

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID : 7NIP

Title: titin N2A unique sequence (UN2A) core

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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
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 (1)) 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: 2.17.1.dev1

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

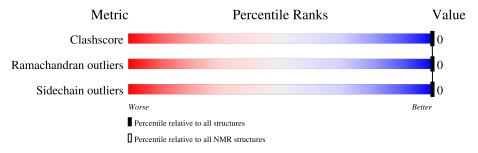
Validation Pipeline (wwPDB-VP) : 2.17.1.dev1

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 1%.

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	NMR archive
IVIETIC	$(\# \mathbf{Entries})$	$(\# \mathrm{Entries})$
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	
4		4-4		
1	A	41	93%	5% •



2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 8 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 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:3-A:40 (38)	0.29	8	

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, 3, 4, 5
2	1, 7, 8, 10
3	6, 9



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 676 atoms, of which 339 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Isoform 11 of Titin.

Mol	Chain	Residues		Atoms				Trace	
1	Λ	40	Total	С	Η	N	О	S	0
1	A	40	676	217	339	54	64	2	U

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	_	initiating methionine	UNP Q8WZ42



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: Isoform 11 of Titin

Chain A: 93% 5%.

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

The representative model is number 8. Colouring as in section 4.1 above.

• Molecule 1: Isoform 11 of Titin

Chain A: 93% 5% •





5 Refinement protocol and experimental data overview (i)



The models were refined using the following method: na.

Of the 32500 calculated structures, 10 were deposited, based on the following criterion: all calculated structures submitted.

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

Software name	Classification	Version
CS-ROSETTA	structure calculation	

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)	$working_cs.cif$
Number of chemical shift lists	1
Total number of shifts	403
Number of shifts mapped to atoms	5
Number of unparsed shifts	0
Number of shifts with mapping errors	398
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	1%



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
All	All	3210	3240	3240	-

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 -.

There are no clashes.

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	${f Analysed}$	Favoured	Allowed	${f Outliers}$	Perce	entiles
1	A	37/41 (90%)	37±0 (100±1%)	0±0 (0±1%)	0±0 (0±0%)	100	100
All	All	370/410 (90%)	369 (100%)	1 (0%)	0 (0%)	100	100

There are no Ramachandran outliers.



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 Outl		Outliers	Perce	$_{ m ntiles}$	
1	A	34/37 (92%)	$34\pm0 \ (100\pm0\%)$	0±0 (0±0%)	100	100
All	All	340/370 (92%)	340 (100%)	0 (0%)	100	100

There are no protein residues with a non-rotameric sidechain to report.

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)

The completeness of assignment taking into account all chemical shift lists is 1% for the well-defined parts and 1% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: $starch_output$

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	403
Number of shifts mapped to atoms	5
Number of unparsed shifts	0
Number of shifts with mapping errors	398
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

• Residue not found in structure. First 5 (of 398) occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	1	MET	CA	56.5	-1.0	2
A	1	MET	СВ	29.96	-1.0	2
A	1	MET	С	176.42	-1.0	2
A	2	ASP	Н	8.103	-1.0	2
A	2	ASP	N	123.071	-1.0	2

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	${\bf Correction}\pm{\bf precision},ppm$	Suggested action
$^{13}\mathrm{C}_{\alpha}$	92	0.00 ± 0.00	None needed ($< 0.5 \text{ ppm}$)
$^{13}C_{\beta}$	86	0.00 ± 0.00	None needed (< 0.5 ppm)
¹³ C′	75	0.00 ± 0.00	None needed ($< 0.5 \text{ ppm}$)

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Nucleus	# values	${\rm Correction}\pm{\rm precision},ppm$	Suggested action
^{15}N	75	0.00 ± 0.00	None needed ($< 0.5 \text{ ppm}$)

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 1%, i.e. 5 atoms were assigned a chemical shift out of a possible 511. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}{ m H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	4/188 (2%)	1/75~(1%)	2/76 (3%)	1/37 (3%)
Sidechain	1/281 (0%)	0/166~(0%)	1/101 (1%)	0/14 (0%)
Aromatic	0/42 (0%)	0/22~(0%)	0/20 (0%)	0/0 (%)
Overall	5/511 (1%)	1/263~(0%)	3/197~(2%)	1/51 (2%)

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (i)

No random coil index (RCI) plot could be generated from the current chemical shift list (starch_output). RCI is only applicable to proteins.

