



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 11:14 PM UTC

PDB ID : 7N87 / pdb_00007n87
BMRB ID : 30926
Title : Solution NMR structure of peptidase domain from Clostridium thermocellum PCAT1
Authors : Bhattacharya, S.; Palillo, A.
Deposited on : 2021-06-13

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

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

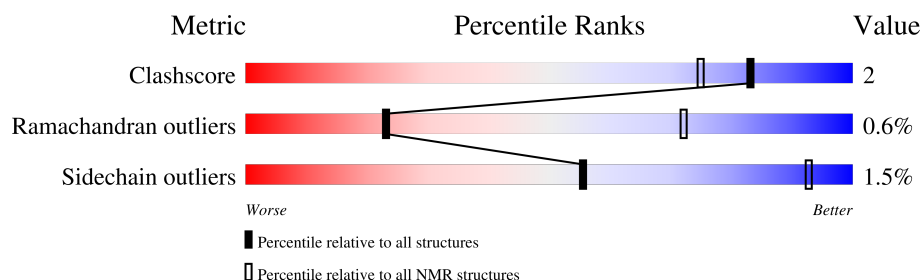
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 93%.

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	151	

2 Ensemble composition and analysis

This entry contains 20 models. Model 19 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:15-A:16, A:24-A:147 (126)	0.73	19

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 3 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2376 atoms, of which 1209 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called ABC-type bacteriocin transporter.

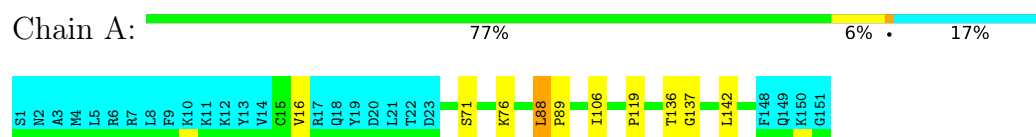
Mol	Chain	Residues	Atoms						Trace
1	A	151	Total	C	H	N	O	S	0
			2376	746	1209	203	211	7	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP A3DCU1
A	2	ASN	-	expression tag	UNP A3DCU1
A	3	ALA	-	expression tag	UNP A3DCU1
A	24	ALA	CYS	engineered mutation	UNP A3DCU1

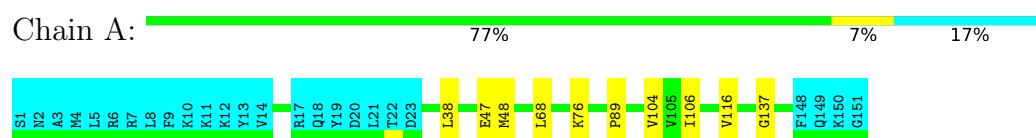
4.2.3 Score per residue for model 3

- Molecule 1: ABC-type bacteriocin transporter



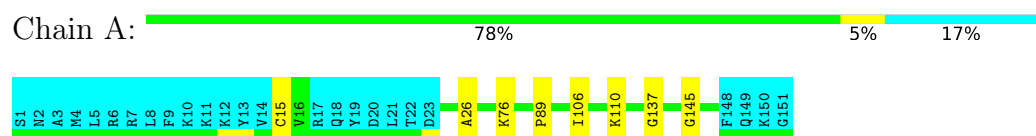
4.2.4 Score per residue for model 4

- Molecule 1: ABC-type bacteriocin transporter



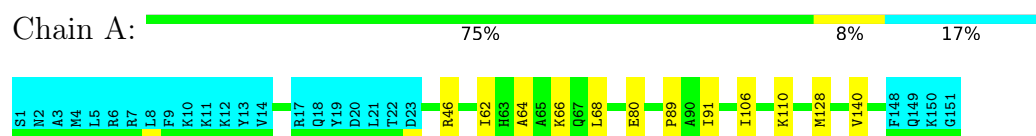
4.2.5 Score per residue for model 5

- Molecule 1: ABC-type bacteriocin transporter



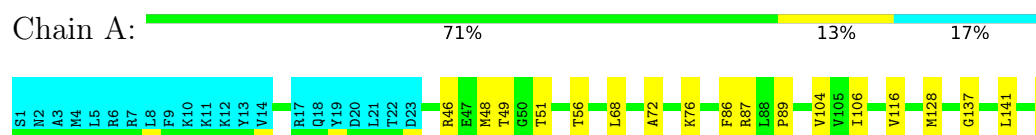
4.2.6 Score per residue for model 6

- Molecule 1: ABC-type bacteriocin transporter



4.2.7 Score per residue for model 7

- Molecule 1: ABC-type bacteriocin transporter

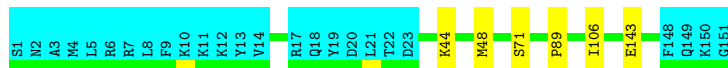




4.2.8 Score per residue for model 8

- Molecule 1: ABC-type bacteriocin transporter

Chain A: 79% 17%



4.2.9 Score per residue for model 9

- Molecule 1: ABC-type bacteriocin transporter

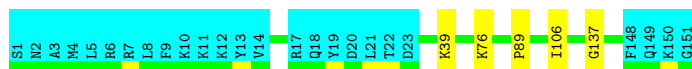
Chain A: 75% 8% 17%



4.2.10 Score per residue for model 10

- Molecule 1: ABC-type bacteriocin transporter

Chain A: 80% 17%



4.2.11 Score per residue for model 11

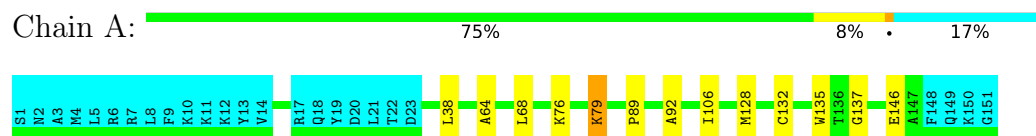
- Molecule 1: ABC-type bacteriocin transporter

Chain A: 77% 6% 17%



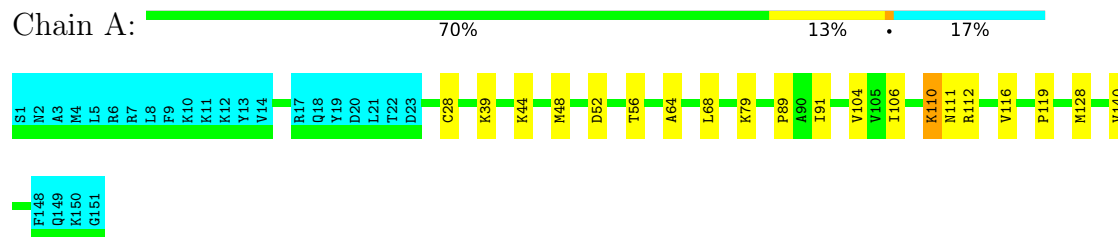
4.2.12 Score per residue for model 12

- Molecule 1: ABC-type bacteriocin transporter



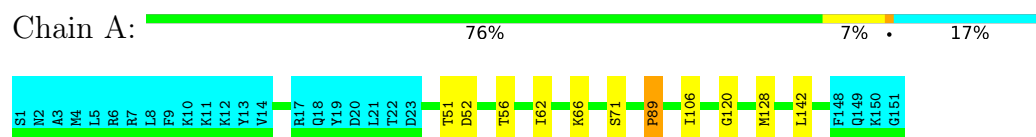
4.2.13 Score per residue for model 13

- Molecule 1: ABC-type bacteriocin transporter



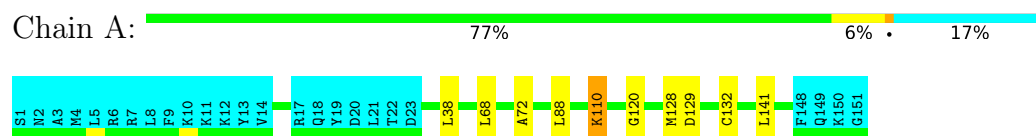
4.2.14 Score per residue for model 14

- Molecule 1: ABC-type bacteriocin transporter



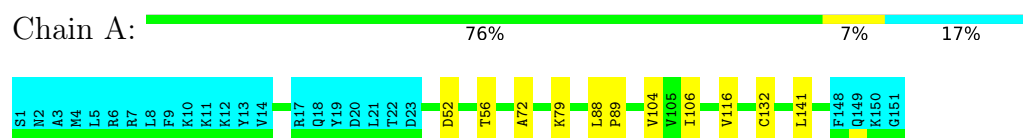
4.2.15 Score per residue for model 15

- Molecule 1: ABC-type bacteriocin transporter



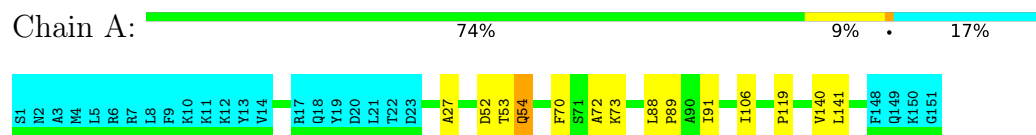
4.2.16 Score per residue for model 16

- Molecule 1: ABC-type bacteriocin transporter



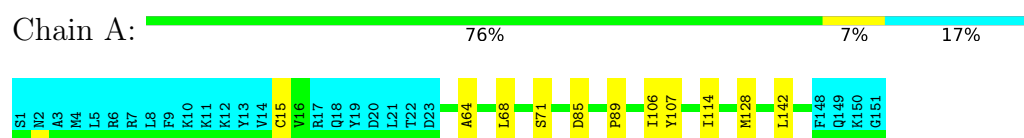
4.2.17 Score per residue for model 17

- Molecule 1: ABC-type bacteriocin transporter



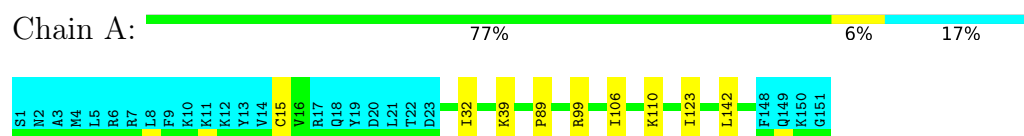
4.2.18 Score per residue for model 18

- Molecule 1: ABC-type bacteriocin transporter



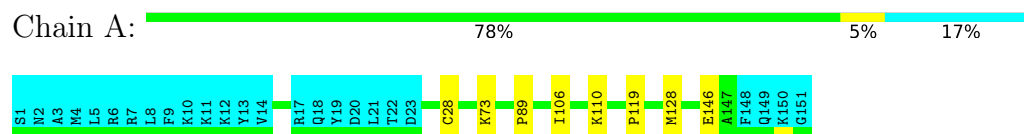
4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: ABC-type bacteriocin transporter



4.2.20 Score per residue for model 20

- Molecule 1: ABC-type bacteriocin transporter



5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 500 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
CYANA	structure calculation	2.1
ARIA	refinement	2.3

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	1830
Number of shifts mapped to atoms	1830
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	93%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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 [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	948	979	977	5±2
All	All	18960	19580	19540	92

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:89:PRO:HA	1:A:106:ILE:O	0.66	1.90	20	18
1:A:51:THR:HG22	1:A:56:THR:HG21	0.57	1.76	7	1
1:A:64:ALA:O	1:A:68:LEU:HG	0.55	2.01	12	7
1:A:79:LYS:HB3	1:A:132:CYS:SG	0.54	2.42	12	2
1:A:28:CYS:SG	1:A:119:PRO:HD3	0.53	2.42	20	1
1:A:76:LYS:HA	1:A:137:GLY:O	0.53	2.04	3	8
1:A:104:VAL:HB	1:A:116:VAL:CG1	0.51	2.34	7	4
1:A:71:SER:O	1:A:142:LEU:HA	0.51	2.05	3	4
1:A:28:CYS:SG	1:A:119:PRO:HG3	0.50	2.47	13	1
1:A:72:ALA:HA	1:A:141:LEU:O	0.50	2.06	16	4
1:A:52:ASP:N	1:A:56:THR:HB	0.49	2.22	11	2
1:A:30:SER:O	1:A:34:GLN:HG3	0.49	2.08	9	1
1:A:114:ILE:HD11	1:A:128:MET:SD	0.48	2.48	18	1
1:A:52:ASP:C	1:A:54:GLN:H	0.48	2.16	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:LEU:HG	1:A:68:LEU:O	0.47	2.10	2	4
1:A:51:THR:HG23	1:A:56:THR:HG21	0.47	1.87	1	1
1:A:62:ILE:O	1:A:66:LYS:HG3	0.47	2.09	6	2
1:A:25:GLY:HA2	1:A:28:CYS:SG	0.47	2.49	1	1
1:A:48:MET:HE1	1:A:68:LEU:HD21	0.47	1.87	7	1
1:A:52:ASP:O	1:A:56:THR:HB	0.47	2.09	13	3
1:A:44:LYS:O	1:A:48:MET:HG2	0.46	2.10	8	1
1:A:52:ASP:H	1:A:56:THR:HB	0.44	1.71	16	1
1:A:47:GLU:HG3	1:A:48:MET:N	0.43	2.28	4	1
1:A:16:VAL:O	1:A:119:PRO:HA	0.43	2.13	3	1
1:A:46:ARG:HA	1:A:49:THR:OG1	0.43	2.12	7	1
1:A:44:LYS:HE3	1:A:48:MET:SD	0.43	2.54	13	1
1:A:86:PHE:O	1:A:87:ARG:HD2	0.43	2.14	7	1
1:A:91:ILE:HB	1:A:140:VAL:HG22	0.43	1.90	13	2
1:A:27:ALA:HB3	1:A:119:PRO:HB3	0.42	1.92	17	1
1:A:15:CYS:HA	1:A:107:TYR:OH	0.42	2.15	18	1
1:A:121:LYS:N	1:A:121:LYS:HD3	0.42	2.28	1	1
1:A:15:CYS:SG	1:A:123:ILE:HD11	0.42	2.55	19	1
1:A:32:ILE:HD13	1:A:142:LEU:CD1	0.41	2.45	19	1
1:A:110:LYS:N	1:A:110:LYS:HD3	0.41	2.30	15	2
1:A:129:ASP:HA	1:A:132:CYS:SG	0.41	2.55	15	1
1:A:91:ILE:HB	1:A:140:VAL:CG2	0.41	2.46	6	1
1:A:58:ALA:O	1:A:62:ILE:HG23	0.41	2.15	2	1
1:A:92:ALA:HB1	1:A:135:TRP:CD1	0.41	2.51	12	1
1:A:71:SER:HB2	1:A:143:GLU:CG	0.41	2.45	8	1
1:A:111:ASN:O	1:A:112:ARG:HB3	0.41	2.16	13	1
1:A:79:LYS:HB2	1:A:128:MET:SD	0.40	2.55	13	1
1:A:110:LYS:HD2	1:A:110:LYS:N	0.40	2.30	13	1
1:A:88:LEU:HB2	1:A:89:PRO:HD3	0.40	1.93	3	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	126/151 (83%)	116±2 (92±2%)	9±2 (7±2%)	1±1 (1±1%)	23	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2520/3020 (83%)	2316 (92%)	188 (7%)	16 (1%)	23 72

All 8 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	88	LEU	4
1	A	39	LYS	3
1	A	145	GLY	3
1	A	120	GLY	2
1	A	89	PRO	1
1	A	53	THR	1
1	A	54	GLN	1
1	A	99	ARG	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	99/122 (81%)	98±1 (99±1%)	1±1 (1±1%)	55 93
All	All	1980/2440 (81%)	1951 (99%)	29 (1%)	55 93

All 12 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	128	MET	8
1	A	110	LYS	7
1	A	70	PHE	3
1	A	146	GLU	2
1	A	73	LYS	2
1	A	130	ASP	1
1	A	136	THR	1
1	A	80	GLU	1
1	A	79	LYS	1
1	A	51	THR	1
1	A	85	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	39	LYS	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 [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 93% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: *starch_output*

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	1830
Number of shifts mapped to atoms	1830
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	146	-0.18 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	133	0.10 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	126	0.05 ± 0.13	None needed (< 0.5 ppm)
^{15}N	139	0.24 ± 0.26	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 93%, i.e. 1559 atoms were assigned a chemical shift out of a possible 1681. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	620/636 (97%)	260/261 (100%)	240/252 (95%)	120/123 (98%)
Sidechain	856/932 (92%)	586/615 (95%)	262/286 (92%)	8/31 (26%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	83/113 (73%)	49/54 (91%)	33/54 (61%)	1/5 (20%)
Overall	1559/1681 (93%)	895/930 (96%)	535/592 (90%)	129/159 (81%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 1830 atoms were assigned a chemical shift out of a possible 2070. 0 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	713/762 (94%)	302/312 (97%)	272/302 (90%)	139/148 (94%)
Sidechain	1016/1157 (88%)	694/758 (92%)	311/352 (88%)	11/47 (23%)
Aromatic	101/151 (67%)	61/72 (85%)	39/74 (53%)	1/5 (20%)
Overall	1830/2070 (88%)	1057/1142 (93%)	622/728 (85%)	151/200 (76%)

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	137	GLY	HA2	1.15	2.15 – 5.77	-7.8
1	A	137	GLY	H	5.07	5.23 – 11.42	-5.3

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:

