wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	1F6V
Title	:	SOLUTION STRUCTURE OF THE C TERMINAL OF MU B TRANSPOSITION PROTEIN
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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:

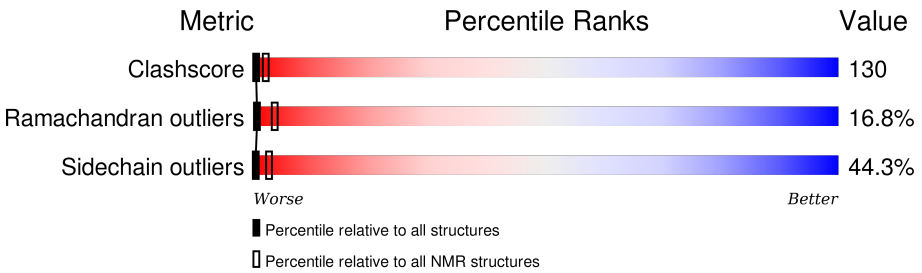
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 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	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	91	9% 42% 29% • 16%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 3 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:11-A:86 (76)	0.30	3

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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1469 atoms, of which 752 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DNA TRANSPOSITION PROTEIN.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	91	1469	446	752	138	132	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	UNP P03763

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: DNA TRANSPOSITION PROTEIN

Chain A: 9% 42% 29% • 16%

G1 S2 R3 I4 A5 K6 R7 T8 A9 I10 N11 K12 T13 K14 K15 A16 D17 V18 K19 A20 I21 A22 D23 A24 W25 Q26 I27 N28 G29 E30 K31 E32 L33 E34 L35 L36 Q37 Q38 I39 A40 Q41 K42 P43 G44 A45 L46 R47 I48 L49 N50 H51 S52 L53 R54 L55 A56 A57 M58 T59 A60

H61 G62 K63 G64 E65 R66 V67 N68 E69 D70 Y71 L72 R73 Q74 A75 F76 R77 E78 L79 D80 L81 D82 V83 D84 I85 S86 T87 L88 L89 R90 N91

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

The representative model is number 3. Colouring as in section 4.1 above.

- Molecule 1: DNA TRANSPOSITION PROTEIN

Chain A: 12% 40% 27% • 16%

G1 S2 R3 I4 A5 K6 R7 T8 A9 I10 N11 K12 T13 K14 K15 A16 D17 V18 K19 A20 I21 A22 D23 A24 W25 Q26 I27 N28 G29 E30 K31 E32 L33 E34 L35 L36 Q37 Q38 I39 A40 Q41 K42 P43 G44 A45 L46 R47 I48 L49 N50 H51 S52 L53 R54 L55 A56 A57 M58 T59 A60

H61 G62 K63 G64 E65 R66 V67 N68 E69 D70 Y71 L72 R73 Q74 A75 F76 R77 E78 L79 D80 L81 D82 V83 D84 I85 S86 T87 L88 L89 R90 N91

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *Simulated annealing.*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with lowest energy and no restraint violations with phi psi angles in allowed regions.*

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

Software name	Classification	Version
X-PLOR	refinement	3.1

No chemical shift data was provided. 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.

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	4.8±0.4
All	All	0	95

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	54	ARG	Sidechain	20
1	A	47	ARG	Sidechain	20
1	A	77	ARG	Sidechain	19
1	A	73	ARG	Sidechain	18
1	A	66	ARG	Sidechain	18

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	602	616	616	159±10
All	All	12040	12320	12320	3176

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 130.

5 of 561 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:ILE:HG21	1:A:76:PHE:CE1	1.09	1.83	15	20
1:A:21:ILE:HG23	1:A:25:TRP:CZ2	1.08	1.83	20	20
1:A:52:SER:CB	1:A:81:LEU:HD22	1.04	1.82	8	20
1:A:46:LEU:HD22	1:A:46:LEU:O	1.01	1.56	19	8
1:A:45:ALA:HB1	1:A:48:ILE:HD12	1.00	1.27	12	2

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	76/91 (84%)	46±2 (60±2%)	17±2 (23±3%)	13±2 (17±2%)	0 3
All	All	1520/1820 (84%)	917 (60%)	347 (23%)	256 (17%)	0 3

5 of 26 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	80	ASP	20
1	A	56	ALA	20
1	A	83	VAL	19
1	A	81	LEU	19
1	A	67	VAL	15

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	62/74 (84%)	35±3 (56±4%)	27±3 (44±4%)	0 3
All	All	1240/1480 (84%)	691 (56%)	549 (44%)	0 3

5 of 49 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	49	LEU	20
1	A	85	ILE	20
1	A	27	ILE	20
1	A	25	TRP	20
1	A	55	LEU	20

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)

No chemical shift data were provided