wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2MWI
Title	:	The structure of the carboxy-terminal domain of DNTTIP1
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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:

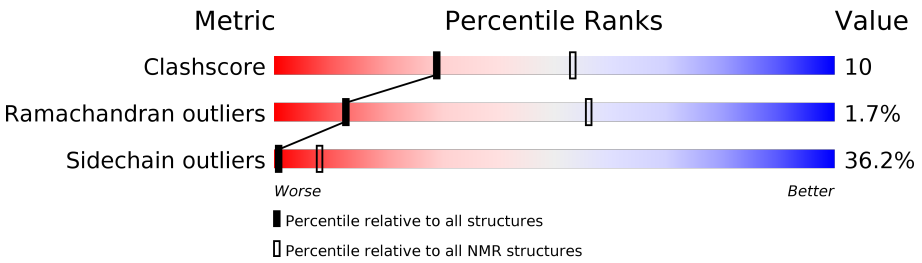
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 80%.

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	122	40% 31% • 25%

2 Ensemble composition and analysis (i)

This entry contains 65 models. Model 2 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:199-A:215, A:222-A:223, A:231-A:253, A:266-A:315 (92)	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 4 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 29, 30, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 42, 43, 45, 46, 48, 49, 50, 51, 52, 53, 54, 55, 56, 60, 61, 62, 63, 65
2	47, 58, 59
3	34, 44
4	17, 28
Single-model clusters	57; 64

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1967 atoms, of which 982 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Deoxynucleotidyltransferase terminal-interacting protein 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	122	1967	623	982	179	176	7	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	GLY	-	EXPRESSION TAG	UNP Q9H147
A	196	ALA	-	EXPRESSION TAG	UNP Q9H147

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: Deoxynucleotidyltransferase terminal-interacting protein 1

Chain A: 40% 31% • 25%

G195 A196 R197 E198 G199 P200 K201 W202 R206 L207 S210 T211 T212 F213 V214 L215 G216 S217 R218 A219 N220 K221 G224 M225 G226 G227 T228 R229 G230 R231 I232 K235 H236 Y242 D245 K249 L252 A253 E254 Q255 H256 H257 M258 R259 A260 T261 G262 G263 K264 M265 A266 Y267

L268 L269 D273 I274 L277 S280 Y283 R284 G285 G286 L289 E292 E293 L294 K295 S296 F297 W298 L299 P300 S301 W302 M303 V304 E305 K306 M307 M311 L314 R315 T316

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

The representative model is number 2. Colouring as in section 4.1 above.

- Molecule 1: Deoxynucleotidyltransferase terminal-interacting protein 1

Chain A: 42% 29% 5% 25%

G195 A196 R197 E198 G199 P200 K201 W202 R206 L207 S210 T211 T212 F213 V214 L215 G216 S217 R218 A219 N220 K221 G224 M225 G226 G227 T228 R229 G230 R231 I232 K235 H236 K241 Y242 D245 P246 Q247 E254 Q255 H256 H257 M258 R259 A260 T261 G262 G263 K264 M265 A266 Y267 L268

L269 D273 I274 L277 S280 Y283 R284 G285 G286 L289 K290 L291 E292 E293 L294 K295 S296 F297 W298 L299 P300 S301 W302 M303 V304 E305 K306 M311 L314 R315 T316

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 65 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	refinement	2.1

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1224
Number of shifts mapped to atoms	1224
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

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	770	772	772	16±3
All	All	50050	50180	50180	1029

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 10.

5 of 96 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:215:LEU:HD21	1:A:252:LEU:HD22	0.85	1.44	61	7
1:A:232:ILE:HD11	1:A:239:LEU:HD22	0.84	1.48	59	3
1:A:215:LEU:HD22	1:A:268:LEU:HD22	0.74	1.58	62	1
1:A:215:LEU:HD22	1:A:252:LEU:HD22	0.72	1.59	14	10
1:A:274:ILE:HG21	1:A:294:LEU:HD11	0.70	1.63	12	15

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	92/122 (75%)	83±1 (90±1%)	8±2 (8±2%)	2±1 (2±1%)	13 56
All	All	5980/7930 (75%)	5380 (90%)	499 (8%)	101 (2%)	13 56

All 4 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	280	SER	44
1	A	284	ARG	44
1	A	234	ILE	8
1	A	202	TRP	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	82/101 (81%)	52±3 (64±3%)	30±3 (36±3%)	1 8
All	All	5330/6565 (81%)	3403 (64%)	1927 (36%)	1 8

5 of 53 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	311	MET	65
1	A	277	LEU	65
1	A	202	TRP	65
1	A	232	ILE	65
1	A	206	ARG	65

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 80% for the well-defined parts and 70% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

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	1224
Number of shifts mapped to atoms	1224
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

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 ± 0.16	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	106	0.20 ± 0.13	None needed (< 0.5 ppm)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	101	0.31 ± 0.38	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 80%, i.e. 976 atoms were assigned a chemical shift out of a possible 1218. 16 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	358/450 (80%)	179/179 (100%)	92/184 (50%)	87/87 (100%)
Sidechain	517/644 (80%)	315/380 (83%)	198/236 (84%)	4/28 (14%)

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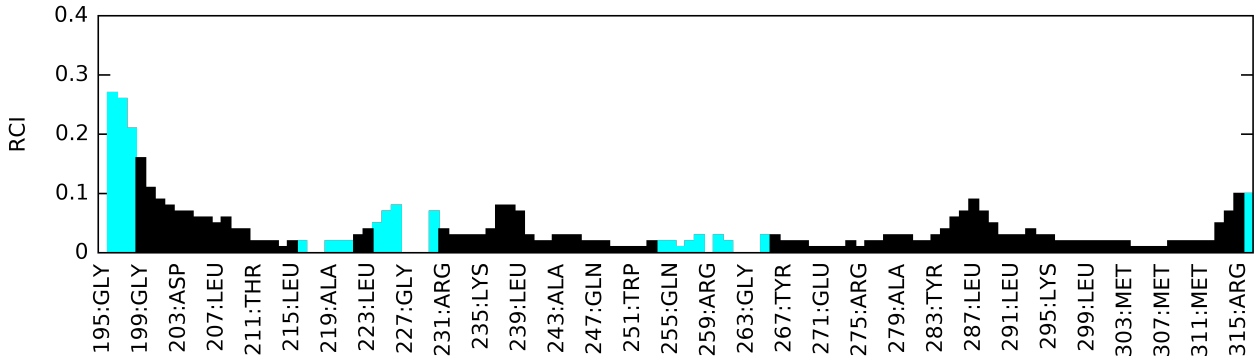
	Total	^{1}H	^{13}C	^{15}N
Aromatic	101/124 (81%)	55/65 (85%)	43/53 (81%)	3/6 (50%)
Overall	976/1218 (80%)	549/624 (88%)	333/473 (70%)	94/121 (78%)

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	300	PRO	HG2	-0.23	3.48 – 0.38	-7.0
1	A	256	HIS	HB3	0.49	5.00 – 1.10	-6.6

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: