wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	1U5M
Title	:	Structure of a Chordin-like Cysteine-rich Repeat (VWC module) from Collagen IIA
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Deposited on	:	2004-07-28

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:

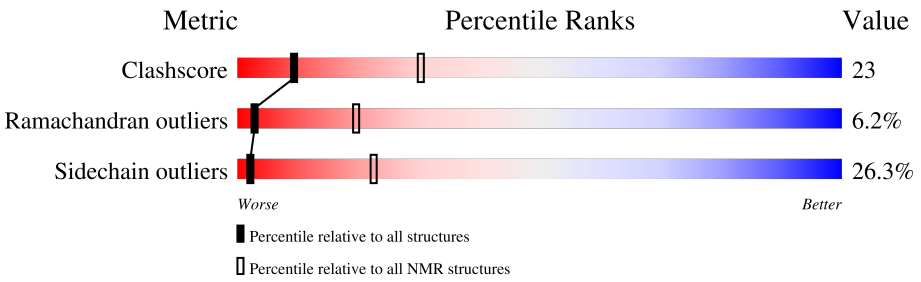
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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	73	29% 36% • 33%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1,2 as representative, based on the following criterion: *closest to the average*.

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:43 (35)	0.31	11
2	A:53-A:66 (14)	0.18	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 3 clusters. No single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1063 atoms, of which 513 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called alpha 1 type II collagen isoform 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	73	1063	340	513	87	113	10	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	TYR	GLY	cloning artifact	UNP P02458
A	2	VAL	GLN	cloning artifact	UNP P02458
A	3	GLU	ASP	cloning artifact	UNP P02458
A	4	PHE	VAL	cloning artifact	UNP P02458
A	67	ALA	THR	engineered mutation	UNP P02458
A	71	ALA	THR	engineered mutation	UNP P02458
A	73	ALA	SER	engineered mutation	UNP P02458

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: alpha 1 type II collagen isoform 1

Chain A: 29% 36% • 33%

Y1 V2 E3 F4 Q5 E6 A7 G8 Q12 D13 G14 Q15 R16 Y17 N18 D19 K20 D21 V22 W23 K24 C28 R29 I30 C31 V32 C33 L39 C40 I43 I44 C45 E46 D47 V48 K49 D50 C51 L52 I56 P57 F58 G59 E60 C61 I64 C65 P66 A67 D68 L69 A70 A71 A72

A73

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

The representative model is number 11. Colouring as in section 4.1 above.

- Molecule 1: alpha 1 type II collagen isoform 1

Chain A: 29% 33% • • 33%

Y1 V2 E3 F4 Q5 E6 A7 G8 S9 Q15 R16 Y17 N18 D19 K20 D21 V22 W23 K24 C28 R29 I30 C31 V32 C33 D34 T35 C40 D41 D42 I43 I44 C45 E46 D47 V48 K49 D50 C51 L52 S53 P57 F58 G59 E60 C61 I64 C65 P66 A67 D68 L69 A70 A71 A72

A73

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *semi-automated assignment and torsion angle dynamics*.

Of the 600 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	1.0.6
CYANA	refinement	1.0.6

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	374	347	342	16±4
All	All	7480	6940	6840	323

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 23.

5 of 129 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:LEU:HD22	1:A:40:CYS:N	0.89	1.82	14	1
1:A:22:VAL:HG22	1:A:32:VAL:HG23	0.83	1.48	4	5
1:A:22:VAL:CG2	1:A:30:ILE:HD11	0.83	2.03	19	2
1:A:28:CYS:C	1:A:43:ILE:HD12	0.80	1.97	20	12
1:A:30:ILE:HG23	1:A:43:ILE:HD11	0.79	1.52	15	6

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	49/73 (67%)	40±2 (83±4%)	6±1 (11±3%)	3±2 (6±3%)	3 19
All	All	980/1460 (67%)	809 (83%)	110 (11%)	61 (6%)	3 19

5 of 7 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	59	GLY	19
1	A	18	ASN	11
1	A	28	CYS	11
1	A	61	CYS	11
1	A	58	PHE	5

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	46/63 (73%)	34±1 (74±3%)	12±1 (26±3%)	2 22
All	All	920/1260 (73%)	678 (74%)	242 (26%)	2 22

5 of 29 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	LYS	20
1	A	29	ARG	17
1	A	40	CYS	16
1	A	19	ASP	14
1	A	64	ILE	14

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