wwPDB NMR Structure Validation Summary Report (i)

Feb 27, 2022 – 05:22 PM EST

PDB ID	:	2DBA
Title	:	The solution structure of the tetratrico peptide repeat of human Smooth muscle cell associated protein-1, isoform 2
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Deposited on	:	2005-12-15

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
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:

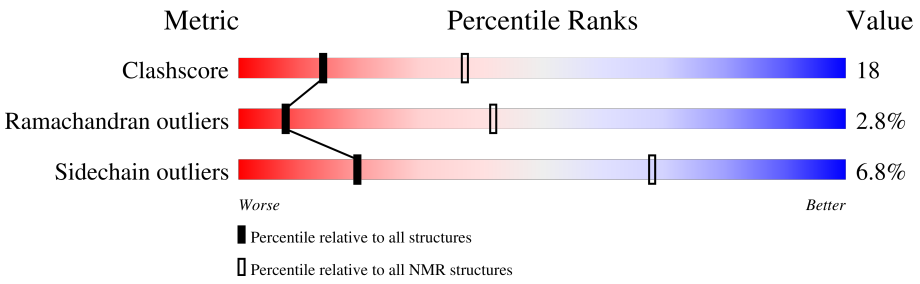
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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	148	55% 23% • 22%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 15 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:27-A:142 (116)	0.33	15

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 6 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2186 atoms, of which 1088 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Smooth muscle cell associated protein-1, isoform 2.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	148	2186	670	1088	201	223	4	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q9H3U1
A	2	SER	-	cloning artifact	UNP Q9H3U1
A	3	SER	-	cloning artifact	UNP Q9H3U1
A	4	GLY	-	cloning artifact	UNP Q9H3U1
A	5	SER	-	cloning artifact	UNP Q9H3U1
A	6	SER	-	cloning artifact	UNP Q9H3U1
A	7	GLY	-	cloning artifact	UNP Q9H3U1
A	143	SER	-	cloning artifact	UNP Q9H3U1
A	144	GLY	-	cloning artifact	UNP Q9H3U1
A	145	PRO	-	cloning artifact	UNP Q9H3U1
A	146	SER	-	cloning artifact	UNP Q9H3U1
A	147	SER	-	cloning artifact	UNP Q9H3U1
A	148	GLY	-	cloning artifact	UNP Q9H3U1

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: Smooth muscle cell associated protein-1, isoform 2

Chain A: 55% 23% • 22%

G1 S2 S3 G4 S5 S6 G7 M8 T9 V10 S11 G12 P13 G14 T15 P16 E17 P18 R19 P20 A21 T22 P23 G24 A25 S26 S27 V28 E29 Q30 L31 R32 K33 E34 G35 N36 F39 D43 G46 A47 A54 A59 T60 Q64 A65 V66 L67 H68 L78 E79 D80 Y81 D82

K83 V99 L102 K111 D121 L122 Q123 L128 K131 N132 K133 V134 F135 L139 S143 G144 P145 S146 S147 G148

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

The representative model is number 15. Colouring as in section 4.1 above.

- Molecule 1: Smooth muscle cell associated protein-1, isoform 2

Chain A: 49% 24% • • 22%

G1 S2 S3 G4 S5 S6 G7 M8 T9 V10 S11 G12 P13 G14 T15 P16 E17 P18 R19 P20 A21 T22 P23 G24 A25 S26 S27 V28 E29 Q30 L31 R32 N36 F39 K40 D43 Y44 G45 G46 A47 L48 A54 A59 D63 Q64 A65 V66 R69 N70 R71 A72 K77

Y81 V99 L102 Y103 R104 R105 K111 Q117 L120 D121 L122 Q123 R124 C125 V126 S127 L128 E129 P130 K131 N132 K133 V134 F135 Q136 L139 S143 G144 P145 S146 S147 G148

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	904	909	907	32±5
All	All	18080	18180	18140	638

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:VAL:HG23	1:A:54:ALA:HB1	1.12	1.20	6	20
1:A:99:VAL:HG13	1:A:128:LEU:HD22	0.90	1.42	20	4
1:A:28:VAL:HG23	1:A:54:ALA:CB	0.83	2.02	17	12
1:A:28:VAL:HG11	1:A:59:ALA:HB2	0.78	1.52	1	13
1:A:48:LEU:C	1:A:48:LEU:HD13	0.70	2.06	5	5

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	116/148 (78%)	91±3 (78±3%)	22±4 (19±3%)	3±2 (3±1%)	8 42
All	All	2320/2960 (78%)	1819 (78%)	435 (19%)	66 (3%)	8 42

5 of 15 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	43	ASP	18
1	A	132	ASN	11
1	A	31	LEU	8
1	A	134	VAL	6
1	A	58	ASP	6

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	93/115 (81%)	87±2 (93±2%)	6±2 (7±2%)	19 68
All	All	1860/2300 (81%)	1734 (93%)	126 (7%)	19 68

5 of 34 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	31	LEU	19
1	A	139	LEU	14
1	A	60	THR	11
1	A	63	ASP	6
1	A	82	ASP	6

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