

# wwPDB NMR Structure Validation Summary Report (i)

#### Oct 17, 2021 – 09:48 AM EDT

PDB ID	:	1J9V
Title	:	Solution structure of a lactam analogue (DabD) of HIV gp41 600-612 loop.
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Deposited on	:	2001-05-29

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:

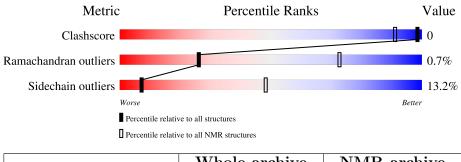
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. $(2010)$
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)		
Validation Pipeline (wwPDB-VP)	:	2.23.2

# 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	$egin{array}{c} { m Whole \ archive}\ (\#{ m Entries}) \end{array}$	${f NMR}  { m archive} \ (\#{ m Entries})$		
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	А	14	71%	29%



## 2 Ensemble composition and analysis (i)

This entry contains 49 models.

Cyrange was unable to find well-defined residues.

Error message: Only domains with < 8 residues could be identified.

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 199 atoms, of which 101 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called DabD (Ace)IWG(DAB)SGKLIDTTA ANALOGUE OF HIV GP41.

Mol	Chain	Residues	Atoms					Trace	
1	٨	1.4	Total	С	Η	Ν	0	0	
1	A	А	A 14	199	63	101	16	19	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	1	ACE	-	insertion	UNP P12488
А	5	DAB	CYS	engineered mutation	UNP P12488
А	11	ASP	CYS	engineered mutation	UNP P12488



# 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: DabD (Ace)IWG(DAB)SGKLIDTTA ANALOGUE OF HIV GP41

Chain A:	71%	29%
ACE1 I2 W3 G4 A5 D11 A14		

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

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

64%

• Molecule 1: DabD (Ace)IWG(DAB)SGKLIDTTA ANALOGUE OF HIV GP41

Chain A:

36%





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

The models were refined using the following method: *Torsion angle dinamics, molecular dynamics, energy minimization.*.

Of the 50 calculated structures, 49 were deposited, based on the following criterion: target function.

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

Software name	Classification	Version
DYANA	refinement	1.5
Discover	refinement	3

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: DAB, ACE

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	В	ond lengths	Bond angles		
	Unam	RMSZ	$\#Z{>}5$	RMSZ	#Z>5	
1	А	$1.45 {\pm} 0.01$	$1{\pm}0/89$ ( $1.1{\pm}$ $0.0\%$ )	$1.32 \pm 0.05$	$1{\pm}0/117~(~0.9{\pm}~0.0\%)$	
All	All	1.45	49/4361 ( $1.1%$ )	1.32	49/5733~(~0.9%)	

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	$Observed(\text{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$	Moo Worst	
1	А	14	ALA	C-OXT	8.17	1.38	1.23	4	49

All unique angle outliers are listed below.

Mo	Chain	Res	Type	Atoms Z		$Observed(^{o})$	$Ideal(^{o})$	Moo Worst	dels Total
1	А	3	TRP	CD1-NE1-CE2	-5.70	103.87	109.00	28	49

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	98	101	98	$0\pm 0$
All	All	4802	4949	4814	1



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.

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

Atom-1	Atom-2	$Clach(\lambda)$	Distance(Å)	Models		
	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:10:ILE:O	1:A:10:ILE:HD12	0.41	2.16	36	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	А	11/14~(79%)	$6\pm1 (51\pm13\%)$	$5\pm1 (48\pm12\%)$	0±0 (1±2%)	26	73	
All	All	539/686~(79%)	276 (51%)	259~(48%)	4 (1%)	26	73	

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	8	LYS	3
1	А	4	GLY	1

#### 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	9/9~(100%)	8±1 (87±8%)	$1 \pm 1 (13 \pm 8\%)$	7	48	
All	All	441/441 (100%)	383~(87%)	58~(13%)	7	48	

All 3 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	А	11	ASP	37
1	А	8	LYS	11
1	А	9	LEU	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)

1 non-standard protein/DNA/RNA residue is 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	Tuno	Chain	Dog	Link		Bond len	ngths
	Type	Ullain	nes	LIIIK	Counts	RMSZ	#Z>2
1	DAB	А	5	1	5,6,7	$1.16{\pm}0.09$	1±0 (13±9%)

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	Type	Chain	Dog	Link		Bond ang	gles
IVIOI			nes	LIUK	Counts	RMSZ	#Z>2
1	DAB	А	5	1	1,6,8	$0.19 {\pm} 0.05$	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	DAB	А	5	1	-	$0\pm0,4,5,7$	-



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Moo Worst	
1	А	5	DAB	CB-CA	2.67	1.57	1.53	27	33

All unique bond outliers are listed below.

There are no bond-angle outliers.

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

