Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2MZS
Title	:	NMR structure of the RRM2 domain of Hrb1
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Deposited on	:	2015-02-23

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

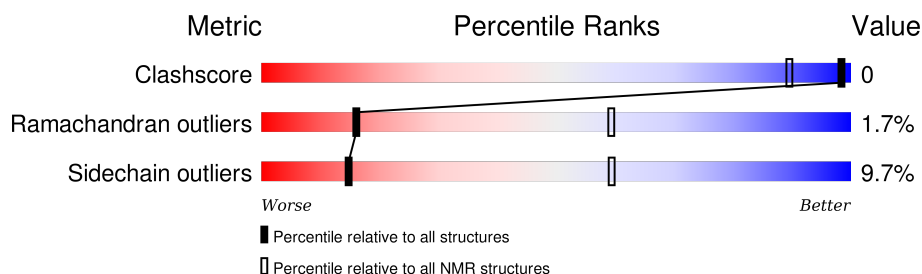|		
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
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 (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 95%.

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	Percentile Ranks	Value
Clashscore		0
Ramachandran outliers		1.7%
Sidechain outliers		9.7%

Worse   *Better*

▌Percentile relative to all structures

▯Percentile relative to all NMR structures

Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	99	71%　　　　5%　24%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 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:262-A:336 (75)	0.50	1

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 5 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1459 atoms, of which 707 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein HRB1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	99	1459	463	707	126	161	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	260	GLY	-	EXPRESSION TAG	UNP P38922
A	261	SER	-	EXPRESSION TAG	UNP P38922

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.
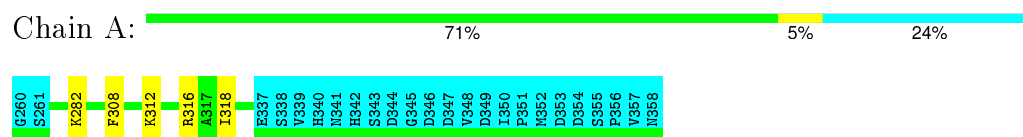
• Molecule 1: Protein HRB1

Chain A:
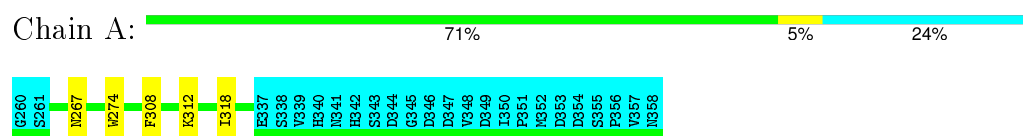
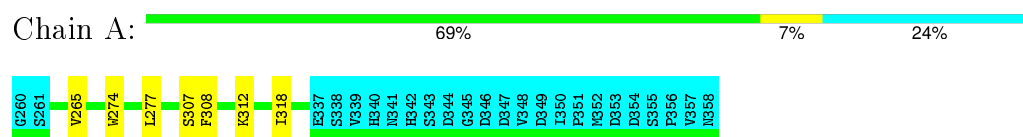## 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

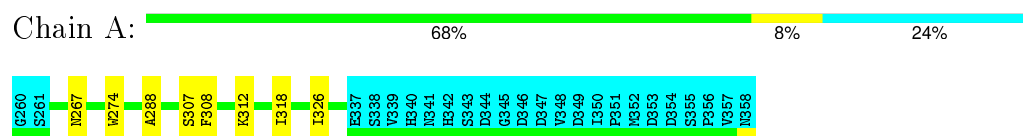### 4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: Protein HRB1

Chain A:

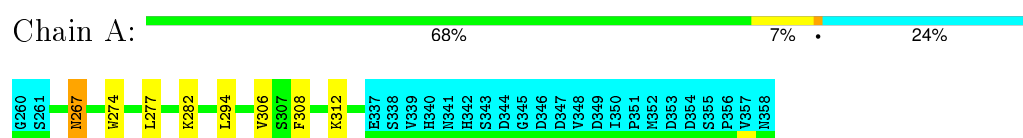### 4.2.2 Score per residue for model 2

• Molecule 1: Protein HRB1

Chain A:

4.2.3 Score per residue for model 3

• Molecule 1: Protein HRB1

Chain A:

4.2.4 Score per residue for model 4

• Molecule 1: Protein HRB1

Chain A:

4.2.5 Score per residue for model 5

• Molecule 1: Protein HRB1

Chain A:
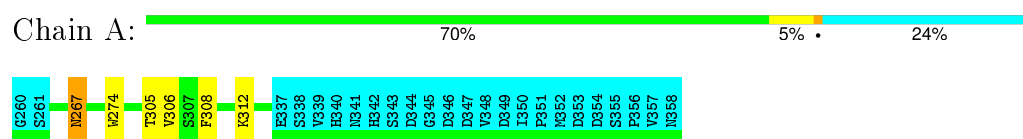
4.2.6 Score per residue for model 6

• Molecule 1: Protein HRB1

Chain A:
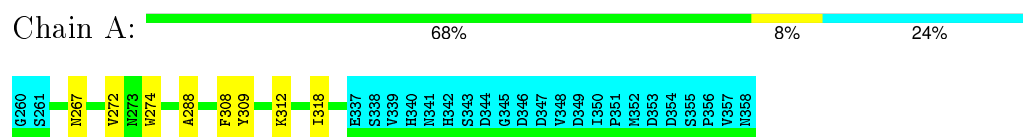
4.2.7 Score per residue for model 7

• Molecule 1: Protein HRB1

Chain A:
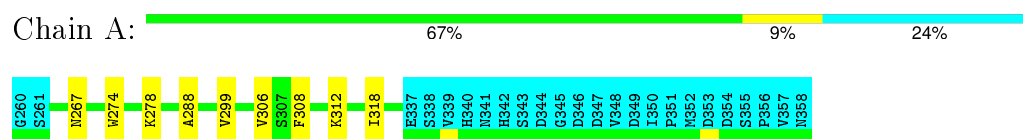
4.2.8 Score per residue for model 8

● Molecule 1: Protein HRB1

Chain A:

4.2.9 Score per residue for model 9

● Molecule 1: Protein HRB1

Chain A:
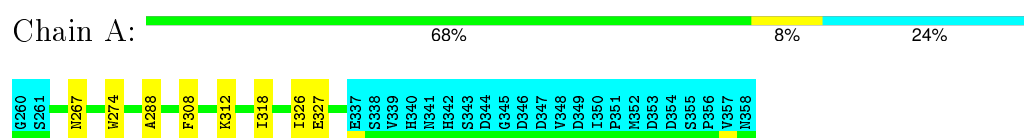
4.2.10 Score per residue for model 10

● Molecule 1: Protein HRB1

Chain A:
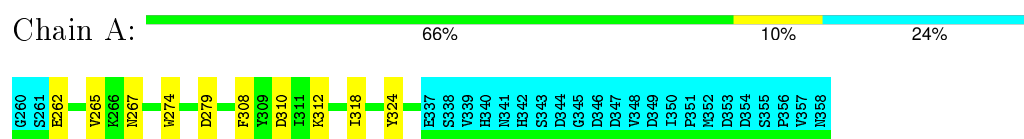
4.2.11 Score per residue for model 11

● Molecule 1: Protein HRB1

Chain A:
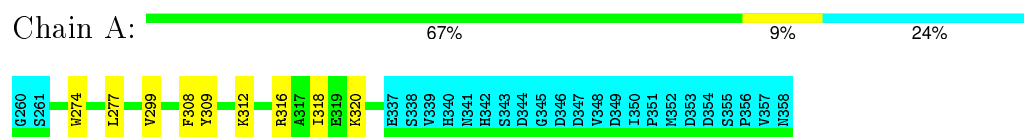
4.2.12 Score per residue for model 12

● Molecule 1: Protein HRB1

Chain A:
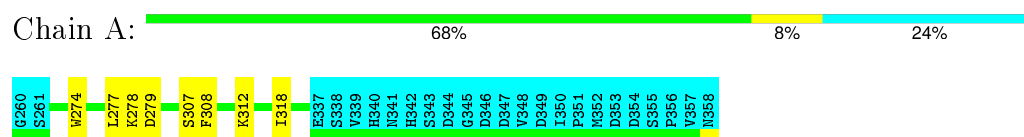
4.2.13   Score per residue for model 13

• Molecule 1: Protein HRB1

Chain A:
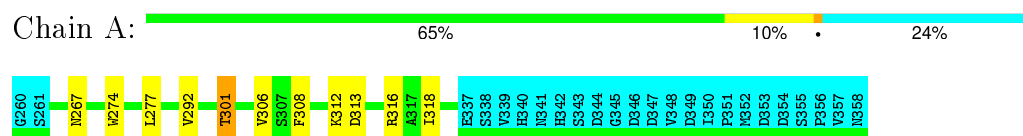
4.2.14   Score per residue for model 14

• Molecule 1: Protein HRB1

Chain A:
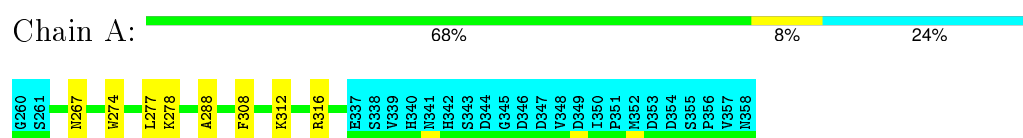
4.2.15   Score per residue for model 15

• Molecule 1: Protein HRB1

Chain A:
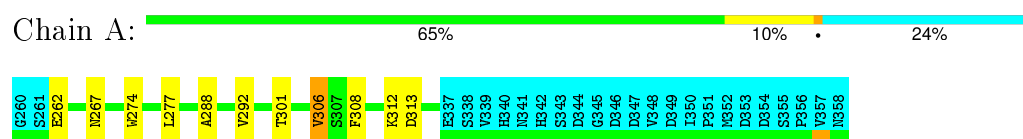
4.2.16   Score per residue for model 16
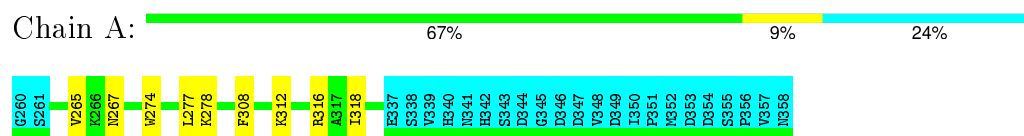
• Molecule 1: Protein HRB1

Chain A:
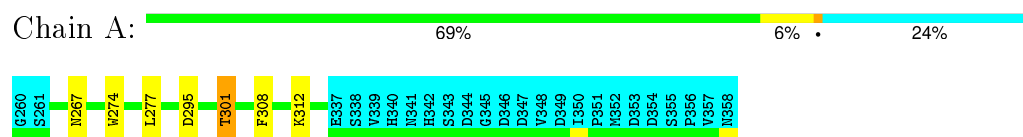
4.2.17   Score per residue for model 17

• Molecule 1: Protein HRB1

Chain A:
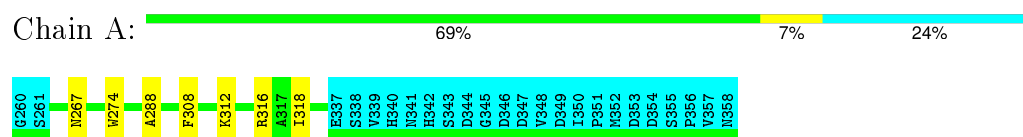
4.2.18 Score per residue for model 18

• Molecule 1: Protein HRB1

Chain A:
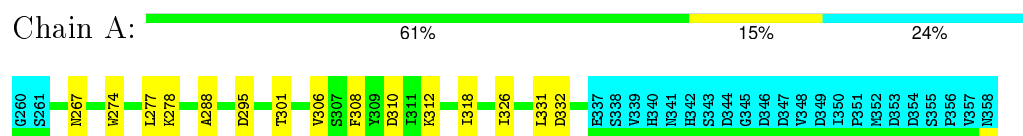
4.2.19 Score per residue for model 19

• Molecule 1: Protein HRB1

Chain A:
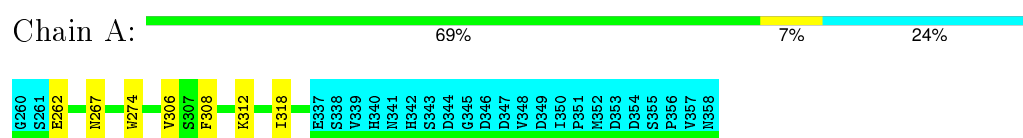
4.2.20 Score per residue for model 20

• Molecule 1: Protein HRB1

Chain A:
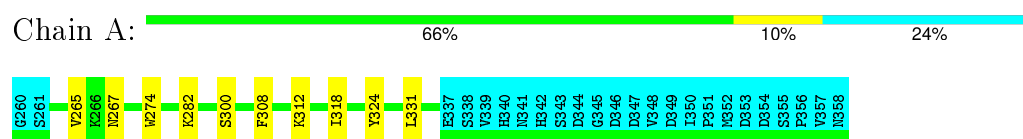
5 Refinement protocol and experimental data overview (i)

Of the 100 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
CYANA	structure solution	
AMBER	refinement	

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)	2mzs_cs.str
Number of chemical shift lists	1
Total number of shifts	1146
Number of shifts mapped to atoms	1146
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	95%

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

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	A	0.71±0.01	0±0/585 (0.0±0.0%)	0.95±0.02	0±1/792 (0.0±0.1%)
All	All	0.71	0/11700 (0.0%)	0.95	6/15840 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.6±0.7
All	All	0	11

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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	316	ARG	NE-CZ-NH1	5.91	123.26	120.30	8	5
1	A	316	ARG	NE-CZ-NH2	-5.13	117.74	120.30	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	A	265	VAL	Peptide	4
1	A	307	SER	Peptide	3
1	A	267	ASN	Peptide	2
1	A	331	LEU	Peptide	1
1	A	309	TYR	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	A	575	562	562	0±1
All	All	11500	11240	11240	9

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	Models Total
1:A:277:LEU:HD21	1:A:306:VAL:HG12	0.61	1.72	18	2
1:A:277:LEU:HD21	1:A:306:VAL:CG1	0.48	2.38	13	3
1:A:277:LEU:HD23	1:A:277:LEU:C	0.44	2.33	2	2
1:A:277:LEU:C	1:A:277:LEU:HD23	0.42	2.34	11	2

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	75/99 (76%)	66±3 (88±4%)	7±3 (10±3%)	1±1 (2±1%)	16	59
All	All	1500/1980 (76%)	1326 (88%)	148 (10%)	26 (2%)	16	59

All 4 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	267	ASN	14
1	A	288	ALA	8
1	A	301	THR	3
1	A	299	VAL	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	63/85 (74%)	57±2 (90±3%)	6±2 (10±3%)	15	59
All	All	1260/1700 (74%)	1138 (90%)	122 (10%)	15	59

All 29 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	308	PHE	20
1	A	312	LYS	20
1	A	274	TRP	19
1	A	318	ILE	15
1	A	278	LYS	5
1	A	306	VAL	4
1	A	262	GLU	3
1	A	282	LYS	3
1	A	301	THR	3
1	A	326	ILE	3
1	A	292	VAL	2
1	A	295	ASP	2
1	A	267	ASN	2
1	A	279	ASP	2
1	A	324	TYR	2
1	A	313	ASP	2
1	A	310	ASP	2
1	A	277	LEU	2
1	A	327	GLU	1
1	A	316	ARG	1
1	A	294	LEU	1
1	A	305	THR	1
1	A	320	LYS	1
1	A	331	LEU	1
1	A	300	SER	1
1	A	309	TYR	1
1	A	299	VAL	1
1	A	332	ASP	1
1	A	272	VAL	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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)

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 (i)

The completeness of assignment taking into account all chemical shift lists is 95% for the well-defined parts and 93% for the entire structure.

7.1 Chemical shift list 1

File name: 2mzs_cs.str

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	1146
Number of shifts mapped to atoms	1146
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
$^{13}C_\alpha$	98	-0.25 ± 0.15	None needed (< 0.5 ppm)
$^{13}C_\beta$	90	0.13 ± 0.14	None needed (< 0.5 ppm)
$^{13}C'$	91	0.01 ± 0.11	None needed (< 0.5 ppm)
^{15}N	92	-0.25 ± 0.38	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 95%, i.e. 826 atoms were assigned a chemical shift out of a possible 874. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	369/373 (99%)	148/149 (99%)	148/150 (99%)	73/74 (99%)
Sidechain	397/433 (92%)	243/249 (98%)	147/168 (88%)	7/16 (44%)

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	Total	**^{1}H**	**^{13}C**	**^{15}N**
Aromatic	60/68 (88%)	32/36 (89%)	27/29 (93%)	1/3 (33%)
Overall	826/874 (95%)	423/434 (97%)	322/347 (93%)	81/93 (87%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 93%, i.e. 1041 atoms were assigned a chemical shift out of a possible 1120. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	**^{1}H**	**^{13}C**	**^{15}N**
Backbone	471/489 (96%)	190/195 (97%)	189/198 (95%)	92/96 (96%)
Sidechain	502/549 (91%)	308/316 (97%)	185/215 (86%)	9/18 (50%)
Aromatic	68/82 (83%)	36/44 (82%)	31/33 (94%)	1/5 (20%)
Overall	1041/1120 (93%)	534/555 (96%)	405/446 (91%)	102/119 (86%)

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: