



# wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2NNT  
Title : General structural motifs of amyloid protofilaments  
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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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : trunk28760  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

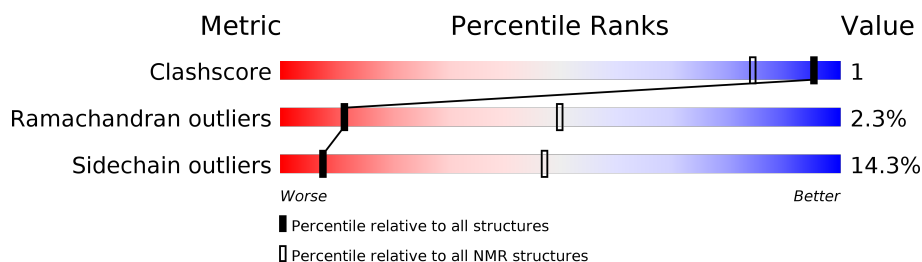
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLID-STATE 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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	40	
1	B	40	
1	C	40	
1	D	40	

## 2 Ensemble composition and analysis

This entry contains 10 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:201-A:230, B:300-B:330, C:400-C:430, D:500-D:530 (123)	0.27	1

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1944 atoms, of which 924 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Transcription elongation regulator 1.

Mol	Chain	Residues	Atoms						Trace
1	A	31	Total	C	H	N	O	S	0
			486	162	231	40	52	1	
1	B	31	Total	C	H	N	O	S	0
			486	162	231	40	52	1	
1	C	31	Total	C	H	N	O	S	0
			486	162	231	40	52	1	
1	D	31	Total	C	H	N	O	S	0
			486	162	231	40	52	1	

There are 16 discrepancies between the modelled and reference sequences:

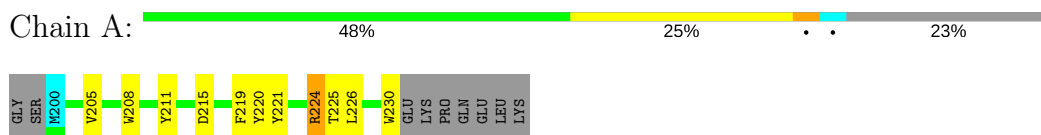
Chain	Residue	Modelled	Actual	Comment	Reference
A	198	GLY	-	CLONING ARTIFACT	UNP O14776
A	199	SER	-	CLONING ARTIFACT	UNP O14776
A	200	MET	-	CLONING ARTIFACT	UNP O14776
A	219	PHE	TYR	ENGINEERED	UNP O14776
B	298	GLY	-	CLONING ARTIFACT	UNP O14776
B	299	SER	-	CLONING ARTIFACT	UNP O14776
B	300	MET	-	CLONING ARTIFACT	UNP O14776
B	319	PHE	TYR	ENGINEERED	UNP O14776
C	398	GLY	-	CLONING ARTIFACT	UNP O14776
C	399	SER	-	CLONING ARTIFACT	UNP O14776
C	400	MET	-	CLONING ARTIFACT	UNP O14776
C	419	PHE	TYR	ENGINEERED	UNP O14776
D	498	GLY	-	CLONING ARTIFACT	UNP O14776
D	499	SER	-	CLONING ARTIFACT	UNP O14776
D	500	MET	-	CLONING ARTIFACT	UNP O14776
D	519	PHE	TYR	ENGINEERED	UNP O14776

## 4 Residue-property plots [i](#)

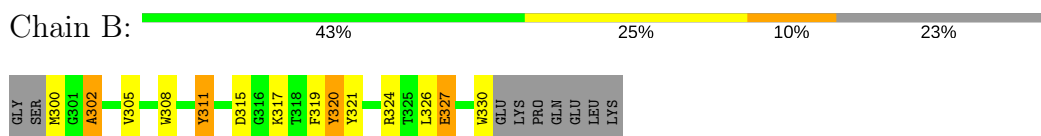
### 4.1 Average score per residue in the NMR ensemble

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: Transcription elongation regulator 1



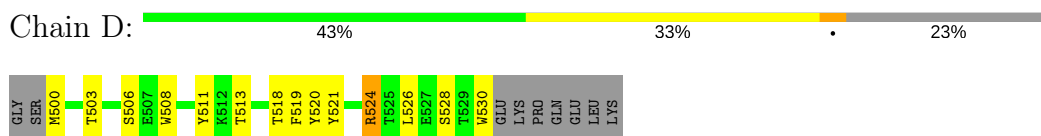
- Molecule 1: Transcription elongation regulator 1



- Molecule 1: Transcription elongation regulator 1



- Molecule 1: Transcription elongation regulator 1

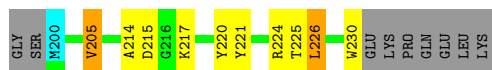


### 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 1. Colouring as in section 4.1 above.

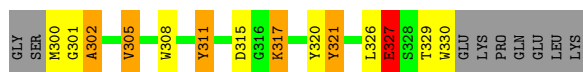
- Molecule 1: Transcription elongation regulator 1

Chain A:  50% 20% 5% • 23%



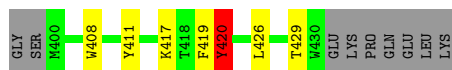
- Molecule 1: Transcription elongation regulator 1

Chain B:  43% 20% 13% • 23%



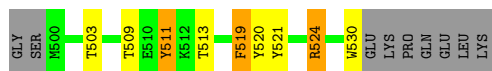
- Molecule 1: Transcription elongation regulator 1

Chain C:  60% 15% • 23%



- Molecule 1: Transcription elongation regulator 1

Chain D:  55% 15% 8% 23%



## 5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *simulated annealing, molecular dynamics*.

Of the 30 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
AMBER	structure solution	7.0
AMBER	refinement	7.0

No chemical shift data was provided. Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.62±0.10	1±1/254 (0.5±0.5%)	2.06±0.15	9±2/346 (2.5±0.6%)
1	B	1.57±0.06	2±1/262 (0.7±0.4%)	2.05±0.11	9±4/356 (2.5±1.0%)
1	C	1.54±0.06	1±1/262 (0.4±0.3%)	2.05±0.11	10±4/356 (2.7±1.0%)
1	D	1.61±0.09	2±1/262 (0.6±0.5%)	2.05±0.14	10±4/356 (2.8±1.2%)
All	All	1.59	57/10400 (0.5%)	2.06	371/14140 (2.6%)

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	2.8±1.0
1	B	0.0±0.0	3.0±1.0
1	C	0.0±0.0	1.6±0.8
1	D	0.0±0.0	1.6±0.8
All	All	0	90

5 of 49 unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	D	511	TYR	CG-CD2	8.40	1.50	1.39	9	2
1	A	228	SER	CA-CB	8.25	1.65	1.52	5	1
1	C	406	SER	CB-OG	7.72	1.52	1.42	4	2
1	A	220	TYR	CD2-CE2	7.25	1.50	1.39	4	1
1	B	307	GLU	CG-CD	6.75	1.62	1.51	2	2

5 of 205 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	224	ARG	NE-CZ-NH1	15.73	128.16	120.30	9	4
1	A	224	ARG	NE-CZ-NH2	-14.85	112.88	120.30	9	6
1	B	311	TYR	CB-CG-CD1	-13.88	112.67	121.00	6	6
1	C	424	ARG	NE-CZ-NH2	-12.74	113.93	120.30	6	4
1	C	424	ARG	NE-CZ-NH1	12.28	126.44	120.30	6	3

There are no chirality outliers.

5 of 30 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	225	THR	Peptide	10
1	B	302	ALA	Peptide,Mainchain	10
1	B	327	GLU	Peptide	8
1	B	320	TYR	Sidechain	5
1	C	420	TYR	Sidechain	5

## 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	247	222	222	0±0
1	B	255	231	230	2±2
1	C	255	231	230	1±1
1	D	255	231	230	0±1
All	All	10120	9150	9120	24

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 1.

5 of 21 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:305:VAL:HB	1:B:326:LEU:HD11	0.53	1.78	4	1
1:B:320:TYR:CE1	1:C:420:TYR:CE1	0.52	2.97	4	2
1:C:420:TYR:CD1	1:D:520:TYR:CD1	0.51	2.98	1	1
1:B:302:ALA:HB3	1:C:402:ALA:H	0.51	1.66	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:326:LEU:N	1:B:326:LEU:HD12	0.50	2.21	5	1

## 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	29/40 (72%)	25±1 (88±5%)	3±2 (11±5%)	0±0 (1±2%)	23	70
1	B	29/40 (72%)	24±1 (81±4%)	4±1 (13±5%)	2±1 (6±3%)	4	23
1	C	29/40 (72%)	27±1 (93±3%)	2±1 (6±3%)	0±0 (1±1%)	30	75
1	D	29/40 (72%)	25±1 (86±4%)	4±1 (12±4%)	1±1 (2±2%)	12	52
All	All	1160/1600 (72%)	1008 (87%)	125 (11%)	27 (2%)	11	50

5 of 12 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	B	302	ALA	6
1	B	317	LYS	5
1	B	316	GLY	3
1	D	529	THR	3
1	A	217	LYS	2

### 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	25/34 (74%)	24±1 (94±4%)	2±1 (6±4%)	27	73
1	B	26/34 (76%)	20±2 (78±6%)	6±2 (22±6%)	4	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	26/34 (76%)	24±1 (91±3%)	2±1 (9±3%)	15	60
1	D	26/34 (76%)	21±2 (80±6%)	5±2 (20±6%)	4	35
All	All	1030/1360 (76%)	883 (86%)	147 (14%)	7	47

5 of 36 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	D	513	THR	10
1	D	524	ARG	10
1	C	429	THR	10
1	C	426	LEU	10
1	B	305	VAL	10

### 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

No chemical shift data were provided