Full wwPDB NMR Structure Validation Report (i)

Apr 27, 2016 – 04:59 AM BST

PDB ID	:	2RNE
Title	:	Solution structure of the second RNA recognition motif (RRM) of TIA-1
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Deposited on	:	2007-12-19

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

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

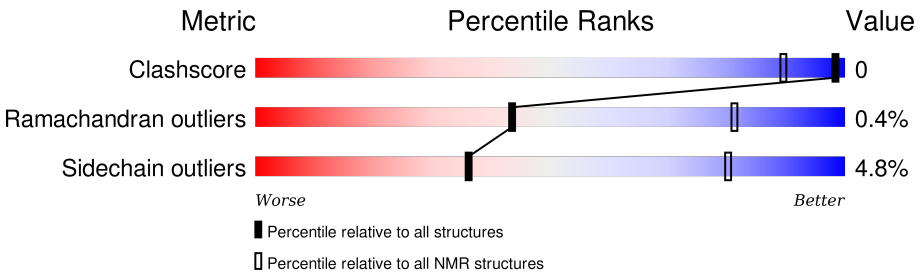
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 92%.

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

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	115	67% • 32%

2 Ensemble composition and analysis (i)

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:96-A:173 (78)	0.22	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 4 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1717 atoms, of which 841 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Tia1 protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	115	1717	546	841	158	170	2	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	GLY	-	EXPRESSION TAG	UNP Q80ZW7
A	83	SER	-	EXPRESSION TAG	UNP Q80ZW7
A	84	SER	-	EXPRESSION TAG	UNP Q80ZW7
A	85	GLY	-	EXPRESSION TAG	UNP Q80ZW7
A	86	SER	-	EXPRESSION TAG	UNP Q80ZW7
A	87	SER	-	EXPRESSION TAG	UNP Q80ZW7
A	88	GLY	-	EXPRESSION TAG	UNP Q80ZW7
A	191	SER	-	EXPRESSION TAG	UNP Q80ZW7
A	192	GLY	-	EXPRESSION TAG	UNP Q80ZW7
A	193	PRO	-	EXPRESSION TAG	UNP Q80ZW7
A	194	SER	-	EXPRESSION TAG	UNP Q80ZW7
A	195	SER	-	EXPRESSION TAG	UNP Q80ZW7
A	196	GLY	-	EXPRESSION TAG	UNP Q80ZW7

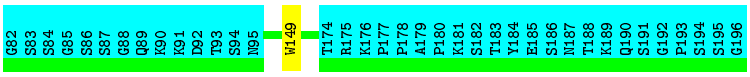
4 Residue-property plots (i)

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: Tia1 protein

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

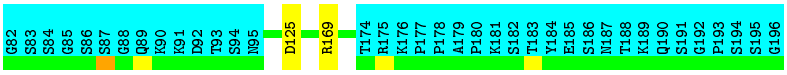
- Molecule 1: Tia1 protein

Chain A:

4.2.2 Score per residue for model 2

- Molecule 1: Tia1 protein

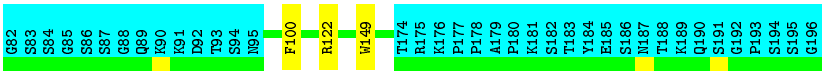
Chain A:



4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Tia1 protein

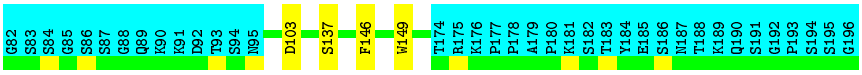
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Tia1 protein

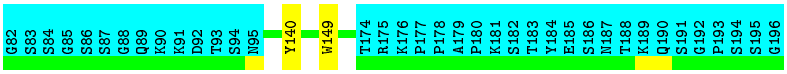
Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: Tia1 protein

Chain A:



4.2.6 Score per residue for model 6

- Molecule 1: Tia1 protein

Chain A:

4.2.7 Score per residue for model 7

- Molecule 1: Tia1 protein

Chain A:

4.2.8 Score per residue for model 8

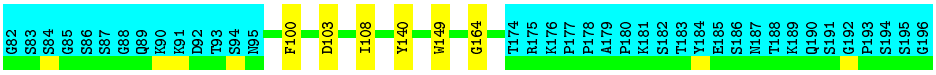
- Molecule 1: Tia1 protein

Chain A: 62% 6% 32%

4.2.9 Score per residue for model 9

- Molecule 1: Tia1 protein

Chain A: 63% 5% 32%



4.2.10 Score per residue for model 10

- Molecule 1: Tia1 protein

Chain A: 63% • 32%

4.2.11 Score per residue for model 11

- Molecule 1: Tia1 protein

Chain A: 62% 6% 32%

4.2.12 Score per residue for model 12

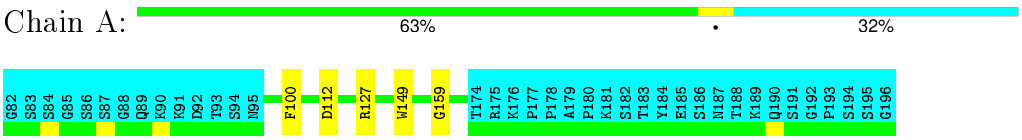
- Molecule 1: Tia1 protein

Chain A: 62% 6% 32%

4.2.13 Score per residue for model 13

- Molecule 1: Tia1 protein

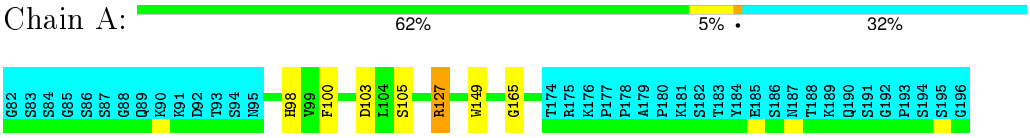
Chain A:



4.2.14 Score per residue for model 14

- Molecule 1: Tia1 protein

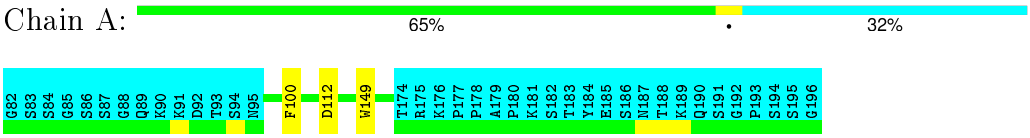
Chain A:



4.2.15 Score per residue for model 15

- Molecule 1: Tia1 protein

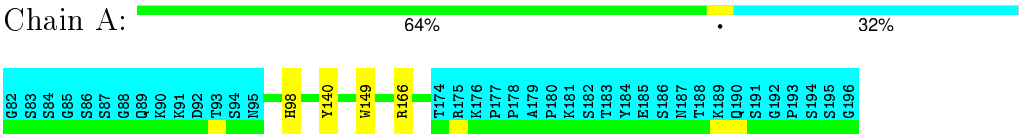
Chain A:



4.2.16 Score per residue for model 16

- Molecule 1: Tia1 protein

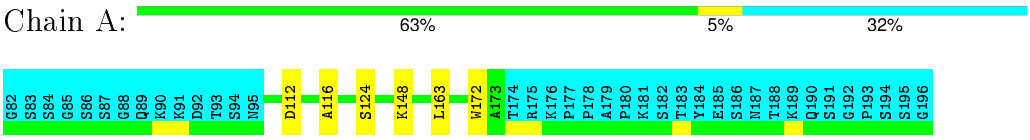
Chain A:



4.2.17 Score per residue for model 17

- Molecule 1: Tia1 protein

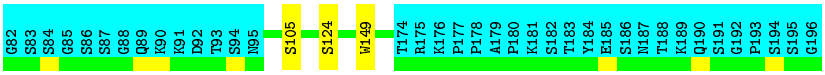
Chain A:



4.2.18 Score per residue for model 18

- Molecule 1: Tia1 protein

Chain A:



4.2.19 Score per residue for model 19

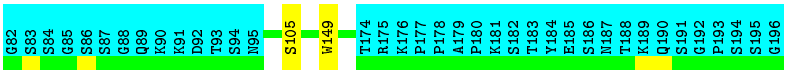
- Molecule 1: Tia1 protein

Chain A:

4.2.20 Score per residue for model 20

- Molecule 1: Tia1 protein

Chain A:



5 Refinement protocol and experimental data overview (i)

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

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
OPAL	structure solution	
OPAL	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)	BMRB entry 11373, BMRB entry 11372, BMRB entry 1137
Number of chemical shift lists	
Total number of shifts	
Number of shifts mapped to atoms	
Number of unparsed shifts	
Number of shifts with mapping errors	
Number of shifts with mapping warnings	
Assignment completeness (well-defined parts)	

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	0.62±0.01	0±0/634 (0.0±0.0%)	1.03±0.03	1±1/856 (0.1±0.1%)
All	All	0.62	0/12680 (0.0%)	1.03	12/17120 (0.1%)

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	0.5±0.5
All	All	0	9

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	100	PHE	CB-CG-CD2	-6.28	116.41	120.80	9	6
1	A	127	ARG	NE-CZ-NH1	5.77	123.19	120.30	14	1
1	A	127	ARG	NE-CZ-NH2	-5.76	117.42	120.30	19	2
1	A	146	PHE	CB-CG-CD2	-5.19	117.17	120.80	4	1
1	A	166	ARG	NE-CZ-NH2	-5.16	117.72	120.30	16	2

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	140	TYR	Sidechain	4
1	A	166	ARG	Sidechain	3
1	A	169	ARG	Sidechain	2

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	616	590	590	0±1
All	All	12320	11800	11800	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	Total
1:A:108:ILE:HD11	1:A:164:GLY:HA3	0.52	1.82	9	3
1:A:148:LYS:HE2	1:A:172:TRP:CH2	0.47	2.44	17	2
1:A:116:ALA:HB2	1:A:163:LEU:HD13	0.46	1.87	17	1
1:A:148:LYS:HE2	1:A:172:TRP:CZ2	0.42	2.48	17	1
1:A:129:VAL:HG12	1:A:138:LYS:HG3	0.42	1.90	1	1
1:A:108:ILE:HD11	1:A:164:GLY:CA	0.41	2.45	9	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	78/115 (68%)	74±1 (94±2%)	4±1 (5±2%)	0±0 (0±1%)	43 81
All	All	1560/2300 (68%)	1473 (94%)	81 (5%)	6 (0%)	43 81

All 2 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	165	GLY	5
1	A	159	GLY	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	61/92 (66%)	58±1 (95±2%)	3±1 (5±2%)	36	80
All	All	1220/1840 (66%)	1161 (95%)	59 (5%)	36	80

All 16 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	149	TRP	18
1	A	103	ASP	7
1	A	98	HIS	5
1	A	124	SER	5
1	A	105	SER	5
1	A	112	ASP	4
1	A	127	ARG	4
1	A	137	SER	2
1	A	138	LYS	2
1	A	171	ASN	1
1	A	132	MET	1
1	A	125	ASP	1
1	A	144	SER	1
1	A	161	GLN	1
1	A	169	ARG	1
1	A	122	ARG	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 92% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 11370

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	410
Number of shifts mapped to atoms	410
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 ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	85	-0.33 ± 0.16	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	76	-0.05 ± 0.10	None needed (< 0.5 ppm)
$^{13}C'$	85	-0.01 ± 0.17	None needed (< 0.5 ppm)
^{15}N	82	0.56 ± 0.36	None needed (imprecise)

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 39%, i.e. 372 atoms were assigned a chemical shift out of a possible 956. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	304/386 (79%)	75/154 (49%)	154/156 (99%)	75/76 (99%)
Sidechain	68/449 (15%)	0/264 (0%)	68/161 (42%)	0/24 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/121 (0%)	0/65 (0%)	0/51 (0%)	0/5 (0%)
Overall	372/956 (39%)	75/483 (16%)	222/368 (60%)	75/105 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 30%, i.e. 410 atoms were assigned a chemical shift out of a possible 1356. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	334/563 (59%)	82/224 (37%)	170/230 (74%)	82/109 (75%)
Sidechain	76/664 (11%)	0/396 (0%)	76/232 (33%)	0/36 (0%)
Aromatic	0/129 (0%)	0/69 (0%)	0/55 (0%)	0/5 (0%)
Overall	410/1356 (30%)	82/689 (12%)	246/517 (48%)	82/150 (55%)

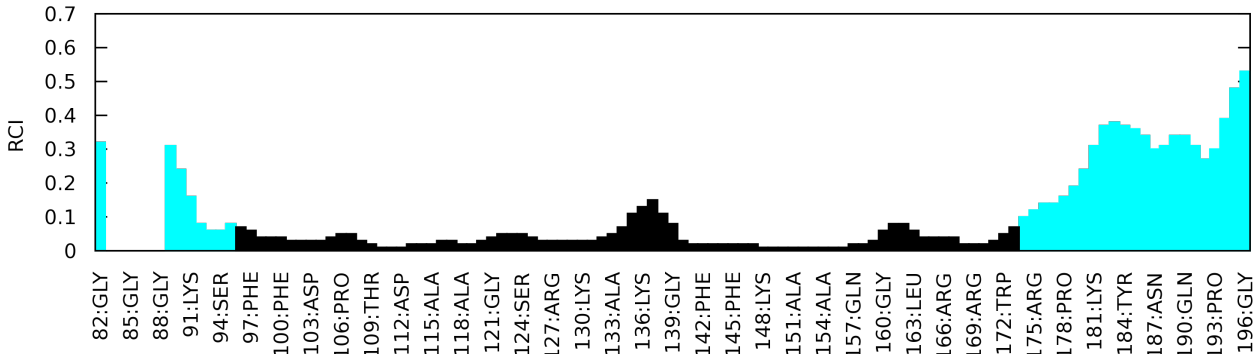
7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 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:



7.2 Chemical shift list 2

File name: BMRB entry 11371

Chemical shift list name: *assigned_chem_shift_list_1*

7.2.1 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	476
Number of shifts mapped to atoms	471
Number of unparsed shifts	0
Number of shifts with mapping errors	5
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 5 occurences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	44	ALA	CB	18.85	0.3	1
A	44	ALA	N	125.018	0.3	1
A	44	ALA	H	8.63	0.03	1
A	44	ALA	CA	51.586	0.3	1
A	44	ALA	C	178.291	0.3	1

7.2.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	100	-0.33 ± 0.19	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	91	0.17 ± 0.29	None needed (< 0.5 ppm)
$^{13}C'$	99	-0.02 ± 0.19	None needed (< 0.5 ppm)
^{15}N	93	0.39 ± 0.27	None needed (< 0.5 ppm)

7.2.3 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 38%, i.e. 362 atoms were assigned a chemical shift out of a possible 956. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	295/386 (76%)	72/154 (47%)	151/156 (97%)	72/76 (95%)
Sidechain	67/449 (15%)	0/264 (0%)	67/161 (42%)	0/24 (0%)
Aromatic	0/121 (0%)	0/65 (0%)	0/51 (0%)	0/5 (0%)
Overall	362/956 (38%)	72/483 (15%)	218/368 (59%)	72/105 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 35%, i.e. 471 atoms were assigned a chemical shift out of a possible 1356. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	381/563 (68%)	92/224 (41%)	197/230 (86%)	92/109 (84%)
Sidechain	90/664 (14%)	0/396 (0%)	90/232 (39%)	0/36 (0%)
Aromatic	0/129 (0%)	0/69 (0%)	0/55 (0%)	0/5 (0%)
Overall	471/1356 (35%)	92/689 (13%)	287/517 (56%)	92/150 (61%)

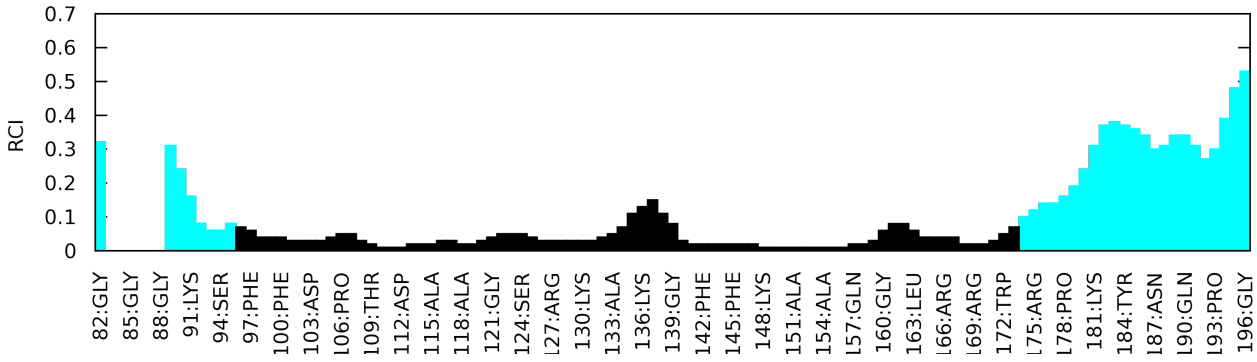
7.2.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.2.5 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:



7.3 Chemical shift list 3

File name: BMRB entry 11372

Chemical shift list name: *assigned_chem_shift_list_1*

7.3.1 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	483
Number of shifts mapped to atoms	478
Number of unparsed shifts	0
Number of shifts with mapping errors	5
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 5 occurences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	51	ALA	CA	52.148	0.3	1
A	51	ALA	C	178.274	0.3	1
A	51	ALA	N	129.733	0.3	1
A	51	ALA	CB	19.294	0.3	1
A	51	ALA	H	9.594	0.03	1

7.3.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	101	-0.38 ± 0.14	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	92	0.21 ± 0.11	None needed (< 0.5 ppm)
$^{13}C'$	100	-0.04 ± 0.19	None needed (< 0.5 ppm)
^{15}N	95	0.33 ± 0.48	None needed (< 0.5 ppm)

7.3.3 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 39%, i.e. 372 atoms were assigned a chemical shift out of a possible 956. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	304/386 (79%)	75/154 (49%)	154/156 (99%)	75/76 (99%)
Sidechain	68/449 (15%)	0/264 (0%)	68/161 (42%)	0/24 (0%)
Aromatic	0/121 (0%)	0/65 (0%)	0/51 (0%)	0/5 (0%)
Overall	372/956 (39%)	75/483 (16%)	222/368 (60%)	75/105 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 35%, i.e. 478 atoms were assigned a chemical shift out of a possible 1356. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	387/563 (69%)	94/224 (42%)	199/230 (87%)	94/109 (86%)
Sidechain	91/664 (14%)	0/396 (0%)	91/232 (39%)	0/36 (0%)
Aromatic	0/129 (0%)	0/69 (0%)	0/55 (0%)	0/5 (0%)
Overall	478/1356 (35%)	94/689 (14%)	290/517 (56%)	94/150 (63%)

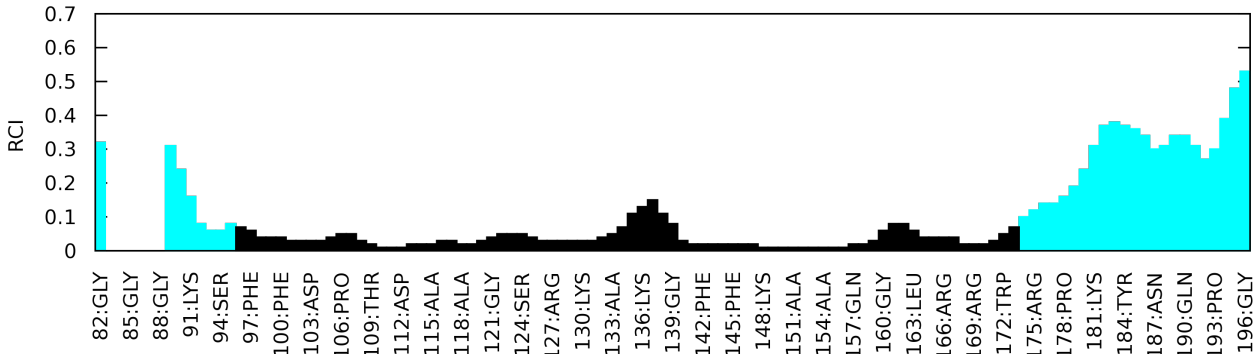
7.3.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.3.5 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:



7.4 Chemical shift list 4

File name: BMRB entry 11373

Chemical shift list name: *assigned_chem_shift_list_1*

7.4.1 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	482
Number of shifts mapped to atoms	477
Number of unparsed shifts	0
Number of shifts with mapping errors	5
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 5 occurences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	47	ALA	H	8.143	0.03	1
A	47	ALA	N	119.675	0.3	1
A	47	ALA	C	178.418	0.3	1
A	47	ALA	CB	19.467	0.3	1
A	47	ALA	CA	52.145	0.3	1

7.4.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	101	-0.32 ± 0.15	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	92	0.27 ± 0.14	None needed (< 0.5 ppm)
$^{13}C'$	99	-0.07 ± 0.11	None needed (< 0.5 ppm)
^{15}N	95	0.37 ± 0.34	None needed (< 0.5 ppm)

7.4.3 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 38%, i.e. 368 atoms were assigned a chemical shift out of a possible 956. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	300/386 (78%)	74/154 (48%)	152/156 (97%)	74/76 (97%)
Sidechain	68/449 (15%)	0/264 (0%)	68/161 (42%)	0/24 (0%)
Aromatic	0/121 (0%)	0/65 (0%)	0/51 (0%)	0/5 (0%)
Overall	368/956 (38%)	74/483 (15%)	220/368 (60%)	74/105 (70%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 35%, i.e. 477 atoms were assigned a chemical shift out of a possible 1356. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	386/563 (69%)	94/224 (42%)	198/230 (86%)	94/109 (86%)
Sidechain	91/664 (14%)	0/396 (0%)	91/232 (39%)	0/36 (0%)
Aromatic	0/129 (0%)	0/69 (0%)	0/55 (0%)	0/5 (0%)
Overall	477/1356 (35%)	94/689 (14%)	289/517 (56%)	94/150 (63%)

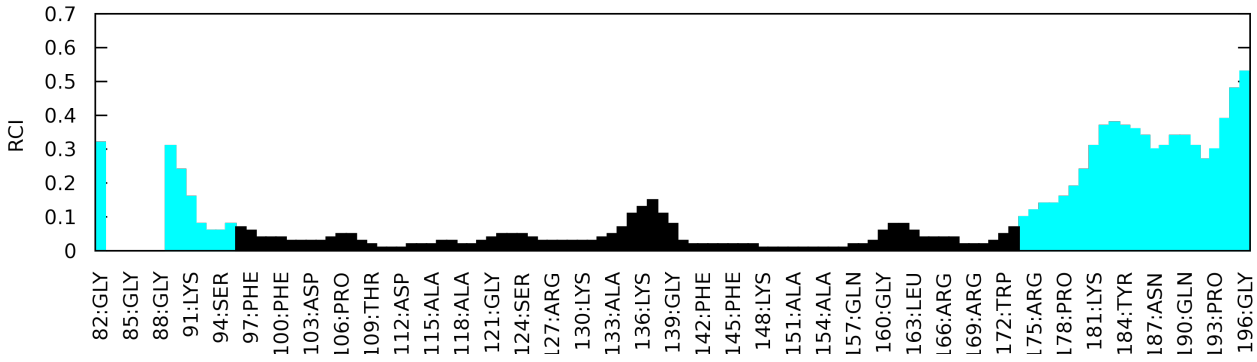
7.4.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.4.5 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:



7.5 Chemical shift list 5

File name: BMRB entry 11374

Chemical shift list name: *assigned_chem_shift_list_1*

7.5.1 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	192
Number of shifts mapped to atoms	192
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

7.5.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	—
$^{13}C_{\beta}$	0	—	—
$^{13}C'$	0	—	—
^{15}N	96	0.14 ± 0.56	None needed (< 0.5 ppm)

7.5.3 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 16%, i.e. 152 atoms were assigned a chemical shift out of a possible 956. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	152/386 (39%)	76/154 (49%)	0/156 (0%)	76/76 (100%)
Sidechain	0/449 (0%)	0/264 (0%)	0/161 (0%)	0/24 (0%)
Aromatic	0/121 (0%)	0/65 (0%)	0/51 (0%)	0/5 (0%)
Overall	152/956 (16%)	76/483 (16%)	0/368 (0%)	76/105 (72%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 14%, i.e. 192 atoms were assigned a chemical shift out of a possible 1356. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	192/563 (34%)	96/224 (43%)	0/230 (0%)	96/109 (88%)

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	Total	^{1}H	^{13}C	^{15}N
Sidechain	0/664 (0%)	0/396 (0%)	0/232 (0%)	0/36 (0%)
Aromatic	0/129 (0%)	0/69 (0%)	0/55 (0%)	0/5 (0%)
Overall	192/1356 (14%)	96/689 (14%)	0/517 (0%)	96/150 (64%)

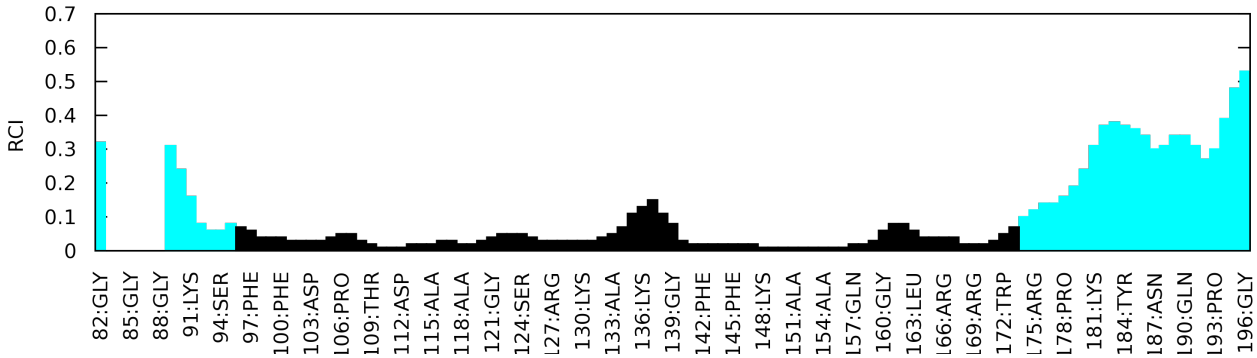
7.5.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.5.5 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:



7.6 Chemical shift list 6

File name: BMRB entry 11375

Chemical shift list name: *assigned_chem_shift_list_1*

7.6.1 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	200
Number of shifts mapped to atoms	200

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

7.6.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	—
$^{13}C_{\beta}$	0	—	—
$^{13}C'$	0	—	—
^{15}N	100	0.05 ± 0.29	None needed (< 0.5 ppm)

7.6.3 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 16%, i.e. 152 atoms were assigned a chemical shift out of a possible 956. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	152/386 (39%)	76/154 (49%)	0/156 (0%)	76/76 (100%)
Sidechain	0/449 (0%)	0/264 (0%)	0/161 (0%)	0/24 (0%)
Aromatic	0/121 (0%)	0/65 (0%)	0/51 (0%)	0/5 (0%)
Overall	152/956 (16%)	76/483 (16%)	0/368 (0%)	76/105 (72%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 15%, i.e. 200 atoms were assigned a chemical shift out of a possible 1356. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	200/563 (36%)	100/224 (45%)	0/230 (0%)	100/109 (92%)
Sidechain	0/664 (0%)	0/396 (0%)	0/232 (0%)	0/36 (0%)
Aromatic	0/129 (0%)	0/69 (0%)	0/55 (0%)	0/5 (0%)
Overall	200/1356 (15%)	100/689 (15%)	0/517 (0%)	100/150 (67%)

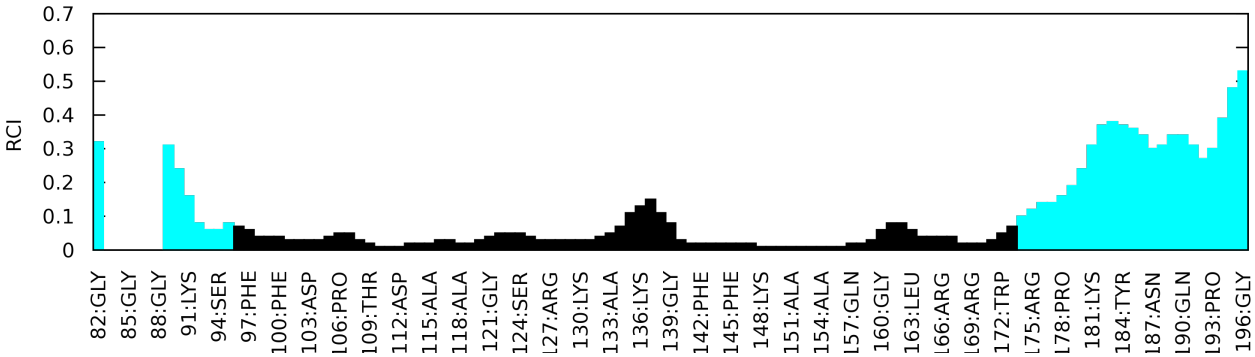
7.6.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.6.5 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:



7.7 Chemical shift list 7

File name: BMRB entry 11376

Chemical shift list name: *assigned_chem_shift_list_1*

7.7.1 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	1305
Number of shifts mapped to atoms	1305
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.7.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

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Nucleus	# values	Correction ± precision, *ppm*	Suggested action

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	109	-0.20 ± 0.15	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	97	0.03 ± 0.09	None needed (< 0.5 ppm)
$^{13}C'$	107	-0.00 ± 0.18	None needed (< 0.5 ppm)
^{15}N	100	0.14 ± 0.48	None needed (< 0.5 ppm)

7.7.3 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 92%, i.e. 880 atoms were assigned a chemical shift out of a possible 956. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	386/386 (100%)	154/154 (100%)	156/156 (100%)	76/76 (100%)
Sidechain	379/449 (84%)	236/264 (89%)	138/161 (86%)	5/24 (21%)
Aromatic	115/121 (95%)	61/65 (94%)	51/51 (100%)	3/5 (60%)
Overall	880/956 (92%)	451/483 (93%)	345/368 (94%)	84/105 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 1190 atoms were assigned a chemical shift out of a possible 1356. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

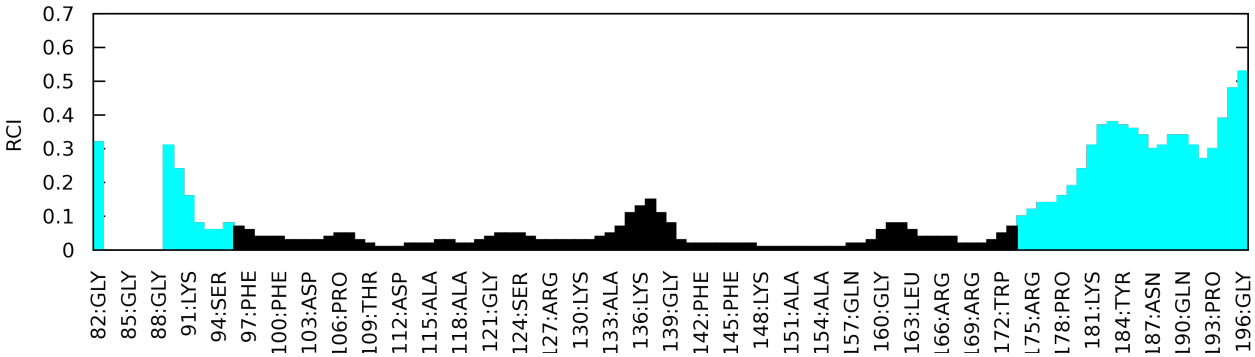
	Total	^{1}H	^{13}C	^{15}N
Backbone	524/563 (93%)	208/224 (93%)	216/230 (94%)	100/109 (92%)
Sidechain	543/664 (82%)	343/396 (87%)	194/232 (84%)	6/36 (17%)
Aromatic	123/129 (95%)	65/69 (94%)	55/55 (100%)	3/5 (60%)
Overall	1190/1356 (88%)	616/689 (89%)	465/517 (90%)	109/150 (73%)

7.7.4 Statistically unusual chemical shifts (i)

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	167	GLN	HG3	0.35	3.75 – 0.85	-6.7
1	A	124	SER	HB3	2.06	5.25 – 2.45	-6.4
1	A	167	GLN	HG2	0.80	3.67 – 0.97	-5.6
1	A	148	LYS	HB3	0.40	3.10 – 0.40	-5.0

7.7.5 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: