



# Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 6SJW  
Title : Structure of the self-processing module of iron-regulated FrpC of *N. Meningitidis* with calcium ions  
Authors : Kuban, V.; Macek, P.; Hritz, J.; Nechvatalova, K.; Nedbalcova, K.; Faldyna, M.; Zidek, L.; Bumba, L.  
Deposited on : 2019-08-14

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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	:	2.20
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.20

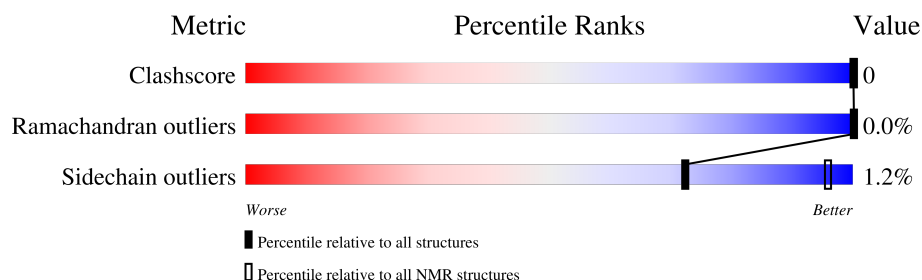
# 1 Overall quality at a glance

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	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  $\geq 3$ , 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	179	<div> <div></div> <div>80%</div> <div>.</div> <div>18%</div> </div>

## 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:1-A:14, A:37-A:168 (146)	0.45	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 2 single-model clusters were found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2624 atoms, of which 1281 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Iron-regulated protein FrpC.

Mol	Chain	Residues	Atoms						Trace
1	A	179	Total	C	H	N	O	S	0
			2620	822	1281	235	281	1	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	SER	ALA	conflict	UNP P55127
A	101	SER	THR	conflict	UNP P55127
A	157	ASN	ASP	conflict	UNP P55127
A	178	LEU	-	expression tag	UNP P55127
A	179	GLU	-	expression tag	UNP P55127

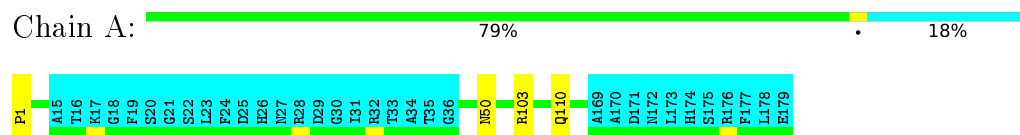
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	
2	A	4	Total	Ca
			4	4



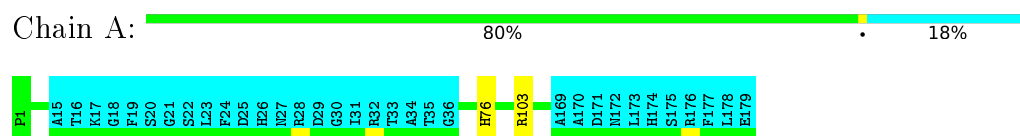
### 4.2.3 Score per residue for model 3

- Molecule 1: Iron-regulated protein FrpC



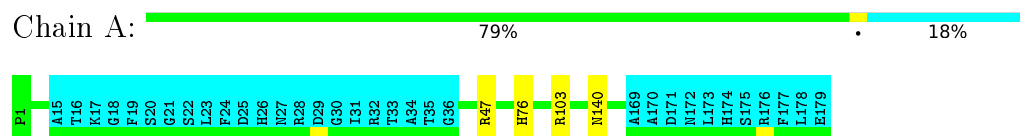
### 4.2.4 Score per residue for model 4

- Molecule 1: Iron-regulated protein FrpC



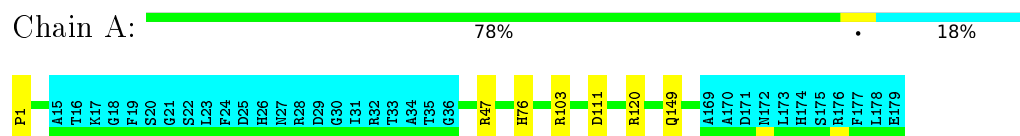
### 4.2.5 Score per residue for model 5

- Molecule 1: Iron-regulated protein FrpC



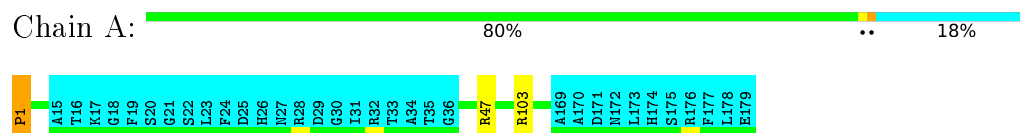
### 4.2.6 Score per residue for model 6

- Molecule 1: Iron-regulated protein FrpC



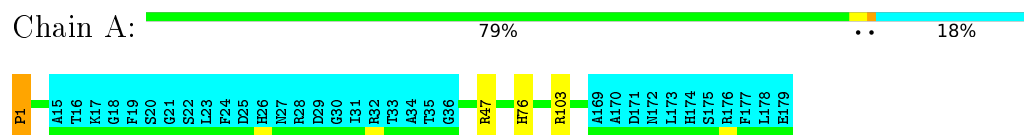
### 4.2.7 Score per residue for model 7

- Molecule 1: Iron-regulated protein FrpC



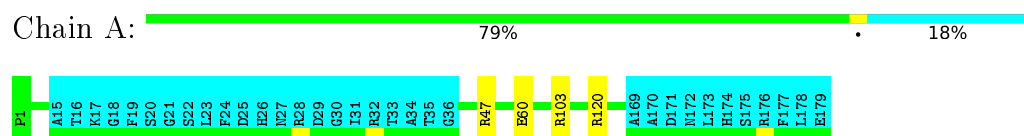
### 4.2.8 Score per residue for model 8

- Molecule 1: Iron-regulated protein FrpC



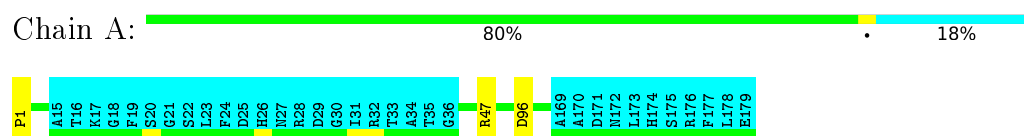
### 4.2.9 Score per residue for model 9

- Molecule 1: Iron-regulated protein FrpC



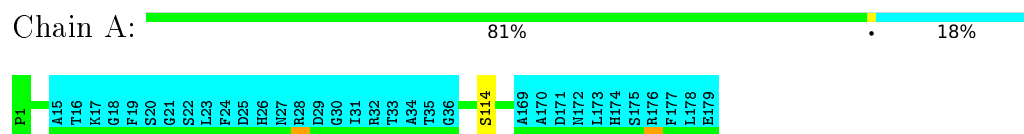
### 4.2.10 Score per residue for model 10

- Molecule 1: Iron-regulated protein FrpC



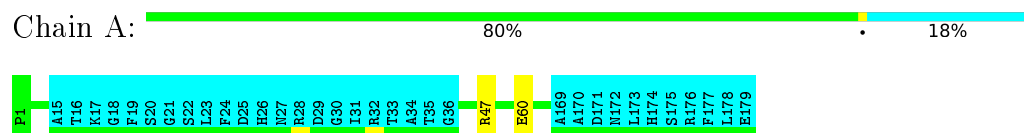
### 4.2.11 Score per residue for model 11

- Molecule 1: Iron-regulated protein FrpC



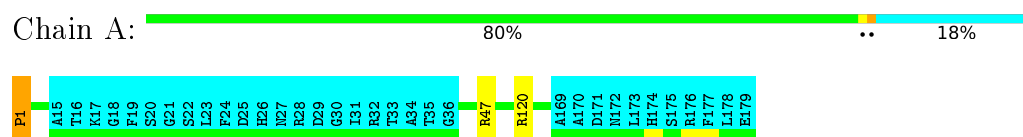
### 4.2.12 Score per residue for model 12

- Molecule 1: Iron-regulated protein FrpC



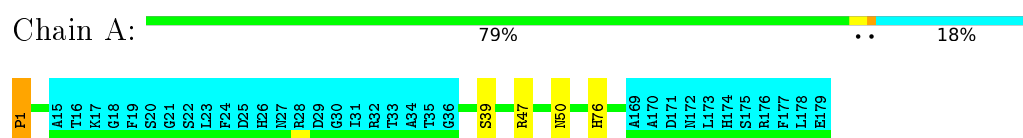
### 4.2.13 Score per residue for model 13

- Molecule 1: Iron-regulated protein FrpC



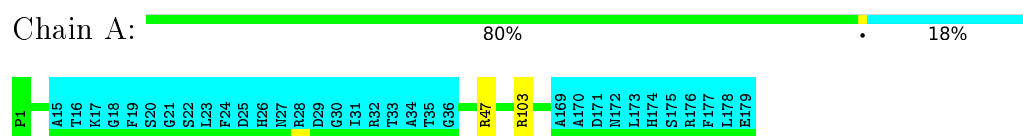
### 4.2.14 Score per residue for model 14

- Molecule 1: Iron-regulated protein FrpC



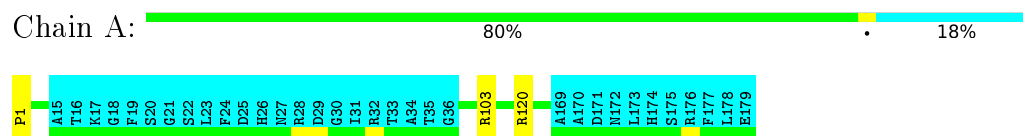
### 4.2.15 Score per residue for model 15

- Molecule 1: Iron-regulated protein FrpC



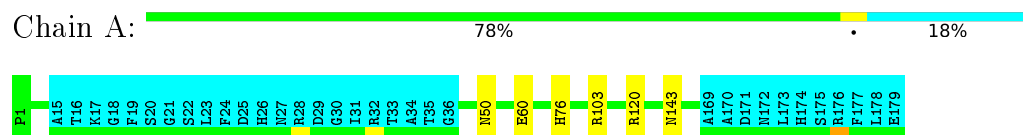
### 4.2.16 Score per residue for model 16

- Molecule 1: Iron-regulated protein FrpC



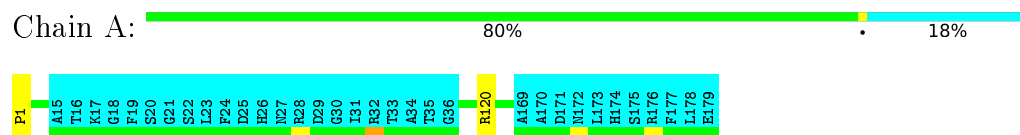
### 4.2.17 Score per residue for model 17

- Molecule 1: Iron-regulated protein FrpC



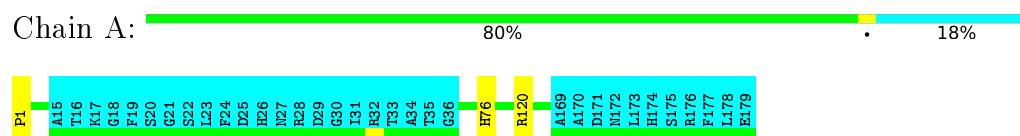
### 4.2.18 Score per residue for model 18

- Molecule 1: Iron-regulated protein FrpC



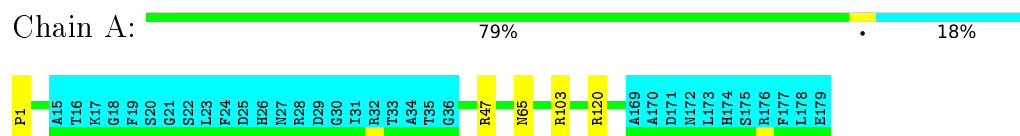
### 4.2.19 Score per residue for model 19

- Molecule 1: Iron-regulated protein FrpC



### 4.2.20 Score per residue for model 20

- Molecule 1: Iron-regulated protein FrpC



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure calculation	3.97
GROMACS	refinement	5.1.1

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	1744
Number of shifts mapped to atoms	1744
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: CA

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	0.48±0.01	0±0/1099 ( 0.0± 0.0%)	1.04±0.02	3±1/1491 ( 0.2± 0.1%)
All	All	0.48	0/21980 ( 0.0%)	1.04	51/29820 ( 0.2%)

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	120	ARG	NE-CZ-NH1	8.50	124.55	120.30	2	6
1	A	120	ARG	NE-CZ-NH2	7.94	124.27	120.30	19	5
1	A	47	ARG	NE-CZ-NH2	7.33	123.96	120.30	13	5
1	A	103	ARG	NE-CZ-NH2	6.86	123.73	120.30	5	3
1	A	103	ARG	NE-CZ-NH1	6.63	123.62	120.30	15	9
1	A	47	ARG	NE-CZ-NH1	6.45	123.53	120.30	5	7
1	A	1	PRO	CA-N-CD	-5.78	103.41	111.50	13	10
1	A	111	ASP	CB-CG-OD1	5.21	122.99	118.30	6	1
1	A	60	GLU	OE1-CD-OE2	-5.21	117.05	123.30	12	3
1	A	118	GLU	OE1-CD-OE2	-5.10	117.18	123.30	2	1
1	A	96	ASP	CB-CG-OD2	5.02	122.81	118.30	10	1

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
All	All	21820	20920	20920	-

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 -.

There are no clashes.

## 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	145/179 (81%)	142±1 (98±1%)	3±1 (2±1%)	0±0 (0±0%)	100	100
All	All	2900/3580 (81%)	2834 (98%)	65 (2%)	1 (0%)	100	100

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	64	ASP	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	113/138 (82%)	112±1 (99±1%)	1±1 (1±1%)	72	96
All	All	2260/2760 (82%)	2232 (99%)	28 (1%)	72	96

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	76	HIS	9
1	A	1	PRO	7
1	A	50	ASN	3
1	A	37	TRP	1
1	A	110	GLN	1
1	A	140	ASN	1
1	A	149	GLN	1
1	A	114	SER	1
1	A	39	SER	1
1	A	47	ARG	1
1	A	143	ASN	1
1	A	65	ASN	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 4 ligands modelled in this entry, 4 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 75% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *NMRStar-CS-spm-wt-3.cif*

#### 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	1744
Number of shifts mapped to atoms	1744
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
$^{13}\text{C}_\alpha$	145	$-0.23 \pm 0.08$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	132	$0.06 \pm 0.16$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	144	$-0.07 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	146	$0.60 \pm 0.29$	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. 1470 atoms were assigned a chemical shift out of a possible 1640. 1 out of 27 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	698/728 (96%)	278/291 (96%)	280/292 (96%)	140/145 (97%)
Sidechain	716/830 (86%)	427/472 (90%)	275/322 (85%)	14/36 (39%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	56/82 (68%)	28/43 (65%)	27/36 (75%)	1/3 (33%)
Overall	1470/1640 (90%)	733/806 (91%)	582/650 (90%)	155/184 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 75%, i.e. 1519 atoms were assigned a chemical shift out of a possible 2026. 1 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	724/893 (81%)	289/357 (81%)	289/358 (81%)	146/178 (82%)
Sidechain	739/1010 (73%)	440/577 (76%)	284/385 (74%)	15/48 (31%)
Aromatic	56/123 (46%)	28/66 (42%)	27/52 (52%)	1/5 (20%)
Overall	1519/2026 (75%)	757/1000 (76%)	600/795 (75%)	162/231 (70%)

#### 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	114	SER	HB2	1.55	5.18 – 2.58	-9.0
1	A	118	GLU	HB3	3.36	3.10 – 0.90	6.2

#### 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:

