Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2RUC
Title	:	Solution structure of the peptidyl prolyl cis-trans isomerase domain of human Pin1 with sulfate ion
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Deposited on	:	2014-03-25

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:

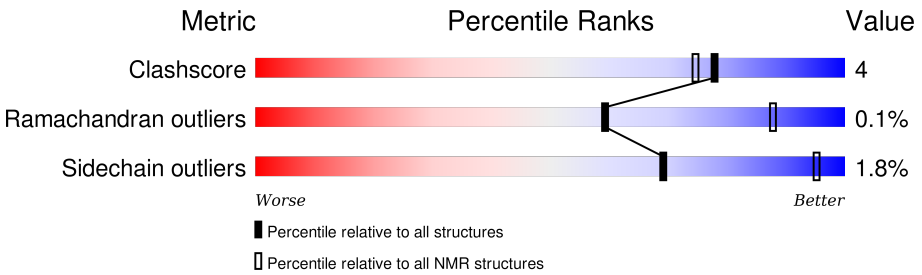
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 91%.

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	117	89% 5% 6%

2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:8-A:117 (110)	0.47	2

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 2 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 5, 7
2	4, 6, 8, 10
Single-model clusters	3; 9

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1825 atoms, of which 906 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	117	1825	565	906	170	179	5	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP Q13526
A	2	SER	-	EXPRESSION TAG	UNP Q13526
A	3	HIS	-	EXPRESSION TAG	UNP Q13526
A	4	MET	-	EXPRESSION TAG	UNP Q13526

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: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

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: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A:

4.2.2 Score per residue for model 2 (medoid)

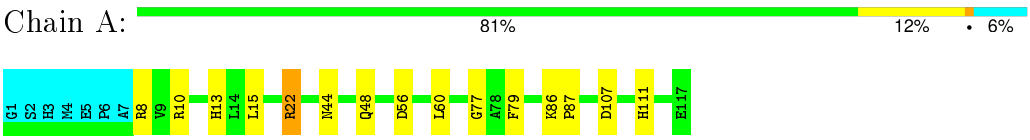
- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A:

4.2.3 Score per residue for model 3

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

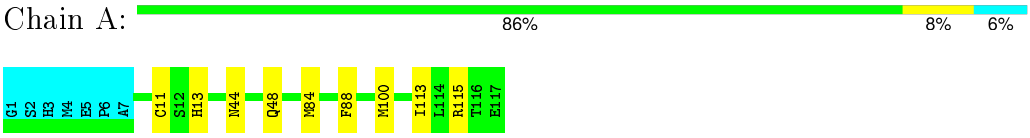
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

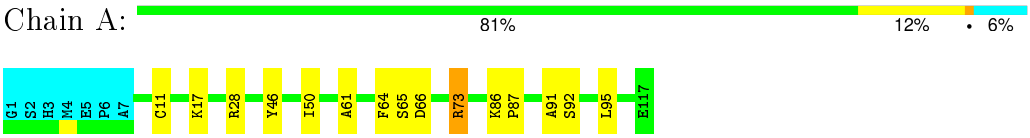
Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

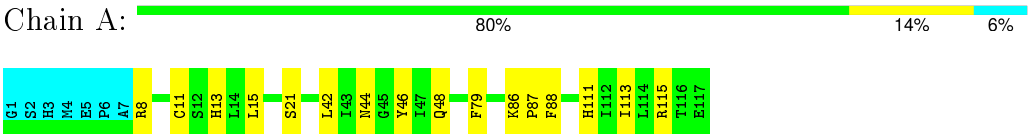
Chain A:



4.2.6 Score per residue for model 6

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

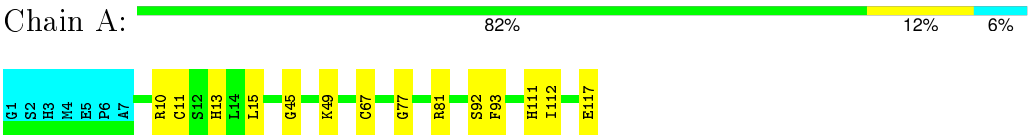
Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

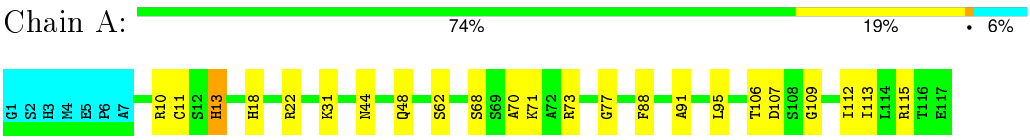
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

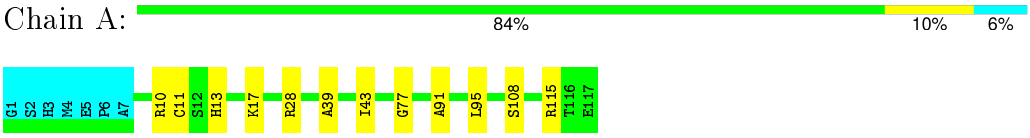
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

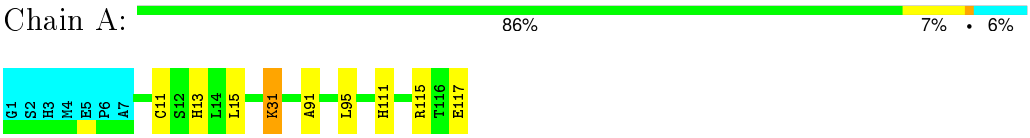
Chain A:



4.2.10 Score per residue for model 10

- Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *distance geometry*.

Of the 40 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR NIH	refinement	
CYANA	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)	2ruc_cs.str
Number of chemical shift lists	1
Total number of shifts	1438
Number of shifts mapped to atoms	1438
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

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)

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	870	861	859	6±2
All	All	8700	8610	8590	63

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:LEU:HD13	1:A:111:HIS:CD2	0.57	2.34	7	2
1:A:11:CYS:SG	1:A:115:ARG:HG2	0.57	2.40	10	5
1:A:88:PHE:CE1	1:A:113:ILE:HG12	0.52	2.39	6	1
1:A:31:LYS:O	1:A:31:LYS:HD2	0.52	2.05	10	1
1:A:73:ARG:HA	1:A:73:ARG:NE	0.51	2.20	5	1
1:A:91:ALA:O	1:A:95:LEU:HG	0.51	2.06	8	4
1:A:13:HIS:HA	1:A:112:ILE:O	0.50	2.05	7	2
1:A:17:LYS:HA	1:A:108:SER:O	0.50	2.06	9	1
1:A:88:PHE:CE2	1:A:113:ILE:HG12	0.49	2.41	4	2
1:A:17:LYS:HE3	1:A:66:ASP:O	0.49	2.06	5	1
1:A:22:ARG:HD2	1:A:107:ASP:OD2	0.49	2.06	8	1
1:A:39:ALA:O	1:A:43:ILE:HG12	0.48	2.08	9	1
1:A:45:GLY:O	1:A:49:LYS:HG3	0.48	2.07	7	1
1:A:15:LEU:HD13	1:A:111:HIS:NE2	0.48	2.23	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:ASN:O	1:A:48:GLN:HG2	0.48	2.07	4	4
1:A:31:LYS:HD2	1:A:31:LYS:O	0.48	2.09	1	1
1:A:61:ALA:O	1:A:65:SER:HB3	0.46	2.11	5	1
1:A:28:ARG:NH1	1:A:64:PHE:HA	0.46	2.25	5	1
1:A:8:ARG:HA	1:A:79:PHE:O	0.46	2.11	3	3
1:A:10:ARG:HA	1:A:77:GLY:O	0.45	2.11	3	5
1:A:62:SER:OG	1:A:73:ARG:HA	0.45	2.11	8	1
1:A:10:ARG:NH2	1:A:77:GLY:HA2	0.44	2.27	1	1
1:A:42:LEU:HG	1:A:46:TYR:CE2	0.44	2.48	6	1
1:A:62:SER:HA	1:A:70:ALA:O	0.43	2.13	8	1
1:A:10:ARG:HD3	1:A:117:GLU:OE1	0.43	2.12	7	1
1:A:84:MET:HG2	1:A:88:PHE:CD1	0.43	2.49	4	1
1:A:86:LYS:N	1:A:87:PRO:HD2	0.43	2.29	6	3
1:A:15:LEU:HD23	1:A:67:CYS:HB2	0.42	1.91	1	2
1:A:56:ASP:O	1:A:60:LEU:HG	0.42	2.15	3	1
1:A:46:TYR:O	1:A:50:ILE:HG13	0.42	2.15	2	2
1:A:15:LEU:HD13	1:A:111:HIS:CE1	0.42	2.50	3	1
1:A:28:ARG:NE	1:A:28:ARG:HA	0.42	2.30	9	1
1:A:68:SER:O	1:A:71:LYS:HG2	0.41	2.15	8	1
1:A:18:HIS:CD2	1:A:109:GLY:HA2	0.41	2.50	8	1
1:A:100:MET:HA	1:A:113:ILE:O	0.41	2.16	4	1
1:A:11:CYS:SG	1:A:92:SER:HB3	0.41	2.56	5	2
1:A:71:LYS:HA	1:A:71:LYS:HE2	0.41	1.93	2	1
1:A:22:ARG:H	1:A:22:ARG:HD3	0.41	1.75	3	1
1:A:81:ARG:HB3	1:A:93:PHE:CZ	0.41	2.50	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	109/117 (93%)	103±1 (94±1%)	6±2 (6±1%)	0±0 (0±0%)	59	88
All	All	1090/1170 (93%)	1028 (94%)	61 (6%)	1 (0%)	59	88

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	21	SER	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	95/100 (95%)	93±1 (98±1%)	2±1 (2±1%)	69 95
All	All	950/1000 (95%)	933 (98%)	17 (2%)	69 95

All 8 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	13	HIS	8
1	A	106	THR	2
1	A	31	LYS	2
1	A	107	ASP	1
1	A	22	ARG	1
1	A	73	ARG	1
1	A	54	GLU	1
1	A	117	GLU	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 91% for the well-defined parts and 90% for the entire structure.

7.1 Chemical shift list 1

File name: 2ruc_cs.str

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	1438
Number of shifts mapped to atoms	1438
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	114	-0.38 ± 0.18	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	106	-0.13 ± 0.19	None needed (< 0.5 ppm)
$^{13}C'$	112	-0.24 ± 0.22	None needed (< 0.5 ppm)
^{15}N	109	0.33 ± 0.57	None needed (< 0.5 ppm)

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 91%, i.e. 1259 atoms were assigned a chemical shift out of a possible 1384. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	541/544 (99%)	217/217 (100%)	218/220 (99%)	106/107 (99%)
Sidechain	632/742 (85%)	396/441 (90%)	219/257 (85%)	17/44 (39%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	86/98 (88%)	46/52 (88%)	39/39 (100%)	1/7 (14%)
Overall	1259/1384 (91%)	659/710 (93%)	476/516 (92%)	124/158 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 1310 atoms were assigned a chemical shift out of a possible 1457. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	560/577 (97%)	225/230 (98%)	226/234 (97%)	109/113 (96%)
Sidechain	660/774 (85%)	414/461 (90%)	229/269 (85%)	17/44 (39%)
Aromatic	90/106 (85%)	48/56 (86%)	41/41 (100%)	1/9 (11%)
Overall	1310/1457 (90%)	687/747 (92%)	496/544 (91%)	127/166 (77%)

7.1.4 Statistically unusual chemical shifts (i)

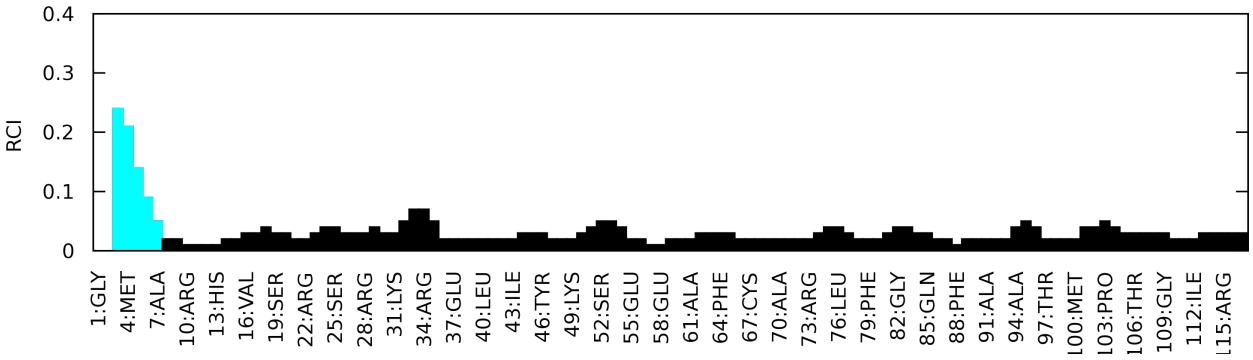
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	28	ARG	HG2	-0.60	2.92 – 0.22	-8.0
1	A	28	ARG	HG3	0.00	3.00 – 0.10	-5.3
1	A	63	GLN	HB2	0.78	3.30 – 0.80	-5.1
1	A	9	VAL	HG21	-0.60	2.20 – -0.60	-5.0
1	A	9	VAL	HG22	-0.60	2.20 – -0.60	-5.0
1	A	9	VAL	HG23	-0.60	2.20 – -0.60	-5.0

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:


RCI
0.4
0.3
0.2
0.1
0
1:GLY
4:MET
7:ALA
10:ARG
13:HIS
16:VAL
19:SER
22:ARG
25:SER
28:ARG
31:LYS
34:ARG
37:GLU
40:LEU
43:ILE
46:TYR
49:LYS
52:SER
55:GLU
58:GLU
61:ALA
64:PHE
67:CYS
70:ALA
73:ARG
76:LEU
79:PHE
82:GLY
85:GLN
88:PHE
91:ALA
94:ALA
97:THR
100:MET
103:PRO
106:THR
109:GLY
112:ILE
115:ARG