

# Full wwPDB NMR Structure Validation Report (i)

### Nov 5, 2023 – 02:18 PM EST

PDB ID	:	1S4A
Title	:	NMR Structure of a D,L alternating decamer of norleucine: double antiparallel
		beta-helix
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Deposited on	:	2004-01-15

This is a Full wwPDB NMR Structure Validation 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. $(2010)$
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

## 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	С	Percent	ile Ranks	Value
Clashscore				3
	Worse	2		Better
	Perc	centile relative to all structures		
	Pero	centile relative to all NMR structures		
				_
<b>Ъ</b> <i>Т</i> / •		Whole archive	NMR archive	

Metric	Whole archive	NMR archive	
Metric	$(\# {\rm Entries})$	$(\# { m Entries})$	
Clashscore	158937	12864	

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	А	10	80%	20%
1	В	10	100%	



## 2 Ensemble composition and analysis (i)

This entry contains 5 models.

Cyrange was unable to find well-defined residues.

Error message: No amino acid residues in sequence.

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust



## 3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 402 atoms, of which 232 are hydrogens and 0 are deuteriums.

Mol	Chain	Residues		Atoms				Trace	
1	I A	Δ	10	Total	С	Н	Ν	0	0
		10	201	63	116	10	12	0	
1	1 B	10	Total	С	Η	Ν	0	0	
		10	201	63	116	10	12	0	

• Molecule 1 is a protein called HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe.



# 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: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe

Chain A:	80%	20%
DNG1 DNM7 LB L10 L10		
• Molecule 1: HCO-	(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-N	lle-L-Nle-OMe
Chain B:		
Cham D.	100%	
There are no outlier	residues in this chain.	

### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

### 4.2.1 Score per residue for model 1

• Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe

Chain A:	80%	20%
DNG1 DNM7 L8 L9 L10		
• Molecule	1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-N	le-OMe
Chain B:	90%	10%
L10		



#### 4.2.2 Score per residue for model 2

• Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe

Chain A:

100%

There are no outlier residues in this chain.

• Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe

Chain B:

100%

There are no outlier residues in this chain.

#### 4.2.3 Score per residue for model 3

• Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe

Chain A:

100%

There are no outlier residues in this chain.

• Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe

Chain B:

100%

There are no outlier residues in this chain.

#### 4.2.4 Score per residue for model 4

• Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe

 Chain A:
 80%
 20%

 E
 E
 80%
 20%

 • Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe
 20%

 Chain B:
 80%
 20%

#### 4.2.5 Score per residue for model 5

• Molecule 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-Nle-OMe



Chain A:	80%	20%
DNG1 DNM7 L8 L9 L9 L10		
• Molecule	e 1: HCO-(D-Nle-L-Nle)3-D-MeNle-L-Nle-D-Nle-L-N	Nle-OMe
Chain B:	80%	20%
DNG1 DNM7 L8 L9 L9 L10		



## 5 Refinement protocol and experimental data overview (i)

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

Of the 50 calculated structures, 5 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
Discover	structure solution	2.9.7
Discover	refinement	2.9.7

No chemical shift data was provided.



## 6 Model quality (i)

## 6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NLE, NLO, DNM, DNE, DNG

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	А	85	116	106	1±1
1	В	85	116	107	0±0
All	All	850	1160	1062	6

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 3.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	m-1 Atom-2 Clash(Å) Distan		Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:7:DNM:H1A	1:A:8:NLE:N	0.56	2.16	1	3	
1:B:7:DNM:H1A	1:B:8:NLE:N	0.52	2.19	4	2	
1:A:7:DNM:C1	1:A:8:NLE:N	0.41	2.84	1	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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	А	0	-	-	-	-
1	В	0	-	-	-	-
All	All	0	-	-	-	-

entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

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	Outliers	Percentiles
1	А	0	-	-	-
1	В	0	-	-	-
All	All	0	-	-	-

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)

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

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Trung	e Chain Res	Dec	Tinle	Bond lengths			
	туре			Counts	RMSZ	#Z>2		
1	NLE	В	4	1	6,7,8	$0.54{\pm}0.02$	0±0 (0±0%)	
1	DNE	А	9	1	6,7,8	$0.55 {\pm} 0.02$	0±0 (0±0%)	



Mol	Tuno	Chain	Res	Link		Bond lengths			
	Type	Ullaili			Counts	RMSZ	#Z>2		
1	DNE	А	5	1	6,7,8	$0.53 {\pm} 0.02$	0±0 (0±0%)		
1	DNM	В	7	1	7,8,9	$0.49 {\pm} 0.01$	0±0 (0±0%)		
1	DNE	В	9	1	6,7,8	$0.54{\pm}0.01$	0±0 (0±0%)		
1	NLO	А	10	1	9,9,9	$0.88 {\pm} 0.01$	0±0 (0±0%)		
1	NLE	А	2	1	6,7,8	$0.62 {\pm} 0.01$	0±0 (0±0%)		
1	DNE	А	3	1	6,7,8	$0.58 {\pm} 0.01$	0±0 (0±0%)		
1	NLE	В	8	1	6,7,8	$0.57 {\pm} 0.03$	0±0 (0±0%)		
1	NLE	А	4	1	6,7,8	$0.53 {\pm} 0.01$	0±0 (0±0%)		
1	NLE	А	8	1	6,7,8	$0.59 {\pm} 0.04$	0±0 (0±0%)		
1	NLE	А	6	1	6,7,8	$0.51 {\pm} 0.02$	0±0 (0±0%)		
1	DNG	А	1	1	8,9,10	$0.45 {\pm} 0.01$	0±0 (0±0%)		
1	DNE	В	3	1	6,7,8	$0.57 {\pm} 0.02$	0±0 (0±0%)		
1	NLE	В	2	1	6,7,8	$0.60 {\pm} 0.02$	0±0 (0±0%)		
1	DNM	А	7	1	7,8,9	$0.50{\pm}0.02$	0±0 (0±0%)		
1	NLO	В	10	1	9,9,9	$0.87 {\pm} 0.02$	0±0 (0±0%)		
1	NLE	В	6	1	6,7,8	$0.51 {\pm} 0.03$	0±0 (0±0%)		
1	DNE	В	5	1	6,7,8	$0.53 {\pm} 0.02$	0±0 (0±0%)		
1	DNG	В	1	1	8,9,10	$0.45 \pm 0.02$	0±0 (0±0%)		

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Turne	Chain	Res Link		Bond angles			
	Type	Chain	nes	LIIIK	Counts	RMSZ	#Z>2	
1	NLE	В	4	1	2,7,9	$0.48 {\pm} 0.12$	0±0 (0±0%)	
1	DNE	А	9	1	2,7,9	$0.51 {\pm} 0.10$	0±0 (0±0%)	
1	DNE	А	5	1	2,7,9	$0.47 {\pm} 0.10$	0±0 (0±0%)	
1	DNM	В	7	1	5,8,10	$0.90 {\pm} 0.09$	0±0 (0±0%)	
1	DNE	В	9	1	2,7,9	$0.45 \pm 0.15$	0±0 (0±0%)	
1	NLO	А	10	1	9,10,10	$0.83 {\pm} 0.06$	0±0 (0±0%)	
1	NLE	А	2	1	2,7,9	$0.30{\pm}0.02$	0±0 (0±0%)	
1	DNE	А	3	1	2,7,9	$0.32{\pm}0.14$	0±0 (0±0%)	
1	NLE	В	8	1	2,7,9	$0.45 {\pm} 0.07$	0±0 (0±0%)	
1	NLE	А	4	1	2,7,9	$0.36 {\pm} 0.12$	0±0 (0±0%)	
1	NLE	А	8	1	2,7,9	$0.40{\pm}0.14$	0±0 (0±0%)	
1	NLE	А	6	1	2,7,9	$0.39 {\pm} 0.13$	0±0 (0±0%)	
1	DNG	А	1	1	7,9,11	$0.97 {\pm} 0.04$	0±0 (0±0%)	
1	DNE	В	3	1	2,7,9	$0.27 {\pm} 0.01$	0±0 (0±0%)	



Mal	Trune	Chain	Dag	Link	Bond angles			
Mol	Type	Chain	$\operatorname{Res}$		Counts	RMSZ	#Z>2	
1	NLE	В	2	1	2,7,9	$0.31 {\pm} 0.01$	0±0 (0±0%)	
1	DNM	А	7	1	5,8,10	$0.84{\pm}0.07$	0±0 (0±0%)	
1	NLO	В	10	1	9,10,10	$0.95 {\pm} 0.13$	$0\pm0~(2\pm4\%)$	
1	NLE	В	6	1	2,7,9	$0.45 \pm 0.13$	0±0 (0±0%)	
1	DNE	В	5	1	2,7,9	$0.50 {\pm} 0.10$	0±0 (0±0%)	
1	DNG	В	1	1	7,9,11	$0.87 {\pm} 0.06$	0±0 (0±0%)	

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	NLO	А	10	1	-	$0\pm0,10,10,10$	-
1	DNE	А	3	1	-	$0\pm 0,5,6,8$	-
1	DNE	А	9	1	-	$0\pm 0,5,6,8$	-
1	NLE	В	2	1	-	$0\pm 0,5,6,8$	-
1	DNG	В	1	1	-	$0\pm 0,7,9,11$	-
1	DNE	В	5	1	-	$0\pm 0,5,6,8$	-
1	DNE	А	5	1	-	$0\pm 0,5,6,8$	-
1	NLE	В	6	1	-	$0\pm 0,5,6,8$	-
1	NLE	А	6	1	-	$0\pm 0,5,6,8$	-
1	DNG	А	1	1	-	$0\pm 0,7,9,11$	-
1	DNE	В	3	1	-	$0\pm 0,5,6,8$	-
1	DNE	В	9	1	-	$0\pm 0,5,6,8$	-
1	DNM	В	7	1	-	$0\pm 0,5,8,10$	-
1	NLE	В	8	1	-	$0\pm 0,5,6,8$	-
1	NLE	А	4	1	-	$0\pm 0,5,6,8$	-
1	NLE	В	4	1	-	$0\pm 0,5,6,8$	-
1	NLO	В	10	1	-	$0\pm0,10,10,10$	-
1	DNM	А	7	1	-	$0\pm 0,5,8,10$	-
1	NLE	А	2	1	-	$0\pm 0,5,6,8$	-
1	NLE	А	8	1	-	$0\pm 0,5,6,8$	_

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$\mathrm{Ideal}(^{o})$	Moo Worst	<b>dels</b> Total
1	В	10	NLO	C1-OXT-C	2.25	110.85	115.94	1	1

There are no chirality outliers.



There are no torsion outliers.

There are no ring outliers.

### 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)

No chemical shift data were provided

