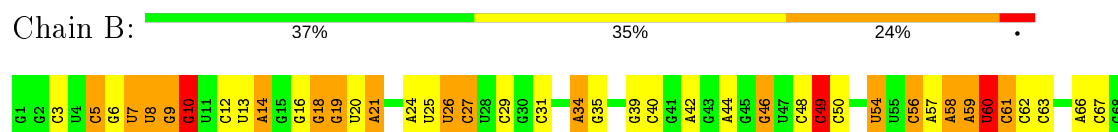


#### 4.2.6 Score per residue for model 6

- Molecule 1: Nucleocapsid protein p10



- Molecule 2: tRNA<sub>Pro</sub>



A69  
G70  
C71  
C72

#### 4.2.7 Score per residue for model 7

- Molecule 1: Nucleocapsid protein p10

Chain A:  29% 70%

A1 T2 V3 V4 S5 S6 G6 G7 R8 R9 Q9 R10 D10 R11 R12 Q12 G13 G14 E15 R16 R17 R18 R19 Q20 L21 L22 D22 R23 D24 K41 K42 P43 R44 G45 P46 R47 G48 P49 R50 P51 Q52 T53 S54 L55 LEU

- Molecule 2: tRNA<sup>Pro</sup>

Chain B:  27% 52% 18%

G1 G2 C3 U4 G5 G6 U7 U8 G9 Q9 R10 G10 U11 C12 U13 U14 A14 G15 G16 G18 G19 U20 A21 A24 U25 U26 C27 U28 C29 G30 C31 A34 G35 G36 G37 U38 R50 G39 C40 G41 A42 G43 A44 G45 G46 U47 C48 C49 C50 U54 U55 C56 A57 A58 A59 U60 G61 C62 C63 G64 G65

A66  
G67  
G68  
A69  
G70  
C71  
C72

#### 4.2.8 Score per residue for model 8

- Molecule 1: Nucleocapsid protein p10

Chain A:  29% 70%

A1 T2 V3 V4 S5 S6 G6 G7 R8 R9 Q9 R10 D10 R11 R12 Q12 G13 G14 E15 R16 R17 R18 R19 Q20 L21 L22 D22 R23 D24 K41 K42 P43 R44 G45 P46 R47 G48 P49 R50 P51 Q52 T53 S54 L55 LEU

- Molecule 2: tRNA<sup>Pro</sup>

Chain B:  27% 54% 17%

G1 G2 C3 U4 G5 G6 U7 U8 G9 Q9 R10 G10 U11 C12 U13 U14 A14 G15 G16 G18 G19 U20 A21 A24 U25 U26 C27 U28 C29 G30 C31 A34 G35 G36 G37 U38 R50 G39 C40 G41 A42 G43 A44 G45 G46 U47 C48 C49 C50 U54 U55 C56 A57 A58 A59 U60 G61 C62 C63 A66

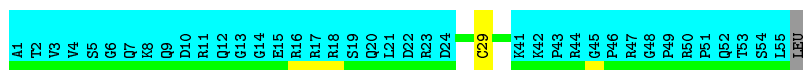
G67  
G68  
A69  
G70  
C71  
C72

#### 4.2.9 Score per residue for model 9

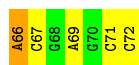
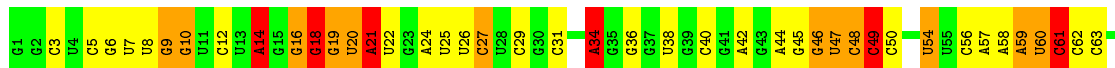
- Molecule 1: Nucleocapsid protein p10

Chain A:  27% 70%





- Molecule 2: tRNA<sup>Pro</sup>

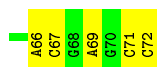


#### 4.2.10 Score per residue for model 10

- Molecule 1: Nucleocapsid protein p10



- Molecule 2: tRNA<sup>Pro</sup>



## 5 Refinement protocol and experimental data overview (i)

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

Of the 20 calculated structures, 10 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
AMBER	refinement	
CYANA	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	4
Total number of shifts	283
Number of shifts mapped to atoms	283
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	15%

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

COVALENT-GEOMETRY INFOmissingINFO

### 5.1 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
2	B	1517	766	766	0±0
All	All	16460	8810	8810	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:13:U:H2'	2:B:14:A:C8	0.46	2.45	10	1
2:B:14:A:N6	2:B:21:A:C2	0.42	2.87	5	2

## 5.2 Torsion angles [i](#)

### 5.2.1 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	
1	A	16/56 (29%)	16±0 (99±2%)	0±0 (1±3%)	0±0 (0±0%)	100	100
All	All	160/560 (29%)	158 (99%)	2 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

### 5.2.2 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	
1	A	13/47 (28%)	12±0 (95±4%)	1±0 (5±4%)	26	75
All	All	130/470 (28%)	123 (95%)	7 (5%)	26	75

All 1 unique residues with a non-rotameric sidechain are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	29	CYS	7

### 5.2.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	70/71 (99%)	16±2 (22±3%)	5±2 (7±2%)	0.52±0.02

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
All	All	700/710 (99%)	156 (22%)	49 (7%)	0.52

The overall RNA backbone suiteness is 0.52.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	59	A	10
2	B	20	U	10
2	B	61	C	9
2	B	8	U	9
2	B	16	G	9
2	B	10	G	8
2	B	19	G	8
2	B	37	G	8
2	B	6	G	8
2	B	49	C	7
2	B	56	C	7
2	B	14	A	7
2	B	9	G	6
2	B	60	U	6
2	B	21	A	6
2	B	45	G	5
2	B	36	G	5
2	B	47	U	5
2	B	7	U	5
2	B	34	A	4
2	B	35	G	3
2	B	48	C	3
2	B	66	A	2
2	B	32	U	1
2	B	18	G	1
2	B	58	A	1
2	B	46	G	1
2	B	33	U	1
2	B	57	A	1

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	6	G	8
2	B	19	G	6
2	B	8	U	5

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Mol	Chain	Res	Type	Models (Total)
2	B	20	U	4
2	B	60	U	4
2	B	47	U	3
2	B	59	A	3
2	B	9	G	2
2	B	16	G	2
2	B	58	A	2
2	B	36	G	2
2	B	32	U	1
2	B	7	U	1
2	B	37	G	1
2	B	46	G	1
2	B	35	G	1
2	B	15	G	1
2	B	18	G	1
2	B	45	G	1

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

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

### 5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.5 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

### 5.6 Other polymers [i](#)

There are no such molecules in this entry.

### 5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 15% for the well-defined parts and 14% for the entire structure.

### 6.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_2*

#### 6.1.1 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	74
Number of shifts mapped to atoms	74
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

#### 6.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

#### 6.1.3 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 3%, i.e. 41 atoms were assigned a chemical shift out of a possible 1537. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	10/78 (13%)	10/31 (32%)	0/32 (0%)	0/15 (0%)
Sidechain	20/91 (22%)	20/56 (36%)	0/31 (0%)	0/4 (0%)
Aromatic	11/27 (41%)	11/14 (79%)	0/11 (0%)	0/2 (0%)
Overall	41/1537 (3%)	41/874 (5%)	0/545 (0%)	0/118 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 5%, i.e. 99 atoms were assigned a chemical shift out of a possible 2061. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	27/265 (10%)	27/105 (26%)	0/110 (0%)	0/50 (0%)
Sidechain	61/428 (14%)	61/259 (24%)	0/133 (0%)	0/36 (0%)
Aromatic	11/27 (41%)	11/14 (79%)	0/11 (0%)	0/2 (0%)
Overall	99/2061 (5%)	99/1151 (9%)	0/725 (0%)	0/185 (0%)

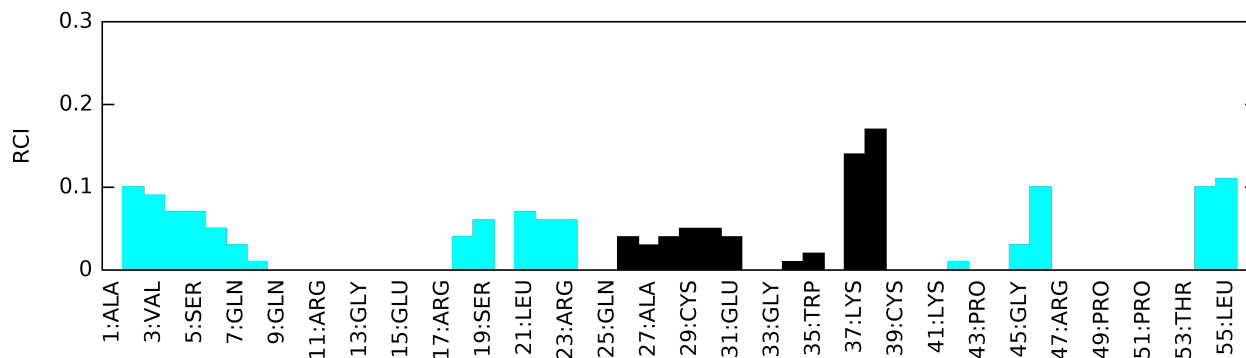
### 6.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 6.1.5 Random Coil Index (RCI) plots [i](#)

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:



## 6.2 Chemical shift list 2

File name: input\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_2\_dup*

### 6.2.1 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	148
Number of shifts mapped to atoms	148

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

### 6.2.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 6.2.3 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 9%, i.e. 134 atoms were assigned a chemical shift out of a possible 1537. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/78 (0%)	0/31 (0%)	0/32 (0%)	0/15 (0%)
Sidechain	0/91 (0%)	0/56 (0%)	0/31 (0%)	0/4 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	134/1537 (9%)	134/874 (15%)	0/545 (0%)	0/118 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 7%, i.e. 134 atoms were assigned a chemical shift out of a possible 2061. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/265 (0%)	0/105 (0%)	0/110 (0%)	0/50 (0%)
Sidechain	0/428 (0%)	0/259 (0%)	0/133 (0%)	0/36 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	134/2061 (7%)	134/1151 (12%)	0/725 (0%)	0/185 (0%)

### 6.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 6.2.5 Random Coil Index (RCI) plots [i](#)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_2\_dup). RCI is only applicable to proteins.



## 6.3 Chemical shift list 3

File name: input\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_2\_dup\_dup*

### 6.3.1 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	33
Number of shifts mapped to atoms	33
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

### 6.3.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 6.3.3 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 2%, i.e. 33 atoms were assigned a chemical shift out of a possible 1537. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/78 (0%)	0/31 (0%)	0/32 (0%)	0/15 (0%)
Sidechain	0/91 (0%)	0/56 (0%)	0/31 (0%)	0/4 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	33/1537 (2%)	0/874 (0%)	33/545 (6%)	0/118 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 2%, i.e. 33 atoms were assigned a chemical shift out of a possible 2061. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/265 (0%)	0/105 (0%)	0/110 (0%)	0/50 (0%)
Sidechain	0/428 (0%)	0/259 (0%)	0/133 (0%)	0/36 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	33/2061 (2%)	0/1151 (0%)	33/725 (5%)	0/185 (0%)

### 6.3.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 6.3.5 Random Coil Index (RCI) plots [i](#)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_2\_dup\_dup). RCI is only applicable to proteins.

## 6.4 Chemical shift list 4

File name: input\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_2\_dup\_dup\_dup*

### 6.4.1 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	28
Number of shifts mapped to atoms	28
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

### 6.4.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 6.4.3 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 2%, i.e. 26 atoms were assigned a chemical shift out of a possible 1537. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/78 (0%)	0/31 (0%)	0/32 (0%)	0/15 (0%)
Sidechain	0/91 (0%)	0/56 (0%)	0/31 (0%)	0/4 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	26/1537 (2%)	26/874 (3%)	0/545 (0%)	0/118 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 1%, i.e. 26 atoms were assigned a chemical shift out of a possible 2061. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	0/265 (0%)	0/105 (0%)	0/110 (0%)	0/50 (0%)
Sidechain	0/428 (0%)	0/259 (0%)	0/133 (0%)	0/36 (0%)
Aromatic	0/27 (0%)	0/14 (0%)	0/11 (0%)	0/2 (0%)
Overall	26/2061 (1%)	26/1151 (2%)	0/725 (0%)	0/185 (0%)

#### 6.4.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 6.4.5 Random Coil Index (RCI) plots [i](#)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_2\_dup\_dup\_dup). RCI is only applicable to proteins.