



Full wwPDB NMR Structure Validation Report ⓘ

Mar 14, 2026 – 10:28 PM UTC

PDB ID : 2M85 / pdb_00002m85
BMRB ID : 19229
Title : PHD Domain from Human SHPRH
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Deposited on : 2013-05-07

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<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

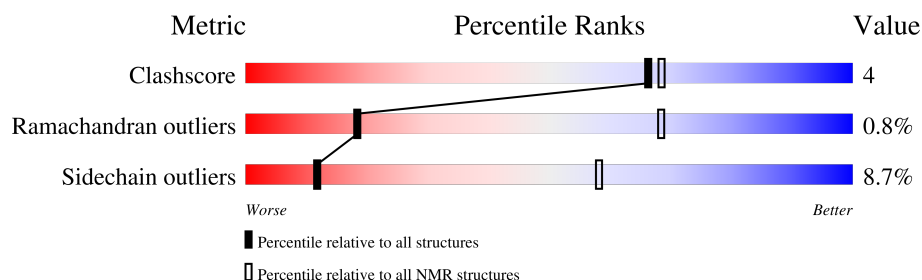
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 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	73	 60% 11% • 16% 11%

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:658-A:710 (53)	0.60	1

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 3 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1068 atoms, of which 525 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called E3 ubiquitin-protein ligase SHPRH.

Mol	Chain	Residues	Atoms						Trace
1	A	65	Total	C	H	N	O	S	0
			1066	342	525	96	95	8	

There are 8 discrepancies between the modelled and reference sequences:

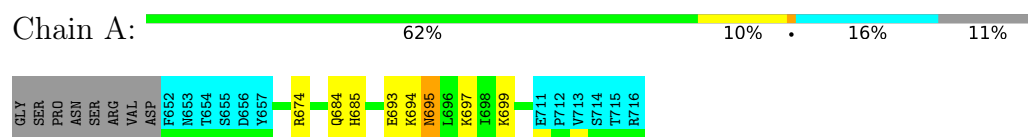
Chain	Residue	Modelled	Actual	Comment	Reference
A	644	GLY	-	expression tag	UNP Q149N8
A	645	SER	-	expression tag	UNP Q149N8
A	646	PRO	-	expression tag	UNP Q149N8
A	647	ASN	-	expression tag	UNP Q149N8
A	648	SER	-	expression tag	UNP Q149N8
A	649	ARG	-	expression tag	UNP Q149N8
A	650	VAL	-	expression tag	UNP Q149N8
A	651	ASP	-	expression tag	UNP Q149N8

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Zn
			2	2

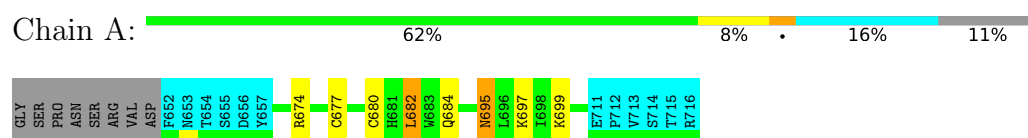
4.2.3 Score per residue for model 3

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



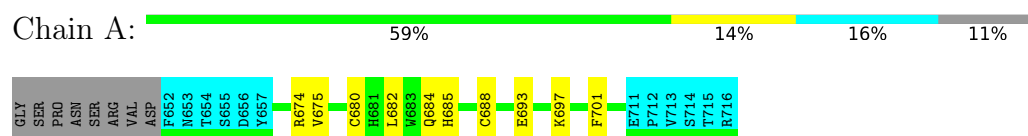
4.2.4 Score per residue for model 4

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



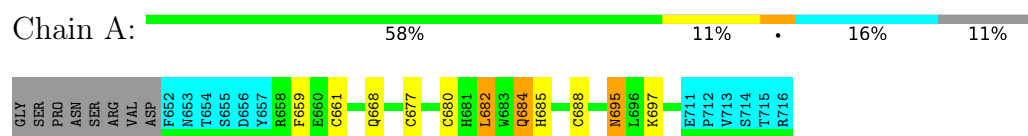
4.2.5 Score per residue for model 5

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



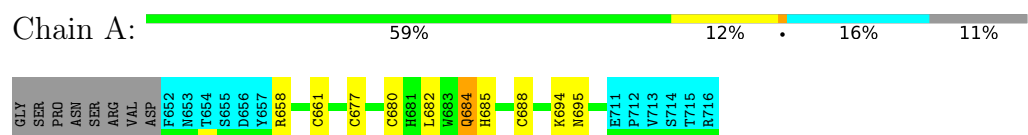
4.2.6 Score per residue for model 6

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



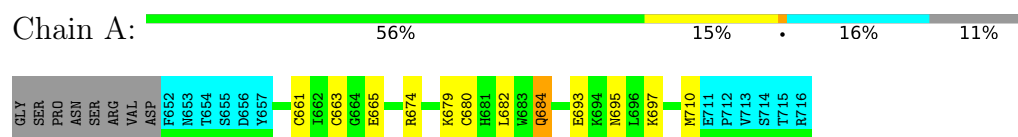
4.2.7 Score per residue for model 7

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



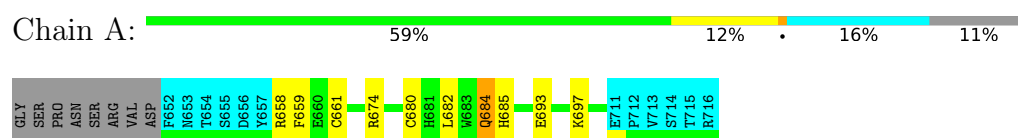
4.2.8 Score per residue for model 8

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



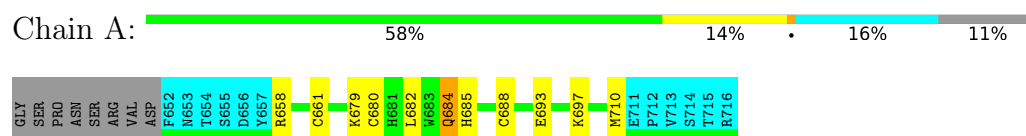
4.2.9 Score per residue for model 9

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



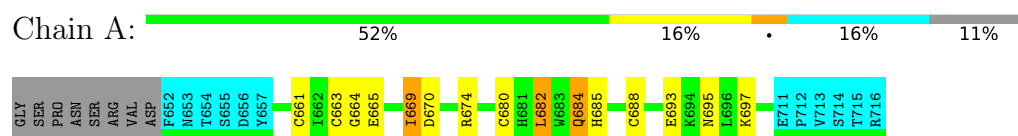
4.2.10 Score per residue for model 10

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



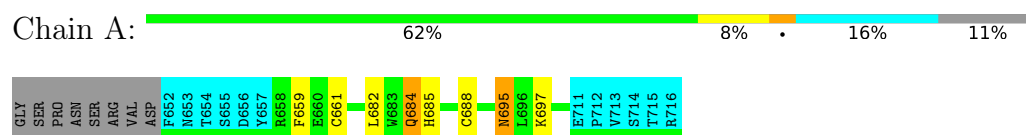
4.2.11 Score per residue for model 11

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



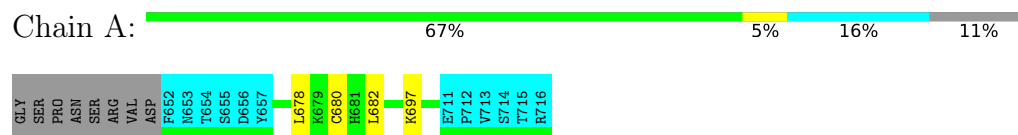
4.2.12 Score per residue for model 12

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



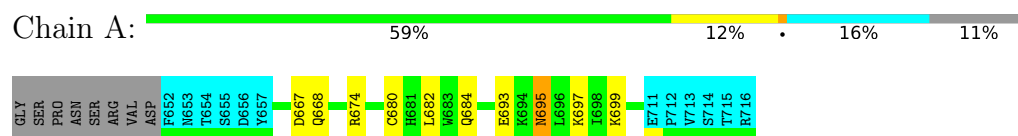
4.2.13 Score per residue for model 13

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



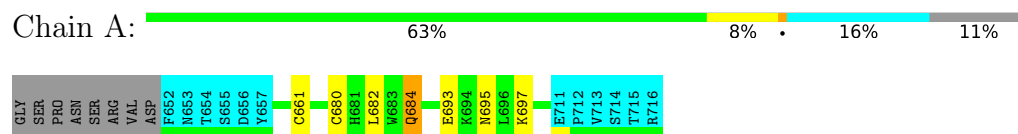
4.2.14 Score per residue for model 14

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



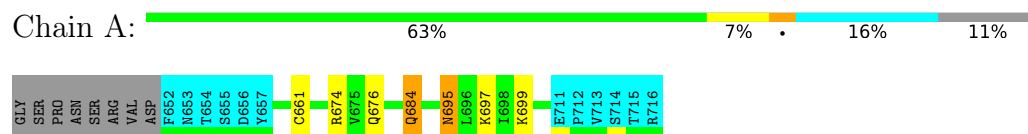
4.2.15 Score per residue for model 15

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



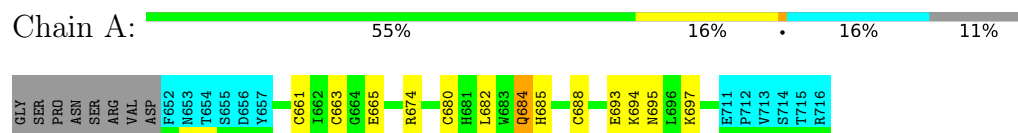
4.2.16 Score per residue for model 16

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



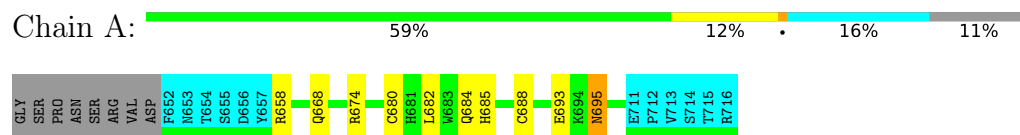
4.2.17 Score per residue for model 17

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



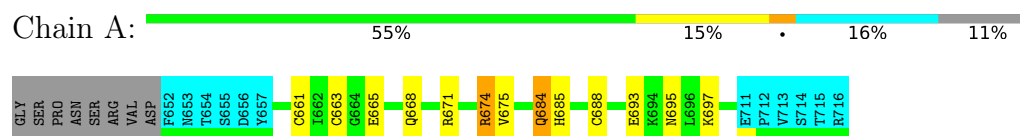
4.2.18 Score per residue for model 18

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



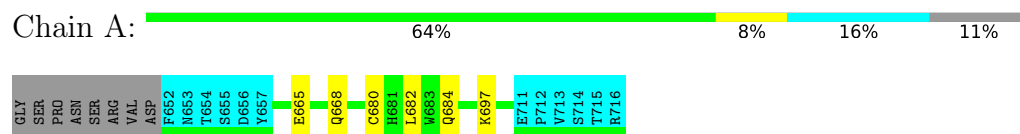
4.2.19 Score per residue for model 19

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



4.2.20 Score per residue for model 20

- Molecule 1: E3 ubiquitin-protein ligase SHPRH



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 100 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
TALOS	structure solution	2.2
CYANA	structure solution	2.1
ABACUS-CNS	geometry optimization	2.5
ABACUS-CNS	refinement	2.5

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	820
Number of shifts mapped to atoms	820
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](#)

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

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	1.32±0.03	0±0/453 (0.0± 0.0%)	1.00±0.03	0±0/610 (0.0± 0.1%)
All	All	1.32	1/9060 (0.0%)	1.00	3/12200 (0.0%)

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	675	VAL	CA-CB	5.03	1.59	1.53	19	1

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	695	ASN	CA-CB-CG	5.14	117.74	112.60	18	3

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	441	438	436	3±2
All	All	8860	8760	8720	69

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 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:680:CYS:SG	1:A:682:LEU:HB2	0.63	2.34	11	15
1:A:661:CYS:SG	1:A:684:GLN:HG3	0.58	2.38	7	10
1:A:663:CYS:SG	1:A:665:GLU:HG2	0.57	2.40	17	1
1:A:685:HIS:HB2	1:A:688:CYS:SG	0.54	2.41	10	10
1:A:663:CYS:SG	1:A:665:GLU:HG3	0.52	2.45	11	3
1:A:674:ARG:HA	1:A:685:HIS:HA	0.50	1.83	11	6
1:A:679:LYS:NZ	1:A:710:MET:SD	0.50	2.85	1	3
1:A:661:CYS:HA	1:A:684:GLN:NE2	0.49	2.22	12	3
1:A:682:LEU:HD11	1:A:684:GLN:NE2	0.47	2.24	1	1
1:A:695:ASN:HB2	1:A:699:LYS:HD3	0.47	1.88	4	4
1:A:679:LYS:HE3	1:A:710:MET:SD	0.46	2.50	2	1
1:A:680:CYS:SG	1:A:682:LEU:CB	0.46	3.03	10	1
1:A:659:PHE:HA	1:A:682:LEU:HD22	0.46	1.88	12	2
1:A:658:ARG:HD2	1:A:658:ARG:N	0.45	2.27	18	1
1:A:675:VAL:HB	1:A:701:PHE:HB2	0.42	1.91	5	1
1:A:674:ARG:HD2	1:A:676:GLN:NE2	0.42	2.30	16	1
1:A:673:PRO:HB3	1:A:693:GLU:HB3	0.41	1.91	2	1
1:A:665:GLU:HB2	1:A:685:HIS:HE1	0.41	1.75	19	1
1:A:665:GLU:HB2	1:A:685:HIS:CE1	0.41	2.51	19	1
1:A:663:CYS:SG	1:A:664:GLY:N	0.41	2.94	11	1
1:A:669:ILE:HD13	1:A:674:ARG:HG3	0.40	1.93	11	1
1:A:680:CYS:SG	1:A:682:LEU:HB3	0.40	2.57	10	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	53/73 (73%)	47±1 (88±3%)	6±1 (11±3%)	0±1 (1±1%)	18	68
All	All	1060/1460 (73%)	931 (88%)	121 (11%)	8 (1%)	18	68

All 5 unique Ramachandran outliers are listed below. They are sorted by the frequency of occur-

rence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	677	CYS	4
1	A	669	ILE	1
1	A	670	ASP	1
1	A	667	ASP	1
1	A	665	GLU	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	50/69 (72%)	46±1 (91±2%)	4±1 (9±2%)	12	58
All	All	1000/1380 (72%)	913 (91%)	87 (9%)	12	58

All 13 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	684	GLN	19
1	A	697	LYS	17
1	A	695	ASN	14
1	A	693	GLU	13
1	A	674	ARG	6
1	A	668	GLN	5
1	A	694	LYS	3
1	A	682	LEU	3
1	A	658	ARG	3
1	A	687	LYS	1
1	A	659	PHE	1
1	A	678	LEU	1
1	A	671	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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 90% for the well-defined parts and 89% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_2*

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	820
Number of shifts mapped to atoms	820
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
$^{13}\text{C}_\alpha$	65	-0.14 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	64	0.15 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	60	0.17 ± 0.21	None needed (< 0.5 ppm)
^{15}N	61	-1.06 ± 0.25	Should be applied

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. 686 atoms were assigned a chemical shift out of a possible 766. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	257/260 (99%)	104/104 (100%)	103/106 (97%)	50/50 (100%)
Sidechain	389/433 (90%)	264/279 (95%)	120/134 (90%)	5/20 (25%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	40/73 (55%)	24/36 (67%)	15/31 (48%)	1/6 (17%)
Overall	686/766 (90%)	392/419 (94%)	238/271 (88%)	56/76 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 89%, i.e. 820 atoms were assigned a chemical shift out of a possible 922. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	313/318 (98%)	127/127 (100%)	125/130 (96%)	61/61 (100%)
Sidechain	456/512 (89%)	309/329 (94%)	141/159 (89%)	6/24 (25%)
Aromatic	51/92 (55%)	31/45 (69%)	19/41 (46%)	1/6 (17%)
Overall	820/922 (89%)	467/501 (93%)	285/330 (86%)	68/91 (75%)

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	659	PHE	CZ	138.04	121.82 – 136.66	5.9
1	A	701	PHE	CZ	137.54	121.82 – 136.66	5.6
1	A	652	PHE	CZ	136.76	121.82 – 136.66	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. 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:

