Full wwPDB NMR Structure Validation Report (i)

Apr 26, 2016 – 04:44 PM BST

PDB ID	:	1R2A
Title	:	THE MOLECULAR BASIS FOR PROTEIN KINASE A ANCHORING REVEALED BY SOLUTION NMR
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Deposited on	:	1998-12-07

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:

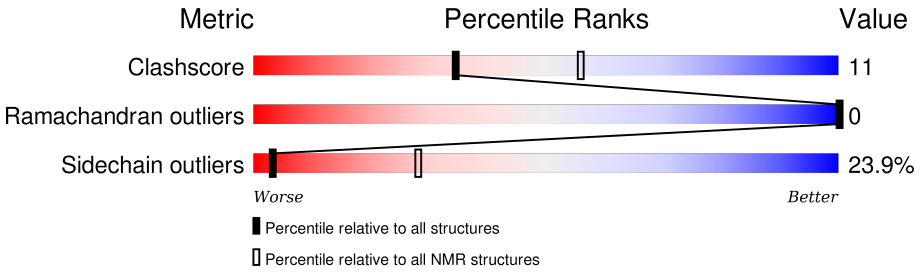
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 81%.

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	46	46% 24% · 26%
1	B	46	43% 26% · 26%

2 Ensemble composition and analysis

This entry contains 17 models. Model 10 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:10-A:43, B:10-B:43 (68)	0.37	10

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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1526 atoms, of which 764 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT).

Mol	Chain	Residues	Atoms						Trace
1	A	46	Total	C	H	N	O	S	0
			763	243	382	69	68	1	
1	B	46	Total	C	H	N	O	S	0
			763	243	382	69	68	1	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	CLONING ARTIFACT	UNP P12367
A	3	GLY	SER	CLONING ARTIFACT	UNP P12367
A	23	LEU	-	INSERTION	UNP P12367
A	24	ARG	GLY	VARIANT	UNP P12367
B	1	HIS	-	CLONING ARTIFACT	UNP P12367
B	3	GLY	SER	CLONING ARTIFACT	UNP P12367
B	23	LEU	-	INSERTION	UNP P12367
B	24	ARG	GLY	VARIANT	UNP P12367

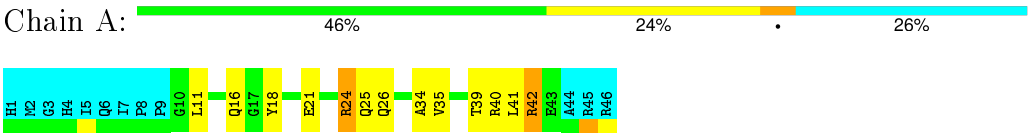
4 Residue-property plots (i)

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.

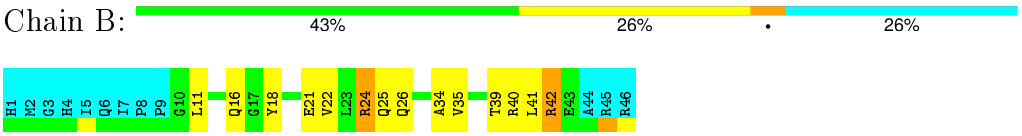
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain B:



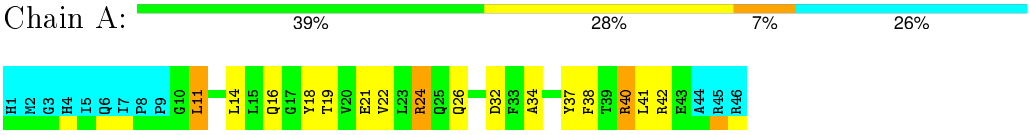
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

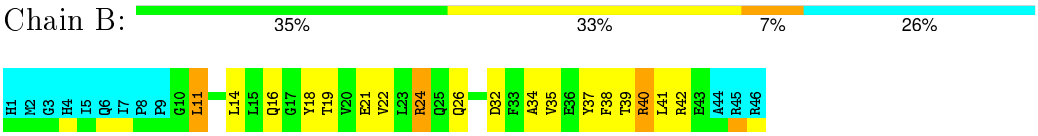
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

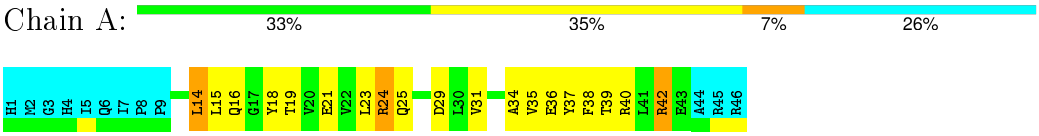
Chain B:



4.2.2 Score per residue for model 2

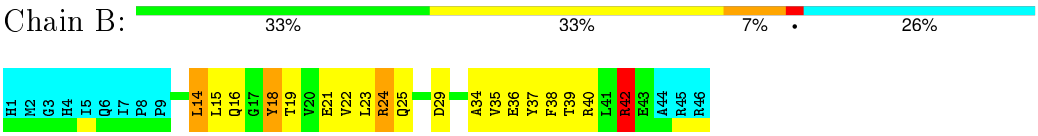
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

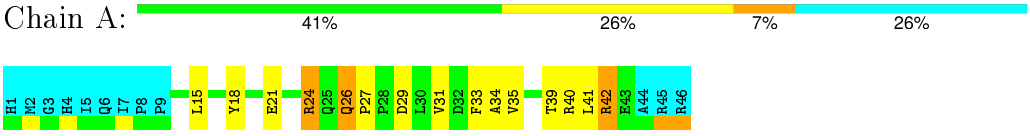
Chain B:



4.2.3 Score per residue for model 3

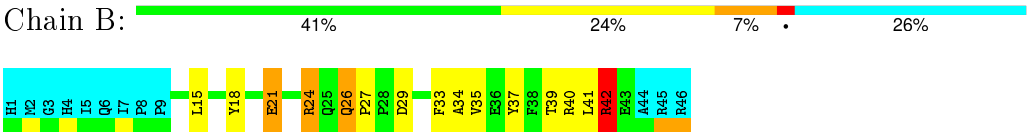
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

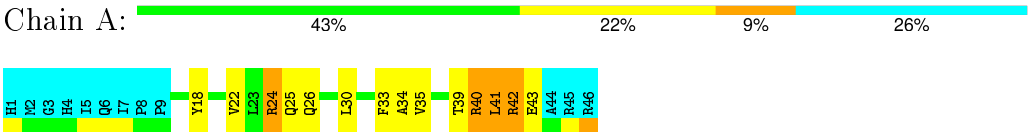
Chain B:



4.2.4 Score per residue for model 4

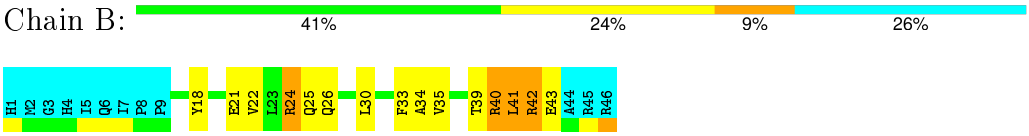
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

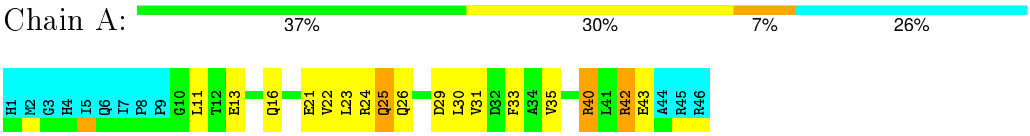
Chain B:



4.2.5 Score per residue for model 5

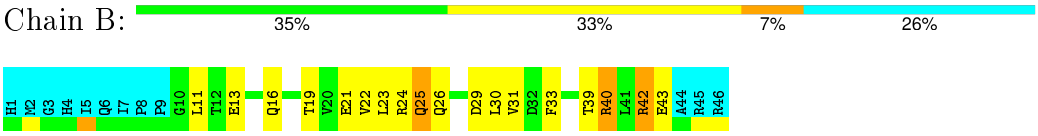
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

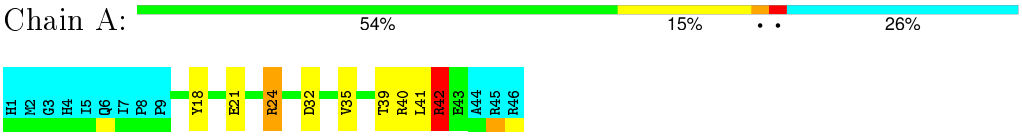
Chain B:



4.2.6 Score per residue for model 6

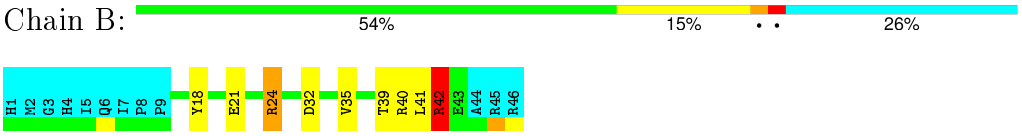
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

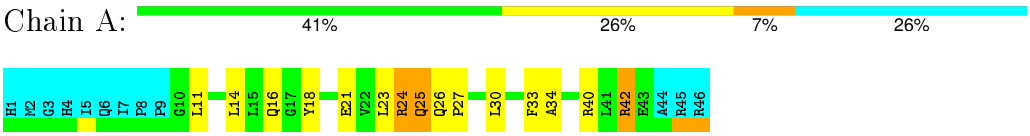
Chain B:



4.2.7 Score per residue for model 7

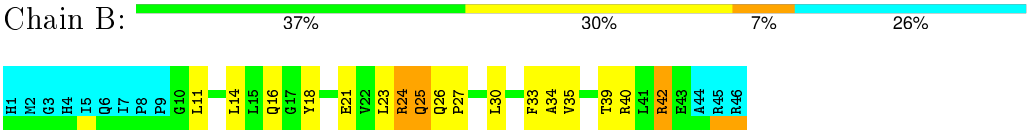
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

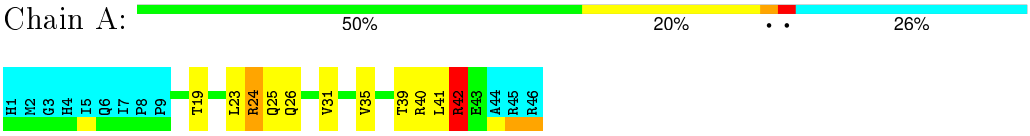
Chain B:



4.2.8 Score per residue for model 8

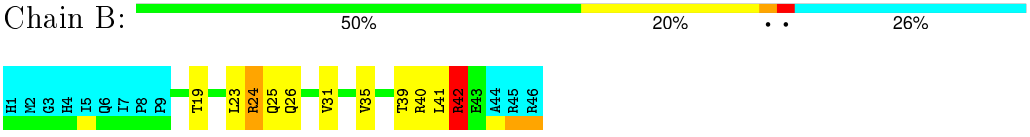
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

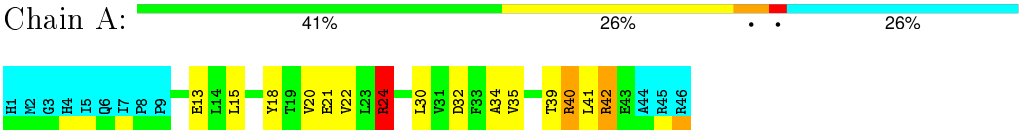
Chain B:



4.2.9 Score per residue for model 9

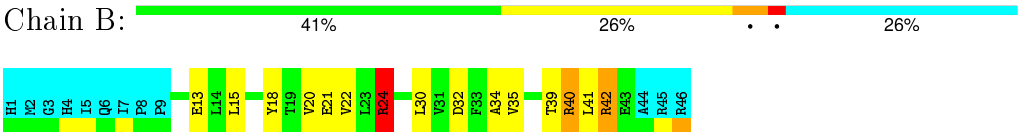
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

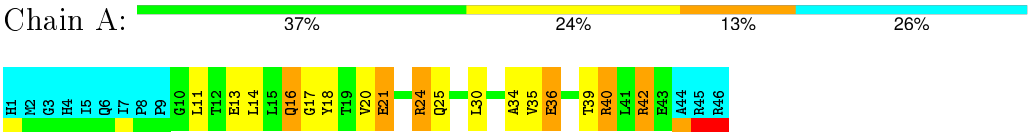
Chain B:



4.2.10 Score per residue for model 10 (medoid)

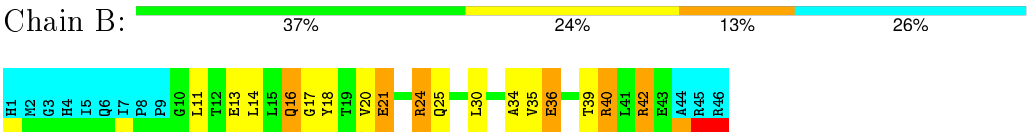
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

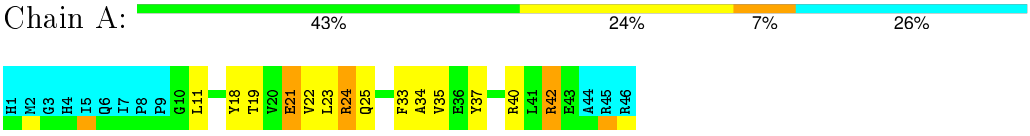
Chain B:



4.2.11 Score per residue for model 11

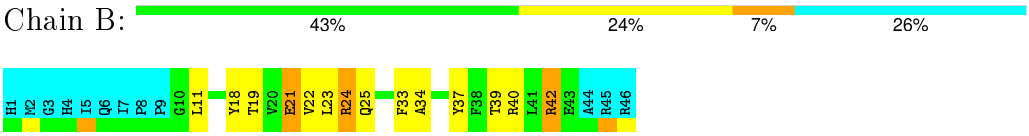
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

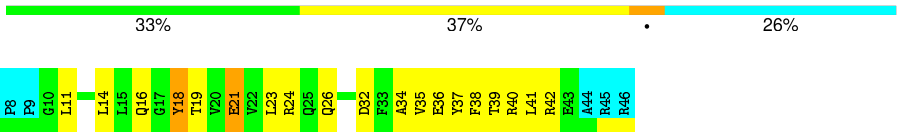
Chain B:



4.2.12 Score per residue for model 12

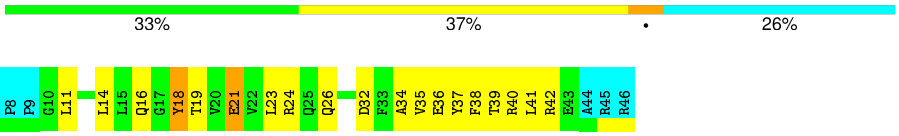
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

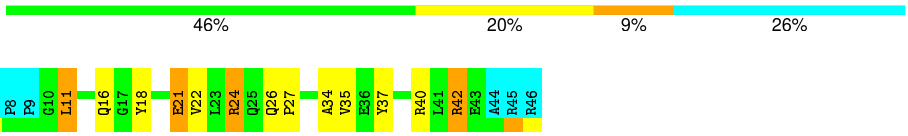
Chain B:



4.2.13 Score per residue for model 13

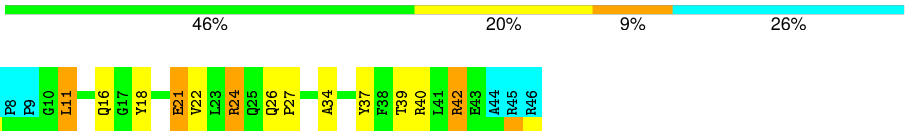
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

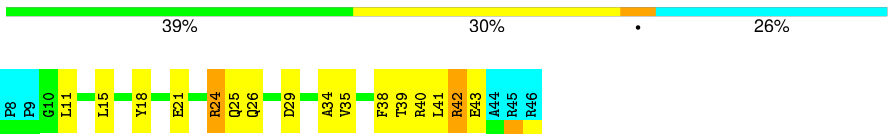
Chain B:



4.2.14 Score per residue for model 14

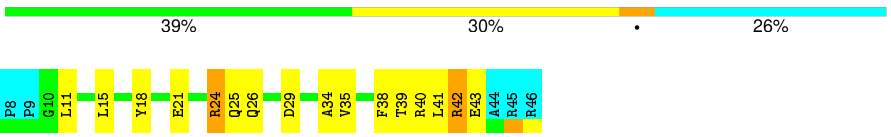
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

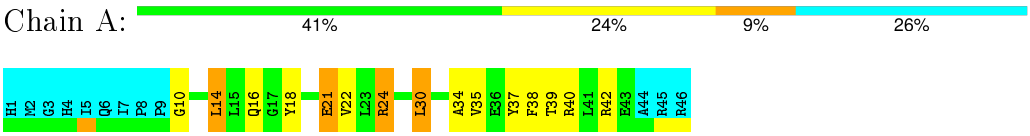
Chain B:



4.2.15 Score per residue for model 15

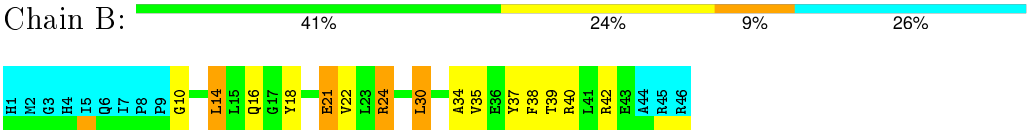
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

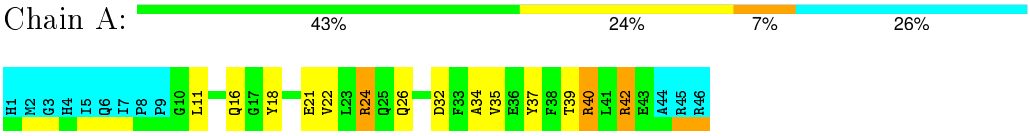
Chain B:



4.2.16 Score per residue for model 16

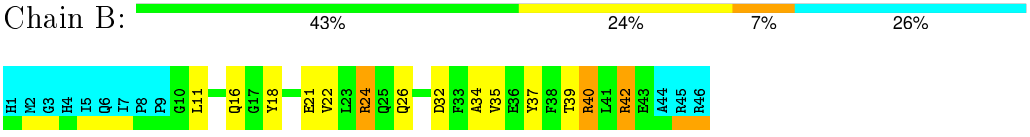
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

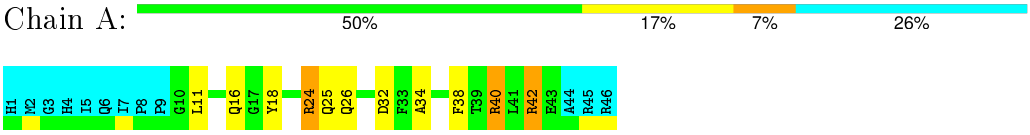
Chain B:



4.2.17 Score per residue for model 17

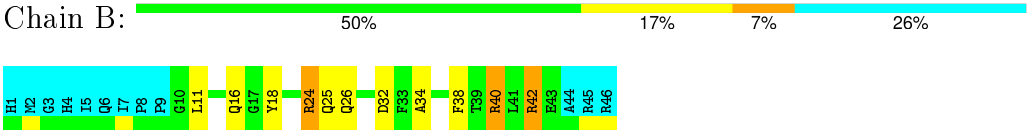
• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain A:



• Molecule 1: PROTEIN (CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY SUBUNIT)

Chain B:


50%
17%
7%
26%
H1
M2
G3
H4
I5
Q6
I7
P8
P9
G10
I11
Q16
G17
Y18
R24
Q25
Q26
D32
F33
A34
F38
T39
R40
L41
R42
F43
A44
R45
R46

5 Refinement protocol and experimental data overview

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

Of the 49 calculated structures, 17 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATION*.

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

Software name	Classification	Version
X-PLOR	refinement	3.851
XPLOR	structure solution	

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 4473
Number of chemical shift lists	1
Total number of shifts	1004
Number of shifts mapped to atoms	1004
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

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

6 Model quality

6.1 Standard geometry

There are no covalent bond-length or bond-angle outliers.

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	3.0±0.0
1	B	0.0±0.0	3.0±0.0
All	All	0	102

There are no bond-length outliers.

There are no bond-angle outliers.

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	B	42	ARG	Sidechain	17
1	B	24	ARG	Sidechain	17
1	B	40	ARG	Sidechain	17
1	A	24	ARG	Sidechain	17
1	A	42	ARG	Sidechain	17
1	A	40	ARG	Sidechain	17

6.2 Too-close contacts

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	282	279	279	7±2
1	B	282	279	279	8±2
All	All	9588	9486	9486	203

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:14:LEU:HD21	1:A:38:PHE:CE1	0.74	2.17	2	1
1:B:14:LEU:HD21	1:B:38:PHE:CE1	0.74	2.17	2	1
1:B:10:GLY:O	1:B:14:LEU:HD12	0.72	1.84	15	1
1:A:10:GLY:O	1:A:14:LEU:HD12	0.70	1.84	15	1
1:B:11:LEU:HD23	1:B:11:LEU:O	0.69	1.88	7	1
1:B:18:TYR:OH	1:B:34:ALA:HB2	0.68	1.88	16	9
1:A:11:LEU:O	1:A:11:LEU:HD23	0.68	1.88	7	1
1:A:18:TYR:OH	1:A:34:ALA:HB2	0.67	1.88	16	9
1:A:15:LEU:HD11	1:B:15:LEU:HD11	0.66	1.65	2	1
1:A:31:VAL:HG12	1:B:42:ARG:HG2	0.66	1.67	5	2
1:A:38:PHE:CD2	1:B:34:ALA:HB1	0.64	2.27	15	6
1:A:34:ALA:HB1	1:B:38:PHE:CD2	0.62	2.29	15	6
1:A:19:THR:O	1:A:23:LEU:HD23	0.57	2.00	11	1
1:A:39:THR:OG1	1:B:35:VAL:HG13	0.56	2.01	16	9
1:A:11:LEU:HD21	1:B:22:VAL:HG11	0.56	1.78	1	1
1:B:19:THR:O	1:B:23:LEU:HD23	0.56	2.01	11	1
1:A:35:VAL:HG13	1:B:39:THR:OG1	0.56	2.00	16	12
1:A:31:VAL:HG12	1:B:42:ARG:HD2	0.55	1.78	8	1
1:A:11:LEU:HD11	1:B:22:VAL:HG11	0.54	1.80	13	1
1:A:22:VAL:HG11	1:B:11:LEU:HD11	0.53	1.79	13	1
1:A:18:TYR:O	1:A:22:VAL:HG23	0.53	2.04	9	6
1:B:18:TYR:O	1:B:22:VAL:HG23	0.52	2.03	9	6
1:A:22:VAL:HG11	1:B:11:LEU:HD21	0.51	1.81	1	1
1:A:42:ARG:HG2	1:B:31:VAL:HG12	0.50	1.82	5	1
1:A:42:ARG:HD2	1:B:31:VAL:HG12	0.50	1.83	8	1
1:B:16:GLN:O	1:B:20:VAL:HG23	0.49	2.08	10	1
1:A:16:GLN:O	1:A:20:VAL:HG23	0.49	2.08	10	1
1:A:30:LEU:HD13	1:A:30:LEU:O	0.48	2.09	15	1
1:A:21:GLU:OE2	1:A:37:TYR:CE1	0.48	2.67	13	2
1:B:21:GLU:OE1	1:B:37:TYR:CE1	0.47	2.68	1	4
1:B:21:GLU:OE2	1:B:37:TYR:CE1	0.47	2.67	13	3
1:B:30:LEU:O	1:B:30:LEU:HD13	0.47	2.08	15	1
1:A:21:GLU:OE2	1:A:37:TYR:CZ	0.47	2.68	15	2
1:A:21:GLU:OE1	1:A:37:TYR:CE1	0.47	2.68	1	4
1:B:21:GLU:OE2	1:B:37:TYR:CZ	0.46	2.68	15	2
1:B:26:GLN:N	1:B:27:PRO:CD	0.46	2.79	3	2
1:A:26:GLN:N	1:A:27:PRO:CD	0.45	2.79	3	2
1:A:15:LEU:HD21	1:B:18:TYR:HD2	0.45	1.72	3	1
1:A:18:TYR:OH	1:A:34:ALA:CA	0.44	2.66	15	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:18:TYR:CE1	1:B:33:PHE:CE2	0.44	3.05	7	4
1:A:25:GLN:OE1	1:A:33:PHE:CZ	0.44	2.71	5	1
1:A:31:VAL:HG12	1:B:42:ARG:CD	0.44	2.42	8	1
1:B:18:TYR:OH	1:B:34:ALA:CA	0.44	2.66	15	8
1:A:18:TYR:CE1	1:A:33:PHE:CE2	0.43	3.05	7	4
1:A:18:TYR:OH	1:A:34:ALA:N	0.43	2.51	4	2
1:B:22:VAL:HG11	1:B:30:LEU:HD21	0.43	1.89	4	1
1:A:35:VAL:CG1	1:B:39:THR:OG1	0.43	2.67	2	2
1:A:11:LEU:C	1:A:11:LEU:HD23	0.43	2.34	12	1
1:B:25:GLN:OE1	1:B:33:PHE:CZ	0.43	2.71	5	1
1:A:35:VAL:O	1:A:39:THR:CB	0.43	2.67	10	4
1:B:18:TYR:OH	1:B:34:ALA:N	0.43	2.52	4	2
1:B:21:GLU:CD	1:B:37:TYR:CE1	0.43	2.92	16	1
1:B:35:VAL:O	1:B:39:THR:CB	0.43	2.67	15	6
1:B:11:LEU:HD23	1:B:11:LEU:C	0.43	2.34	12	1
1:A:18:TYR:OH	1:A:34:ALA:CB	0.43	2.67	17	4
1:A:18:TYR:CE2	1:A:30:LEU:HD11	0.43	2.49	9	1
1:B:18:TYR:CE2	1:B:30:LEU:HD11	0.43	2.49	9	1
1:B:31:VAL:O	1:B:35:VAL:HG23	0.43	2.14	8	1
1:B:18:TYR:CE1	1:B:33:PHE:CD2	0.42	3.07	4	1
1:A:20:VAL:O	1:A:24:ARG:CB	0.42	2.67	9	1
1:B:36:GLU:N	1:B:36:GLU:OE1	0.42	2.53	10	1
1:A:31:VAL:O	1:A:35:VAL:HG23	0.42	2.14	8	1
1:A:39:THR:OG1	1:B:35:VAL:CG1	0.42	2.67	2	1
1:A:21:GLU:CD	1:A:37:TYR:CE1	0.42	2.93	16	1
1:A:18:TYR:CE1	1:A:33:PHE:CD2	0.42	3.08	4	1
1:B:18:TYR:OH	1:B:34:ALA:CB	0.42	2.68	7	4
1:A:36:GLU:OE1	1:A:36:GLU:N	0.42	2.53	10	1
1:B:20:VAL:O	1:B:24:ARG:CB	0.42	2.67	9	1
1:A:22:VAL:HG11	1:A:30:LEU:HD21	0.42	1.89	4	1
1:A:19:THR:O	1:A:23:LEU:HD12	0.42	2.15	8	1
1:A:42:ARG:NH1	1:B:32:ASP:OD1	0.42	2.52	6	1
1:B:17:GLY:O	1:B:21:GLU:CG	0.42	2.67	10	1
1:A:17:GLY:O	1:A:21:GLU:CG	0.42	2.68	10	1
1:A:18:TYR:HD2	1:B:15:LEU:HD21	0.42	1.75	3	1
1:B:19:THR:O	1:B:23:LEU:HD12	0.42	2.14	8	1
1:B:25:GLN:O	1:B:27:PRO:N	0.41	2.53	7	1
1:B:19:THR:O	1:B:23:LEU:CB	0.41	2.68	12	2
1:A:25:GLN:O	1:A:27:PRO:CD	0.41	2.68	7	1
1:A:25:GLN:O	1:A:27:PRO:N	0.41	2.53	7	1
1:B:22:VAL:HG11	1:B:30:LEU:CD2	0.41	2.45	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:THR:O	1:A:23:LEU:CB	0.41	2.68	12	2
1:B:15:LEU:CD2	1:B:15:LEU:N	0.41	2.83	14	1
1:B:41:LEU:HD23	1:B:41:LEU:O	0.41	2.16	4	1
1:A:22:VAL:HG11	1:A:30:LEU:CD2	0.41	2.45	5	1
1:B:25:GLN:O	1:B:27:PRO:CD	0.41	2.68	7	1
1:B:18:TYR:HE2	1:B:30:LEU:HD11	0.41	1.76	15	1
1:B:18:TYR:CD2	1:B:22:VAL:HG21	0.41	2.51	2	1
1:A:41:LEU:O	1:A:41:LEU:HD23	0.41	2.16	4	1
1:B:15:LEU:HD22	1:B:15:LEU:N	0.41	2.31	14	1
1:A:15:LEU:CD2	1:A:15:LEU:N	0.41	2.83	14	1
1:A:32:ASP:OD1	1:B:42:ARG:NH1	0.40	2.54	6	1
1:B:30:LEU:C	1:B:30:LEU:HD13	0.40	2.36	15	1
1:B:14:LEU:HD21	1:B:38:PHE:HE1	0.40	1.69	2	1
1:A:42:ARG:CD	1:B:31:VAL:HG12	0.40	2.45	8	1
1:A:31:VAL:HG12	1:B:42:ARG:HD3	0.40	1.94	2	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	34/46 (74%)	31±1 (92±3%)	3±1 (8±3%)	0±0 (0±0%)	100	100
1	B	34/46 (74%)	31±1 (92±3%)	3±1 (8±3%)	0±0 (0±0%)	100	100
All	All	1156/1564 (74%)	1062 (92%)	94 (8%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	31/41 (76%)	24±2 (76±7%)	7±2 (24±7%)	3 28
1	B	31/41 (76%)	24±2 (76±7%)	7±2 (24±7%)	3 28
All	All	1054/1394 (76%)	802 (76%)	252 (24%)	3 28

All 40 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	24	ARG	15
1	B	24	ARG	15
1	B	42	ARG	13
1	A	42	ARG	13
1	B	21	GLU	12
1	A	21	GLU	11
1	B	26	GLN	10
1	A	16	GLN	10
1	A	26	GLN	10
1	B	16	GLN	10
1	B	25	GLN	9
1	A	25	GLN	9
1	A	11	LEU	8
1	B	11	LEU	8
1	B	41	LEU	7
1	A	41	LEU	7
1	A	40	ARG	7
1	B	40	ARG	7
1	B	14	LEU	6
1	A	14	LEU	6
1	B	32	ASP	5
1	A	32	ASP	5
1	A	29	ASP	4
1	B	29	ASP	4
1	B	18	TYR	4
1	A	18	TYR	4
1	A	30	LEU	3
1	A	43	GLU	3
1	B	43	GLU	3
1	A	13	GLU	3
1	A	36	GLU	3
1	B	13	GLU	3
1	B	36	GLU	3
1	B	30	LEU	3

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Mol	Chain	Res	Type	Models (Total)
1	A	23	LEU	2
1	B	19	THR	2
1	B	23	LEU	2
1	B	15	LEU	1
1	A	15	LEU	1
1	A	19	THR	1

6.3.3 RNA

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 81% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4473

Chemical shift list name: *assigned_chem_shift_list_1*

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	1004
Number of shifts mapped to atoms	1004
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	92	-0.55 ± 0.22	Should be applied
$^{13}C_{\beta}$	86	0.60 ± 0.06	Should be applied
$^{13}C'$	0	—	—
^{15}N	82	0.12 ± 0.46	None needed (< 0.5 ppm)

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 81%, i.e. 718 atoms were assigned a chemical shift out of a possible 884. 2 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	264/332 (80%)	132/132 (100%)	68/136 (50%)	64/64 (100%)
Sidechain	388/484 (80%)	240/280 (86%)	148/180 (82%)	0/24 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	66/68 (97%)	34/36 (94%)	32/32 (100%)	0/0 (—%)
Overall	718/884 (81%)	406/448 (91%)	248/348 (71%)	64/88 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 948 atoms were assigned a chemical shift out of a possible 1220. 2 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	348/444 (78%)	174/176 (99%)	92/184 (50%)	82/84 (98%)
Sidechain	534/680 (79%)	334/400 (84%)	200/242 (83%)	0/38 (0%)
Aromatic	66/96 (69%)	34/52 (65%)	32/40 (80%)	0/4 (0%)
Overall	948/1220 (78%)	542/628 (86%)	324/466 (70%)	82/126 (65%)

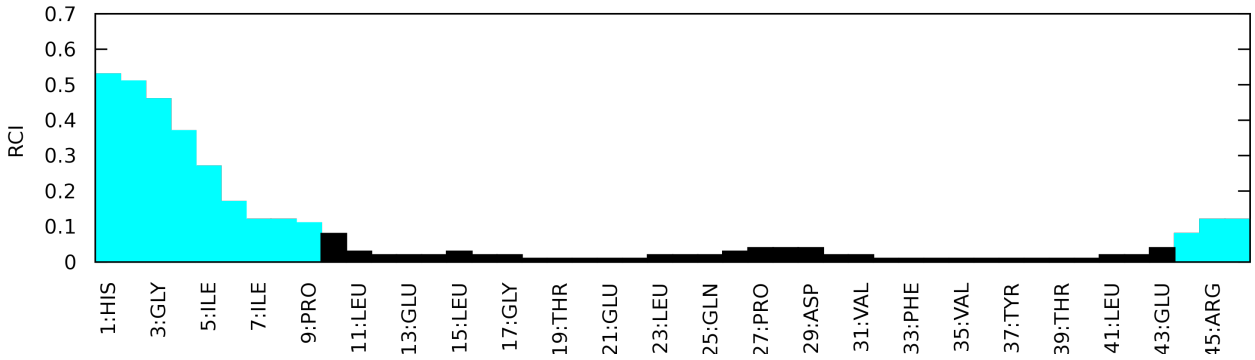
7.1.4 Statistically unusual chemical shifts

There are no statistically unusual chemical shifts.

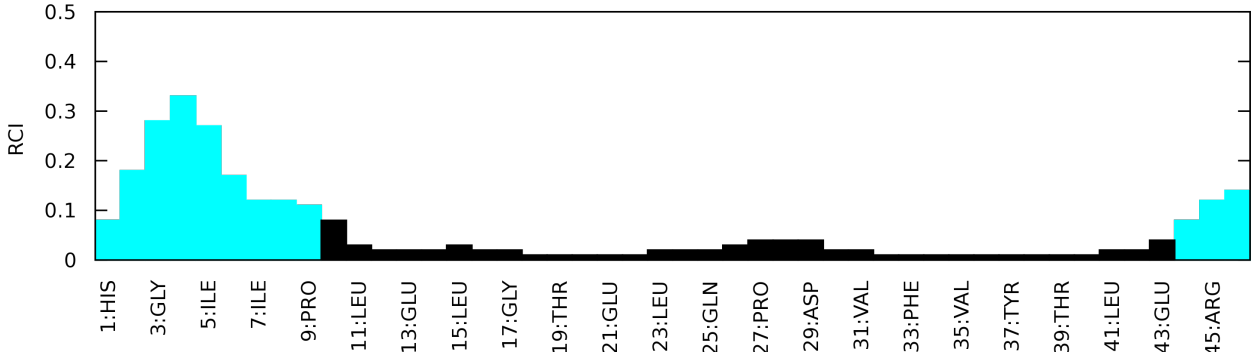
7.1.5 Random Coil Index (RCI) plots

The images below report *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:



Random coil index (RCI) for chain B:


RCI
0.5
0.4
0.3
0.2
0.1
0
1:HIS
3:GLY
5:ILE
7:ILE
9:PRO
11:LEU
13:GLU
15:LEU
17:GLY
19:THR
21:GLU
23:LEU
25:GLN
27:PRO
29:ASP
31:VAL
33:PHE
35:VAL
37:TYR
39:THR
41:LEU
43:GLU
45:ARG