



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 07:44 PM UTC

PDB ID : 6CAH / pdb_00006cah
BMRB ID : 30399
Title : NMR-based structure of the FHA-2 domain from Mycobacterium tuberculosis ABC transporter Rv1747
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Deposited on : 2018-01-30

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A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

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
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
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

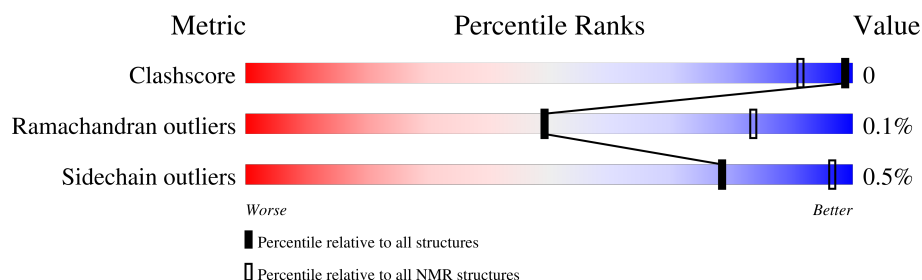
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 90%.

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	108	

2 Ensemble composition and analysis

This entry contains 20 models. Model 8 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:229-A:307 (79)	0.69	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 3 clusters and 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1633 atoms, of which 819 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called ABC transporter ATP-binding/permease protein Rv1747.

Mol	Chain	Residues	Atoms						Trace
1	A	108	Total	C	H	N	O	S	
			1633	501	819	156	154	3	0

There are 4 discrepancies between the modelled and reference sequences:

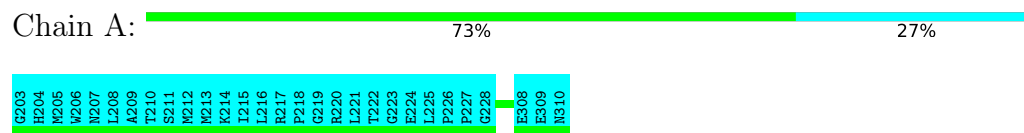
Chain	Residue	Modelled	Actual	Comment	Reference
A	203	GLY	-	expression tag	UNP O65934
A	204	HIS	-	expression tag	UNP O65934
A	205	MET	-	expression tag	UNP O65934
A	206	TRP	-	expression tag	UNP O65934

4 Residue-property plots

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: ABC transporter ATP-binding/permease protein Rv1747

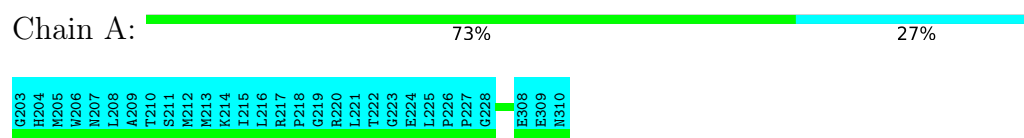


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

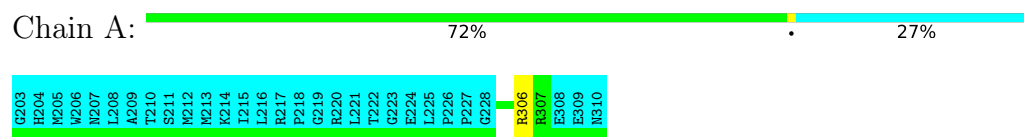
4.2.1 Score per residue for model 1

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



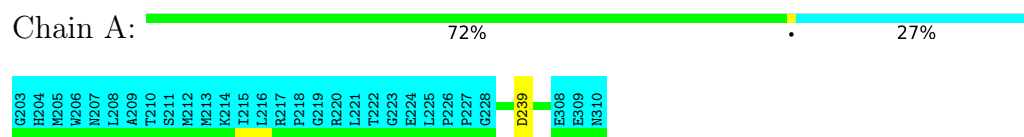
4.2.2 Score per residue for model 2

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



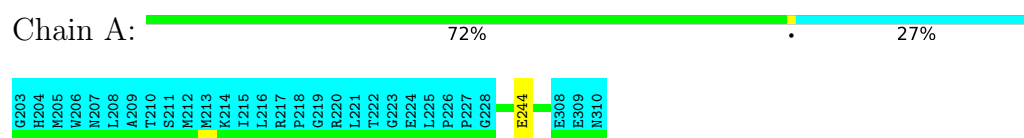
4.2.3 Score per residue for model 3

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



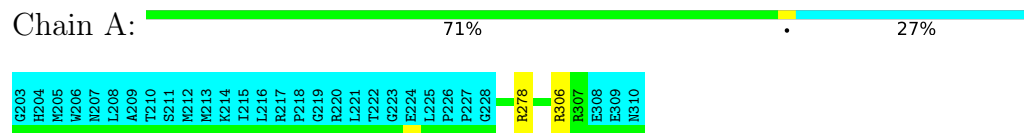
4.2.4 Score per residue for model 4

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



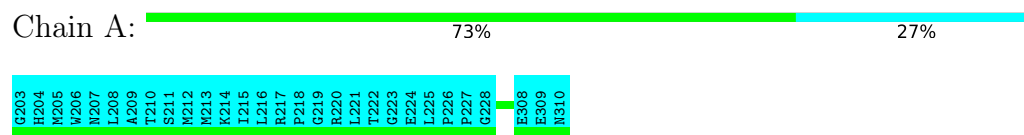
4.2.5 Score per residue for model 5

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



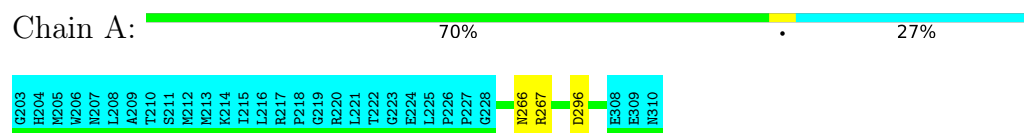
4.2.6 Score per residue for model 6

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



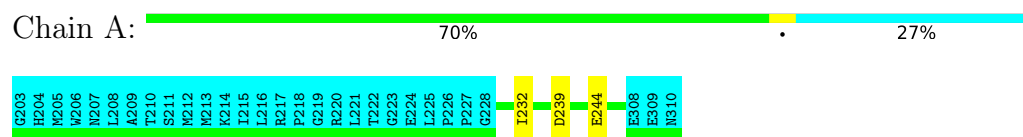
4.2.7 Score per residue for model 7

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



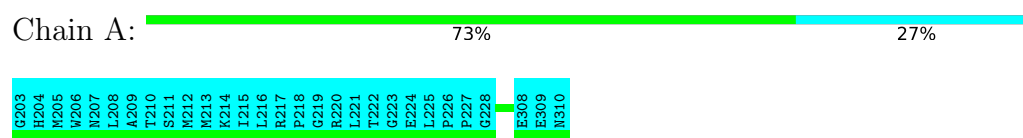
4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



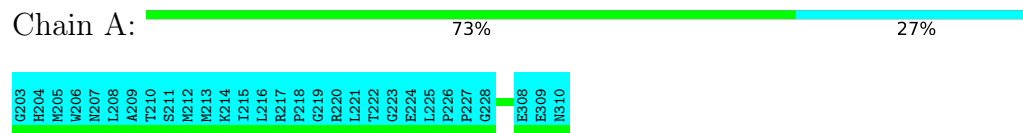
4.2.9 Score per residue for model 9

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



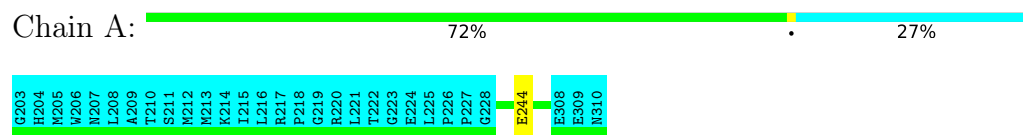
4.2.10 Score per residue for model 10

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



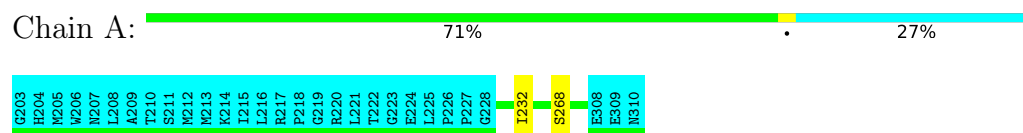
4.2.11 Score per residue for model 11

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



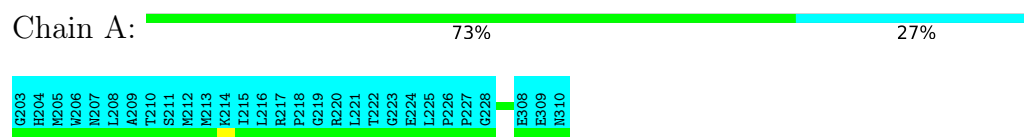
4.2.12 Score per residue for model 12

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



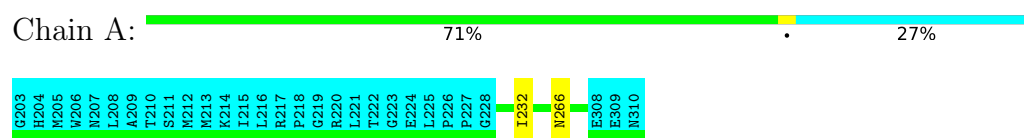
4.2.13 Score per residue for model 13

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



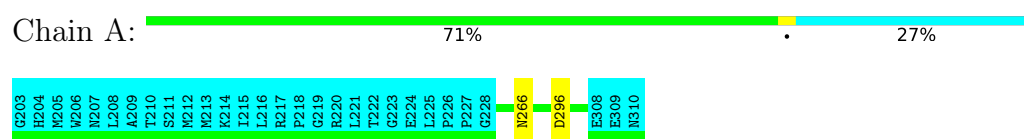
4.2.14 Score per residue for model 14

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



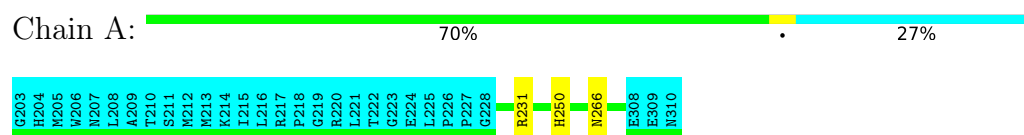
4.2.15 Score per residue for model 15

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



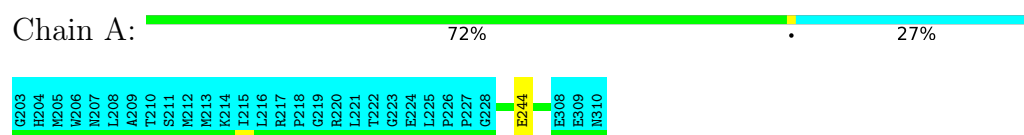
4.2.16 Score per residue for model 16

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



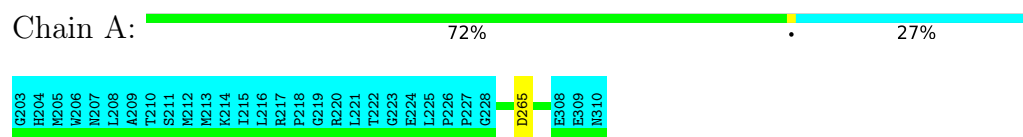
4.2.17 Score per residue for model 17

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



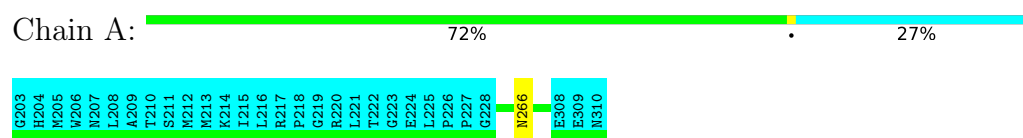
4.2.18 Score per residue for model 18

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



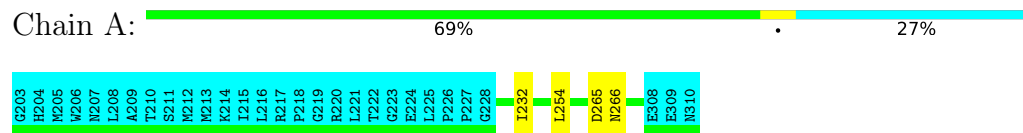
4.2.19 Score per residue for model 19

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



4.2.20 Score per residue for model 20

- Molecule 1: ABC transporter ATP-binding/permease protein Rv1747



5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CYANA	structure calculation	
NMRe	refinement	

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	1161
Number of shifts mapped to atoms	1161
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

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	1.16±0.01	0±0/597 (0.0± 0.0%)	1.25±0.04	1±1/815 (0.1± 0.2%)
All	All	1.16	0/11940 (0.0%)	1.26	24/16300 (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	0.1±0.3
All	All	0	2

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	296	ASP	CA-CB-CG	7.89	120.49	112.60	15	2
1	A	266	ASN	N-CA-C	-6.14	98.99	109.24	20	1
1	A	266	ASN	CA-C-N	6.01	128.33	120.28	15	5
1	A	266	ASN	C-N-CA	6.01	128.33	120.28	15	5
1	A	244	GLU	CA-C-N	5.51	128.01	120.46	17	4
1	A	244	GLU	C-N-CA	5.51	128.01	120.46	17	4
1	A	267	ARG	CA-C-N	5.06	127.06	120.28	7	1
1	A	267	ARG	C-N-CA	5.06	127.06	120.28	7	1
1	A	268	SER	N-CA-C	5.03	116.45	111.07	12	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	265	ASP	Peptide	2

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	589	591	589	0±0
All	All	11780	11820	11780	2

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:232:ILE:HD11	1:A:254:LEU:HD23	0.44	1.89	20	1
1:A:231:ARG:HG3	1:A:250:HIS:CE1	0.41	2.50	16	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	79/108 (73%)	78±0 (99±1%)	1±1 (1±1%)	0±0 (0±0%)	49	83
All	All	1580/2160 (73%)	1557 (99%)	21 (1%)	2 (0%)	49	83

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	239	ASP	2

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	62/86 (72%)	62±1 (100±1%)	0±1 (0±1%)	78	96
All	All	1240/1720 (72%)	1234 (100%)	6 (0%)	78	96

All 3 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	232	ILE	3
1	A	306	ARG	2
1	A	278	ARG	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 oligosaccharides 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 ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 90% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *fha_2_shifts*

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	1161
Number of shifts mapped to atoms	1161
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

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	107	-0.16 ± 0.22	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	94	0.17 ± 0.27	None needed (< 0.5 ppm)
$^{13}\text{C}'$	97	0.10 ± 0.09	None needed (< 0.5 ppm)
^{15}N	101	-0.42 ± 0.47	None needed (< 0.5 ppm)

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 90%, i.e. 949 atoms were assigned a chemical shift out of a possible 1051. 0 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	397/397 (100%)	163/163 (100%)	158/158 (100%)	76/76 (100%)
Sidechain	518/611 (85%)	355/399 (89%)	157/182 (86%)	6/30 (20%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	34/43 (79%)	17/22 (77%)	16/16 (100%)	1/5 (20%)
Overall	949/1051 (90%)	535/584 (92%)	331/356 (93%)	83/111 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1161 atoms were assigned a chemical shift out of a possible 1445. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	509/540 (94%)	204/222 (92%)	204/216 (94%)	101/102 (99%)
Sidechain	614/842 (73%)	411/550 (75%)	195/253 (77%)	8/39 (21%)
Aromatic	38/63 (60%)	19/32 (59%)	18/23 (78%)	1/8 (12%)
Overall	1161/1445 (80%)	634/804 (79%)	417/492 (85%)	110/149 (74%)

7.1.4 Statistically unusual chemical shifts ⓘ

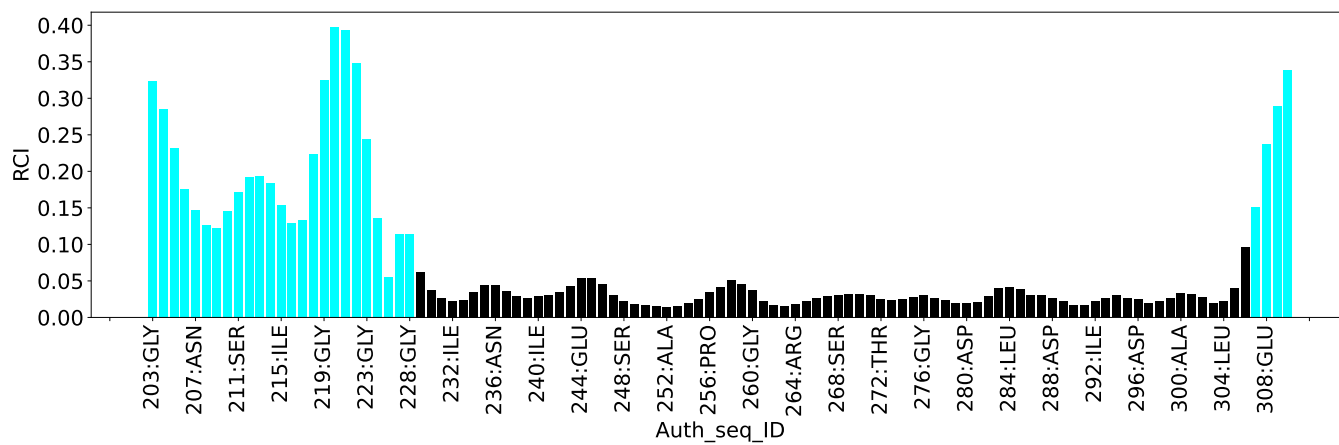
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	203	GLY	CA	55.46	38.93 – 51.79	7.8
1	A	248	SER	H	12.14	5.45 – 11.10	6.8
1	A	251	HIS	HE1	10.77	5.13 – 10.76	5.0

7.1.5 Random Coil Index (RCI) plots ⓘ

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:



8 NMR restraints analysis [i](#)

8.1 Conformationally restricting restraints [i](#)

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	1209
Intra-residue ($ i-j =0$)	305
Sequential ($ i-j =1$)	343
Medium range ($ i-j >1$ and $ i-j <5$)	128
Long range ($ i-j \geq 5$)	433
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	11.2
Number of long range restraints per residue ¹	4.0

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations [i](#)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model [i](#)

Distance violations less than 0.1 Å are not included in the calculation. There are no distance violations

8.2.2 Average number of dihedral-angle violations per model [i](#)

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis

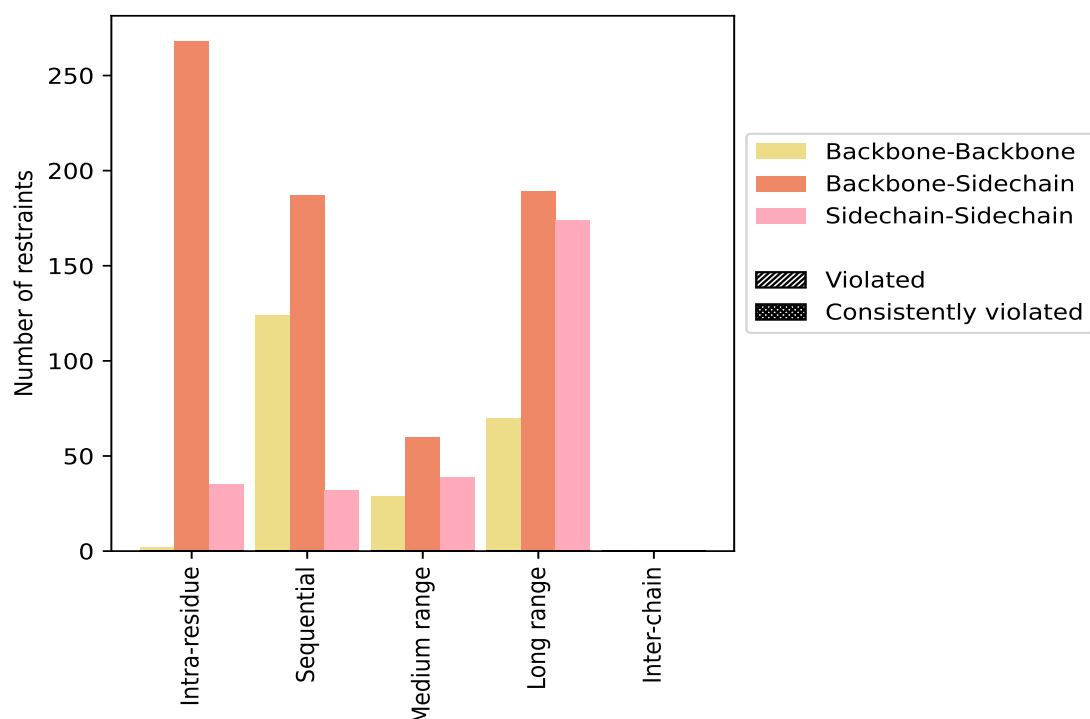
9.1 Summary of distance violations

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	305	25.2	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	2	0.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	268	22.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	35	2.9	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	343	28.4	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	124	10.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	187	15.5	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	32	2.6	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	128	10.6	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	29	2.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	60	5.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	39	3.2	0	0.0	0.0	0	0.0	0.0
Long range (i-j ≥5)	433	35.8	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	70	5.8	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	189	15.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	174	14.4	0	0.0	0.0	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1209	100.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	225	18.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	704	58.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	280	23.2	0	0.0	0.0	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfide bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model [i](#)

No violations found

9.3 Distance violation statistics for the ensemble [i](#)

No violations found

9.4 Most violated distance restraints in the ensemble [i](#)

No violations found

9.5 All violated distance restraints [i](#)

No violations found

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found