wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2YRY
Title	:	Solution structure of the PH domain of Pleckstrin homology domain-containing family A member 6 from human
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This is a wwPDB NMR Structure Validation Summary 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:

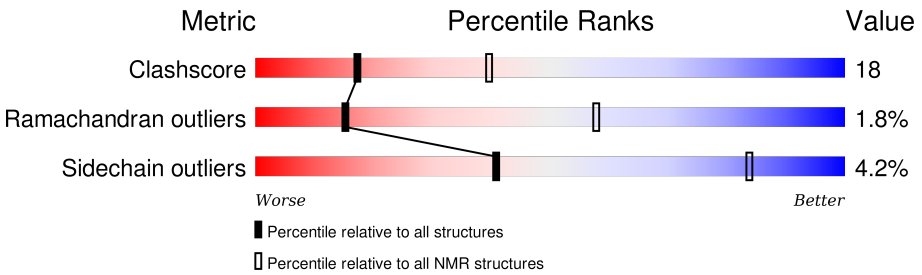
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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	122	53% 29% • 17%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 13 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:15-A:32, A:38-A:120 (101)	0.30	13

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 16 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1917 atoms, of which 949 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Pleckstrin homology domain-containing family A member 6.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	122	1917	612	949	176	177	3	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP Q9Y2H5
A	2	SER	-	EXPRESSION TAG	UNP Q9Y2H5
A	3	SER	-	EXPRESSION TAG	UNP Q9Y2H5
A	4	GLY	-	EXPRESSION TAG	UNP Q9Y2H5
A	5	SER	-	EXPRESSION TAG	UNP Q9Y2H5
A	6	SER	-	EXPRESSION TAG	UNP Q9Y2H5
A	7	GLY	-	EXPRESSION TAG	UNP Q9Y2H5

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: Pleckstrin homology domain-containing family A member 6

Chain A: 53% 29% • 17%

G1 S2 S3 G4 S5 S6 G7 G8 K9 R10 S11 H12 S13 M14 K15 R16 V22 T23 K24 W27 S33 S34 G35 V36 K37 W43 F44 V45 L46 V47 C50 L51 F52 Y53 Y54 K55 D56 E57 I62 L63 L68 L69 S70 F71 V76 T87 F88 K89 H92 A93

G94 V95 R96 F99 F100 E109 A110 W111 I112 G116 V121 Q122

4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 13. Colouring as in section 4.1 above.

- Molecule 1: Pleckstrin homology domain-containing family A member 6

Chain A: 55% 26% •• 17%

G1 S2 S3 G4 S5 S6 G7 G8 K9 R10 S11 H12 S13 M14 K15 R16 V22 F29 K30 Q31 A32 S33 S34 G35 V36 K37 Q38 W39 N40 K41 F44 V45 L46 V47 C50 L51 F52 Y53 L63 G64 L68 L69 S70 F71 A75 V76 T87 F88 K89 H92 A93

G94 V95 R96 F99 F100 E109 A110 W111 I112 G116 A119 R120 V121 Q122

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: *structures with the least restraint violations,target function*.

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

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 11089
Number of chemical shift lists	1
Total number of shifts	1441
Number of shifts mapped to atoms	1441
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	830	812	810	29±6
All	All	16600	16240	16200	588

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 18.

5 of 197 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:PHE:O	1:A:119:ALA:HB1	0.86	1.69	16	7
1:A:76:VAL:HG22	1:A:87:THR:O	0.82	1.74	2	7
1:A:25:ALA:HB1	1:A:43:TRP:CZ2	0.81	2.10	5	8
1:A:46:LEU:HD12	1:A:50:CYS:O	0.75	1.82	19	10
1:A:44:PHE:CD2	1:A:51:LEU:HD21	0.72	2.19	3	12

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	101/122 (83%)	86±4 (85±4%)	13±4 (13±4%)	2±1 (2±1%)	15 58
All	All	2020/2440 (83%)	1726 (85%)	258 (13%)	36 (2%)	15 58

5 of 8 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	94	GLY	15
1	A	120	ARG	6
1	A	75	ALA	6
1	A	93	ALA	3
1	A	73	VAL	2

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	85/101 (84%)	81±2 (96±2%)	4±2 (4±2%)	41 84
All	All	1700/2020 (84%)	1628 (96%)	72 (4%)	41 84

5 of 20 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	89	LYS	17
1	A	69	LEU	7
1	A	15	LYS	7
1	A	88	PHE	6
1	A	57	GLU	5

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 86% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 11089

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	1441
Number of shifts mapped to atoms	1441
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	21

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	112	-0.14 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	106	-0.14 ± 0.18	None needed (< 0.5 ppm)
$^{13}C'$	108	0.15 ± 0.19	None needed (< 0.5 ppm)
^{15}N	100	-0.17 ± 0.56	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. 1198 atoms were assigned a chemical shift out of a possible 1316. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	484/495 (98%)	195/197 (99%)	197/202 (98%)	92/96 (96%)
Sidechain	574/670 (86%)	360/398 (90%)	203/234 (87%)	11/38 (29%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	140/151 (93%)	75/79 (95%)	61/64 (95%)	4/8 (50%)
Overall	1198/1316 (91%)	630/674 (93%)	461/500 (92%)	107/142 (75%)

7.1.4 Statistically unusual chemical shifts (i)

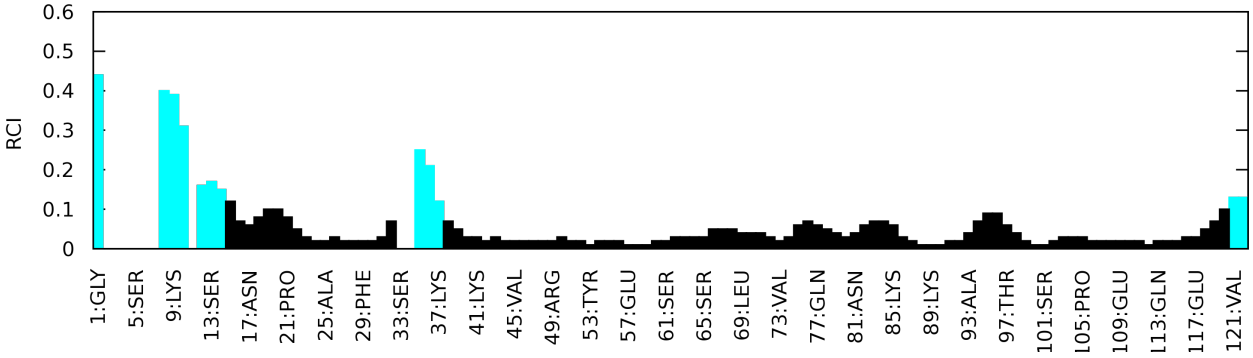
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	24	LYS	HE3	1.01	3.86 – 1.96	-10.0
1	A	84	ARG	HD2	0.88	4.27 – 1.97	-9.8
1	A	24	LYS	HD2	-0.51	2.76 – 0.46	-9.2
1	A	84	ARG	HD3	1.22	4.36 – 1.86	-7.6
1	A	28	LEU	HD12	-1.30	2.16 – -0.64	-7.4
1	A	28	LEU	HD11	-1.30	2.16 – -0.64	-7.4
1	A	28	LEU	HD13	-1.30	2.16 – -0.64	-7.4
1	A	24	LYS	HE2	1.54	3.87 – 1.97	-7.2
1	A	31	GLN	HB3	0.12	3.37 – 0.67	-7.1
1	A	59	GLU	HG2	0.84	3.33 – 1.23	-6.9
1	A	57	GLU	HB3	0.57	3.10 – 0.90	-6.5
1	A	57	GLU	HB2	0.71	3.08 – 0.98	-6.3
1	A	57	GLU	HA	1.73	6.30 – 2.20	-6.1
1	A	100	PHE	HB2	0.77	4.85 – 1.15	-6.0
1	A	57	GLU	HG2	1.07	3.33 – 1.23	-5.8
1	A	16	ARG	HB3	0.16	3.17 – 0.37	-5.8
1	A	24	LYS	HG3	-0.20	2.76 – -0.04	-5.6
1	A	43	TRP	HE3	5.16	9.33 – 5.33	-5.4
1	A	41	LYS	HE2	1.91	3.87 – 1.97	-5.3
1	A	31	GLN	HG3	0.83	3.75 – 0.85	-5.1
1	A	85	LYS	HB2	0.52	3.03 – 0.53	-5.1

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
0.6
0.5
0.4
0.3
0.2
0.1
0
1:GLY
5:SER
9:LYS
13:SER
17:ASN
21:PRO
25:ALA
29:PHE
33:SER
37:LYS
41:LYS
45:VAL
49:ARG
53:TYR
57:GLU
61:SER
65:SER
69:LEU
73:VAL
77:GLN
81:ASN
85:LYS
89:LYS
93:ALA
97:THR
101:SER
105:PRO
109:GLU
113:GLN
117:GLU
121:VAL