Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	1BH1
Title	:	STRUCTURAL STUDIES OF D-PRO MELITTIN, NMR, 20 STRUCTURES
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Deposited on	:	1998-06-11

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
http://wwpdb.org/validation/2016/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

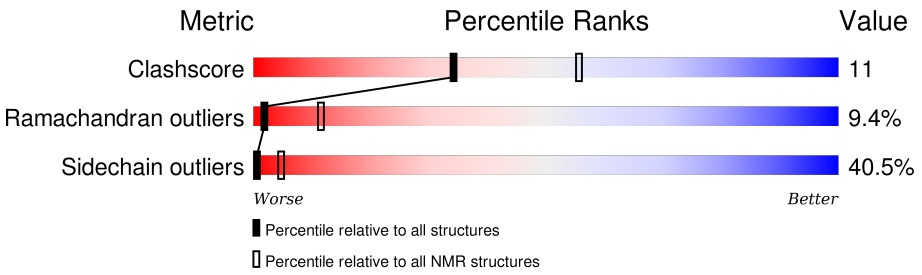
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

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 34%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	27	44% 33% 11% • 7%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 14 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:2-A:26 (25)	0.54	14

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 436 atoms, of which 235 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MELITTIN.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	27	436	131	235	39	31	1

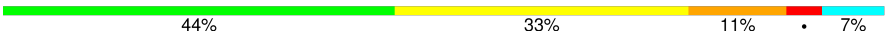
4 Residue-property plots (i)

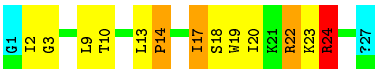
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: MELITTIN

Chain A:





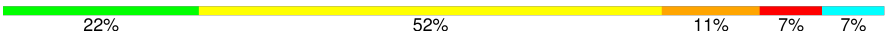
4.2 Scores per residue for each member of the ensemble

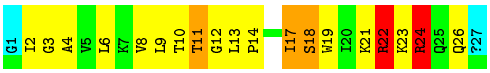
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: MELITTIN

Chain A:

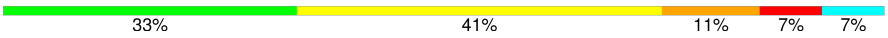


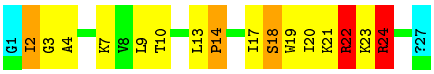


4.2.2 Score per residue for model 2

- Molecule 1: MELITTIN

Chain A:





4.2.3 Score per residue for model 3

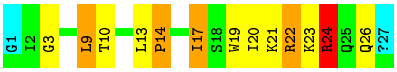
- Molecule 1: MELITTIN

Chain A: 41% 33% 11% 7% 7%

4.2.4 Score per residue for model 4

- Molecule 1: MELITTIN

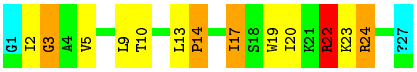
Chain A: 44% 30% 15% • 7%



4.2.5 Score per residue for model 5

- Molecule 1: MELITTIN

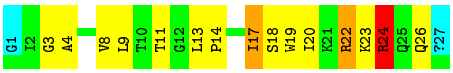
Chain A: 44% 30% 15% • 7%



4.2.6 Score per residue for model 6

- Molecule 1: MELITTIN

Chain A: 37% 44% 7% • 7%



4.2.7 Score per residue for model 7

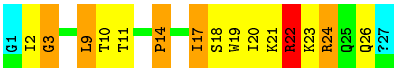
- Molecule 1: MELITTIN

Chain A: 37% 30% 26% 7%

4.2.8 Score per residue for model 8

- Molecule 1: MELITTIN

Chain A: 37% 33% 19% • 7%



4.2.9 Score per residue for model 9

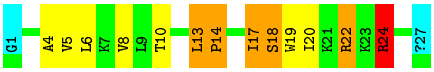
- Molecule 1: MELITTIN

Chain A: 33% 41% 15% • 7%

4.2.10 Score per residue for model 10

- Molecule 1: MELITTIN

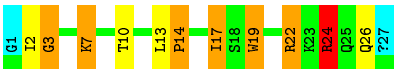
Chain A: 44% 26% 19% • 7%



4.2.11 Score per residue for model 11

- Molecule 1: MELITTIN

Chain A: 52% 15% 22% • 7%



4.2.12 Score per residue for model 12

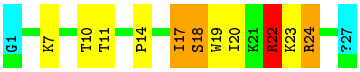
- Molecule 1: MELITTIN

Chain A: 33% 44% 7% 7% 7%

4.2.13 Score per residue for model 13

- Molecule 1: MELITTIN

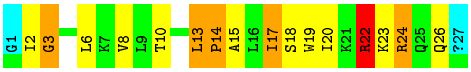
Chain A: 52% 26% 11% • 7%



4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: MELITTIN

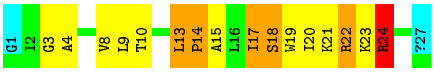
Chain A: 33% 37% 19% • 7%



4.2.15 Score per residue for model 15

- Molecule 1: MELITTIN

Chain A: 33% 37% 19% • 7%



4.2.16 Score per residue for model 16

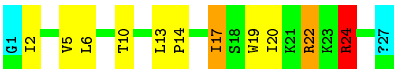
- Molecule 1: MELITTIN

Chain A: 48% 30% 11% • 7%

4.2.17 Score per residue for model 17

- Molecule 1: MELITTIN

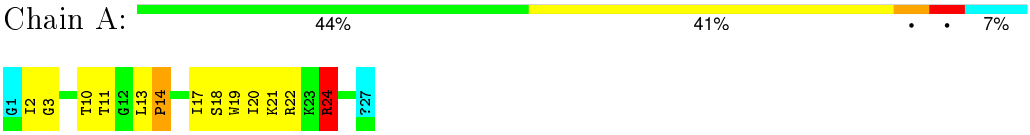
Chain A: 52% 30% 7% • 7%



4.2.18 Score per residue for model 18

- Molecule 1: MELITTIN

Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: MELITTIN

Chain A:

4.2.20 Score per residue for model 20

- Molecule 1: MELITTIN

Chain A:

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DISTANCE GEOMETRY*.

Of the 1000 calculated structures, 20 were deposited, based on the following criterion: *LOWEST STEREOCHEMICAL AND NOE ENERGIES*.

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

Software name	Classification	Version
X-PLOR	refinement	3.8
DYANA	structure solution	1.4
X-PLOR	structure solution	3.8

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)	BMRB entry 4194
Number of chemical shift lists	1
Total number of shifts	150
Number of shifts mapped to atoms	143
Number of unparsed shifts	0
Number of shifts with mapping errors	7
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	34%

No validations of the models with respect to experimental NMR restraints is performed at this time.

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: NH2

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	1.28±0.02	0±0/198 (0.0±0.1%)	1.40±0.07	3±1/266 (1.0±0.3%)
All	All	1.28	1/3960 (0.0%)	1.41	51/5320 (1.0%)

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	1.0±0.0	2.0±0.0
All	All	20	40

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	19	TRP	NE1-CE2	-5.20	1.30	1.37	11	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	22	ARG	NE-CZ-NH2	-10.73	114.94	120.30	20	6
1	A	22	ARG	NE-CZ-NH1	-8.48	116.06	120.30	9	12
1	A	24	ARG	NE-CZ-NH1	-8.32	116.14	120.30	3	15
1	A	24	ARG	NE-CZ-NH2	-8.13	116.24	120.30	19	7
1	A	22	ARG	NH1-CZ-NH2	6.01	126.01	119.40	17	3
1	A	22	ARG	N-CA-C	-5.65	95.73	111.00	20	1
1	A	24	ARG	NH1-CZ-NH2	5.36	125.30	119.40	12	7

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	14	PRO	CA	20

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	24	ARG	Sidechain	20
1	A	22	ARG	Sidechain	20

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	196	228	228	5±1
All	All	3920	4560	4560	91

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:ILE:HD12	1:A:17:ILE:H	0.70	1.47	15	3
1:A:14:PRO:O	1:A:17:ILE:HD11	0.67	1.90	5	10
1:A:17:ILE:HD12	1:A:18:SER:H	0.65	1.51	10	7
1:A:2:ILE:HD12	1:A:3:GLY:N	0.65	2.06	5	6
1:A:17:ILE:H	1:A:17:ILE:HD12	0.62	1.53	1	3
1:A:6:LEU:HD23	1:A:6:LEU:H	0.61	1.55	17	1
1:A:17:ILE:HD12	1:A:18:SER:N	0.60	2.12	18	5
1:A:4:ALA:O	1:A:8:VAL:HG23	0.59	1.98	1	4
1:A:2:ILE:H	1:A:2:ILE:HD13	0.59	1.57	9	2
1:A:2:ILE:HD13	1:A:6:LEU:HD11	0.59	1.74	14	1
1:A:17:ILE:H	1:A:17:ILE:CD1	0.56	2.09	15	3
1:A:13:LEU:N	1:A:14:PRO:CD	0.55	2.70	3	6
1:A:13:LEU:HD23	1:A:13:LEU:N	0.52	2.20	3	1
1:A:17:ILE:HD12	1:A:17:ILE:N	0.51	2.19	15	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:VAL:HG13	1:A:14:PRO:CG	0.49	2.37	14	1
1:A:18:SER:O	1:A:22:ARG:NH1	0.49	2.45	13	2
1:A:17:ILE:CD1	1:A:17:ILE:H	0.49	2.17	17	2
1:A:18:SER:OG	1:A:22:ARG:NH1	0.48	2.45	3	3
1:A:2:ILE:HD13	1:A:2:ILE:H	0.48	1.67	20	1
1:A:2:ILE:HD12	1:A:3:GLY:H	0.47	1.68	19	1
1:A:14:PRO:O	1:A:16:LEU:N	0.46	2.48	3	1
1:A:9:LEU:CD2	1:A:9:LEU:H	0.46	2.24	4	2
1:A:6:LEU:H	1:A:6:LEU:CD2	0.46	2.23	17	1
1:A:11:THR:OG1	1:A:12:GLY:N	0.45	2.50	1	1
1:A:16:LEU:HA	1:A:19:TRP:HB2	0.44	1.87	7	2
1:A:2:ILE:HD13	1:A:2:ILE:N	0.44	2.28	20	3
1:A:16:LEU:HA	1:A:19:TRP:CB	0.44	2.43	7	1
1:A:7:LYS:NZ	1:A:10:THR:HG21	0.44	2.28	11	1
1:A:4:ALA:O	1:A:6:LEU:N	0.44	2.51	10	1
1:A:2:ILE:HD12	1:A:6:LEU:HD11	0.43	1.89	1	1
1:A:2:ILE:O	1:A:4:ALA:N	0.43	2.51	2	1
1:A:13:LEU:O	1:A:15:ALA:N	0.42	2.51	15	2
1:A:2:ILE:O	1:A:5:VAL:N	0.42	2.52	12	3
1:A:9:LEU:CD2	1:A:9:LEU:N	0.41	2.83	4	1
1:A:8:VAL:CG1	1:A:14:PRO:HG2	0.41	2.45	12	1
1:A:8:VAL:HG13	1:A:14:PRO:HG2	0.41	1.93	14	1
1:A:23:LYS:C	1:A:23:LYS:CD	0.41	2.89	7	1
1:A:6:LEU:HD23	1:A:6:LEU:N	0.41	2.28	17	1
1:A:8:VAL:HG13	1:A:14:PRO:HD2	0.40	1.93	7	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	25/27 (93%)	18±2 (70±6%)	5±1 (21±6%)	2±1 (9±3%)	2 11
All	All	500/540 (93%)	350 (70%)	103 (21%)	47 (9%)	2 11

All 9 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	14	PRO	20
1	A	3	GLY	14
1	A	5	VAL	4
1	A	24	ARG	2
1	A	2	ILE	2
1	A	13	LEU	2
1	A	26	GLN	1
1	A	12	GLY	1
1	A	15	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	21/21 (100%)	13±2 (60±8%)	9±2 (40±8%)	0 5
All	All	420/420 (100%)	250 (60%)	170 (40%)	0 5

All 18 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	19	TRP	20
1	A	20	ILE	16
1	A	17	ILE	16
1	A	10	THR	16
1	A	23	LYS	14
1	A	24	ARG	14
1	A	13	LEU	13
1	A	18	SER	10
1	A	9	LEU	10
1	A	21	LYS	9
1	A	11	THR	8
1	A	22	ARG	7
1	A	26	GLN	6
1	A	7	LYS	3
1	A	2	ILE	3
1	A	16	LEU	2
1	A	25	GLN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	14	PRO	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 carbohydrates 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 34% for the well-defined parts and 34% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4194

Chemical shift list name: *assigned_chem_shift_list_1*

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	150
Number of shifts mapped to atoms	143
Number of unparsed shifts	0
Number of shifts with mapping errors	7
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 7 occurences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	14	DPR	HB2	2.31	-1.0	2
A	14	DPR	HD2	3.73	-1.0	2
A	14	DPR	HG3	2.17	-1.0	2
A	14	DPR	HB3	2.09	-1.0	2
A	14	DPR	HD3	3.98	-1.0	2
A	14	DPR	HG2	2.17	-1.0	2
A	14	DPR	HA	4.41	-1.0	1

7.1.2 Chemical shift referencing (i)

No chemical shift referencing corrections were calculated (not enough data).

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 34%, i.e. 113 atoms were assigned a chemical shift out of a possible 332. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	36/123 (29%)	36/49 (73%)	0/50 (0%)	0/24 (0%)
Sidechain	71/197 (36%)	71/115 (62%)	0/71 (0%)	0/11 (0%)
Aromatic	6/12 (50%)	6/6 (100%)	0/5 (0%)	0/1 (0%)
Overall	113/332 (34%)	113/170 (66%)	0/126 (0%)	0/36 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 34%, i.e. 114 atoms were assigned a chemical shift out of a possible 337. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	37/128 (29%)	37/51 (73%)	0/52 (0%)	0/25 (0%)
Sidechain	71/197 (36%)	71/115 (62%)	0/71 (0%)	0/11 (0%)
Aromatic	6/12 (50%)	6/6 (100%)	0/5 (0%)	0/1 (0%)
Overall	114/337 (34%)	114/172 (66%)	0/128 (0%)	0/37 (0%)

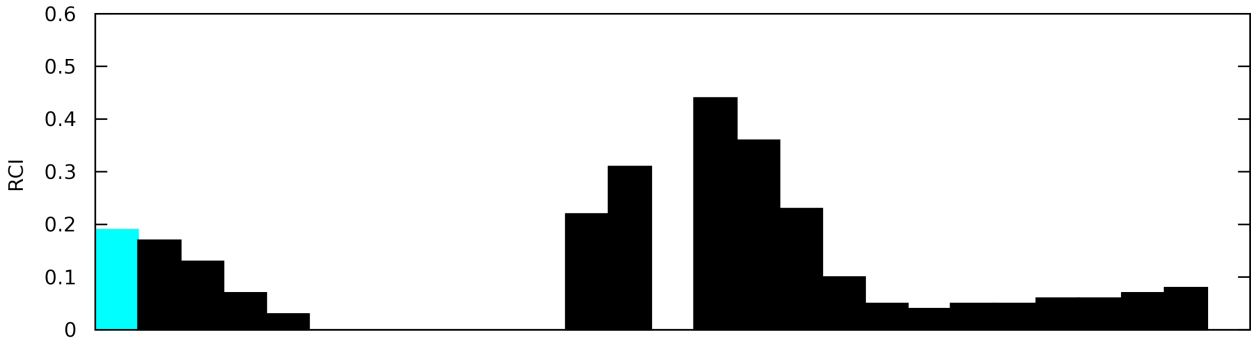
7.1.4 Statistically unusual chemical shifts (i)

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.

Random coil index (RCI) for chain A:


0.6
0.5
0.4
0.3
0.2
0.1
0
RCI