



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 10, 2026 – 07:29 AM UTC

PDB ID : 5OAY / pdb_00005oay
BMRB ID : 34153
Title : M. tuberculosis [4Fe-4S] protein WhiB1 is a four-helix bundle that forms a NO-sensitive complex with sigmaA and regulates the major virulence factor ESX-1
Authors : Williamson, M.P.; Green, J.; Hounslow, A.M.
Deposited on : 2017-06-25

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with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

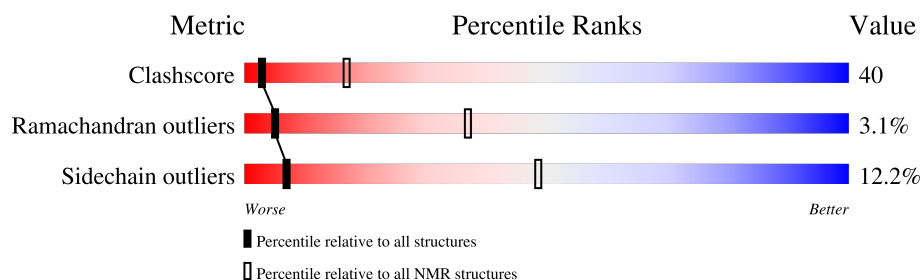
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 66%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	94	

2 Ensemble composition and analysis

This entry contains 10 models. Model 4 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:1-A:55, A:62-A:76 (70)	0.91	4

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 and 5 single-model clusters were found.

Cluster number	Models
1	2, 3, 8
2	4, 9
Single-model clusters	1; 5; 6; 7; 10

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1160 atoms, of which 563 are hydrogens and 0 are deuteriums.

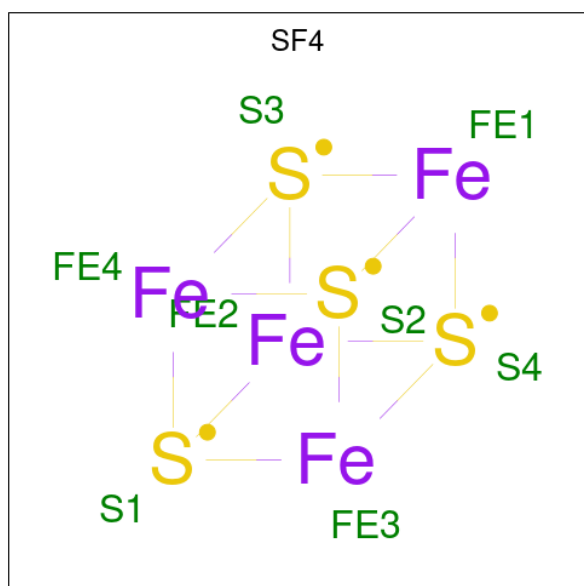
- Molecule 1 is a protein called Transcriptional regulator WhiB1.

Mol	Chain	Residues	Atoms						Trace
1	A	76	Total	C	H	N	O	S	0
			1152	361	563	111	111	6	

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	ALA	-	expression tag	UNP P9WF43
A	-8	GLY	-	expression tag	UNP P9WF43
A	-7	GLU	-	expression tag	UNP P9WF43
A	-6	ASN	-	expression tag	UNP P9WF43
A	-5	LEU	-	expression tag	UNP P9WF43
A	-4	TYR	-	expression tag	UNP P9WF43
A	-3	PHE	-	expression tag	UNP P9WF43
A	-2	GLN	-	expression tag	UNP P9WF43
A	-1	GLY	-	expression tag	UNP P9WF43
A	0	ALA	-	expression tag	UNP P9WF43

- Molecule 2 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



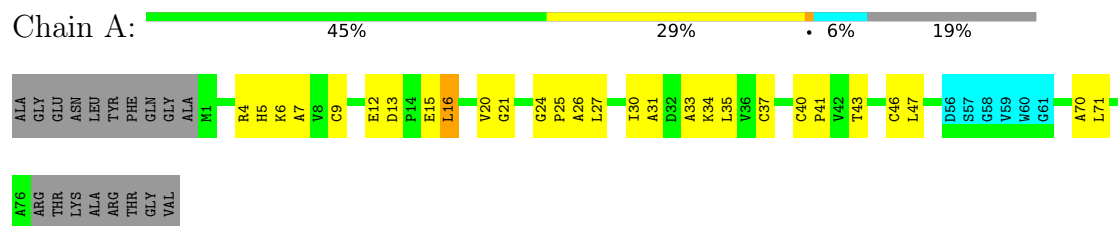
Mol	Chain	Residues	Atoms		
			Total	Fe	S
2	A	1	8	4	4

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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.

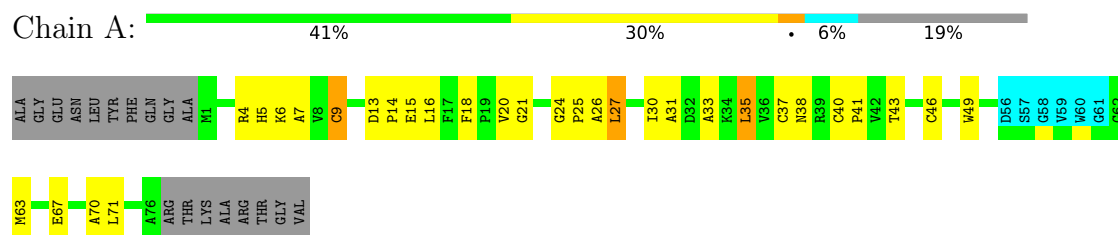
- Molecule 1: Transcriptional regulator WhiB1



4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 4. Colouring as in section 4.1 above.

- Molecule 1: Transcriptional regulator WhiB1



5 Refinement protocol and experimental data overview

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

Of the 62 calculated structures, 10 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
CNS	structure calculation	1.2

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	859
Number of shifts mapped to atoms	677
Number of unparsed shifts	0
Number of shifts with mapping errors	182
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	66%

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	546	529	0	39±20
2	A	8	0	0	3±1
All	All	5540	5290	4240	388

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 40.

5 of 127 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:LEU:HD22	1:A:30:ILE:HG23	1.01	1.32	6	7
1:A:16:LEU:HD11	1:A:30:ILE:HG23	0.98	1.33	4	1
1:A:16:LEU:CD1	1:A:30:ILE:HG23	0.90	1.95	4	1
1:A:37:CYS:O	2:A:101:SF4:S3	0.90	2.29	1	5
1:A:31:ALA:O	1:A:35:LEU:HD23	0.88	1.66	8	3

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	63/94 (67%)	63±2 (100±3%)	2±1 (4±1%)	2±1 (3±1%)	5	35
All	All	675/940 (72%)	631 (93%)	23 (3%)	21 (3%)	5	37

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	21	GLY	8
1	A	12	GLU	6
1	A	41	PRO	4
1	A	42	VAL	2
1	A	62	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	53/74 (72%)	50±2 (95±5%)	7±1 (13±3%)	6	46
All	All	575/740 (78%)	505 (88%)	70 (12%)	7	48

5 of 18 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	16	LEU	9
1	A	46	CYS	9
1	A	40	CYS	8
1	A	9	CYS	7
1	A	27	LEU	7

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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	SF4	A	101	1	0,12,12	0.00±0.00	-

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	SF4	A	101	1	-	-	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means

no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SF4	A	101	1	-	-	0±0,6,5,5

There are no bond-length outliers.

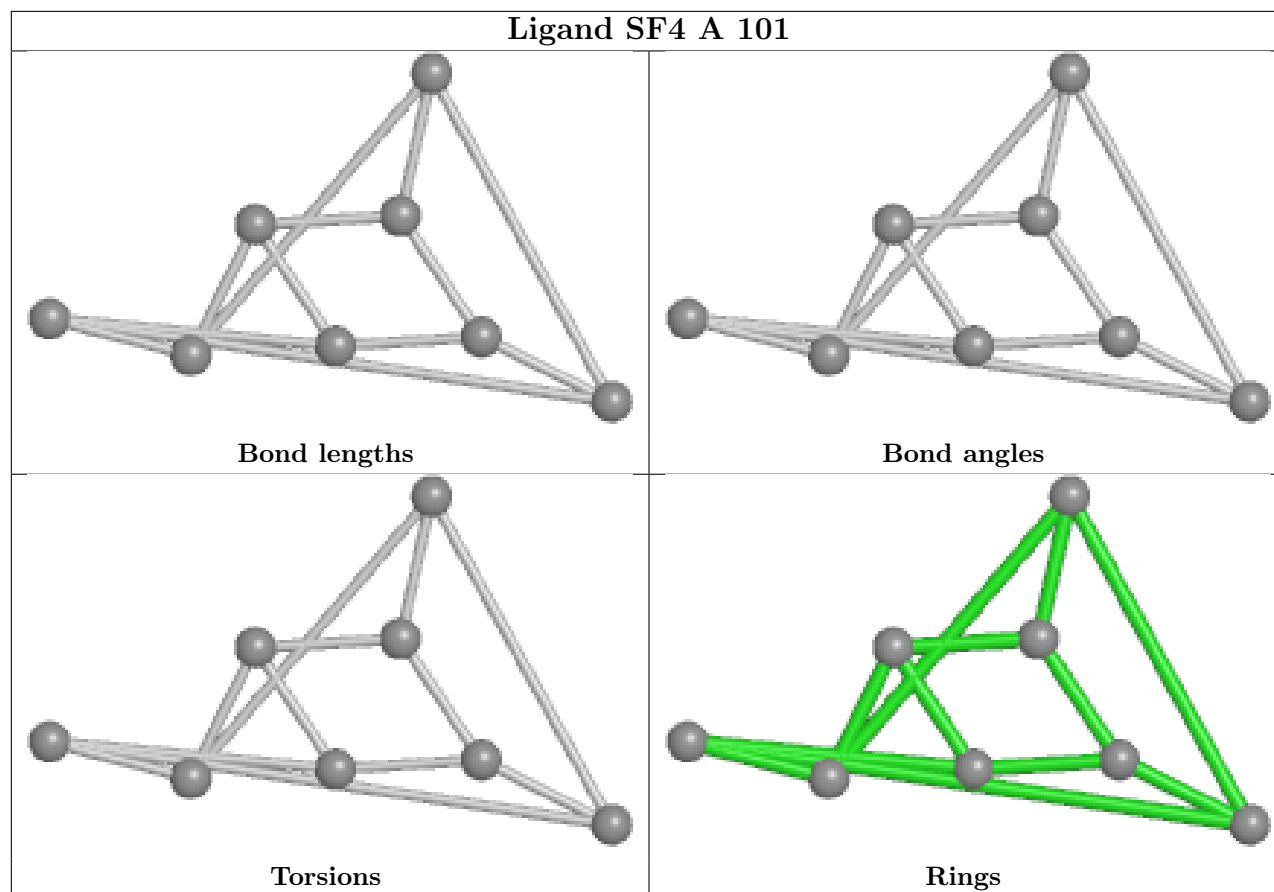
There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 66% for the well-defined parts and 67% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *WhiB1_new_STAR_3.1*

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	859
Number of shifts mapped to atoms	677
Number of unparsed shifts	0
Number of shifts with mapping errors	182
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

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

- No matching atom found in the structure. First 5 (of 182) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-9	ALA	H	7.88	0.005	1
1	A	-9	ALA	HA	4.33	0.005	1
1	A	-9	ALA	HB1	1.55	0.005	1
1	A	-9	ALA	HB2	1.55	0.005	1
1	A	-9	ALA	HB3	1.55	0.005	1
1	A	-9	ALA	C	179.362	0.050	1
1	A	-9	ALA	CA	52.661	0.050	1
1	A	-9	ALA	CB	19.087	0.050	1
1	A	-9	ALA	N	123.531	0.050	1
1	A	-8	GLY	H	7.712	0.005	1
1	A	-8	GLY	HA2	3.89	0.005	2
1	A	-8	GLY	HA3	3.79	0.005	2
1	A	-8	GLY	C	174.294	0.050	1
1	A	-8	GLY	CA	46.39	0.050	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-8	GLY	N	105.109	0.050	1
1	A	-7	GLU	H	8.385	0.005	1
1	A	-7	GLU	HA	4.27	0.005	1
1	A	-7	GLU	C	176.459	0.050	1
1	A	-7	GLU	CA	56.53	0.050	1
1	A	-7	GLU	N	120.085	0.050	1
1	A	-6	ASN	H	8.561	0.005	1
1	A	-6	ASN	HA	4.47	0.005	1
1	A	-6	ASN	HB2	2.73	0.005	2
1	A	-6	ASN	HB3	2.73	0.005	2
1	A	-6	ASN	C	175.023	0.050	1
1	A	-6	ASN	CA	53.552	0.050	1
1	A	-6	ASN	CB	38.214	0.050	1
1	A	-6	ASN	N	119.735	0.050	1
1	A	-5	LEU	H	7.9	0.005	1
1	A	-5	LEU	HA	4.09	0.005	1
1	A	-5	LEU	HB2	1.15	0.005	2
1	A	-5	LEU	HB3	1.3	0.005	2
1	A	-5	LEU	HD11	0.61	0.005	2
1	A	-5	LEU	HD12	0.61	0.005	2
1	A	-5	LEU	HD13	0.61	0.005	2
1	A	-5	LEU	HD21	0.7	0.005	2
1	A	-5	LEU	HD22	0.7	0.005	2
1	A	-5	LEU	HD23	0.7	0.005	2
1	A	-5	LEU	HG	1.25	0.005	1
1	A	-5	LEU	C	176.716	0.050	1
1	A	-5	LEU	CA	55.406	0.050	1
1	A	-5	LEU	CB	42.151	0.050	1
1	A	-5	LEU	CD1	23.3	0.050	2
1	A	-5	LEU	CD2	24.7	0.050	2
1	A	-5	LEU	CG	26.6	0.050	1
1	A	-5	LEU	N	121.239	0.050	1
1	A	-4	TYR	H	7.994	0.005	1
1	A	-4	TYR	HA	4.42	0.005	1
1	A	-4	TYR	HB2	2.75	0.005	2
1	A	-4	TYR	HB3	2.9	0.005	2
1	A	-4	TYR	HD1	6.95	0.005	1
1	A	-4	TYR	HD2	6.95	0.005	1
1	A	-4	TYR	HE1	6.74	0.005	1
1	A	-4	TYR	HE2	6.74	0.005	1
1	A	-4	TYR	C	175.573	0.050	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	-4	TYR	CA	57.816	0.050	1
1	A	-4	TYR	CB	38.175	0.050	1
1	A	-4	TYR	CD1	133.0	0.050	1
1	A	-4	TYR	CD2	133.0	0.050	1
1	A	-4	TYR	CE1	118.1	0.050	1
1	A	-4	TYR	CE2	118.1	0.050	1
1	A	-4	TYR	N	118.927	0.050	1
1	A	-3	PHE	H	7.846	0.005	1
1	A	-3	PHE	HA	4.53	0.005	1
1	A	-3	PHE	HB2	2.92	0.005	2
1	A	-3	PHE	HB3	3.1	0.005	2
1	A	-3	PHE	HD1	7.1	0.005	1
1	A	-3	PHE	HD2	7.1	0.005	1
1	A	-3	PHE	C	175.588	0.050	1
1	A	-3	PHE	CA	57.633	0.050	1
1	A	-3	PHE	CB	39.406	0.050	1
1	A	-3	PHE	CD1	131.7	0.050	1
1	A	-3	PHE	CD2	131.7	0.050	1
1	A	-3	PHE	N	121.185	0.050	1
1	A	-2	GLN	H	8.559	0.005	1
1	A	-2	GLN	HA	4.56	0.005	1
1	A	-2	GLN	HB2	2.14	0.005	2
1	A	-2	GLN	HB3	1.93	0.005	2
1	A	-2	GLN	HG2	2.3	0.005	2
1	A	-2	GLN	HG3	2.3	0.005	2
1	A	-2	GLN	C	176.193	0.050	1
1	A	-2	GLN	CA	55.901	0.050	1
1	A	-2	GLN	CB	28.849	0.050	1
1	A	-2	GLN	CG	33.7	0.050	1
1	A	-2	GLN	N	121.583	0.050	1
1	A	-1	GLY	H	8.108	0.005	1
1	A	-1	GLY	HA2	3.84	0.005	2
1	A	-1	GLY	HA3	4.08	0.005	2
1	A	-1	GLY	C	174.238	0.050	1
1	A	-1	GLY	CA	45.317	0.050	1
1	A	-1	GLY	N	109.719	0.050	1
1	A	0	ALA	H	8.306	0.005	1
1	A	0	ALA	HA	4.21	0.005	1
1	A	0	ALA	HB1	1.31	0.005	1
1	A	0	ALA	HB2	1.31	0.005	1
1	A	0	ALA	HB3	1.31	0.005	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	0	ALA	C	177.771	0.050	1
1	A	0	ALA	CA	52.95	0.050	1
1	A	0	ALA	CB	18.976	0.050	1
1	A	0	ALA	N	123.594	0.050	1
1	A	77	ARG	H	8.075	0.005	1
1	A	77	ARG	HA	4.32	0.005	1
1	A	77	ARG	HB2	1.94	0.005	2
1	A	77	ARG	HB3	1.88	0.005	2
1	A	77	ARG	C	177.144	0.050	1
1	A	77	ARG	CA	56.761	0.050	1
1	A	77	ARG	CB	30.367	0.050	1
1	A	77	ARG	N	119.026	0.050	1
1	A	78	THR	H	8.062	0.005	1
1	A	78	THR	HA	4.25	0.005	1
1	A	78	THR	HB	4.25	0.005	1
1	A	78	THR	HG21	1.19	0.005	1
1	A	78	THR	HG22	1.19	0.005	1
1	A	78	THR	HG23	1.19	0.005	1
1	A	78	THR	C	174.815	0.050	1
1	A	78	THR	CA	62.486	0.050	1
1	A	78	THR	CB	69.579	0.050	1
1	A	78	THR	CG2	21.55	0.050	1
1	A	78	THR	N	114.814	0.050	1
1	A	79	LYS	H	8.224	0.005	1
1	A	79	LYS	HA	4.28	0.005	1
1	A	79	LYS	HB2	1.84	0.005	2
1	A	79	LYS	HB3	1.78	0.005	2
1	A	79	LYS	C	176.461	0.050	1
1	A	79	LYS	CA	56.526	0.050	1
1	A	79	LYS	CB	32.697	0.050	1
1	A	79	LYS	N	123.629	0.050	1
1	A	80	ALA	H	8.232	0.005	1
1	A	80	ALA	HA	4.28	0.005	1
1	A	80	ALA	HB1	1.41	0.005	1
1	A	80	ALA	HB2	1.41	0.005	1
1	A	80	ALA	HB3	1.41	0.005	1
1	A	80	ALA	C	177.8	0.050	1
1	A	80	ALA	CA	52.548	0.050	1
1	A	80	ALA	CB	18.99	0.050	1
1	A	80	ALA	N	124.872	0.050	1
1	A	81	ARG	H	8.327	0.005	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	81	ARG	HA	4.39	0.005	1
1	A	81	ARG	HB2	1.78	0.005	2
1	A	81	ARG	HB3	1.88	0.005	2
1	A	81	ARG	HD2	2.84	0.005	2
1	A	81	ARG	HD3	3.19	0.005	2
1	A	81	ARG	HG2	1.62	0.005	2
1	A	81	ARG	HG3	1.67	0.005	2
1	A	81	ARG	C	176.563	0.050	1
1	A	81	ARG	CA	56.151	0.050	1
1	A	81	ARG	CB	30.577	0.050	1
1	A	81	ARG	CD	43.22	0.050	1
1	A	81	ARG	CG	27.11	0.050	1
1	A	81	ARG	N	120.331	0.050	1
1	A	82	THR	H	8.209	0.005	1
1	A	82	THR	HA	4.39	0.005	1
1	A	82	THR	HB	4.25	0.005	1
1	A	82	THR	HG21	1.22	0.005	1
1	A	82	THR	HG22	1.22	0.005	1
1	A	82	THR	HG23	1.22	0.005	1
1	A	82	THR	C	175.058	0.050	1
1	A	82	THR	CA	61.809	0.050	1
1	A	82	THR	CB	69.784	0.050	1
1	A	82	THR	CG2	21.44	0.050	1
1	A	82	THR	N	114.6	0.050	1
1	A	83	GLY	H	8.442	0.005	1
1	A	83	GLY	HA2	3.95	0.005	2
1	A	83	GLY	HA3	4.07	0.005	2
1	A	83	GLY	C	173.255	0.050	1
1	A	83	GLY	CA	45.352	0.050	1
1	A	83	GLY	N	111.727	0.050	1
1	A	84	VAL	H	7.63	0.005	1
1	A	84	VAL	HA	4.08	0.005	1
1	A	84	VAL	HB	2.11	0.005	1
1	A	84	VAL	HG11	0.85	0.005	2
1	A	84	VAL	HG12	0.85	0.005	2
1	A	84	VAL	HG13	0.85	0.005	2
1	A	84	VAL	HG21	0.89	0.005	2
1	A	84	VAL	HG22	0.89	0.005	2
1	A	84	VAL	HG23	0.89	0.005	2
1	A	84	VAL	C	181.186	0.050	1
1	A	84	VAL	CA	63.526	0.050	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	84	VAL	CB	32.81	0.050	1
1	A	84	VAL	CG1	19.91	0.050	2
1	A	84	VAL	CG2	21.52	0.050	2
1	A	84	VAL	N	122.733	0.050	1

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
$^{13}\text{C}_\alpha$	89	-0.51 ± 0.26	None needed (imprecise)
$^{13}\text{C}_\beta$	71	0.51 ± 0.08	Should be checked
$^{13}\text{C}'$	88	-0.51 ± 0.23	Should be applied
^{15}N	83	0.37 ± 0.48	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 66%, i.e. 624 atoms were assigned a chemical shift out of a possible 939. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	311/346 (90%)	120/140 (86%)	131/140 (94%)	60/66 (91%)
Sidechain	279/541 (52%)	189/348 (54%)	90/163 (55%)	0/30 (0%)
Aromatic	34/52 (65%)	17/26 (65%)	15/22 (68%)	2/4 (50%)
Overall	624/939 (66%)	326/514 (63%)	236/325 (73%)	62/100 (62%)

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	4	ARG	HB2	3.09	0.52 – 3.08	5.0

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

