



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 06:53 PM BST

PDB ID : 1XYQ  
Title : NMR structure of the pig prion protein  
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Deposited on : 2004-11-10

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A user guide is available at  
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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  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

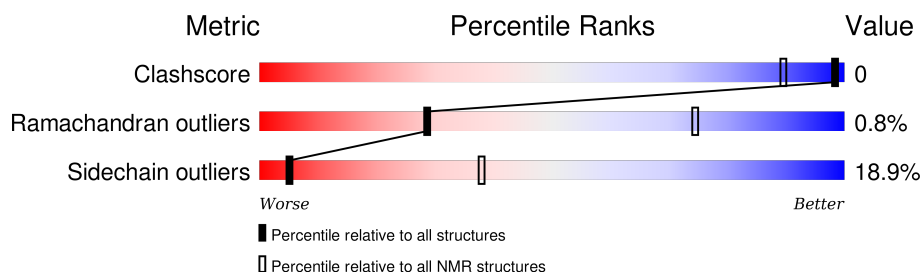
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 73%.

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  $\geq 3$ , 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	111	

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 19 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:127-A:167, A:171-A:225 (96)	0.38	19

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 5 single-model clusters were found.

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

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

There is only 1 type of molecule in this entry. The entry contains 1763 atoms, of which 854 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Major prion protein.

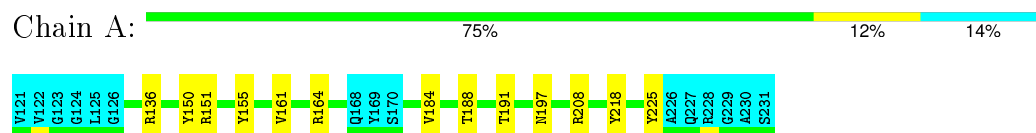
Mol	Chain	Residues	Atoms							Trace
1	A	111	Total	C	H	N	O	S		0
			1763	568	854	156	178	7		

## 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: Major prion protein

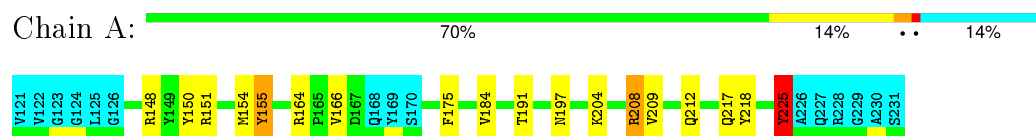


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

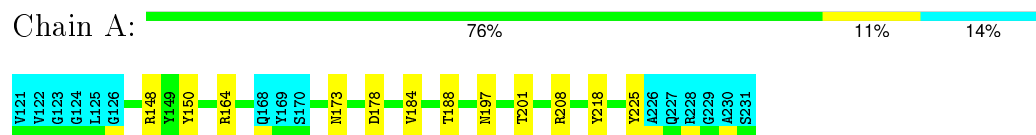
#### 4.2.1 Score per residue for model 1

- Molecule 1: Major prion protein



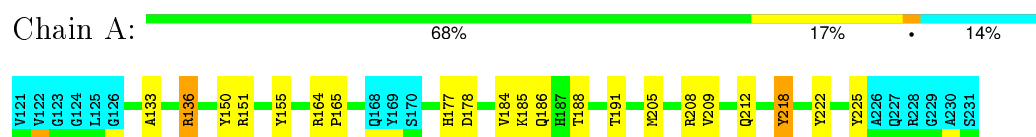
#### 4.2.2 Score per residue for model 2

- Molecule 1: Major prion protein



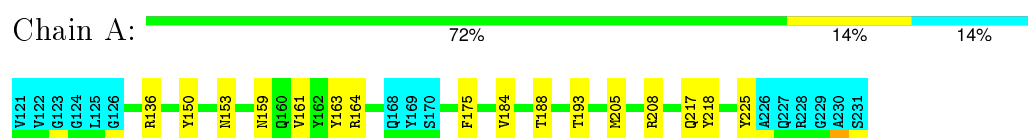
### 4.2.3 Score per residue for model 3

- Molecule 1: Major prion protein



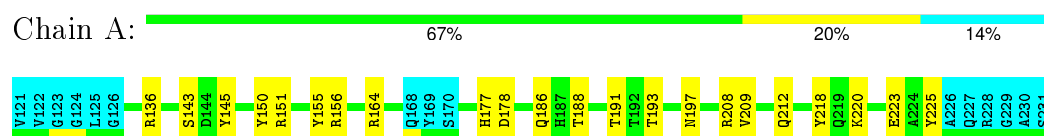
### 4.2.4 Score per residue for model 4

- Molecule 1: Major prion protein



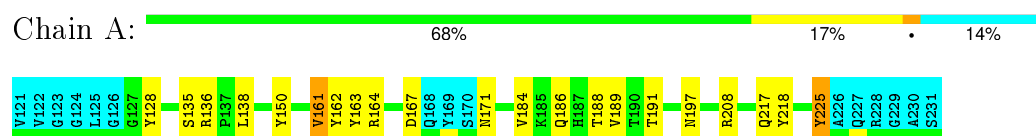
### 4.2.5 Score per residue for model 5

- Molecule 1: Major prion protein



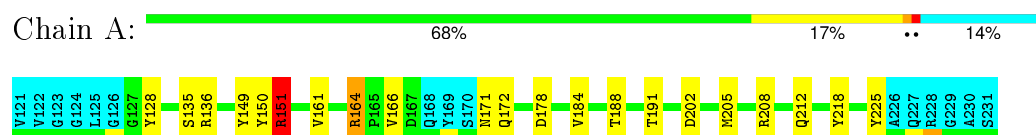
### 4.2.6 Score per residue for model 6

- Molecule 1: Major prion protein



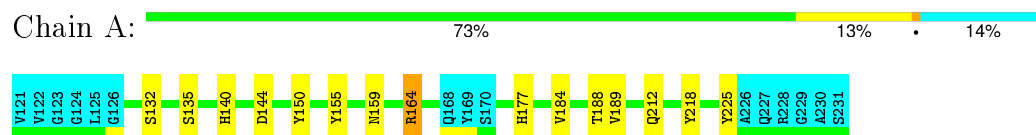
### 4.2.7 Score per residue for model 7

- Molecule 1: Major prion protein



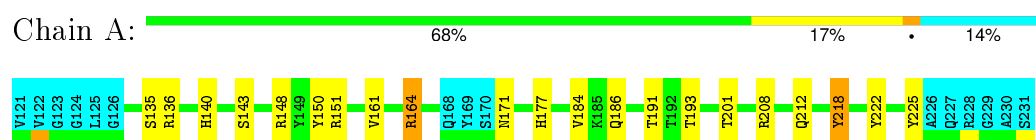
### 4.2.8 Score per residue for model 8

- Molecule 1: Major prion protein



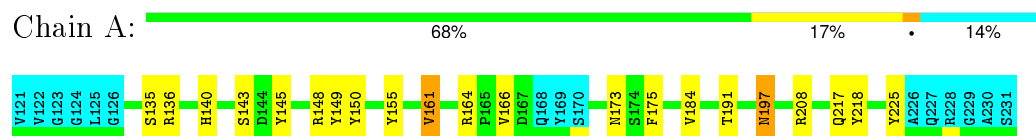
### 4.2.9 Score per residue for model 9

- Molecule 1: Major prion protein



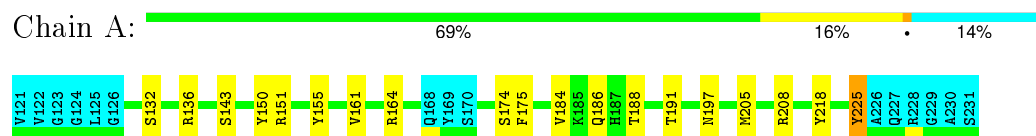
### 4.2.10 Score per residue for model 10

- Molecule 1: Major prion protein



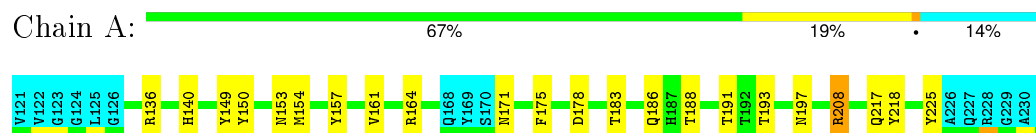
### 4.2.11 Score per residue for model 11

- Molecule 1: Major prion protein



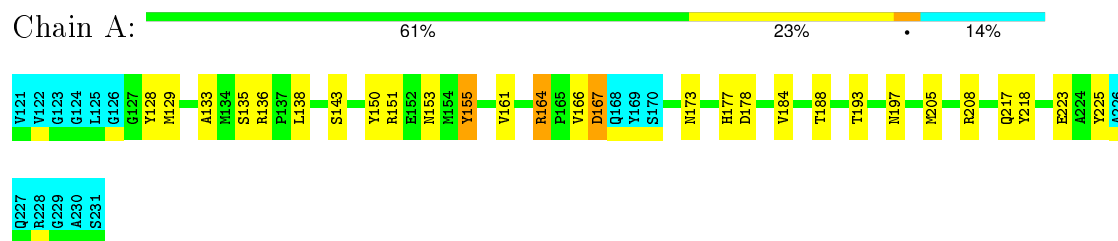
### 4.2.12 Score per residue for model 12

- Molecule 1: Major prion protein



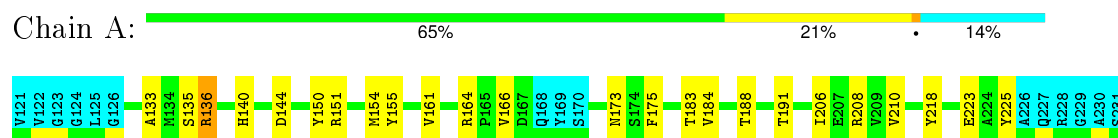
### 4.2.13 Score per residue for model 13

- Molecule 1: Major prion protein



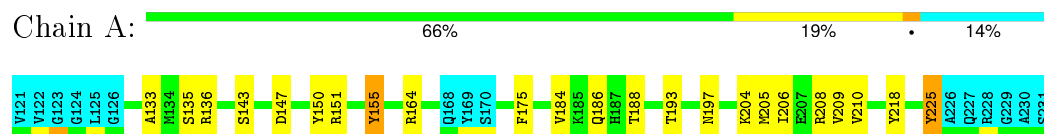
### 4.2.14 Score per residue for model 14

- Molecule 1: Major prion protein



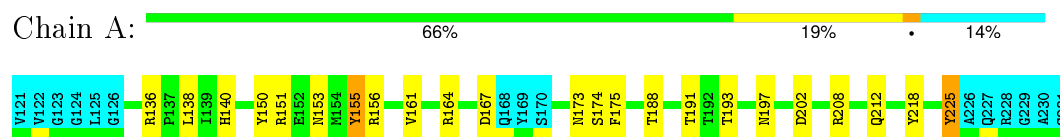
### 4.2.15 Score per residue for model 15

- Molecule 1: Major prion protein



### 4.2.16 Score per residue for model 16

- Molecule 1: Major prion protein



### 4.2.17 Score per residue for model 17

- Molecule 1: Major prion protein

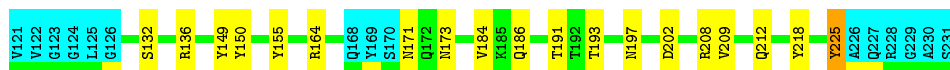






#### 4.2.18 Score per residue for model 18

- Molecule 1: Major prion protein



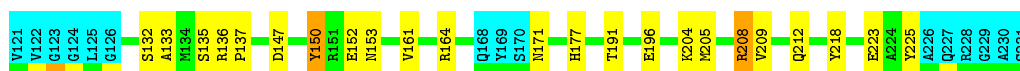
#### 4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: Major prion protein



#### 4.2.20 Score per residue for model 20

- Molecule 1: Major prion protein



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle 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
DYANA	structure solution	6.2
CANDID	refinement	1.0

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 6380
Number of chemical shift lists	1
Total number of shifts	1146
Number of shifts mapped to atoms	1136
Number of unparsed shifts	0
Number of shifts with mapping errors	10
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	73%

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	0.69±0.01	0±0/828 (0.0±0.0%)	1.08±0.02	1±1/1122 (0.1±0.1%)
All	All	0.69	0/16560 (0.0%)	1.08	20/22440 (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	1.9±1.4
All	All	0	39

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	225	TYR	CB-CG-CD2	-6.50	117.10	121.00	18	6
1	A	209	VAL	CA-CB-CG2	6.17	120.16	110.90	15	1
1	A	225	TYR	CB-CG-CD1	-6.09	117.35	121.00	15	2
1	A	161	VAL	CA-CB-CG1	5.93	119.79	110.90	10	2
1	A	208	ARG	NE-CZ-NH2	-5.90	117.35	120.30	12	1
1	A	178	ASP	CB-CG-OD1	5.85	123.57	118.30	3	1
1	A	151	ARG	NE-CZ-NH1	5.83	123.22	120.30	7	1
1	A	149	TYR	CB-CG-CD1	-5.52	117.69	121.00	7	2
1	A	136	ARG	NE-CZ-NH2	-5.39	117.61	120.30	19	1
1	A	136	ARG	CD-NE-CZ	5.27	130.98	123.60	12	1
1	A	164	ARG	NE-CZ-NH2	-5.21	117.69	120.30	9	1
1	A	150	TYR	CB-CG-CD1	-5.04	117.98	121.00	20	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	151	ARG	Sidechain	6
1	A	155	TYR	Sidechain	5
1	A	148	ARG	Sidechain	4
1	A	222	TYR	Sidechain	3
1	A	136	ARG	Sidechain	3
1	A	128	TYR	Sidechain	2
1	A	156	ARG	Sidechain	2
1	A	218	TYR	Sidechain	2
1	A	149	TYR	Sidechain	2
1	A	208	ARG	Sidechain	2
1	A	164	ARG	Sidechain	2
1	A	163	TYR	Sidechain	1
1	A	225	TYR	Sidechain	1
1	A	157	TYR	Sidechain	1
1	A	133	ALA	Peptide	1
1	A	162	TYR	Sidechain	1
1	A	135	SER	Peptide	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	808	755	755	1±1
All	All	16160	15100	15100	12

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:206:ILE:O	1:A:210:VAL:HG23	0.57	2.00	15	2
1:A:137:PRO:HG2	1:A:209:VAL:HG22	0.55	1.78	20	1
1:A:184:VAL:HG23	1:A:210:VAL:HG21	0.48	1.84	14	1
1:A:161:VAL:HG12	1:A:183:THR:HG21	0.46	1.88	12	2
1:A:133:ALA:HB1	1:A:159:ASN:HD22	0.45	1.71	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:143:SER:HB3	1:A:145:TYR:CE1	0.44	2.47	10	1
1:A:163:TYR:CE1	1:A:217:GLN:NE2	0.43	2.86	4	1
1:A:152:GLU:HG3	1:A:153:ASN:HD22	0.42	1.75	20	1
1:A:143:SER:HB3	1:A:145:TYR:CE2	0.40	2.51	5	1
1:A:128:TYR:CE1	1:A:164:ARG:HG2	0.40	2.51	7	1

## 6.3 Torsion angles ⓘ

### 6.3.1 Protein backbone ⓘ

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	96/111 (86%)	85±2 (88±2%)	11±2 (11±2%)	1±1 (1±1%)	29	74
All	All	1920/2220 (86%)	1693 (88%)	211 (11%)	16 (1%)	29	74

All 6 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	171	ASN	5
1	A	133	ALA	4
1	A	197	ASN	3
1	A	132	SER	2
1	A	196	GLU	1
1	A	165	PRO	1

### 6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	90/99 (91%)	73±3 (81±3%)	17±3 (19±3%)	5	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1800/1980 (91%)	1460 (81%)	340 (19%)	<b>5</b> 38

All 48 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	164	ARG	20
1	A	150	TYR	20
1	A	218	TYR	20
1	A	208	ARG	18
1	A	225	TYR	18
1	A	188	THR	15
1	A	191	THR	14
1	A	136	ARG	14
1	A	184	VAL	14
1	A	197	ASN	11
1	A	155	TYR	11
1	A	161	VAL	11
1	A	212	GLN	10
1	A	186	GLN	9
1	A	193	THR	9
1	A	135	SER	9
1	A	175	PHE	8
1	A	205	MET	8
1	A	177	HIS	7
1	A	166	VAL	6
1	A	140	HIS	6
1	A	153	ASN	6
1	A	173	ASN	6
1	A	178	ASP	5
1	A	217	GLN	5
1	A	151	ARG	5
1	A	202	ASP	5
1	A	143	SER	4
1	A	209	VAL	4
1	A	223	GLU	4
1	A	167	ASP	4
1	A	174	SER	4
1	A	138	LEU	3
1	A	154	MET	3
1	A	204	LYS	3
1	A	132	SER	3

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Mol	Chain	Res	Type	Models (Total)
1	A	144	ASP	2
1	A	159	ASN	2
1	A	189	VAL	2
1	A	201	THR	2
1	A	171	ASN	2
1	A	147	ASP	2
1	A	129	MET	1
1	A	172	GLN	1
1	A	196	GLU	1
1	A	220	LYS	1
1	A	185	LYS	1
1	A	149	TYR	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

The completeness of assignment taking into account all chemical shift lists is 73% for the well-defined parts and 73% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 6380

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 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	1146
Number of shifts mapped to atoms	1136
Number of unparsed shifts	0
Number of shifts with mapping errors	10
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

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

- Residue not found in structure. All 10 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	1	GLY	HA2	3.89	0.01	1
A	1	GLY	CA	43.0	0.1	1
A	2	SER	N	116.0	0.1	1
A	2	SER	CB	63.7	0.1	1
A	2	SER	HB3	3.81	0.01	1
A	2	SER	H	8.65	0.01	1
A	2	SER	HB2	3.81	0.01	1
A	2	SER	HA	4.57	0.01	1
A	2	SER	CA	57.8	0.1	1
A	1	GLY	HA3	3.89	0.01	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
$^{13}\text{C}_\alpha$	101	$-0.05 \pm 0.10$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	85	$0.77 \pm 0.14$	Should be applied
$^{13}\text{C}'$	0	—	—
$^{15}\text{N}$	106	$0.04 \pm 0.14$	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 73%, i.e. 901 atoms were assigned a chemical shift out of a possible 1232. 7 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	363/474 (77%)	185/189 (98%)	87/192 (45%)	91/93 (98%)
Sidechain	482/622 (77%)	315/366 (86%)	151/222 (68%)	16/34 (47%)
Aromatic	56/136 (41%)	30/71 (42%)	26/62 (42%)	0/3 (0%)
Overall	901/1232 (73%)	530/626 (85%)	264/476 (55%)	107/130 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 73%, i.e. 1008 atoms were assigned a chemical shift out of a possible 1387. 10 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	417/549 (76%)	213/219 (97%)	99/222 (45%)	105/108 (97%)
Sidechain	531/694 (77%)	348/408 (85%)	166/247 (67%)	17/39 (44%)
Aromatic	60/144 (42%)	32/75 (43%)	28/66 (42%)	0/3 (0%)
Overall	1008/1387 (73%)	593/702 (84%)	293/535 (55%)	122/150 (81%)

### 7.1.4 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	228	ARG	HD2	1.61	4.27 – 1.97	-6.6
1	A	228	ARG	HD3	1.61	4.36 – 1.86	-6.0
1	A	220	LYS	HD2	2.85	2.76 – 0.46	5.4

### 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:

