



# Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1TL4  
Title : Solution structure of Cu(I) HAH1  
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Deposited on : 2004-06-09

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

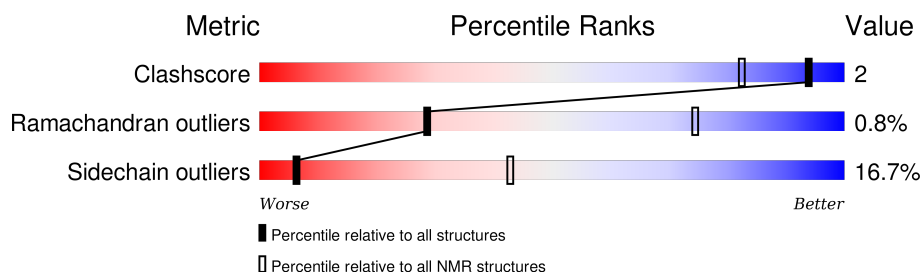
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 51%.

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	68	 84% 13% •

## 2 Ensemble composition and analysis

This entry contains 30 models. Model 8 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:68 (66)	0.32	8

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 5 clusters and 12 single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 7, 8, 9, 12, 20, 21, 29
2	2, 26
3	5, 15
4	6, 19
5	10, 23
Single-model clusters	11; 13; 14; 16; 17; 18; 22; 24; 25; 27; 28; 30

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1044 atoms, of which 529 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Copper transport protein ATOX1.

Mol	Chain	Residues	Atoms						Trace
1	A	68	Total	C	H	N	O	S	0
			1043	322	529	85	101	6	

- Molecule 2 is COPPER (I) ION (three-letter code: CU1) (formula: Cu).

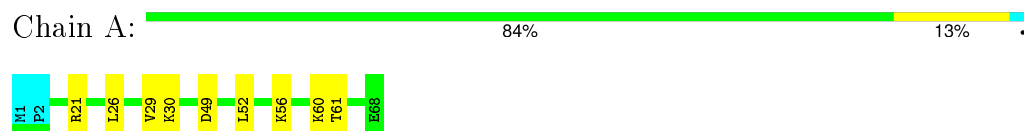
Mol	Chain	Residues	Atoms	
2	A	1	Total	Cu
			1	1

## 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: Copper transport protein ATOX1

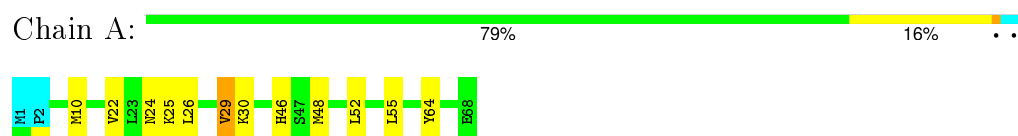


### 4.2 Scores per residue for each member of the ensemble

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

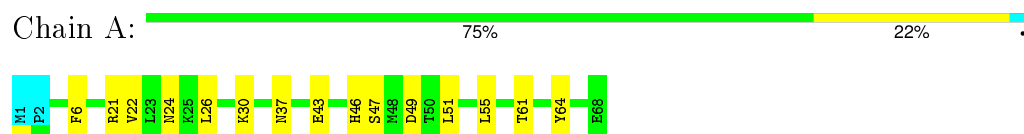
#### 4.2.1 Score per residue for model 1

- Molecule 1: Copper transport protein ATOX1



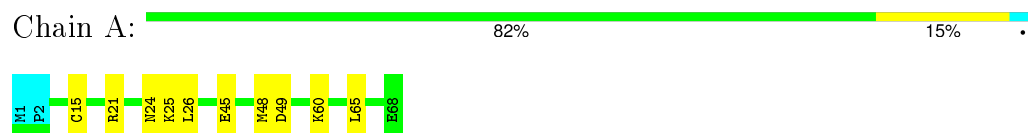
#### 4.2.2 Score per residue for model 2

- Molecule 1: Copper transport protein ATOX1



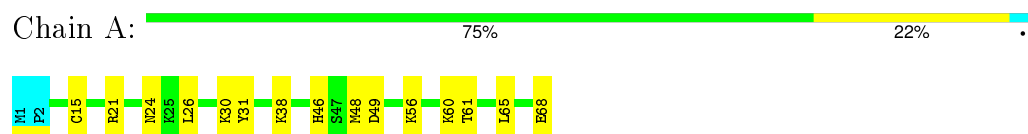
### 4.2.3 Score per residue for model 3

- Molecule 1: Copper transport protein ATOX1



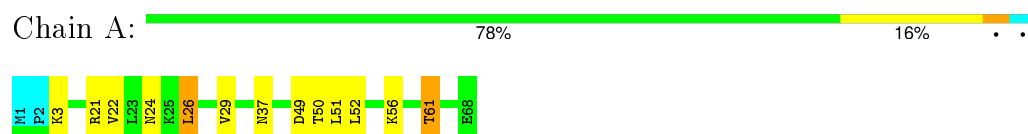
### 4.2.4 Score per residue for model 4

- Molecule 1: Copper transport protein ATOX1



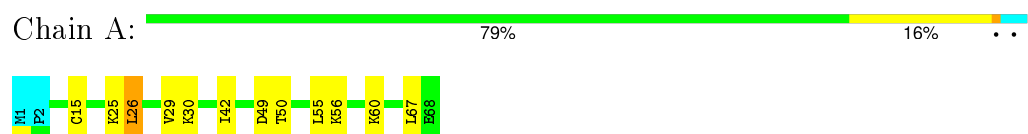
### 4.2.5 Score per residue for model 5

- Molecule 1: Copper transport protein ATOX1



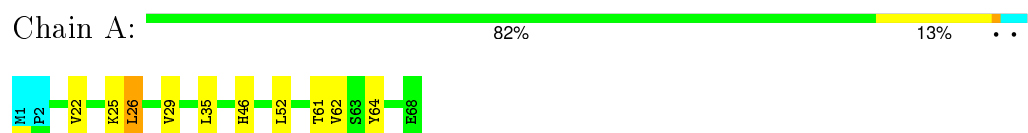
### 4.2.6 Score per residue for model 6

- Molecule 1: Copper transport protein ATOX1



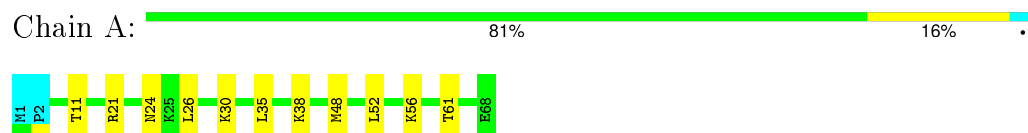
### 4.2.7 Score per residue for model 7

- Molecule 1: Copper transport protein ATOX1



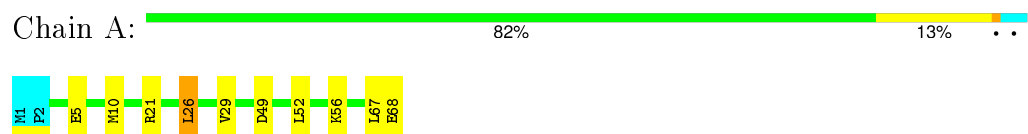
#### 4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: Copper transport protein ATOX1



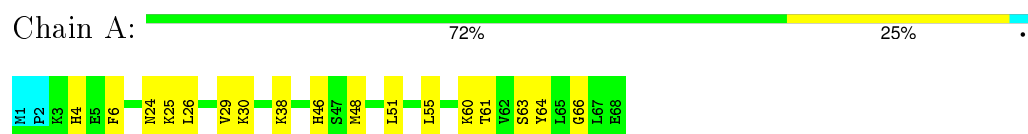
#### 4.2.9 Score per residue for model 9

- Molecule 1: Copper transport protein ATOX1



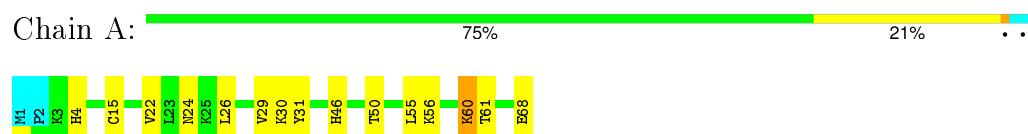
#### 4.2.10 Score per residue for model 10

- Molecule 1: Copper transport protein ATOX1



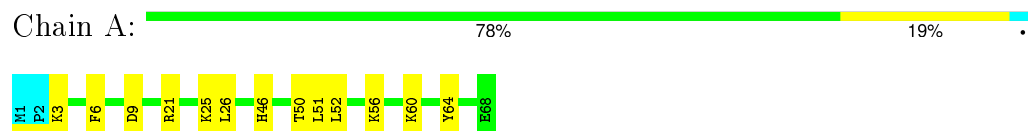
#### 4.2.11 Score per residue for model 11

- Molecule 1: Copper transport protein ATOX1



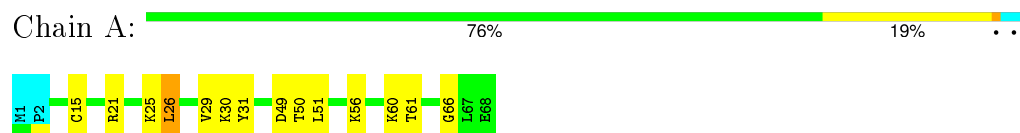
#### 4.2.12 Score per residue for model 12

- Molecule 1: Copper transport protein ATOX1



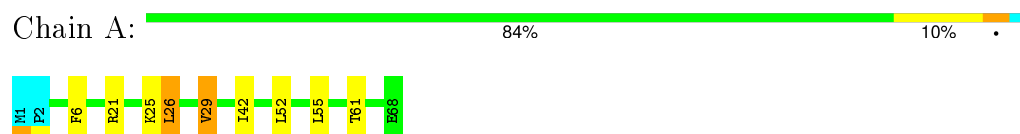
#### 4.2.13 Score per residue for model 13

- Molecule 1: Copper transport protein ATOX1



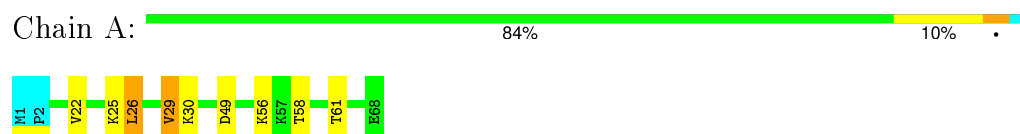
#### 4.2.14 Score per residue for model 14

- Molecule 1: Copper transport protein ATOX1



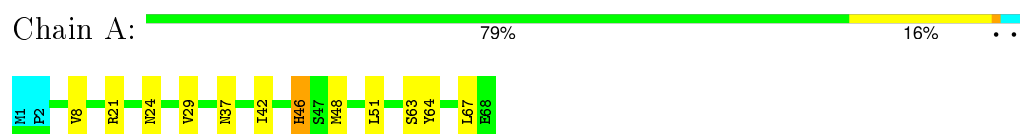
#### 4.2.15 Score per residue for model 15

- Molecule 1: Copper transport protein ATOX1



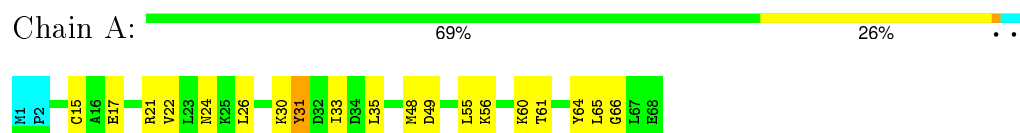
#### 4.2.16 Score per residue for model 16

- Molecule 1: Copper transport protein ATOX1



#### 4.2.17 Score per residue for model 17

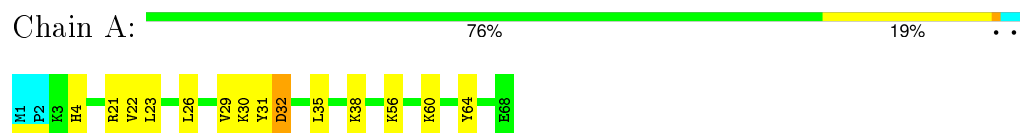
- Molecule 1: Copper transport protein ATOX1





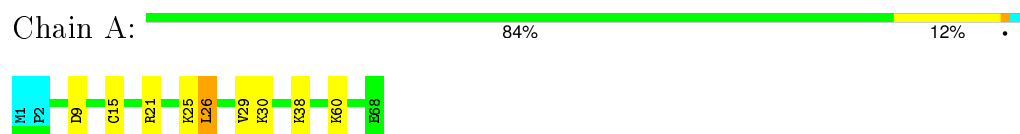
#### 4.2.18 Score per residue for model 18

- Molecule 1: Copper transport protein ATOX1



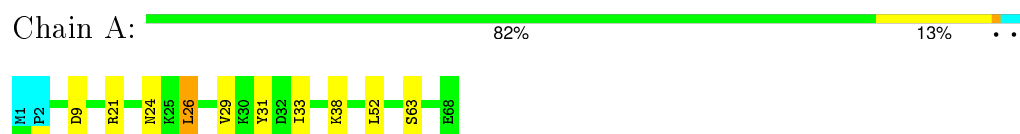
#### 4.2.19 Score per residue for model 19

- Molecule 1: Copper transport protein ATOX1



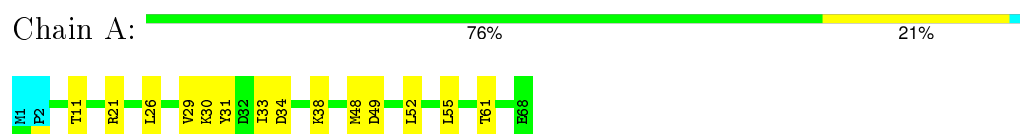
#### 4.2.20 Score per residue for model 20

- Molecule 1: Copper transport protein ATOX1



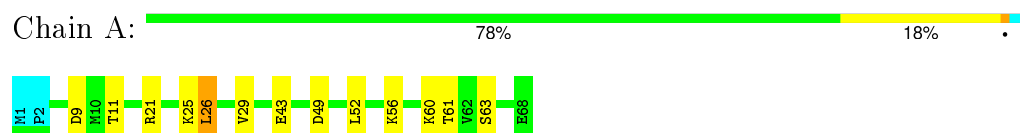
#### 4.2.21 Score per residue for model 21

- Molecule 1: Copper transport protein ATOX1



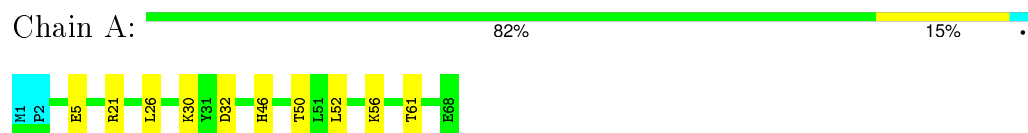
#### 4.2.22 Score per residue for model 22

- Molecule 1: Copper transport protein ATOX1



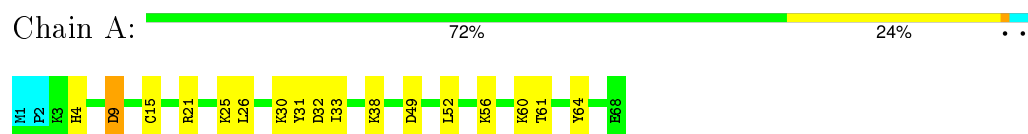
#### 4.2.23 Score per residue for model 23

- Molecule 1: Copper transport protein ATOX1



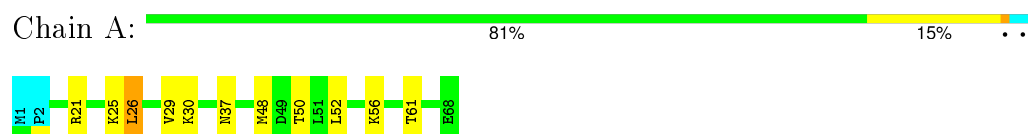
#### 4.2.24 Score per residue for model 24

- Molecule 1: Copper transport protein ATOX1



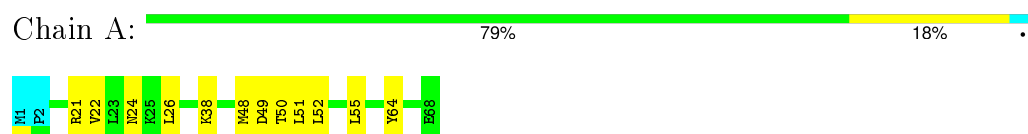
#### 4.2.25 Score per residue for model 25

- Molecule 1: Copper transport protein ATOX1



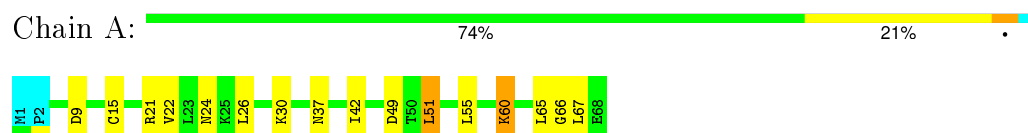
#### 4.2.26 Score per residue for model 26

- Molecule 1: Copper transport protein ATOX1



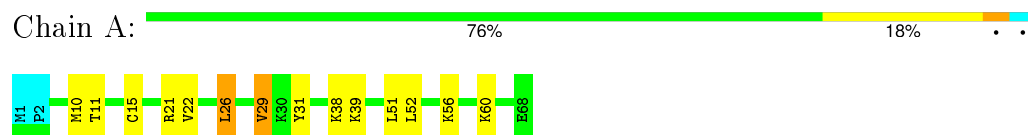
#### 4.2.27 Score per residue for model 27

- Molecule 1: Copper transport protein ATOX1



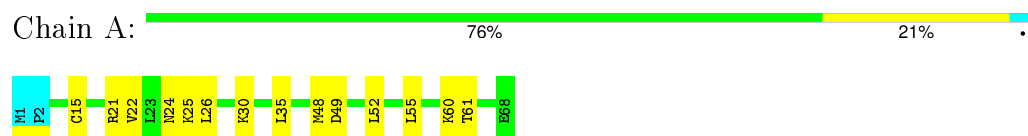
#### 4.2.28 Score per residue for model 28

- Molecule 1: Copper transport protein ATOX1



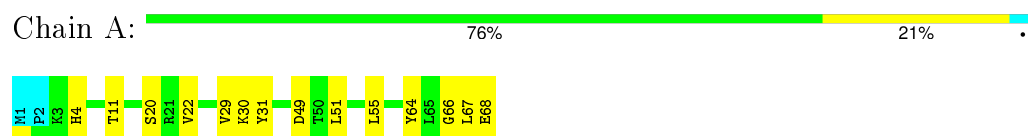
#### 4.2.29 Score per residue for model 29

- Molecule 1: Copper transport protein ATOX1



#### 4.2.30 Score per residue for model 30

- Molecule 1: Copper transport protein ATOX1



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics coupled with simulated annealing followed by restrained energy minimization*.

Of the 400 calculated structures, 30 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
DIANA	structure solution	1.5
CYANA	structure solution	1.0
AMBER	refinement	5.0

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 6266
Number of chemical shift lists	1
Total number of shifts	486
Number of shifts mapped to atoms	486
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	51%

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CU1

There are no covalent bond-length or bond-angle outliers.

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	1.2±1.0
All	All	0	35

There are no bond-length outliers.

There are no bond-angle outliers.

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	64	TYR	Sidechain	9
1	A	31	TYR	Sidechain	6
1	A	29	VAL	Peptide	6
1	A	6	PHE	Sidechain	4
1	A	46	HIS	Sidechain	3
1	A	32	ASP	Peptide	3
1	A	67	LEU	Peptide	2
1	A	65	LEU	Peptide	1
1	A	8	VAL	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	499	511	511	2±1
All	All	15000	15330	15330	50

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:LEU:HD12	1:A:29:VAL:HG13	0.79	1.54	14	12
1:A:42:ILE:HD11	1:A:55:LEU:HD11	0.49	1.83	6	2
1:A:15:CYS:SG	1:A:60:LYS:NZ	0.48	2.85	24	11
1:A:26:LEU:HD13	1:A:26:LEU:C	0.48	2.28	7	4
1:A:26:LEU:C	1:A:26:LEU:HD13	0.48	2.29	20	4
1:A:42:ILE:HG21	1:A:51:LEU:CD1	0.48	2.38	27	1
1:A:26:LEU:CD1	1:A:29:VAL:HG13	0.48	2.37	25	7
1:A:31:TYR:CE2	1:A:33:ILE:HD11	0.47	2.43	24	4
1:A:4:HIS:CD2	1:A:64:TYR:CE1	0.45	3.05	24	1
1:A:46:HIS:CE1	1:A:51:LEU:HD21	0.43	2.48	16	1
1:A:26:LEU:HD12	1:A:29:VAL:CG1	0.41	2.46	22	1
1:A:23:LEU:O	1:A:26:LEU:HB3	0.40	2.16	18	1
1:A:42:ILE:HD13	1:A:51:LEU:HD13	0.40	1.92	16	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	65/68 (96%)	57±2 (88±3%)	7±2 (11±3%)	1±1 (1±1%)	29	74
All	All	1950/2040 (96%)	1721 (88%)	214 (11%)	15 (1%)	29	74

All 5 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	9	ASP	5

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Mol	Chain	Res	Type	Models (Total)
1	A	66	GLY	5
1	A	46	HIS	2
1	A	29	VAL	2
1	A	61	THR	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	57/59 (97%)	48±2 (83±4%)	10±2 (17±4%)	6	43
All	All	1710/1770 (97%)	1425 (83%)	285 (17%)	6	43

All 42 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	26	LEU	26
1	A	21	ARG	23
1	A	30	LYS	19
1	A	61	THR	17
1	A	52	LEU	16
1	A	56	LYS	16
1	A	49	ASP	16
1	A	25	LYS	14
1	A	24	ASN	14
1	A	22	VAL	13
1	A	48	MET	11
1	A	55	LEU	10
1	A	38	LYS	10
1	A	51	LEU	9
1	A	50	THR	8
1	A	60	LYS	6
1	A	37	ASN	5
1	A	11	THR	5
1	A	35	LEU	5
1	A	46	HIS	4
1	A	63	SER	4

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Mol	Chain	Res	Type	Models (Total)
1	A	4	HIS	4
1	A	65	LEU	3
1	A	10	MET	3
1	A	5	GLU	2
1	A	29	VAL	2
1	A	43	GLU	2
1	A	9	ASP	2
1	A	3	LYS	2
1	A	67	LEU	2
1	A	17	GLU	1
1	A	58	THR	1
1	A	39	LYS	1
1	A	34	ASP	1
1	A	45	GLU	1
1	A	31	TYR	1
1	A	68	GLU	1
1	A	64	TYR	1
1	A	32	ASP	1
1	A	47	SER	1
1	A	62	VAL	1
1	A	20	SER	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.



## 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 51% for the well-defined parts and 50% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 6266

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	486
Number of shifts mapped to atoms	486
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
$^{13}\text{C}_\alpha$	0	—	—
$^{13}\text{C}_\beta$	0	—	—
$^{13}\text{C}'$	0	—	—
$^{15}\text{N}$	64	$-0.96 \pm 0.60$	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 51%, i.e. 392 atoms were assigned a chemical shift out of a possible 770. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	192/328 (59%)	128/131 (98%)	0/132 (0%)	64/65 (98%)
Sidechain	192/403 (48%)	190/234 (81%)	0/156 (0%)	2/13 (15%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	8/39 (21%)	8/21 (38%)	0/16 (0%)	0/2 (0%)
Overall	392/770 (51%)	326/386 (84%)	0/304 (0%)	66/80 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 50%, i.e. 398 atoms were assigned a chemical shift out of a possible 795. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	193/336 (57%)	129/134 (96%)	0/136 (0%)	64/66 (97%)
Sidechain	197/420 (47%)	195/245 (80%)	0/162 (0%)	2/13 (15%)
Aromatic	8/39 (21%)	8/21 (38%)	0/16 (0%)	0/2 (0%)
Overall	398/795 (50%)	332/400 (83%)	0/314 (0%)	66/81 (81%)

#### 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:

