



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 04:40 PM BST

PDB ID : 1RHX  
Title : HIGH-RESOLUTION NMR STRUCTURE OF A PUTATIVE SULFUR  
TRANSFERASE (TM0979) FROM THERMOTOGA MARITIMA  
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Deposited on : 2003-11-14

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

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
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

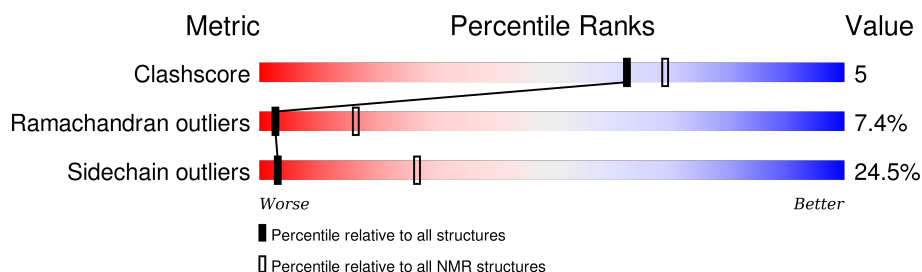
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 85%.

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	87	 63% 30% 5% •

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 9 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:3-A:87 (85)	0.27	9

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 3 single-model clusters were found.

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

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

There is only 1 type of molecule in this entry. The entry contains 1404 atoms, of which 707 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called conserved hypothetical protein TM0979.

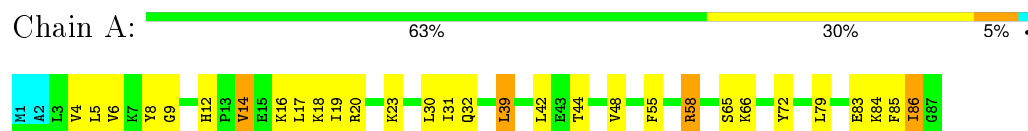
Mol	Chain	Residues	Atoms							Trace
1	A	87	Total	C	H	N	O	S		0
			1404	455	707	107	134	1		

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

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

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: conserved hypothetical protein TM0979

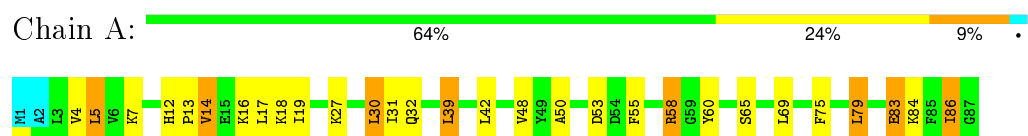


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

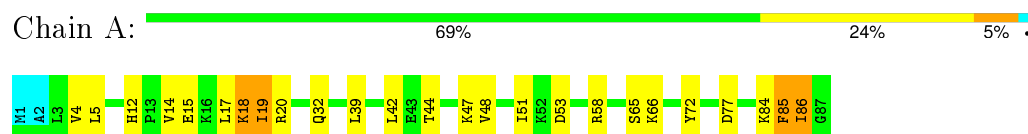
#### 4.2.1 Score per residue for model 1

- Molecule 1: conserved hypothetical protein TM0979



#### 4.2.2 Score per residue for model 2

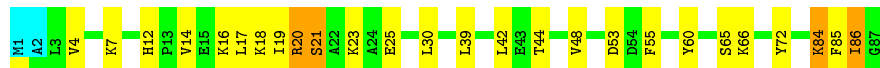
- Molecule 1: conserved hypothetical protein TM0979



### 4.2.3 Score per residue for model 3

- Molecule 1: conserved hypothetical protein TM0979

Chain A:  68% 25% 5% .



### 4.2.4 Score per residue for model 4

- Molecule 1: conserved hypothetical protein TM0979

Chain A:  57% 36% 5% .



### 4.2.5 Score per residue for model 5

- Molecule 1: conserved hypothetical protein TM0979

Chain A:  54% 34% 9% .



### 4.2.6 Score per residue for model 6

- Molecule 1: conserved hypothetical protein TM0979

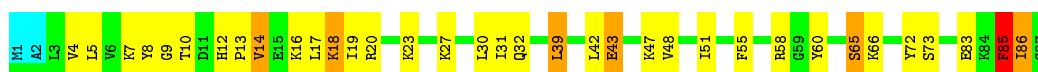
Chain A:  67% 26% . . .



### 4.2.7 Score per residue for model 7

- Molecule 1: conserved hypothetical protein TM0979

Chain A:  57% 32% 7% . .



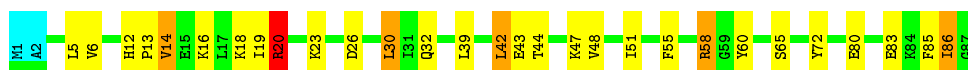
#### 4.2.8 Score per residue for model 8

- Molecule 1: conserved hypothetical protein TM0979



#### 4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: conserved hypothetical protein TM0979



#### 4.2.10 Score per residue for model 10

- Molecule 1: conserved hypothetical protein TM0979



#### 4.2.11 Score per residue for model 11

- Molecule 1: conserved hypothetical protein TM0979



#### 4.2.12 Score per residue for model 12

- Molecule 1: conserved hypothetical protein TM0979





#### 4.2.13 Score per residue for model 13

- Molecule 1: conserved hypothetical protein TM0979

Chain A: 66% 25% 6% ..



#### 4.2.14 Score per residue for model 14

- Molecule 1: conserved hypothetical protein TM0979

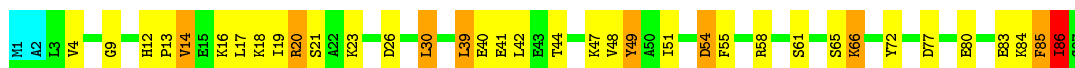
Chain A: 62% 31% 5% ..



#### 4.2.15 Score per residue for model 15

- Molecule 1: conserved hypothetical protein TM0979

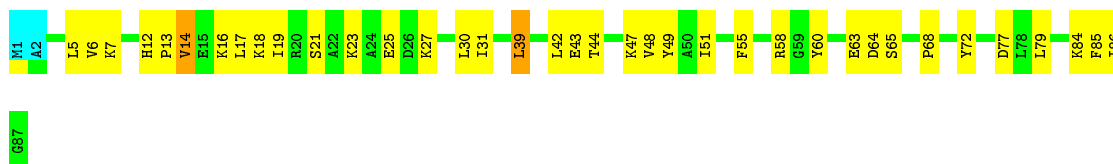
Chain A: 56% 31% 9% ..



#### 4.2.16 Score per residue for model 16

- Molecule 1: conserved hypothetical protein TM0979

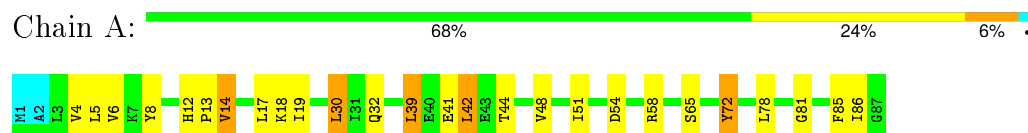
Chain A: 55% 40% ..





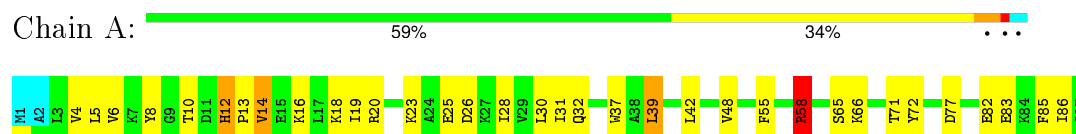
### 4.2.17 Score per residue for model 17

- Molecule 1: conserved hypothetical protein TM0979



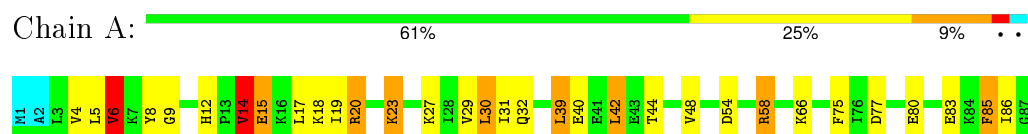
### 4.2.18 Score per residue for model 18

- Molecule 1: conserved hypothetical protein TM0979



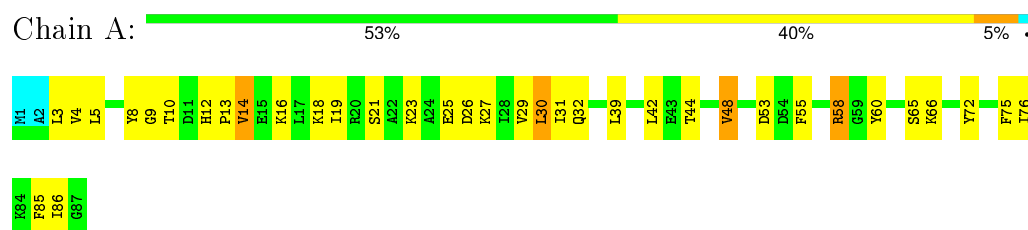
### 4.2.19 Score per residue for model 19

- Molecule 1: conserved hypothetical protein TM0979



### 4.2.20 Score per residue for model 20

- Molecule 1: conserved hypothetical protein TM0979



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

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	refinement	6.0

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 6010
Number of chemical shift lists	1
Total number of shifts	1032
Number of shifts mapped to atoms	1032
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	85%

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	0.65±0.01	0±0/697 (0.0±0.0%)	1.14±0.04	1±1/941 (0.1±0.1%)
All	All	0.65	0/13940 (0.0%)	1.14	19/18820 (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	2.0±1.4
All	All	0	41

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	72	TYR	CB-CG-CD2	-7.72	116.36	121.00	10	1
1	A	58	ARG	NE-CZ-NH2	-6.68	116.96	120.30	5	3
1	A	77	ASP	CB-CG-OD1	6.58	124.22	118.30	15	4
1	A	49	TYR	CB-CG-CD1	-6.42	117.14	121.00	8	2
1	A	78	LEU	CB-CG-CD1	6.15	121.46	111.00	17	1
1	A	72	TYR	CB-CG-CD1	5.72	124.43	121.00	10	1
1	A	58	ARG	CD-NE-CZ	5.55	131.37	123.60	11	2
1	A	20	ARG	NE-CZ-NH2	-5.40	117.60	120.30	8	1
1	A	20	ARG	CD-NE-CZ	5.37	131.12	123.60	9	1
1	A	54	ASP	CA-CB-CG	-5.24	101.88	113.40	15	1
1	A	58	ARG	NE-CZ-NH1	5.20	122.90	120.30	1	1
1	A	20	ARG	NE-CZ-NH1	5.00	122.80	120.30	3	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	86	ILE	Peptide	10
1	A	72	TYR	Sidechain	7
1	A	58	ARG	Sidechain	7
1	A	20	ARG	Sidechain	6
1	A	9	GLY	Peptide	6
1	A	49	TYR	Sidechain	1
1	A	81	GLY	Peptide	1
1	A	82	GLU	Peptide	1
1	A	75	PHE	Sidechain	1
1	A	85	PHE	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	684	693	693	7±3
All	All	13680	13860	13860	149

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:THR:HG21	1:A:48:VAL:HG11	0.82	1.51	13	3
1:A:44:THR:HG21	1:A:48:VAL:HG21	0.68	1.66	15	3
1:A:14:VAL:HG22	1:A:48:VAL:HG12	0.67	1.65	20	5
1:A:18:LYS:HE3	1:A:19:ILE:HD12	0.64	1.69	11	1
1:A:18:LYS:HE3	1:A:19:ILE:CD1	0.62	2.25	11	1
1:A:83:GLU:HA	1:A:86:ILE:HD11	0.62	1.69	9	9
1:A:14:VAL:HG22	1:A:48:VAL:HG22	0.58	1.75	15	6
1:A:6:VAL:HG23	1:A:12:HIS:NE2	0.58	2.13	19	1
1:A:23:LYS:HE3	1:A:23:LYS:HA	0.57	1.77	8	1
1:A:4:VAL:HG13	1:A:86:ILE:HB	0.56	1.78	14	9
1:A:75:PHE:CE1	1:A:79:LEU:HD21	0.56	2.35	10	4
1:A:13:PRO:O	1:A:14:VAL:HG23	0.54	2.01	18	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:VAL:HG22	1:A:48:VAL:CG1	0.53	2.32	1	2
1:A:55:PHE:CE2	1:A:65:SER:HB2	0.53	2.39	1	7
1:A:51:ILE:HG21	1:A:72:TYR:CE1	0.53	2.38	2	8
1:A:79:LEU:CD1	1:A:86:ILE:HD12	0.53	2.33	13	1
1:A:6:VAL:HG23	1:A:12:HIS:CD2	0.51	2.40	19	1
1:A:4:VAL:HG12	1:A:4:VAL:O	0.51	2.05	2	2
1:A:14:VAL:HG22	1:A:48:VAL:CG2	0.50	2.37	18	3
1:A:44:THR:CG2	1:A:48:VAL:CG2	0.49	2.89	4	6
1:A:44:THR:CG2	1:A:48:VAL:HG11	0.49	2.31	13	3
1:A:14:VAL:HG21	1:A:30:LEU:HD21	0.49	1.83	1	3
1:A:23:LYS:HE2	1:A:23:LYS:HA	0.48	1.85	19	2
1:A:14:VAL:HG21	1:A:30:LEU:CD2	0.48	2.38	17	7
1:A:29:VAL:HG21	1:A:75:PHE:CD1	0.48	2.43	10	3
1:A:44:THR:HG21	1:A:48:VAL:CG2	0.48	2.37	9	2
1:A:44:THR:HG22	1:A:48:VAL:HG21	0.48	1.86	10	2
1:A:6:VAL:HG22	1:A:34:GLY:HA3	0.48	1.85	8	1
1:A:44:THR:CG2	1:A:48:VAL:CG1	0.47	2.92	17	3
1:A:4:VAL:O	1:A:4:VAL:HG23	0.47	2.10	10	4
1:A:49:TYR:CD2	1:A:68:PRO:HG2	0.47	2.45	5	1
1:A:55:PHE:CE1	1:A:60:TYR:CG	0.47	3.03	5	9
1:A:6:VAL:O	1:A:6:VAL:HG22	0.47	2.10	19	1
1:A:18:LYS:CE	1:A:19:ILE:HD12	0.46	2.41	10	2
1:A:49:TYR:CD1	1:A:68:PRO:HG2	0.46	2.46	16	3
1:A:83:GLU:CA	1:A:86:ILE:HD11	0.46	2.41	14	1
1:A:15:GLU:O	1:A:42:LEU:HD22	0.46	2.11	19	1
1:A:76:ILE:HA	1:A:79:LEU:HD23	0.45	1.87	20	1
1:A:18:LYS:HE3	1:A:43:GLU:O	0.44	2.12	7	1
1:A:40:GLU:H	1:A:66:LYS:HE2	0.44	1.73	15	2
1:A:22:ALA:O	1:A:23:LYS:HE3	0.43	2.13	5	1
1:A:55:PHE:CE1	1:A:60:TYR:HB3	0.43	2.49	7	1
1:A:79:LEU:HD11	1:A:86:ILE:HD12	0.43	1.91	13	1
1:A:14:VAL:CG2	1:A:48:VAL:HG11	0.43	2.44	4	1
1:A:47:LYS:HE3	1:A:49:TYR:CE2	0.43	2.49	15	1
1:A:14:VAL:O	1:A:44:THR:HB	0.42	2.15	15	1
1:A:51:ILE:HG22	1:A:54:ASP:H	0.41	1.74	15	2
1:A:50:ALA:HB3	1:A:69:LEU:HD23	0.41	1.92	1	1
1:A:4:VAL:HG23	1:A:4:VAL:O	0.41	2.16	6	1
1:A:23:LYS:HE3	1:A:23:LYS:CA	0.41	2.44	8	1
1:A:14:VAL:HG21	1:A:48:VAL:HG11	0.41	1.93	4	1
1:A:44:THR:HG22	1:A:48:VAL:CG2	0.41	2.46	11	1
1:A:12:HIS:CE1	1:A:37:TRP:CD1	0.40	3.10	18	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	84/87 (97%)	59±2 (70±2%)	19±2 (22±2%)	6±1 (7±1%)	3	16
All	All	1680/1740 (97%)	1184 (70%)	372 (22%)	124 (7%)	3	16

All 19 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	14	VAL	20
1	A	39	LEU	20
1	A	32	GLN	16
1	A	85	PHE	14
1	A	16	LYS	11
1	A	6	VAL	9
1	A	80	GLU	7
1	A	21	SER	6
1	A	79	LEU	5
1	A	9	GLY	5
1	A	42	LEU	3
1	A	84	LYS	1
1	A	43	GLU	1
1	A	34	GLY	1
1	A	5	LEU	1
1	A	22	ALA	1
1	A	81	GLY	1
1	A	86	ILE	1
1	A	48	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	74/75 (99%)	56±2 (76±3%)	18±2 (24±3%)	3	27
All	All	1480/1500 (99%)	1118 (76%)	362 (24%)	3	27

All 45 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	18	LYS	20
1	A	19	ILE	20
1	A	42	LEU	20
1	A	12	HIS	19
1	A	58	ARG	19
1	A	30	LEU	19
1	A	23	LYS	17
1	A	5	LEU	15
1	A	17	LEU	14
1	A	84	LYS	12
1	A	20	ARG	12
1	A	39	LEU	12
1	A	31	ILE	11
1	A	66	LYS	11
1	A	8	TYR	11
1	A	65	SER	10
1	A	86	ILE	10
1	A	53	ASP	10
1	A	27	LYS	9
1	A	25	GLU	8
1	A	47	LYS	8
1	A	10	THR	7
1	A	15	GLU	6
1	A	26	ASP	6
1	A	85	PHE	6
1	A	43	GLU	5
1	A	7	LYS	5
1	A	83	GLU	5
1	A	41	GLU	4
1	A	54	ASP	4
1	A	14	VAL	3
1	A	77	ASP	3
1	A	28	ILE	3
1	A	73	SER	2
1	A	71	THR	2
1	A	61	SER	2

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Mol	Chain	Res	Type	Models (Total)
1	A	72	TYR	2
1	A	21	SER	2
1	A	64	ASP	2
1	A	6	VAL	1
1	A	3	LEU	1
1	A	55	PHE	1
1	A	63	GLU	1
1	A	33	ASN	1
1	A	82	GLU	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 85% for the well-defined parts and 84% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 6010

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	1032
Number of shifts mapped to atoms	1032
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	86	$-0.06 \pm 0.06$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	81	$0.58 \pm 0.17$	Should be applied
$^{13}\text{C}'$	82	$-0.08 \pm 0.20$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	82	$1.16 \pm 0.32$	Should be applied

#### 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 85%, i.e. 901 atoms were assigned a chemical shift out of a possible 1065. 17 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	414/419 (99%)	166/167 (99%)	166/170 (98%)	82/82 (100%)
Sidechain	461/559 (82%)	266/324 (82%)	193/218 (89%)	2/17 (12%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	26/87 (30%)	25/46 (54%)	0/39 (0%)	1/2 (50%)
Overall	901/1065 (85%)	457/537 (85%)	359/427 (84%)	85/101 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 84%, i.e. 906 atoms were assigned a chemical shift out of a possible 1085. 17 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	417/429 (97%)	167/171 (98%)	168/174 (97%)	82/84 (98%)
Sidechain	463/569 (81%)	267/330 (81%)	194/222 (87%)	2/17 (12%)
Aromatic	26/87 (30%)	25/46 (54%)	0/39 (0%)	1/2 (50%)
Overall	906/1085 (84%)	459/547 (84%)	362/435 (83%)	85/103 (83%)

#### 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:

