Full wwPDB NMR Structure Validation Report (i)

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Title	:	PHD Domain from Human SHPRH
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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 (i) 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 (i)) were used in the production of this report:

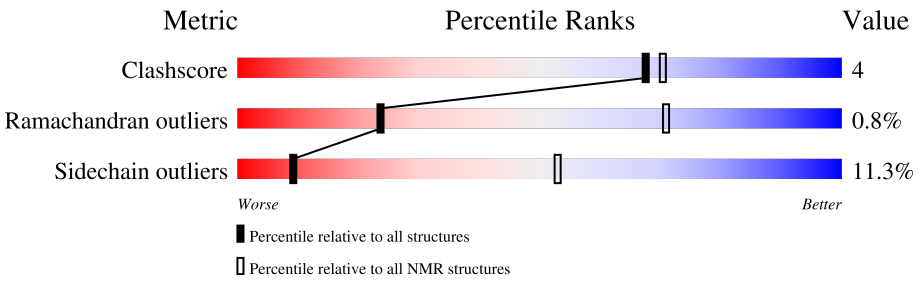
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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	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 <=5%

Mol	Chain	Length	Quality of chain
1	A	73	60% 11% • 16% 11%

2 Ensemble composition and analysis (i)

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 (i)

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
			Total	C	H	N	O	S	
1	A	65	1066	342	525	96	95	8	0

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 (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	2	2	2

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: E3 ubiquitin-protein ligase SHPRH

Chain A: 60% 11% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 C661 R674 C680 H681 L682 W683 Q684 H685 E693 K694 N695 L696 K697 E711 P712 V713 S714 T715 R716

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 (medoid)

• Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 56% 15% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 C661 R674 C677 L678 K679 C680 H681 L682 W683 Q684 H685 E693 K694 N695 M710 E711 P712 V713 S714 T715 R716

4.2.2 Score per residue for model 2

• Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 53% 16% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 C661 P673 L678 K679 C680 H681 L682 W683 Q684 H685 A686 K687 C688 E693 K694 K697 M710 E711 P712 V713 S714 T715 R716

4.2.3 Score per residue for model 3

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 59% 12% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 R658 R674 L678 Q684 H685 E693 K694 N695 L696 K697 I698 K699 E711 P712 V713 S714 T715 R716

4.2.4 Score per residue for model 4

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 62% 8% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 R674 C677 C680 H681 L682 W683 Q684 N695 L696 K697 I698 K699 E711 P712 V713 S714 T715 R716

4.2.5 Score per residue for model 5

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 58% 15% 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 R674 V675 C680 H681 L682 W683 Q684 H685 C688 E693 K694 K697 F701 E711 P712 V713 S714 T715 R716

4.2.6 Score per residue for model 6

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 58% 12% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 R658 F659 E660 C661 Q668 C677 C680 H681 L682 W683 Q684 H685 C688 N695 L696 K697 E711 P712 V713 S714 T715 R716

4.2.7 Score per residue for model 7

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 58% 14% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 C661 C677 L678 K679 C680 H681 L682 W683 Q684 H685 C688 E693 K694 N695 E711 P712 V713 S714 T715 R716

4.2.8 Score per residue for model 8

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 53% 18% • 16% 11%

4.2.9 Score per residue for model 9

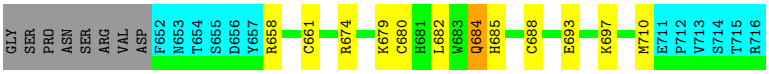
- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 58% 14% • 16% 11%

4.2.10 Score per residue for model 10

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 56% 15% • 16% 11%



4.2.11 Score per residue for model 11

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 49% 19% • 16% 11%

4.2.12 Score per residue for model 12

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 60% 10% • 16% 11%

4.2.13 Score per residue for model 13

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 67% 5% 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 L678 K679 C680 H681 L682 K697 E711 P712 V713 S714 T715 R716

4.2.14 Score per residue for model 14

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 59% 11% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 D667 Q668 R674 C680 H681 L682 W683 Q684 E693 K694 N695 L696 K697 I698 K699 E711 P712 V713 S714 T715 R716

4.2.15 Score per residue for model 15

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 59% 12% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 C661 R671 R674 L678 K679 C680 H681 L682 W683 Q684 E693 K694 N695 L696 K697 E711 P712 V713 S714 T715 R716

4.2.16 Score per residue for model 16

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 62% 8% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 C661 R671 R674 V675 Q676 Q684 N695 L696 K697 I698 K699 E711 P712 V713 S714 T715 R716

4.2.17 Score per residue for model 17

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 55% 16% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 C661 I662 C663 G664 E665 R674 C680 H681 L682 W683 Q684 H685 C688 E693 K694 N695 L696 K697 E711 P712 V713 S714 T715 R716

4.2.18 Score per residue for model 18

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 55% 18% 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 R658 F659 E660 Q668 R674 L678 K679 C680 H681 L682 W683 Q684 H685 C688 E693 K694 N695 E711 P712 V713 S714 T715 R716

4.2.19 Score per residue for model 19

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 55% 15% • 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 E660 C661 I662 C663 G664 E665 Q668 R671 R674 Q684 H685 C688 E693 K694 N695 L696 K697 E711 P712 V713 S714 T715 R716

4.2.20 Score per residue for model 20

- Molecule 1: E3 ubiquitin-protein ligase SHPRH

Chain A: 62% 11% 16% 11%

GLY SER PRO ASN SER ARG VAL ASP F652 N653 T654 S655 D656 Y657 R658 E665 Q668 L678 K679 C680 H681 L682 W683 Q684 K697 E711 P712 V713 S714 T715 R716

5 Refinement protocol and experimental data overview (i)

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

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	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

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
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 (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	53/73 (73%)	47±1 (88±3%)	6±1 (11±3%)	0±1 (1±1%)	24	71
All	All	1060/1460 (73%)	931 (88%)	121 (11%)	8 (1%)	24	71

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	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 (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	50/69 (72%)	44±1 (89±3%)	6±1 (11±3%)	9 53
All	All	1000/1380 (72%)	887 (89%)	113 (11%)	9 53

All 16 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	693	GLU	14
1	A	695	ASN	14
1	A	674	ARG	9
1	A	678	LEU	8
1	A	694	LYS	7
1	A	659	PHE	5
1	A	668	GLN	5
1	A	658	ARG	4
1	A	682	LEU	3
1	A	671	ARG	3
1	A	660	GLU	2
1	A	687	LYS	1
1	A	701	PHE	1
1	A	667	ASP	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 monosaccharides 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 (i)

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 (i)

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 (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	65	-0.14 ± 0.16	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	64	0.15 ± 0.06	None needed (< 0.5 ppm)
$^{13}C'$	60	0.17 ± 0.21	None needed (< 0.5 ppm)
^{15}N	61	-1.07 ± 0.39	Should be applied

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 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	^{1}H	^{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 (i)

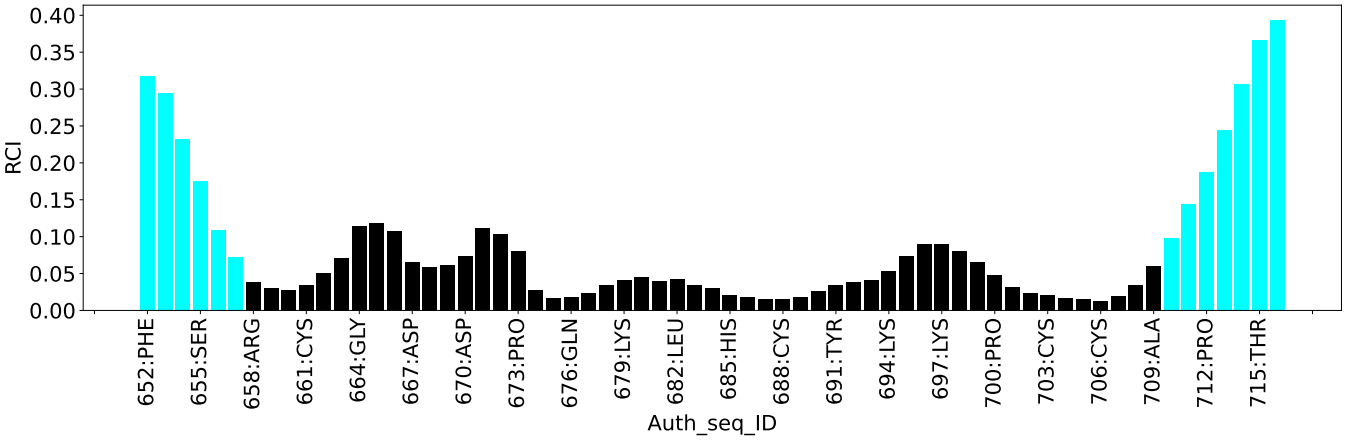
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	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 (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:


RCI
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
652:PHE
655:SER
658:ARG
661:CYS
664:GLY
667:ASP
670:ASP
673:PRO
676:GLN
679:LYS
682:LEU
685:HIS
688:CYS
691:TYR
694:LYS
697:LYS
700:PRO
703:CYS
706:CYS
709:ALA
712:PRO
715:THR
Auth_seq_ID