



Full wwPDB NMR Structure Validation Report ⓘ

Feb 18, 2018 – 02:32 AM EST

PDB ID : 5OBN
Title : NMR solution structure of U11/U12 65K protein's C-terminal RRM domain (381-516)
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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
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20030736
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030736

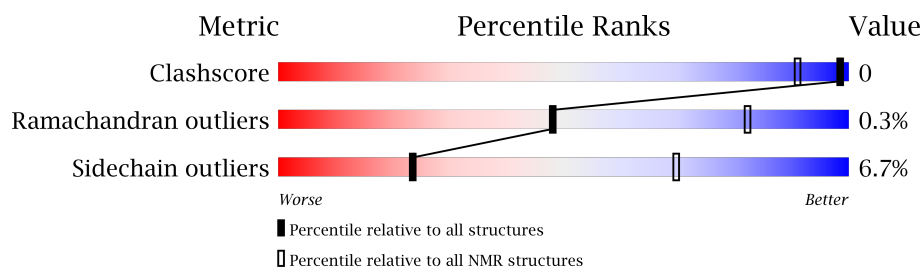
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 88%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	136	

2 Ensemble composition and analysis

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models).

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:387-A:501 (115)	0.37	6

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 2 clusters and 1 single-model cluster was found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2231 atoms, of which 1127 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RNA-binding protein 40.

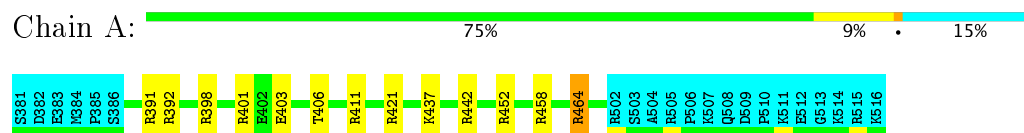
Mol	Chain	Residues	Atoms						Trace
1	A	136	Total	C	H	N	O	S	0
			2231	694	1127	201	201	8	

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: RNA-binding protein 40

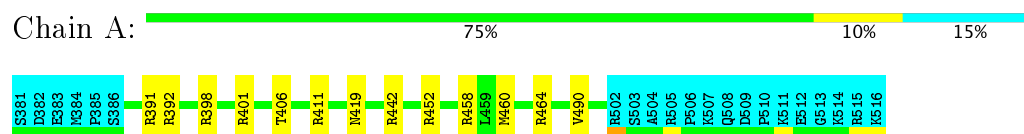


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

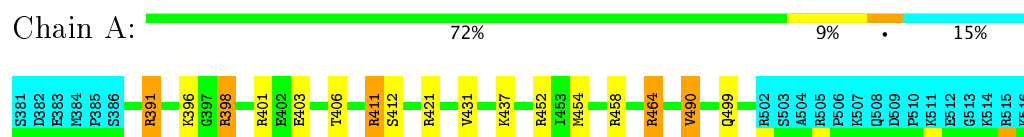
4.2.1 Score per residue for model 1

- Molecule 1: RNA-binding protein 40



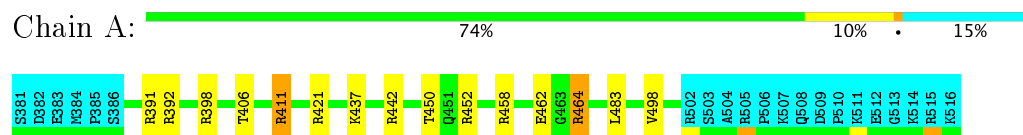
4.2.2 Score per residue for model 2

- Molecule 1: RNA-binding protein 40



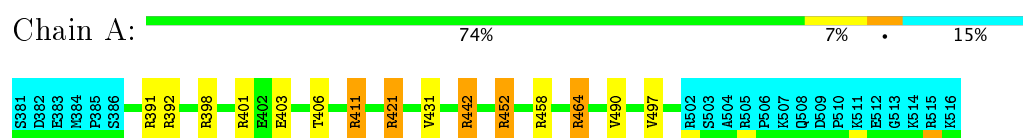
4.2.3 Score per residue for model 3

- Molecule 1: RNA-binding protein 40



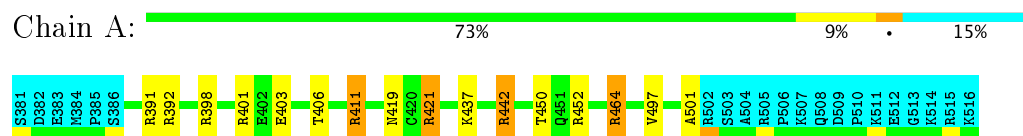
4.2.4 Score per residue for model 4

- Molecule 1: RNA-binding protein 40



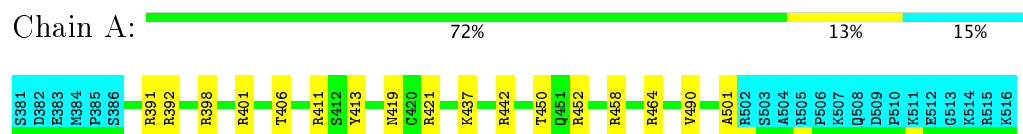
4.2.5 Score per residue for model 5

- Molecule 1: RNA-binding protein 40



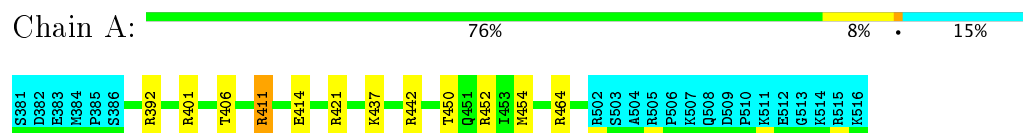
4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: RNA-binding protein 40



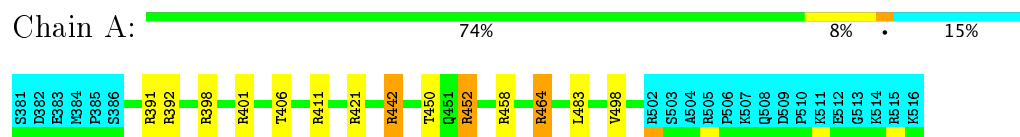
4.2.7 Score per residue for model 7

- Molecule 1: RNA-binding protein 40



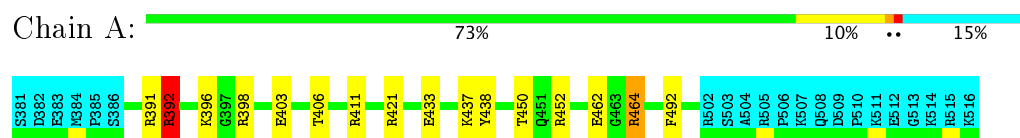
4.2.8 Score per residue for model 8

- Molecule 1: RNA-binding protein 40



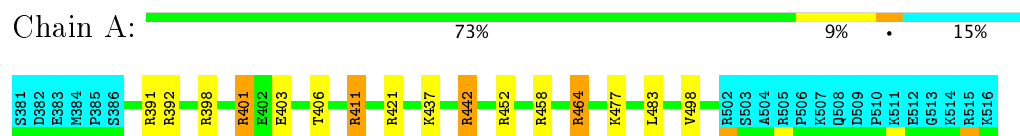
4.2.9 Score per residue for model 9

- Molecule 1: RNA-binding protein 40



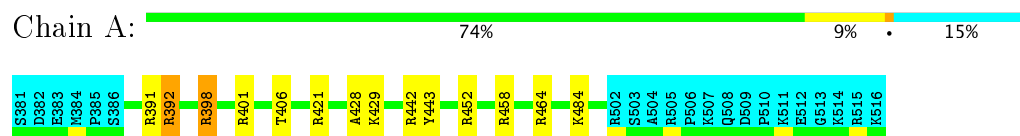
4.2.10 Score per residue for model 10

- Molecule 1: RNA-binding protein 40



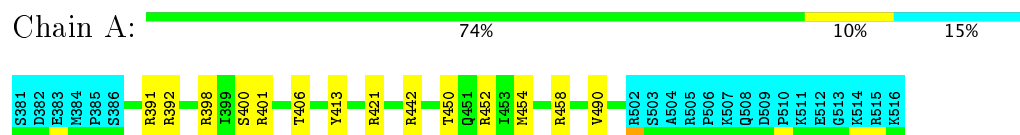
4.2.11 Score per residue for model 11

- Molecule 1: RNA-binding protein 40



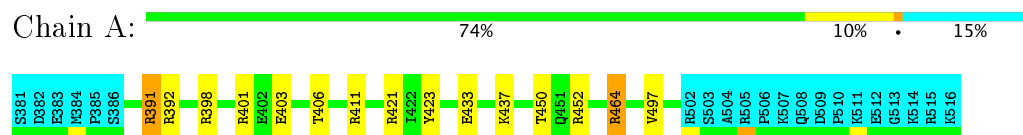
4.2.12 Score per residue for model 12

- Molecule 1: RNA-binding protein 40



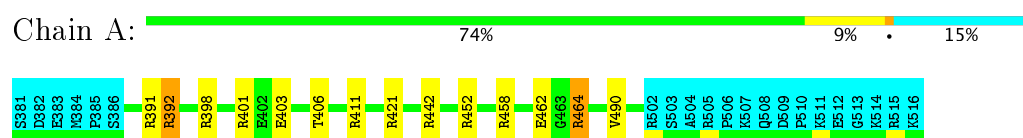
4.2.13 Score per residue for model 13

- Molecule 1: RNA-binding protein 40



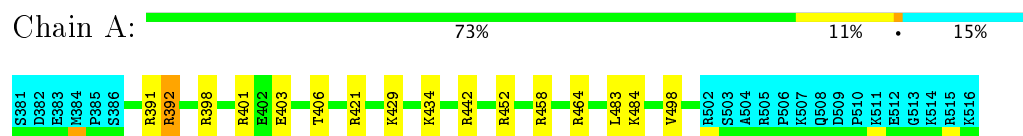
4.2.14 Score per residue for model 14

- Molecule 1: RNA-binding protein 40



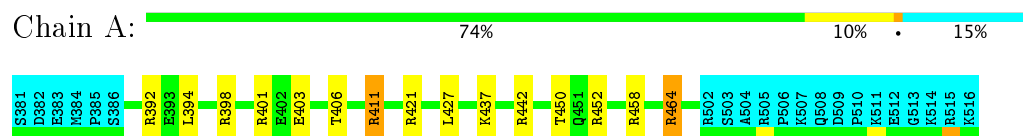
4.2.15 Score per residue for model 15

- Molecule 1: RNA-binding protein 40



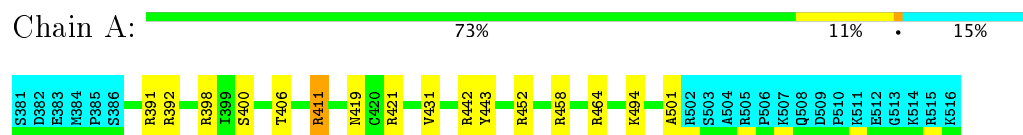
4.2.16 Score per residue for model 16

- Molecule 1: RNA-binding protein 40



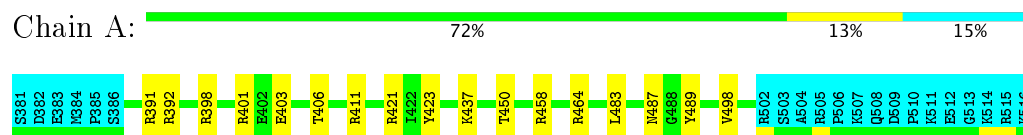
4.2.17 Score per residue for model 17

- Molecule 1: RNA-binding protein 40



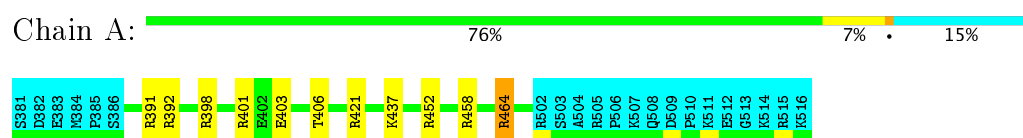
4.2.18 Score per residue for model 18

- Molecule 1: RNA-binding protein 40



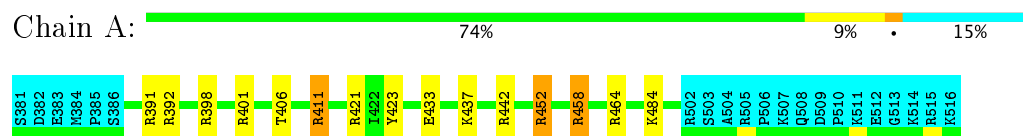
4.2.19 Score per residue for model 19

- Molecule 1: RNA-binding protein 40



4.2.20 Score per residue for model 20

- Molecule 1: RNA-binding protein 40



5 Refinement protocol and experimental data overview

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
AMBER	refinement	14.0
CYANA	structure calculation	3.0
TALOS	structure calculation	N

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)	5obn_cs.cif
Number of chemical shift lists	1
Total number of shifts	1714
Number of shifts mapped to atoms	1714
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

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

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	0.75±0.01	0±0/953 (0.0±0.0%)	1.18±0.03	9±1/1272 (0.7±0.1%)
All	All	0.75	0/19060 (0.0%)	1.18	173/25440 (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	A	0.0±0.0	0.9±0.9
All	All	0	19

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	452	ARG	NE-CZ-NH1	10.26	125.43	120.30	7	19
1	A	458	ARG	NE-CZ-NH1	9.98	125.29	120.30	11	16
1	A	398	ARG	NE-CZ-NH1	9.97	125.29	120.30	5	18
1	A	401	ARG	NE-CZ-NH1	9.40	125.00	120.30	11	17
1	A	464	ARG	NE-CZ-NH1	9.36	124.98	120.30	13	13
1	A	391	ARG	NE-CZ-NH1	9.35	124.97	120.30	8	17
1	A	421	ARG	NE-CZ-NH1	9.33	124.97	120.30	12	19
1	A	442	ARG	NE-CZ-NH1	8.56	124.58	120.30	4	15
1	A	392	ARG	NE-CZ-NH1	7.74	124.17	120.30	19	18
1	A	411	ARG	NE-CZ-NH1	7.34	123.97	120.30	5	13
1	A	398	ARG	NE-CZ-NH2	-5.93	117.34	120.30	12	2
1	A	452	ARG	NE-CZ-NH2	-5.78	117.41	120.30	19	2
1	A	391	ARG	NE-CZ-NH2	-5.54	117.53	120.30	4	1
1	A	421	ARG	NE-CZ-NH2	-5.30	117.65	120.30	8	1
1	A	438	TYR	CB-CG-CD1	-5.27	117.84	121.00	9	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	492	PHE	CB-CA-C	5.00	120.40	110.40	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)
1	A	501	ALA	Peptide	3
1	A	398	ARG	Sidechain	2
1	A	443	TYR	Sidechain	2
1	A	391	ARG	Sidechain	2
1	A	413	TYR	Sidechain	2
1	A	442	ARG	Sidechain	2
1	A	421	ARG	Sidechain	1
1	A	423	TYR	Sidechain	1
1	A	452	ARG	Sidechain	1
1	A	458	ARG	Sidechain	1
1	A	489	TYR	Sidechain	1
1	A	392	ARG	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	936	953	953	0±0
All	All	18720	19060	19060	6

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
1:A:483:LEU:HD23	1:A:498:VAL:HG12	0.52	1.81	10	5
1:A:419:ASN:ND2	1:A:421:ARG:H	0.41	2.13	5	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	
1	A	115/136 (85%)	107±2 (93±2%)	8±2 (7±2%)	0±1 (0±1%)	48	82
All	All	2300/2720 (85%)	2138 (93%)	154 (7%)	8 (0%)	48	82

All 3 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	490	VAL	6
1	A	429	LYS	1
1	A	428	ALA	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	
1	A	99/118 (84%)	92±2 (93±2%)	7±2 (7±2%)	23	70
All	All	1980/2360 (84%)	1847 (93%)	133 (7%)	23	70

All 34 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	406	THR	20
1	A	464	ARG	17
1	A	437	LYS	12
1	A	411	ARG	12
1	A	403	GLU	11
1	A	450	THR	10
1	A	392	ARG	5

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Mol	Chain	Res	Type	Models (Total)
1	A	484	LYS	3
1	A	462	GLU	3
1	A	454	MET	3
1	A	497	VAL	3
1	A	419	ASN	3
1	A	431	VAL	3
1	A	433	GLU	3
1	A	400	SER	2
1	A	452	ARG	2
1	A	423	TYR	2
1	A	396	LYS	2
1	A	442	ARG	2
1	A	477	LYS	1
1	A	434	LYS	1
1	A	460	MET	1
1	A	394	LEU	1
1	A	427	LEU	1
1	A	414	GLU	1
1	A	499	GLN	1
1	A	412	SER	1
1	A	494	LYS	1
1	A	429	LYS	1
1	A	401	ARG	1
1	A	398	ARG	1
1	A	391	ARG	1
1	A	490	VAL	1
1	A	487	ASN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 carbohydrates 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

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 87% for the entire structure.

7.1 Chemical shift list 1

File name: 5obn_cs.cif

Chemical shift list name: *CRRM_121217*

7.1.1 Bookkeeping

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	1714
Number of shifts mapped to atoms	1714
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	136	-0.02 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	126	0.01 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}'$	135	0.31 ± 0.11	None needed (< 0.5 ppm)
^{15}N	131	0.26 ± 0.32	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 88%, i.e. 1335 atoms were assigned a chemical shift out of a possible 1511. 15 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	560/567 (99%)	223/226 (99%)	229/230 (100%)	108/111 (97%)
Sidechain	700/834 (84%)	437/495 (88%)	256/290 (88%)	7/49 (14%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	75/110 (68%)	49/59 (83%)	26/50 (52%)	0/1 (0%)
Overall	1335/1511 (88%)	709/780 (91%)	511/570 (90%)	115/161 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 1566 atoms were assigned a chemical shift out of a possible 1794. 15 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	654/666 (98%)	259/265 (98%)	271/272 (100%)	124/129 (96%)
Sidechain	837/1018 (82%)	527/608 (87%)	302/347 (87%)	8/63 (13%)
Aromatic	75/110 (68%)	49/59 (83%)	26/50 (52%)	0/1 (0%)
Overall	1566/1794 (87%)	835/932 (90%)	599/669 (90%)	132/193 (68%)

7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	430	HIS	CE1	118.59	149.70 – 125.30	-7.8

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:

