



Full wwPDB NMR Structure Validation Report ⓘ

Feb 3, 2021 – 01:09 PM GMT

PDB ID : 6FFU
Title : Solution NMR structure of CBM64 from *S.thermophila* using 20% ¹³C, 100% ¹⁵N
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Deposited on : 2018-01-09

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

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	:	2.16
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

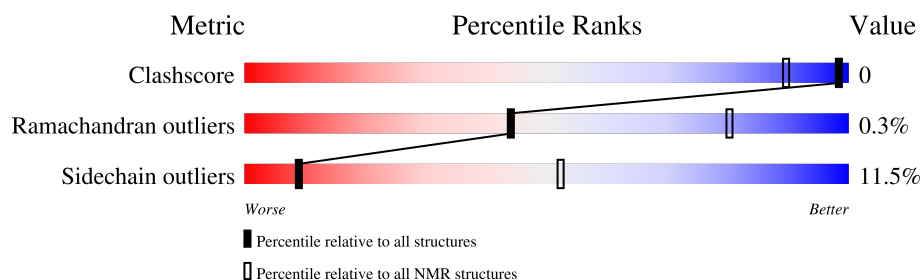
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR


The overall completeness of chemical shifts assignment is 91%.

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 ≥ 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	86	

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 14 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:459-A:541 (83)	0.27	14

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 2 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1347 atoms, of which 632 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Glycosyl hydrolase family 5 cellulase CBM64.

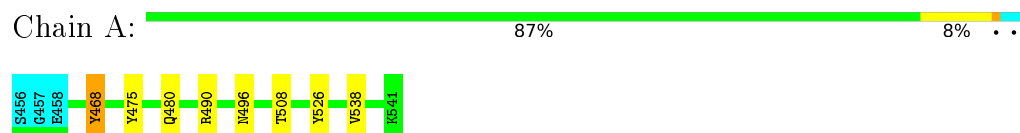
Mol	Chain	Residues	Atoms					Trace
1	A	86	Total	C	H	N	O	0
			1347	462	632	112	141	

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: Glycosyl hydrolase family 5 cellulase CBM64

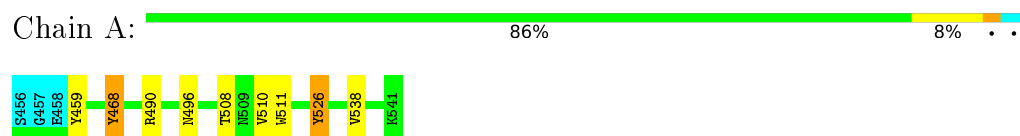


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

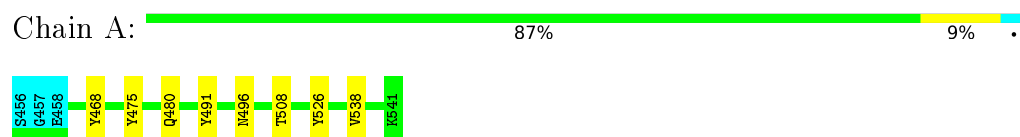
4.2.1 Score per residue for model 1

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



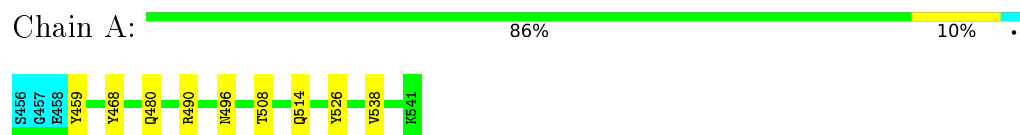
4.2.2 Score per residue for model 2

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



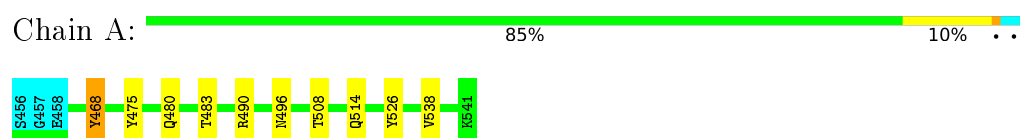
4.2.3 Score per residue for model 3

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



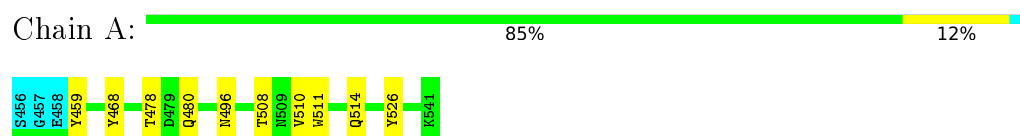
4.2.4 Score per residue for model 4

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



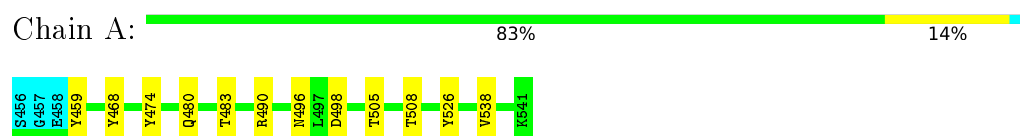
4.2.5 Score per residue for model 5

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



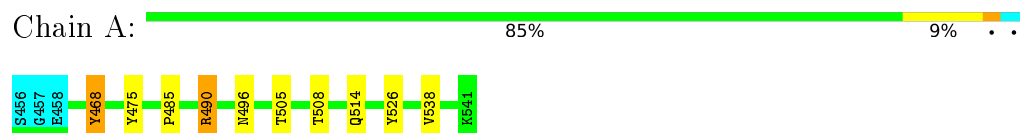
4.2.6 Score per residue for model 6

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



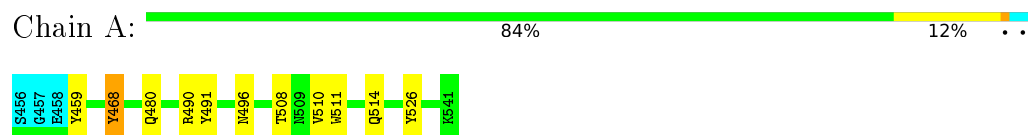
4.2.7 Score per residue for model 7

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



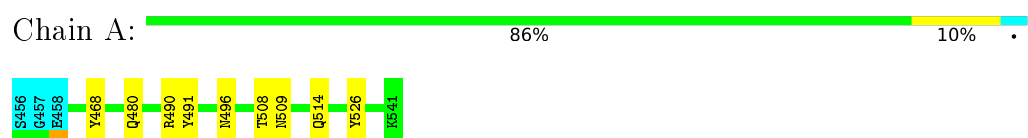
4.2.8 Score per residue for model 8

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



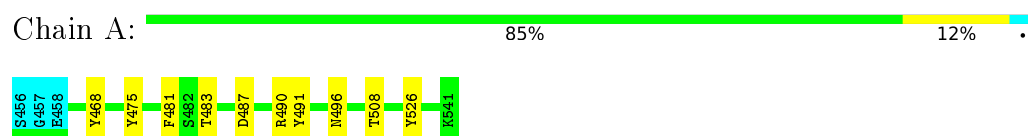
4.2.9 Score per residue for model 9

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



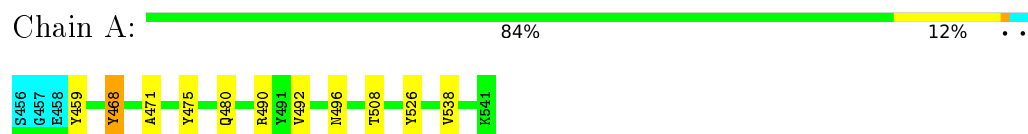
4.2.10 Score per residue for model 10

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



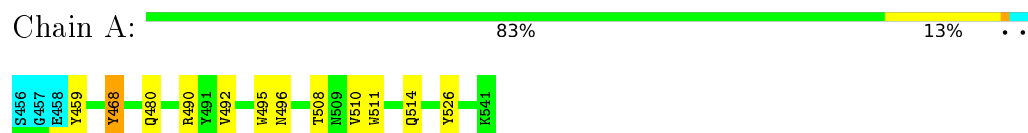
4.2.11 Score per residue for model 11

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



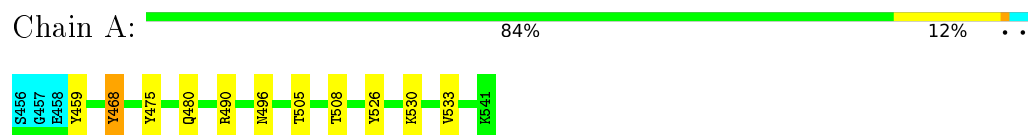
4.2.12 Score per residue for model 12

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



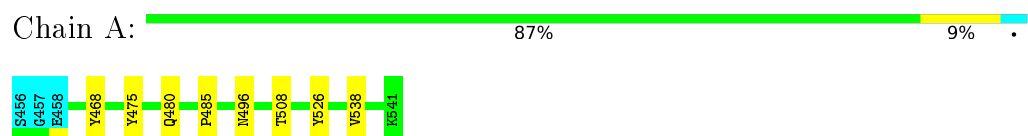
4.2.13 Score per residue for model 13

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



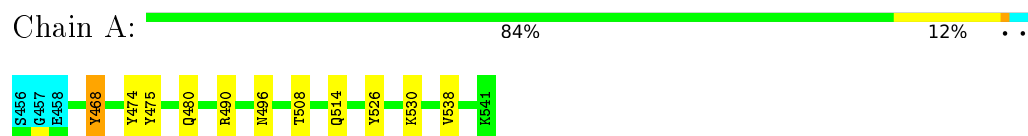
4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



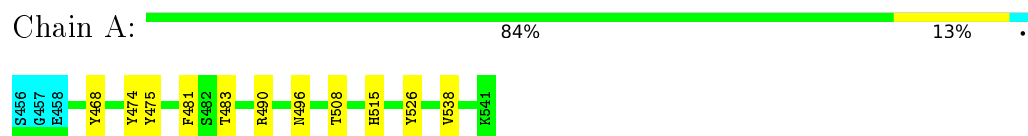
4.2.15 Score per residue for model 15

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



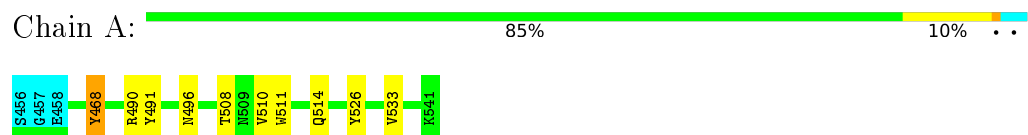
4.2.16 Score per residue for model 16

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



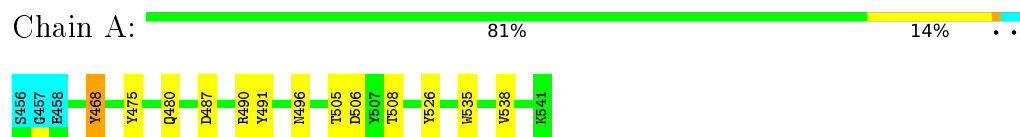
4.2.17 Score per residue for model 17

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



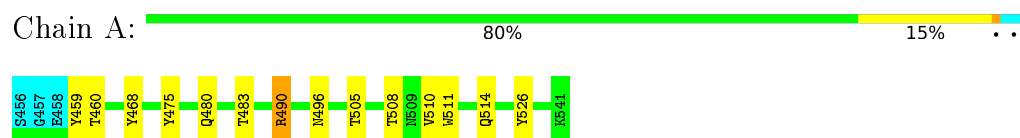
4.2.18 Score per residue for model 18

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



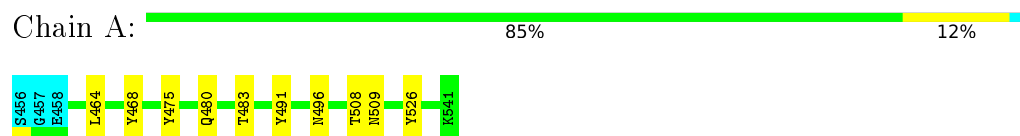
4.2.19 Score per residue for model 19

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



4.2.20 Score per residue for model 20

- Molecule 1: Glycosyl hydrolase family 5 cellulase CBM64



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
Amber	refinement	14
CYANA	structure calculation	3.97

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	1030
Number of shifts mapped to atoms	1030
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

6 Model quality

6.1 Standard geometry

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	0.80±0.01	0±0/724 (0.0± 0.0%)	1.16±0.02	1±1/993 (0.1± 0.1%)
All	All	0.80	0/14480 (0.0%)	1.16	23/19860 (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	0.8±0.7
All	All	0	16

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	490	ARG	NE-CZ-NH1	9.47	125.03	120.30	10	16
1	A	526	TYR	CB-CG-CD1	-5.62	117.63	121.00	1	1
1	A	468	TYR	CB-CG-CD2	-5.61	117.64	121.00	13	6

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	491	TYR	Peptide,Sidechain	7
1	A	468	TYR	Sidechain	4
1	A	474	TYR	Peptide,Sidechain	3
1	A	490	ARG	Sidechain	1
1	A	475	TYR	Sidechain	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	696	616	616	0±0
All	All	13920	12320	12320	6

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:510:VAL:HG22	1:A:511:TRP:H	0.48	1.67	8	6

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	82/86 (95%)	77±1 (94±1%)	5±1 (6±1%)	0±0 (0±1%)	44	80
All	All	1640/1720 (95%)	1542 (94%)	93 (6%)	5 (0%)	44	80

All 3 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	485	PRO	2
1	A	487	ASP	2
1	A	471	ALA	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	72/74 (97%)	64±1 (89±2%)	8±1 (11±2%)	9	52
All	All	1440/1480 (97%)	1275 (89%)	165 (11%)	9	52

All 25 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	526	TYR	20
1	A	496	ASN	20
1	A	508	THR	20
1	A	468	TYR	20
1	A	480	GLN	15
1	A	538	VAL	11
1	A	514	GLN	10
1	A	475	TYR	10
1	A	459	TYR	9
1	A	483	THR	6
1	A	505	THR	5
1	A	530	LYS	2
1	A	533	VAL	2
1	A	492	VAL	2
1	A	509	ASN	2
1	A	481	PHE	2
1	A	535	TRP	1
1	A	464	LEU	1
1	A	478	THR	1
1	A	506	ASP	1
1	A	495	TRP	1
1	A	498	ASP	1
1	A	515	HIS	1
1	A	460	THR	1
1	A	490	ARG	1

6.3.3 RNA ⓘ

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 monosaccharides 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 91% for the well-defined parts and 90% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *TMB_31.bmrB*

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	1030
Number of shifts mapped to atoms	1030
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	85	0.07 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	78	-0.08 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}'$	84	0.58 ± 0.19	Should be applied
^{15}N	81	-0.24 ± 0.16	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 91%, i.e. 923 atoms were assigned a chemical shift out of a possible 1019. 9 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	408/409 (100%)	163/163 (100%)	165/166 (99%)	80/80 (100%)
Sidechain	379/427 (89%)	232/250 (93%)	141/163 (87%)	6/14 (43%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	136/183 (74%)	79/94 (84%)	51/80 (64%)	6/9 (67%)
Overall	923/1019 (91%)	474/507 (93%)	357/409 (87%)	92/103 (89%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 937 atoms were assigned a chemical shift out of a possible 1044. 9 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	416/424 (98%)	166/169 (98%)	169/172 (98%)	81/83 (98%)
Sidechain	385/437 (88%)	236/256 (92%)	143/167 (86%)	6/14 (43%)
Aromatic	136/183 (74%)	79/94 (84%)	51/80 (64%)	6/9 (67%)
Overall	937/1044 (90%)	481/519 (93%)	363/419 (87%)	93/106 (88%)

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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	481	PHE	HB2	-0.46	4.85 – 1.15	-9.4
1	A	524	TYR	CE2	129.13	124.68 – 111.18	8.3
1	A	479	ASP	HB3	0.94	4.07 – 1.27	-6.2
1	A	514	GLN	HG3	0.59	3.75 – 0.85	-5.9
1	A	474	TYR	HB3	0.65	4.75 – 0.95	-5.8
1	A	519	ALA	HA	1.90	6.46 – 2.06	-5.4
1	A	476	TRP	HZ2	5.65	8.89 – 5.69	-5.1

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.

Random coil index (RCI) for chain A:

