



# Full wwPDB NMR Structure Validation Report ⓘ

May 30, 2020 – 02:09 am BST

PDB ID : 6JTF  
Title : Complex of MarH and L-Trp  
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Deposited on : 2019-04-10

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

<https://www.wwpdb.org/validation/2017/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  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

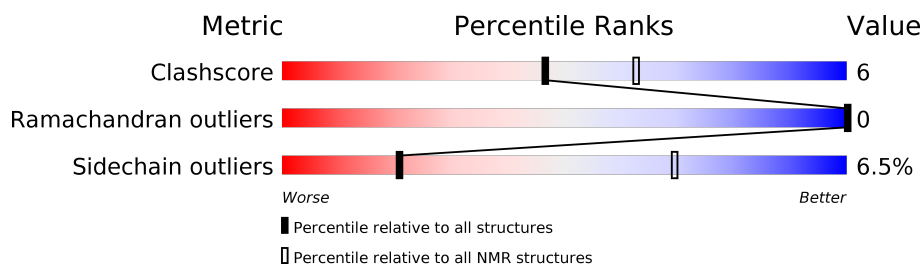
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 62%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	126	<div>81% 14% ..</div>

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 2 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:7-A:129 (123)	0.01	2

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 2 clusters. No single-model clusters were found.

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

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

There are 3 unique types of molecules in this entry. The entry contains 1863 atoms, of which 930 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cupin superfamily protein.

Mol	Chain	Residues	Atoms						Trace
1	A	123	Total	C	H	N	O	S	0
			1835	589	918	156	168	4	

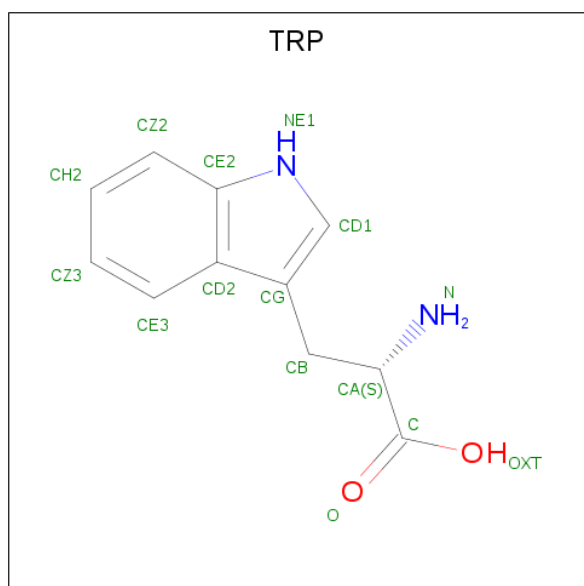
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	GLY	-	expression tag	UNP X2D812
A	5	SER	-	expression tag	UNP X2D812

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

- Molecule 3 is TRYPTOPHAN (three-letter code: TRP) (formula: C<sub>11</sub>H<sub>12</sub>N<sub>2</sub>O<sub>2</sub>).

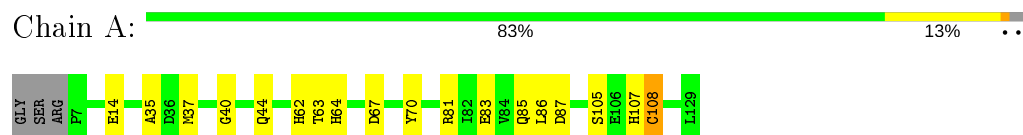


Mol	Chain	Residues	Atoms				
3	A	1	Total	C	H	N	O
			27	11	12	2	2



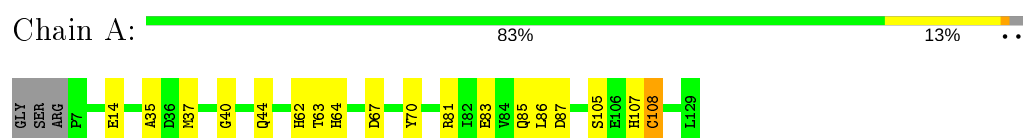
### 4.2.3 Score per residue for model 3

- Molecule 1: Cupin superfamily protein



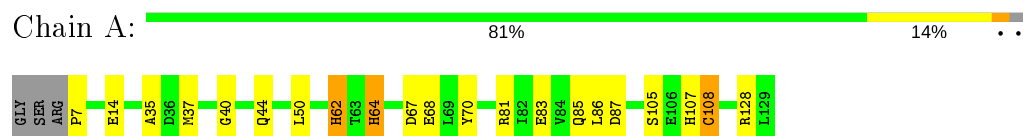
### 4.2.4 Score per residue for model 4

- Molecule 1: Cupin superfamily protein



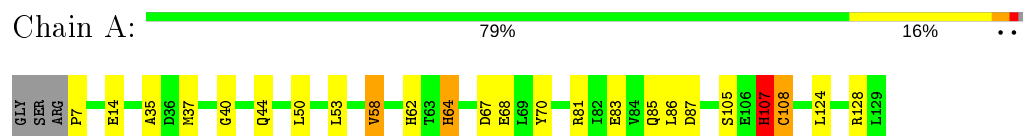
### 4.2.5 Score per residue for model 5

- Molecule 1: Cupin superfamily protein



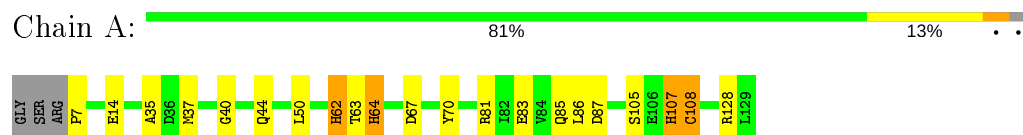
### 4.2.6 Score per residue for model 6

- Molecule 1: Cupin superfamily protein



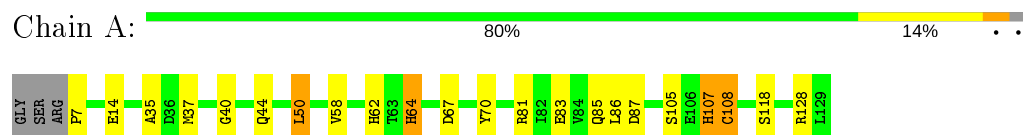
### 4.2.7 Score per residue for model 7

- Molecule 1: Cupin superfamily protein



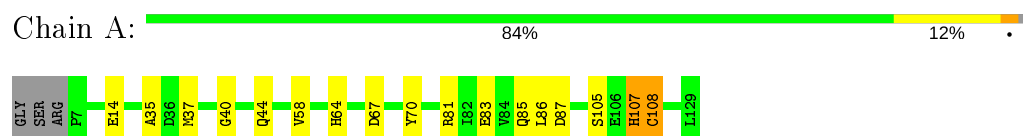
### 4.2.8 Score per residue for model 8

- Molecule 1: Cupin superfamily protein



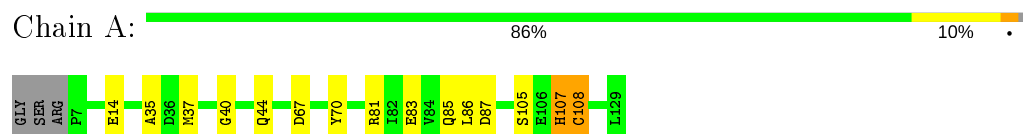
### 4.2.9 Score per residue for model 9

- Molecule 1: Cupin superfamily protein



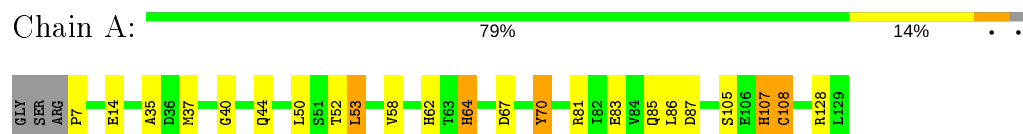
### 4.2.10 Score per residue for model 10

- Molecule 1: Cupin superfamily protein



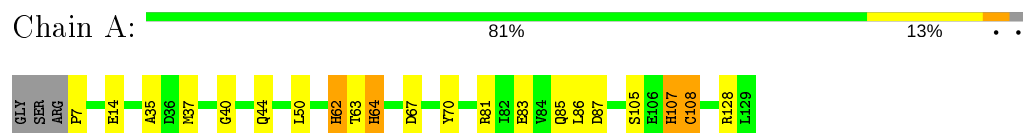
### 4.2.11 Score per residue for model 11

- Molecule 1: Cupin superfamily protein



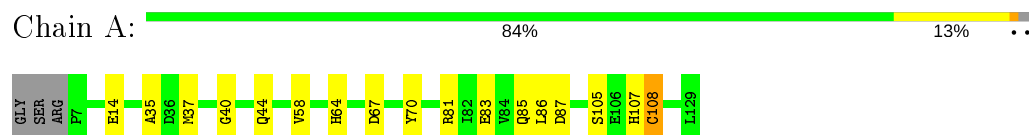
### 4.2.12 Score per residue for model 12

- Molecule 1: Cupin superfamily protein



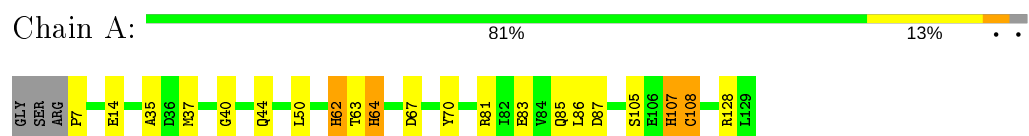
### 4.2.13 Score per residue for model 13

- Molecule 1: Cupin superfamily protein



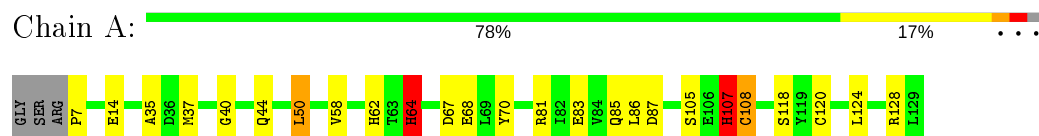
### 4.2.14 Score per residue for model 14

- Molecule 1: Cupin superfamily protein



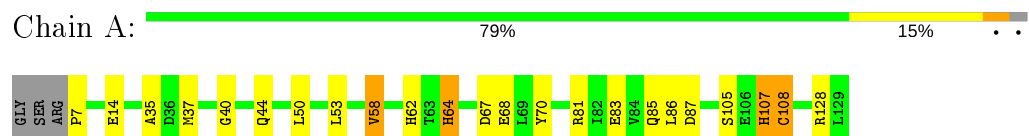
### 4.2.15 Score per residue for model 15

- Molecule 1: Cupin superfamily protein



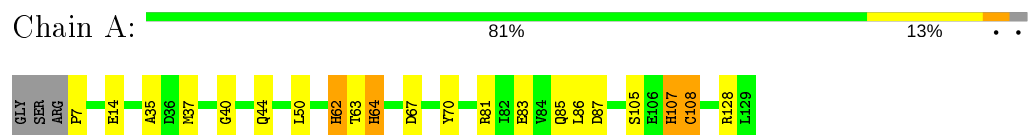
### 4.2.16 Score per residue for model 16

- Molecule 1: Cupin superfamily protein



### 4.2.17 Score per residue for model 17

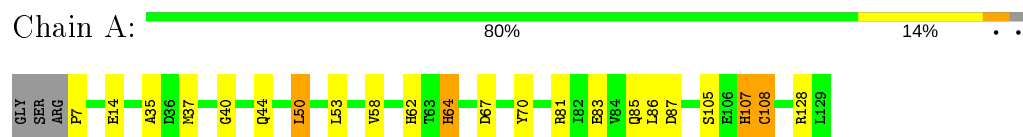
- Molecule 1: Cupin superfamily protein





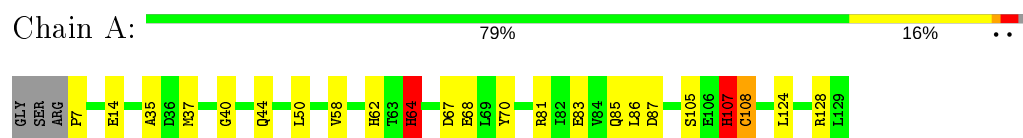
#### 4.2.18 Score per residue for model 18

- Molecule 1: Cupin superfamily protein



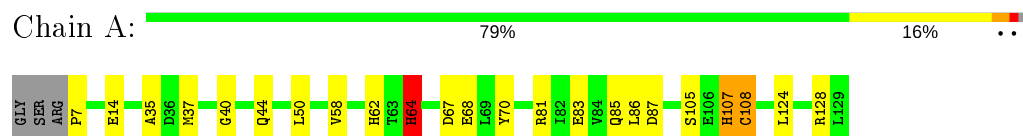
#### 4.2.19 Score per residue for model 19

- Molecule 1: Cupin superfamily protein



#### 4.2.20 Score per residue for model 20

- Molecule 1: Cupin superfamily protein



## 5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR NIH	structure calculation	
X-PLOR NIH	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	978
Number of shifts mapped to atoms	978
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	62%

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

COVALENT-GEOMETRY INFOmissingINFO

### 5.1 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	917	918	917	12±2
3	A	15	12	9	0±0
All	All	18660	18600	18520	240

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:HIS:ND1	1:A:64:HIS:N	0.88	2.20	4	7
1:A:64:HIS:N	1:A:64:HIS:ND1	0.88	2.20	2	8
1:A:70:TYR:OH	1:A:107:HIS:CE1	0.76	2.37	4	20
1:A:107:HIS:ND1	1:A:107:HIS:C	0.76	2.39	12	10
1:A:107:HIS:C	1:A:107:HIS:ND1	0.76	2.40	4	10
1:A:107:HIS:HD1	1:A:108:CYS:N	0.71	1.83	12	16
1:A:107:HIS:ND1	1:A:108:CYS:N	0.67	2.42	13	20
1:A:64:HIS:HD1	1:A:64:HIS:N	0.62	1.91	12	4
1:A:64:HIS:N	1:A:64:HIS:HD1	0.61	1.92	3	4
1:A:64:HIS:CE1	1:A:68:GLU:CD	0.58	2.77	19	4
1:A:107:HIS:HD1	1:A:108:CYS:CA	0.58	2.10	3	10
1:A:64:HIS:CE1	1:A:68:GLU:OE1	0.58	2.56	6	4
1:A:58:VAL:HG11	3:A:202:TRP:CZ3	0.56	2.34	13	6
1:A:68:GLU:HB3	1:A:124:LEU:HD23	0.56	1.76	6	4
1:A:68:GLU:OE2	1:A:70:TYR:CE2	0.55	2.59	5	1
1:A:63:THR:C	1:A:64:HIS:ND1	0.55	2.59	12	7
1:A:64:HIS:CD2	1:A:68:GLU:OE1	0.52	2.63	6	1
1:A:83:GLU:OE2	1:A:85:GLN:NE2	0.49	2.42	1	20
1:A:50:LEU:HD12	1:A:118:SER:O	0.49	2.08	15	2
1:A:62:HIS:CE1	1:A:64:HIS:NE2	0.47	2.82	12	7
1:A:35:ALA:H	1:A:44:GLN:HE21	0.46	1.53	1	20
1:A:64:HIS:CG	1:A:68:GLU:OE1	0.45	2.69	6	1
1:A:107:HIS:ND1	1:A:108:CYS:CA	0.44	2.80	17	9
1:A:62:HIS:CE1	1:A:64:HIS:CD2	0.43	3.06	5	1
1:A:50:LEU:HB3	1:A:53:LEU:HD12	0.42	1.90	18	1
1:A:86:LEU:CD1	1:A:105:SER:OG	0.41	2.69	1	20
1:A:35:ALA:H	1:A:44:GLN:NE2	0.41	2.13	1	20
1:A:50:LEU:HD21	1:A:120:CYS:CB	0.41	2.45	15	1
1:A:50:LEU:HD21	1:A:120:CYS:HB2	0.40	1.91	15	1
1:A:70:TYR:OH	1:A:107:HIS:HE1	0.40	1.94	19	1

## 5.2 Torsion angles ⓘ

### 5.2.1 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	121/126 (96%)	96±48 (79±40%)	1±0 (1±0%)	0±0 (0±0%)	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1936/2520 (77%)	1920 (99%)	16 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

### 5.2.2 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	97/99 (98%)	64±42 (65±43%)	4±3 (5±3%)	31	80
All	All	1358/1980 (69%)	1270 (94%)	88 (6%)	21	69

All 9 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	50	LEU	14
1	A	64	HIS	14
1	A	62	HIS	14
1	A	7	PRO	14
1	A	128	ARG	14
1	A	107	HIS	8
1	A	58	VAL	6
1	A	53	LEU	3
1	A	68	GLU	1

### 5.2.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.3 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.4 Carbohydrates

There are no carbohydrates in this entry.

## 5.5 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Other polymers

There are no such molecules in this entry.

## 5.7 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 62% for the well-defined parts and 62% for the entire structure.

### 6.1 Chemical shift list 1

File name: input\_cs.cif

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

#### 6.1.1 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	978
Number of shifts mapped to atoms	978
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

#### 6.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	118	$0.17 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	102	$-0.29 \pm 0.16$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	99	$0.40 \pm 0.20$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	103	$-0.44 \pm 0.32$	None needed ( $< 0.5$ ppm)

#### 6.1.3 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 62%, i.e. 886 atoms were assigned a chemical shift out of a possible 1427. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	519/589 (88%)	201/233 (86%)	216/246 (88%)	102/110 (93%)
Sidechain	367/736 (50%)	200/432 (46%)	167/283 (59%)	0/21 (0%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	0/102 (0%)	0/56 (0%)	0/40 (0%)	0/6 (0%)
Overall	886/1427 (62%)	401/721 (56%)	383/569 (67%)	102/137 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 62%, i.e. 886 atoms were assigned a chemical shift out of a possible 1427. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	519/589 (88%)	201/233 (86%)	216/246 (88%)	102/110 (93%)
Sidechain	367/736 (50%)	200/432 (46%)	167/283 (59%)	0/21 (0%)
Aromatic	0/102 (0%)	0/56 (0%)	0/40 (0%)	0/6 (0%)
Overall	886/1427 (62%)	401/721 (56%)	383/569 (67%)	102/137 (74%)

#### 6.1.4 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	46	ALA	HB1	-0.04	2.61 – 0.11	-5.6
1	A	46	ALA	HB3	-0.04	2.61 – 0.11	-5.6
1	A	46	ALA	HB2	-0.04	2.61 – 0.11	-5.6

#### 6.1.5 Random Coil Index (RCI) plots [i](#)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_1). RCI is only applicable to proteins.