Full wwPDB NMR Structure Validation Report (i)

Feb 26, 2022 – 06:06 PM EST

PDB ID	:	2CT4
Title	:	Solution Strutcure of the SH3 domain of the Cdc42-interacting protein 4
Authors	:	Miyamoto, K.; Tomizawa, T.; Koshiba, S.; Inoue, M.; Kigawa, T.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2005-05-23

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

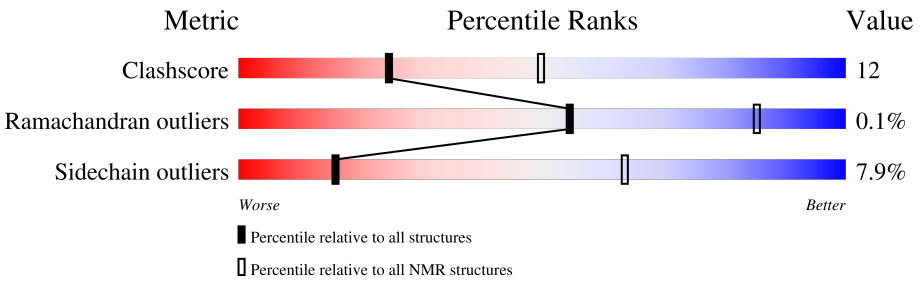
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 was not calculated.

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	70	50% 13% • 36%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 18 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:9-A:17, A:24-A:48, A:53-A:63 (45)	0.14	18

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 4 clusters and 3 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 977 atoms, of which 468 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cdc42-interacting protein 4.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	70	977	306	468	89	111	3	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q15642
A	2	SER	-	cloning artifact	UNP Q15642
A	3	SER	-	cloning artifact	UNP Q15642
A	4	GLY	-	cloning artifact	UNP Q15642
A	5	SER	-	cloning artifact	UNP Q15642
A	6	SER	-	cloning artifact	UNP Q15642
A	7	GLY	-	cloning artifact	UNP Q15642
A	65	SER	-	cloning artifact	UNP Q15642
A	66	GLY	-	cloning artifact	UNP Q15642
A	67	PRO	-	cloning artifact	UNP Q15642
A	68	SER	-	cloning artifact	UNP Q15642
A	69	SER	-	cloning artifact	UNP Q15642
A	70	GLY	-	cloning artifact	UNP Q15642

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: Cdc42-interacting protein 4

Chain A: 50% 13% • 36%

G1 S2 S3 G4 S5 S6 G7 G8 G18 S19 S20 E21 G22 T23 I24 L32 S33 L34 M35 E36 E37 D38 T44 R45 V46 R47 R48 K49 E50 G51 G52 V56 L61 T64 S65 G66 P67 S68 S69 G70

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: Cdc42-interacting protein 4

Chain A: 50% 13% • 36%

G1 S2 S3 G4 S5 S6 G7 G8 G18 S19 S20 E21 G22 T23 I24 L32 S33 L34 M35 D38 T44 R45 V46 R47 R48 K49 E50 G51 G52 V56 L61 T64 S65 G66 P67 S68 S69 G70

4.2.2 Score per residue for model 2

• Molecule 1: Cdc42-interacting protein 4

Chain A: 56% 7% • 36%

G1 S2 S3 G4 S5 S6 G7 G8 H9 G18 S19 S20 E21 G22 T23 I24 L34 D38 R48 K49 E50 G51 G52 E53 T64 S65 G66 P67 S68 S69 G70

4.2.3 Score per residue for model 3

- Molecule 1: Cdc42-interacting protein 4

Chain A: 43% 17% • 36%

G1 S2 S3 G4 S5 S6 G7 G8 H9 C10 V11 F16 E17 G18 S19 S20 E21 G22 T23 I24 D31 L32 S33 L34 M35 D38 T44 R45 V46 R47 R48 K49 E50 G51 G52 V56 P57 T58 T64 S65 G66 P67 S68 S69 G70

4.2.4 Score per residue for model 4

- Molecule 1: Cdc42-interacting protein 4

Chain A: 50% 14% 36%

G1 S2 S3 G4 S5 S6 G7 G8 G18 S19 S20 E21 G22 T23 I24 L32 S33 L34 M35 E36 E37 D38 T44 R45 V46 K49 E50 G51 G52 E53 G54 Y55 V56 T64 S65 G66 P67 S68 S69 G70

4.2.5 Score per residue for model 5

- Molecule 1: Cdc42-interacting protein 4

Chain A: 41% 20% • 36%

G1 S2 S3 G4 S5 S6 G7 G8 G18 S19 S20 E21 G22 T23 I24 S25 D31 L32 S33 L34 M35 E36 E37 D38 T44 R45 V46 R47 R48 K49 E50 G51 G52 E53 G54 Y55 V56 L61 T64 S65 G66 P67 S68 S69 G70

4.2.6 Score per residue for model 6

- Molecule 1: Cdc42-interacting protein 4

Chain A: 43% 20% • 36%

G1 S2 S3 G4 S5 S6 G7 G8 A12 I13 Y14 H15 F16 E17 G18 S19 S20 E21 G22 T23 I24 A27 D31 L32 S33 L34 M35 E36 E37 D38 T44 R45 V46 K49 E50 G51 G52 V56 P57 Y60 T64 S65 G66 P67 S68 S69 G70

4.2.7 Score per residue for model 7

- Molecule 1: Cdc42-interacting protein 4

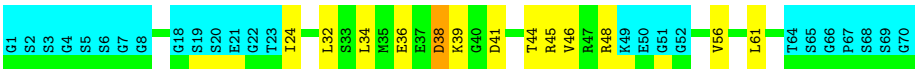
Chain A: 49% 13% • 36%

G1 S2 S3 G4 S5 S6 G7 G8 G18 S19 S20 E21 G22 T23 I24 L34 M35 E36 E37 D38 T44 R45 R48 K49 E50 G51 G52 Y55 V56 L61 T64 S65 G66 P67 S68 S69 G70

4.2.8 Score per residue for model 8

- Molecule 1: Cdc42-interacting protein 4

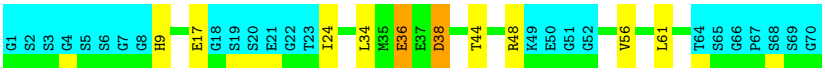
Chain A: 46% 17% • 36%



4.2.9 Score per residue for model 9

- Molecule 1: Cdc42-interacting protein 4

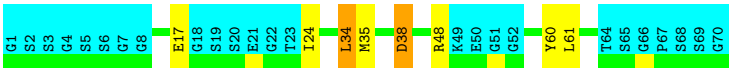
Chain A: 50% 11% • 36%



4.2.10 Score per residue for model 10

- Molecule 1: Cdc42-interacting protein 4

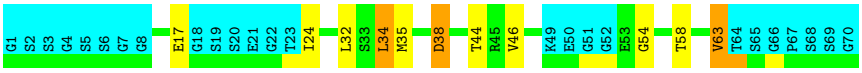
Chain A: 53% 9% • 36%



4.2.11 Score per residue for model 11

- Molecule 1: Cdc42-interacting protein 4

Chain A: 49% 11% • 36%



4.2.12 Score per residue for model 12

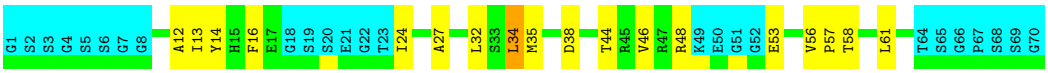
- Molecule 1: Cdc42-interacting protein 4

Chain A: 46% 16% • 36%

4.2.13 Score per residue for model 13

- Molecule 1: Cdc42-interacting protein 4

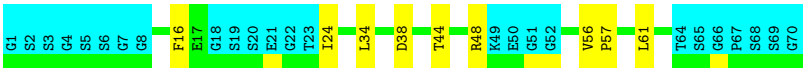
Chain A: 39% 24% • 36%



4.2.14 Score per residue for model 14

- Molecule 1: Cdc42-interacting protein 4

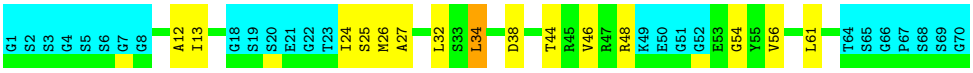
Chain A: 51% 13% 36%



4.2.15 Score per residue for model 15

- Molecule 1: Cdc42-interacting protein 4

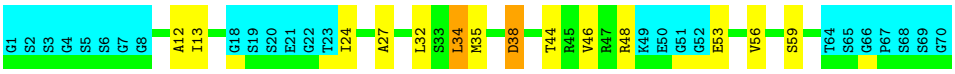
Chain A: 43% 20% • 36%



4.2.16 Score per residue for model 16

- Molecule 1: Cdc42-interacting protein 4

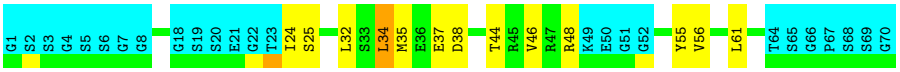
Chain A: 44% 17% • 36%



4.2.17 Score per residue for model 17

- Molecule 1: Cdc42-interacting protein 4

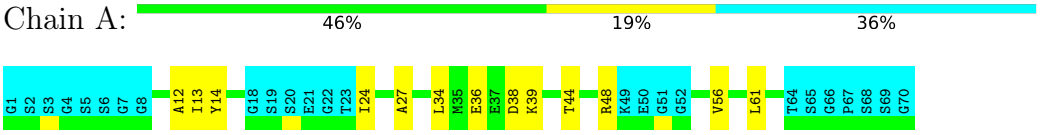
Chain A: 46% 17% • 36%



4.2.18 Score per residue for model 18 (medoid)

- Molecule 1: Cdc42-interacting protein 4

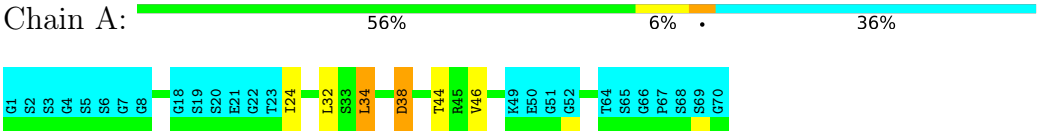
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: Cdc42-interacting protein 4

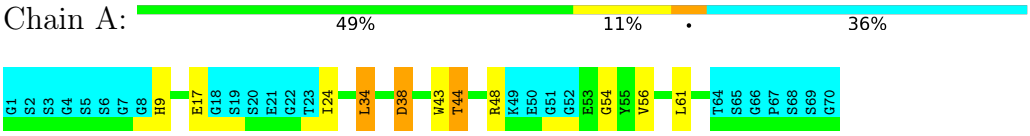
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Cdc42-interacting protein 4

Chain A:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

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

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

Software name	Classification	Version
CYANA	structure solution	2.0.17
CYANA	refinement	2.0.17

No chemical shift data was provided.

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	367	347	345	8±3
All	All	7340	6940	6900	167

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:ILE:HD11	1:A:48:ARG:CD	0.78	2.08	14	16
1:A:36:GLU:O	1:A:44:THR:HG23	0.74	1.83	7	5
1:A:24:ILE:HD11	1:A:48:ARG:HD3	0.71	1.60	3	13
1:A:12:ALA:HB3	1:A:27:ALA:O	0.68	1.89	15	5
1:A:32:LEU:HD13	1:A:46:VAL:HG21	0.65	1.66	1	12
1:A:56:VAL:HG23	1:A:61:LEU:HD11	0.65	1.68	5	8
1:A:34:LEU:HD21	1:A:44:THR:HG21	0.61	1.69	7	12
1:A:56:VAL:CG2	1:A:61:LEU:HD11	0.59	2.28	7	7
1:A:13:ILE:HD11	1:A:61:LEU:C	0.58	2.19	15	2
1:A:24:ILE:HG23	1:A:56:VAL:CG1	0.58	2.28	3	4
1:A:44:THR:O	1:A:56:VAL:HG22	0.57	2.00	20	8
1:A:34:LEU:HD13	1:A:35:MET:N	0.57	2.15	3	8
1:A:24:ILE:HD11	1:A:48:ARG:HD2	0.56	1.78	18	5
1:A:11:VAL:HG12	1:A:31:ASP:HA	0.55	1.77	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:LEU:HD21	1:A:44:THR:CG2	0.53	2.31	15	3
1:A:34:LEU:CD2	1:A:44:THR:HG21	0.50	2.37	7	4
1:A:16:PHE:CE1	1:A:57:PRO:HG3	0.49	2.43	13	2
1:A:24:ILE:HG22	1:A:54:GLY:HA3	0.49	1.85	4	3
1:A:13:ILE:HD12	1:A:59:SER:O	0.48	2.07	16	1
1:A:24:ILE:HG22	1:A:54:GLY:CA	0.48	2.39	20	2
1:A:24:ILE:CG2	1:A:56:VAL:HG13	0.47	2.39	17	3
1:A:9:HIS:H	1:A:9:HIS:CD2	0.46	2.28	2	2
1:A:16:PHE:CE2	1:A:57:PRO:HG3	0.45	2.46	14	1
1:A:24:ILE:CG2	1:A:56:VAL:CG1	0.45	2.94	16	3
1:A:13:ILE:HG22	1:A:14:TYR:CZ	0.45	2.46	18	2
1:A:44:THR:O	1:A:56:VAL:CG2	0.45	2.65	15	2
1:A:38:ASP:O	1:A:38:ASP:CG	0.45	2.55	12	6
1:A:16:PHE:CZ	1:A:57:PRO:HD3	0.45	2.47	3	2
1:A:45:ARG:NH2	1:A:55:TYR:CE2	0.45	2.84	7	2
1:A:41:ASP:OD1	1:A:41:ASP:N	0.45	2.49	8	1
1:A:13:ILE:HG22	1:A:14:TYR:CE1	0.44	2.48	13	2
1:A:38:ASP:CG	1:A:38:ASP:O	0.44	2.55	3	3
1:A:35:MET:C	1:A:36:GLU:OE1	0.43	2.56	5	1
1:A:14:TYR:HB2	1:A:60:TYR:CD2	0.43	2.49	6	1
1:A:35:MET:C	1:A:36:GLU:OE2	0.43	2.57	7	1
1:A:24:ILE:HG22	1:A:54:GLY:C	0.43	2.34	15	1
1:A:25:SER:O	1:A:48:ARG:NH1	0.43	2.52	15	1
1:A:58:THR:O	1:A:61:LEU:N	0.43	2.52	13	1
1:A:24:ILE:CG1	1:A:25:SER:N	0.42	2.82	12	3
1:A:13:ILE:CG2	1:A:14:TYR:CZ	0.42	3.02	18	2
1:A:17:GLU:O	1:A:17:GLU:CG	0.42	2.67	9	1
1:A:60:TYR:O	1:A:61:LEU:HD23	0.41	2.16	10	1
1:A:39:LYS:N	1:A:41:ASP:OD1	0.41	2.54	8	1
1:A:38:ASP:CB	1:A:43:TRP:O	0.41	2.69	20	1
1:A:36:GLU:CB	1:A:45:ARG:HB3	0.40	2.46	8	1
1:A:36:GLU:N	1:A:36:GLU:CD	0.40	2.75	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	45/70 (64%)	41±1 (92±2%)	4±1 (8±2%)	0±0 (0±0%)	54 85
All	All	900/1400 (64%)	826 (92%)	73 (8%)	1 (0%)	54 85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	63	VAL	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	39/54 (72%)	36±1 (92±2%)	3±1 (8±2%)	16 63
All	All	780/1080 (72%)	718 (92%)	62 (8%)	16 63

All 13 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	34	LEU	20
1	A	38	ASP	20
1	A	53	GLU	5
1	A	36	GLU	3
1	A	17	GLU	3
1	A	9	HIS	2
1	A	58	THR	2
1	A	31	ASP	2
1	A	41	ASP	1
1	A	26	MET	1
1	A	37	GLU	1
1	A	39	LYS	1
1	A	44	THR	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)

No chemical shift data were provided