Full wwPDB NMR Structure Validation Report (i)

May 7, 2024 – 03:08 pm BST

PDB ID	:	6QF8
BMRB ID	:	34351
Title	:	Solution NMR ensemble for human ubiquitin at 298K compiled using the CoMAND method
Authors	:	ElGamacy, M.; Truffault, V.; Zhu, H.; Coles, M.
Deposited on	:	2019-01-09

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 (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:

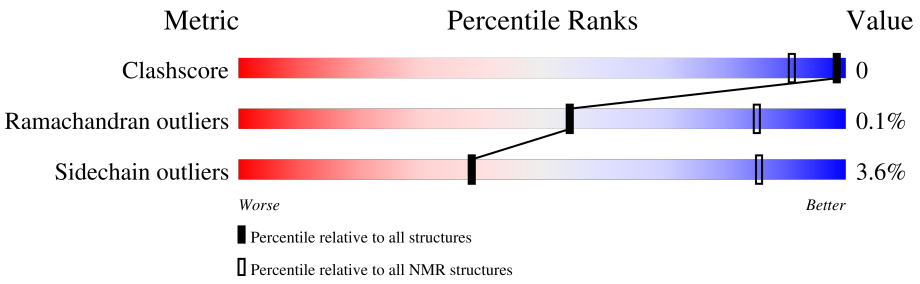
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson 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 69%.

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	79	85% · 8% ·

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:1-A:70 (70)	0.71	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 4 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1229 atoms, of which 627 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	76	1229	378	627	105	118	1	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	expression tag	UNP J3QS39
A	-1	MET	-	expression tag	UNP J3QS39
A	0	GLY	-	expression tag	UNP J3QS39

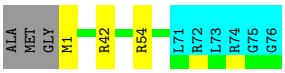
4 Residue-property plots (i)

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: Polyubiquitin-B

Chain A:



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)

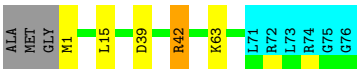
• Molecule 1: Polyubiquitin-B

Chain A:

4.2.2 Score per residue for model 2

• Molecule 1: Polyubiquitin-B

Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: Polyubiquitin-B

Chain A: 76% 13% 8% •

ALA MET GLY M1 E18 P19 S20 R42 L43 T44 F45 R54 Y59 L67 H68 L69 V70 L71 R72 L73 R74 G75 G76

4.2.4 Score per residue for model 4

- Molecule 1: Polyubiquitin-B

Chain A: 75% 11% • 8% •

ALA MET GLY M1 Q2 L15 V26 P37 P38 D39 R42 F45 R54 K63 H68 L71 R72 L73 R74 G75 G76

4.2.5 Score per residue for model 5

- Molecule 1: Polyubiquitin-B

Chain A: 80% 6% • 8% •

ALA MET GLY M1 Q31 R42 R54 Y59 E64 V70 L71 R72 L73 R74 G75 G76

4.2.6 Score per residue for model 6

- Molecule 1: Polyubiquitin-B

Chain A: 78% 8% • 8% •

ALA MET GLY M1 L15 V26 P38 R42 D52 G53 R54 Y59 L71 R72 L73 R74 G75 G76

4.2.7 Score per residue for model 7

- Molecule 1: Polyubiquitin-B

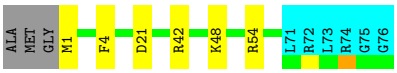
Chain A: 81% 8% 8% •

ALA MET GLY M1 F4 P37 R54 K63 L67 L71 R72 L73 R74 G75 G76

4.2.8 Score per residue for model 8

- Molecule 1: Polyubiquitin-B

Chain A:



4.2.9 Score per residue for model 9

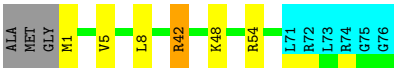
- Molecule 1: Polyubiquitin-B

Chain A:

4.2.10 Score per residue for model 10

- Molecule 1: Polyubiquitin-B

Chain A:



4.2.11 Score per residue for model 11

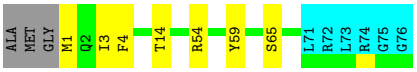
- Molecule 1: Polyubiquitin-B

Chain A:

4.2.12 Score per residue for model 12

- Molecule 1: Polyubiquitin-B

Chain A:



4.2.13 Score per residue for model 13

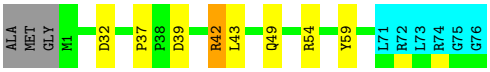
- Molecule 1: Polyubiquitin-B

Chain A:

4.2.14 Score per residue for model 14

- Molecule 1: Polyubiquitin-B

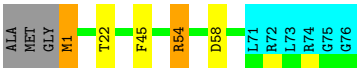
Chain A:



4.2.15 Score per residue for model 15

- Molecule 1: Polyubiquitin-B

Chain A:



4.2.16 Score per residue for model 16

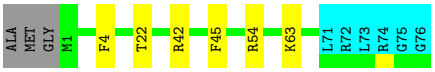
- Molecule 1: Polyubiquitin-B

Chain A:

4.2.17 Score per residue for model 17

- Molecule 1: Polyubiquitin-B

Chain A:



4.2.18 Score per residue for model 18

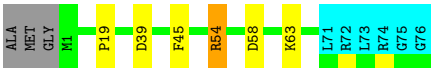
- Molecule 1: Polyubiquitin-B

Chain A:

4.2.19 Score per residue for model 19

- Molecule 1: Polyubiquitin-B

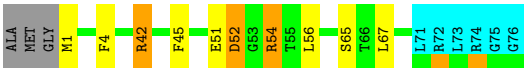
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Polyubiquitin-B

Chain A:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *R-factor based frame picking.*

Of the 10000 calculated structures, 20 were deposited, based on the following criterion: *NOESY-based R-factor selection.*

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

Software name	**Classification**	**Version**
Rosetta	structure calculation	3.6
NAMD 2.12	refinement	
Shine	refinement	
CoMAND	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	728
Number of shifts mapped to atoms	728
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	69%

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	1.39±0.06	0±1/562 (0.1± 0.1%)	1.54±0.09	6±2/759 (0.7± 0.2%)
All	All	1.40	7/11240 (0.1%)	1.54	112/15180 (0.7%)

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	1.1±0.7
All	All	0	21

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	54	ARG	CZ-NH2	-6.52	1.24	1.33	9	1
1	A	64	GLU	CB-CG	6.32	1.64	1.52	5	1
1	A	51	GLU	CG-CD	5.51	1.60	1.51	20	1
1	A	18	GLU	CB-CG	5.45	1.62	1.52	3	1
1	A	70	VAL	CB-CG1	5.32	1.64	1.52	5	1
1	A	34	GLU	CG-CD	5.31	1.59	1.51	1	1
1	A	51	GLU	CB-CG	5.05	1.61	1.52	9	1

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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	42	ARG	NE-CZ-NH1	18.57	129.58	120.30	1	10
1	A	54	ARG	NE-CZ-NH2	-15.85	112.38	120.30	4	9
1	A	54	ARG	NE-CZ-NH1	15.02	127.81	120.30	12	15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	59	TYR	CB-CG-CD2	-11.33	114.20	121.00	1	6
1	A	45	PHE	CB-CG-CD2	10.10	127.87	120.80	15	5
1	A	42	ARG	NH1-CZ-NH2	-9.82	108.60	119.40	18	5
1	A	45	PHE	CB-CG-CD1	-9.66	114.04	120.80	15	4
1	A	59	TYR	CB-CG-CD1	-9.65	115.21	121.00	3	3
1	A	42	ARG	NE-CZ-NH2	-8.86	115.87	120.30	17	7
1	A	54	ARG	NH1-CZ-NH2	-8.61	109.92	119.40	17	5
1	A	4	PHE	CB-CG-CD1	8.23	126.56	120.80	7	2
1	A	1	MET	CG-SD-CE	-7.94	87.50	100.20	18	3
1	A	67	LEU	CB-CG-CD1	6.67	122.33	111.00	3	2
1	A	39	ASP	CB-CG-OD1	-6.50	112.45	118.30	1	2
1	A	39	ASP	CB-CG-OD2	6.47	124.12	118.30	1	3
1	A	52	ASP	CB-CG-OD1	6.36	124.03	118.30	20	2
1	A	65	SER	N-CA-CB	-6.25	101.13	110.50	20	1
1	A	26	VAL	CA-CB-CG2	-6.23	101.55	110.90	6	1
1	A	69	LEU	CB-CG-CD1	6.23	121.59	111.00	3	1
1	A	4	PHE	CB-CG-CD2	-6.15	116.50	120.80	16	4
1	A	22	THR	CA-CB-CG2	-5.99	104.02	112.40	11	4
1	A	21	ASP	CB-CG-OD1	5.95	123.66	118.30	1	2
1	A	62	GLN	OE1-CD-NE2	-5.86	108.42	121.90	1	1
1	A	21	ASP	CB-CG-OD2	-5.56	113.30	118.30	8	1
1	A	32	ASP	CB-CG-OD2	-5.54	113.31	118.30	14	1
1	A	58	ASP	CB-CG-OD1	-5.41	113.43	118.30	19	3
1	A	70	VAL	CA-CB-CG2	-5.39	102.82	110.90	18	1
1	A	59	TYR	CG-CD1-CE1	-5.38	116.99	121.30	6	1
1	A	14	THR	CA-CB-CG2	-5.37	104.88	112.40	12	1
1	A	55	THR	CA-CB-CG2	-5.35	104.91	112.40	11	2
1	A	61	ILE	CA-CB-CG1	5.26	121.00	111.00	1	1
1	A	1	MET	CA-CB-CG	5.20	122.13	113.30	15	1
1	A	15	LEU	CB-CG-CD2	5.14	119.74	111.00	2	1
1	A	22	THR	N-CA-CB	5.05	119.89	110.30	9	1
1	A	25	ASN	CB-CA-C	5.02	120.44	110.40	13	1

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	42	ARG	Sidechain	8
1	A	54	ARG	Sidechain	7
1	A	59	TYR	Sidechain	3

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	4	PHE	Sidechain	2
1	A	62	GLN	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	555	573	575	0±0
All	All	11100	11460	11500	3

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:23:ILE:HD12	1:A:50:LEU:HD13	0.46	1.88	18	1
1:A:3:ILE:HG22	1:A:65:SER:HB2	0.41	1.91	12	1
1:A:15:LEU:HD11	1:A:26:VAL:HG13	0.41	1.91	4	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	69/79 (87%)	67±1 (97±2%)	2±1 (3±2%)	0±0 (0±0%)	54	85
All	All	1380/1580 (87%)	1343 (97%)	35 (3%)	2 (0%)	54	85

All 2 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	52	ASP	1
1	A	46	ALA	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	64/69 (93%)	62±1 (96±2%)	2±1 (4±2%)	38 86
All	All	1280/1380 (93%)	1234 (96%)	46 (4%)	38 86

All 22 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	1	MET	14
1	A	63	LYS	7
1	A	37	PRO	3
1	A	48	LYS	2
1	A	49	GLN	2
1	A	9	THR	2
1	A	20	SER	1
1	A	44	ILE	1
1	A	2	GLN	1
1	A	68	HIS	1
1	A	31	GLN	1
1	A	15	LEU	1
1	A	38	PRO	1
1	A	62	GLN	1
1	A	5	VAL	1
1	A	60	ASN	1
1	A	39	ASP	1
1	A	43	LEU	1
1	A	19	PRO	1
1	A	52	ASP	1
1	A	56	LEU	1
1	A	67	LEU	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)

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 (i)

The completeness of assignment taking into account all chemical shift lists is 69% for the well-defined parts and 68% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *Ub_bmrb.str*

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	728
Number of shifts mapped to atoms	728
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	76	-0.11 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	70	0.16 ± 0.19	None needed (< 0.5 ppm)
$^{13}C'$	68	-0.11 ± 0.17	None needed (< 0.5 ppm)
^{15}N	71	0.76 ± 0.32	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 69%, i.e. 673 atoms were assigned a chemical shift out of a possible 977. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	334/348 (96%)	136/141 (96%)	133/140 (95%)	65/67 (97%)
Sidechain	339/593 (57%)	164/383 (43%)	167/189 (88%)	8/21 (38%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/36 (0%)	0/18 (0%)	0/17 (0%)	0/1 (0%)
Overall	673/977 (69%)	300/542 (55%)	300/346 (87%)	73/89 (82%)

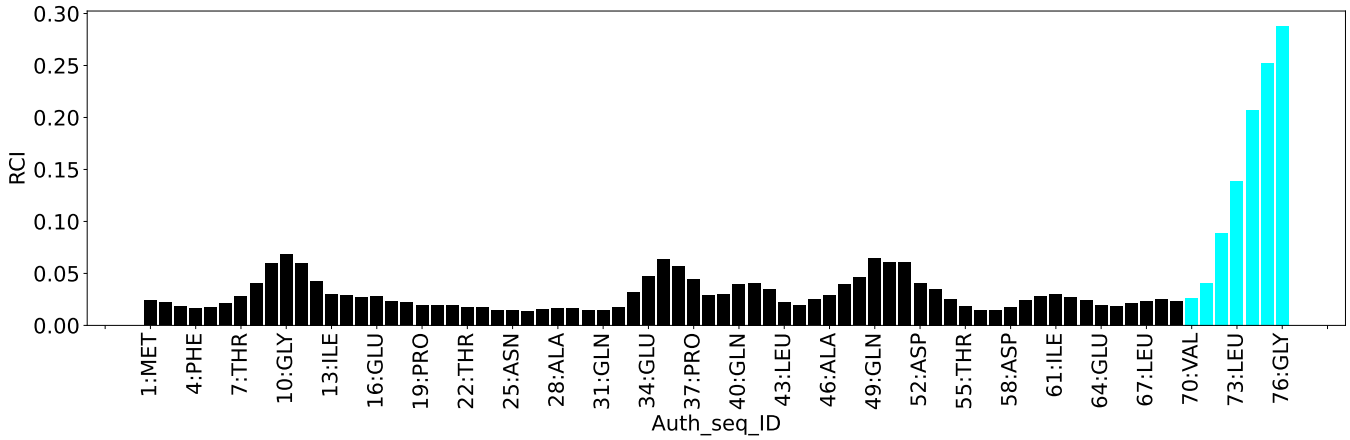
The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 68%, i.e. 728 atoms were assigned a chemical shift out of a possible 1071. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	363/380 (96%)	148/155 (95%)	144/152 (95%)	71/73 (97%)
Sidechain	365/655 (56%)	176/423 (42%)	181/205 (88%)	8/27 (30%)
Aromatic	0/36 (0%)	0/18 (0%)	0/17 (0%)	0/1 (0%)
Overall	728/1071 (68%)	324/596 (54%)	325/374 (87%)	79/101 (78%)

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

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: