



# wwPDB NMR Structure Validation Summary Report ⓘ

Jun 15, 2020 – 10:41 pm BST

PDB ID : 2N1E  
Title : MAX1 peptide fibril  
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Deposited on : 2015-03-30

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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 : 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

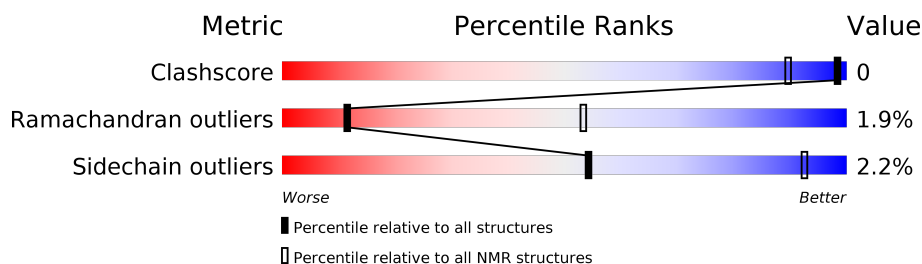
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLID-STATE NMR*

The overall completeness of chemical shifts assignment is 2%.

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  $\geq 3$ , 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	21	86% 5% 10%
1	B	21	90% 10%
1	C	21	86% 5% 10%
1	D	21	90% 10%
1	E	21	90% 10%
1	F	21	86% 5% 10%
1	G	21	90% 10%
1	H	21	86% 5% 10%

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *last structure from namd trajectory*.

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:1-A:9, A:11-A:20, B:1-B:9, B:11-B:20, C:1-C:9, C:11-C:20, D:1-D:9, D:11-D:20, E:1-E:9, E:11-E:20, F:1-F:9, F:11-F:20, G:1-G:9, G:11-G:20, H:1-H:9, H:11-H:20 (152)	0.37	13

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, 6, 7, 8, 9, 10, 11
2	1, 16, 17, 18, 19, 20
3	12, 13, 14, 15

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2936 atoms, of which 1680 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MAX1 peptide.

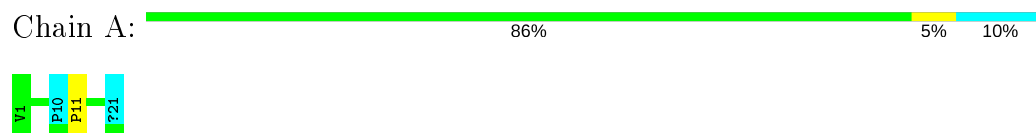
Mol	Chain	Residues	Atoms					Trace
1	A	21	Total	C	H	N	O	1
			367	107	210	29	21	
1	B	21	Total	C	H	N	O	1
			367	107	210	29	21	
1	C	21	Total	C	H	N	O	1
			367	107	210	29	21	
1	D	21	Total	C	H	N	O	1
			367	107	210	29	21	
1	E	21	Total	C	H	N	O	1
			367	107	210	29	21	
1	F	21	Total	C	H	N	O	1
			367	107	210	29	21	
1	G	21	Total	C	H	N	O	1
			367	107	210	29	21	
1	H	21	Total	C	H	N	O	1
			367	107	210	29	21	

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

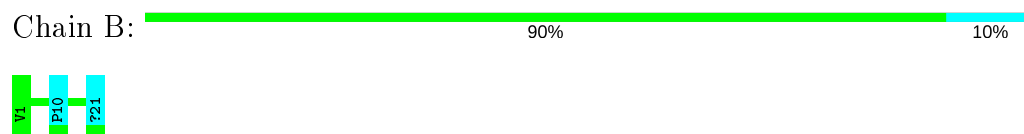
### 4.1 Average score per residue in the NMR ensemble

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.

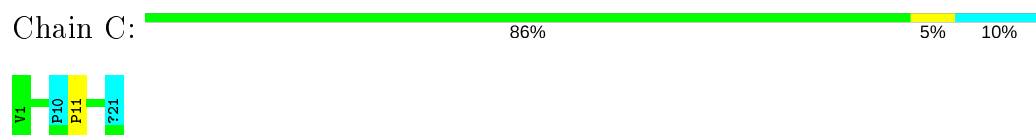
- Molecule 1: MAX1 peptide



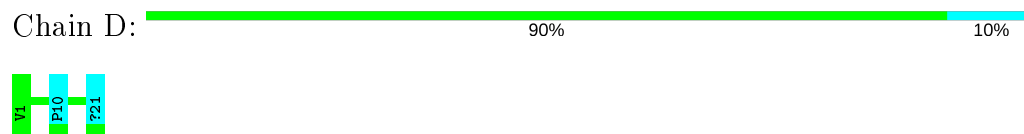
- Molecule 1: MAX1 peptide



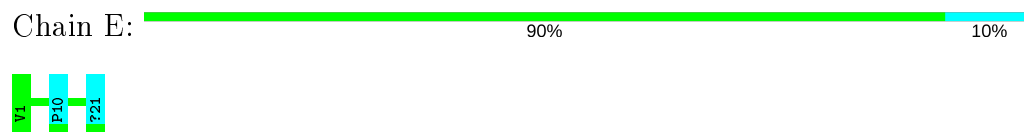
- Molecule 1: MAX1 peptide




- Molecule 1: MAX1 peptide

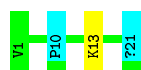


- Molecule 1: MAX1 peptide



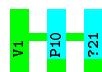
- Molecule 1: MAX1 peptide

Chain F:  86% 5% 10%




- Molecule 1: MAX1 peptide

Chain G:  90% 10%



- Molecule 1: MAX1 peptide


Chain H:  86% 5% 10%

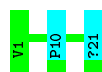


## 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 13. Colouring as in section 4.1 above.

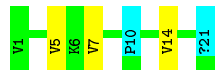
- Molecule 1: MAX1 peptide

Chain A:  90% 10%




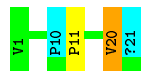
- Molecule 1: MAX1 peptide

Chain B:  76% 14% 10%



- Molecule 1: MAX1 peptide

Chain C:  81% 5% 5% 10%



- Molecule 1: MAX1 peptide

Chain D:  71% 19% 10%



- Molecule 1: MAX1 peptide

Chain E: 76% 14% 10%



- Molecule 1: MAX1 peptide

Chain F: 86% 5% 10%



- Molecule 1: MAX1 peptide

Chain G: 81% 10% 10%



- Molecule 1: MAX1 peptide

Chain H: 86% 5% 10%



## 5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 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
X-PLOR NIH	structure solution	
NAMD	structure solution	
NAMD	refinement	

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	41
Number of shifts mapped to atoms	41
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	2%

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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: DPR, NH2

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	1.53±0.10	0±0/148 ( 0.1± 0.2%)	1.72±0.09	2±1/193 ( 0.9± 0.6%)
1	B	1.50±0.08	0±0/148 ( 0.1± 0.2%)	1.72±0.10	1±1/193 ( 0.6± 0.5%)
1	C	1.54±0.08	0±1/148 ( 0.3± 0.5%)	1.72±0.09	1±1/193 ( 0.6± 0.5%)
1	D	1.57±0.11	0±1/148 ( 0.3± 0.4%)	1.80±0.09	2±1/193 ( 1.0± 0.5%)
1	E	1.50±0.12	0±0/148 ( 0.2± 0.3%)	1.76±0.07	2±1/193 ( 0.8± 0.6%)
1	F	1.50±0.12	0±1/148 ( 0.1± 0.3%)	1.75±0.07	2±1/193 ( 0.8± 0.5%)
1	G	1.55±0.12	0±0/148 ( 0.1± 0.3%)	1.74±0.06	1±1/193 ( 0.6± 0.6%)
1	H	1.53±0.08	0±0/148 ( 0.2± 0.3%)	1.76±0.10	1±1/193 ( 0.7± 0.6%)
All	All	1.53	43/23680 ( 0.2%)	1.75	229/30880 ( 0.7%)

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	G	0.0±0.0	0.2±0.4
1	E	0.0±0.0	0.1±0.2
1	H	0.0±0.0	0.1±0.3
1	F	0.0±0.0	0.1±0.3
1	B	0.0±0.0	0.1±0.2
1	D	0.0±0.0	0.1±0.3
All	All	0	12

5 of 37 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	C	9	VAL	CB-CG1	7.51	1.68	1.52	1	1
1	C	14	VAL	CB-CG1	7.01	1.67	1.52	17	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	D	1	VAL	N-CA	6.44	1.59	1.46	14	2
1	B	1	VAL	CB-CG1	6.33	1.66	1.52	17	1
1	F	1	VAL	N-CA	6.15	1.58	1.46	19	1

5 of 185 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	F	7	VAL	CG1-CB-CG2	10.08	127.03	110.90	12	1
1	D	14	VAL	CA-CB-CG1	-8.04	98.85	110.90	19	3
1	D	20	VAL	CA-CB-CG1	-7.61	99.48	110.90	14	2
1	A	7	VAL	CA-CB-CG2	7.57	122.26	110.90	17	1
1	A	7	VAL	CA-CB-CG1	7.31	121.86	110.90	9	1

There are no chirality outliers.

5 of 7 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	G	9	VAL	Peptide	4
1	H	9	VAL	Peptide	2
1	F	9	VAL	Peptide	2
1	D	14	VAL	Peptide	1
1	D	13	LYS	Mainchain	1

## 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	G	149	201	201	0±0
1	H	149	201	201	0±0
1	C	149	201	201	0±1
1	D	149	201	201	0±1
1	A	149	201	201	0±0
1	E	149	201	201	0±0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	F	149	201	201	0±0
1	B	149	201	201	0±0
All	All	23840	32160	32160	13

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 0.

5 of 13 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:E:7:VAL:HG23	1:F:14:VAL:HG22	0.53	1.81	15	1
1:G:1:VAL:HG22	1:H:20:VAL:HG13	0.51	1.82	19	1
1:C:3:VAL:HG22	1:D:18:VAL:HG13	0.50	1.84	10	1
1:G:3:VAL:HG22	1:H:18:VAL:HG22	0.49	1.84	2	1
1:C:3:VAL:HG21	1:G:9:VAL:HG13	0.48	1.84	17	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	18/21 (86%)	17±1 (94±4%)	1±1 (4±4%)	0±0 (2±3%)	9	45
1	B	18/21 (86%)	17±1 (96±4%)	1±1 (4±4%)	0±0 (0±1%)	44	80
1	C	18/21 (86%)	16±1 (89±3%)	1±1 (4±4%)	1±1 (6±3%)	3	19
1	D	18/21 (86%)	18±1 (98±3%)	0±1 (2±3%)	0±0 (0±1%)	44	80
1	E	18/21 (86%)	18±1 (97±3%)	0±0 (2±3%)	0±0 (1±2%)	18	66
1	F	18/21 (86%)	17±1 (97±4%)	1±1 (3±4%)	0±0 (0±1%)	44	80
1	G	18/21 (86%)	17±1 (94±4%)	1±1 (5±5%)	0±0 (1±2%)	18	66
1	H	18/21 (86%)	16±1 (87±5%)	2±1 (10±6%)	1±1 (3±3%)	7	39
All	All	2880/3360 (86%)	2707 (94%)	119 (4%)	54 (2%)	11	53

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	C	11	PRO	18
1	A	11	PRO	9
1	H	11	PRO	9
1	E	11	PRO	4
1	C	20	VAL	4

### 6.3.2 Protein sidechains ⓘ

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	19/19 (100%)	19±0 (98±3%)	0±0 (2±3%)	61	94
1	B	19/19 (100%)	19±0 (99±2%)	0±0 (1±2%)	89	97
1	C	19/19 (100%)	19±1 (99±3%)	0±1 (1±3%)	70	96
1	D	19/19 (100%)	19±0 (99±2%)	0±0 (1±2%)	70	96
1	E	19/19 (100%)	19±0 (99±2%)	0±0 (1±2%)	74	96
1	F	19/19 (100%)	18±1 (94±4%)	1±1 (6±4%)	24	73
1	G	19/19 (100%)	18±1 (97±3%)	1±1 (3±3%)	45	89
1	H	19/19 (100%)	18±1 (97±4%)	1±1 (3±4%)	42	88
All	All	3040/3040 (100%)	2972 (98%)	68 (2%)	54	92

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	F	13	LYS	17
1	H	9	VAL	5
1	G	12	THR	5
1	A	11	PRO	3
1	G	18	VAL	3

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues are modelled in this entry.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 6.7 Other polymers ⓘ

There are no such molecules in this entry.

## 6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 2% for the well-defined parts and 2% 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

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	41
Number of shifts mapped to atoms	41
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

#### 7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

#### 7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 2%, i.e. 38 atoms were assigned a chemical shift out of a possible 2112. 0 out of 72 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	17/744 (2%)	0/296 (0%)	14/304 (5%)	3/144 (2%)
Sidechain	21/1368 (2%)	0/792 (0%)	21/512 (4%)	0/64 (0%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	38/2112 (2%)	0/1088 (0%)	35/816 (4%)	3/208 (1%)

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.

#### 7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 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:

