

# Full wwPDB NMR Structure Validation Report (i)

#### Mar 6, 2022 – 07:58 AM EST

PDB ID	:	2K8U
Title	:	Solution NMR structure of trans-4-hydroxynonenal derived dG adduct of (6S
		,8R,11S)-configuration matched with dC
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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 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	:	2.27
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

Clashscore

## 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.

Metrie	С	Percent	ile Ranks	Value
Clashscore				0
	Worse	2		Better
	Perc	centile relative to all structures		
	Perc	centile relative to all NMR structures		
				-
Metri	c	Whole archive	NMR archive	

(# Entries)

158937

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%

(#Entries)

12864

Mol	Chain	Length	Quality of chain
1	А	12	100%
2	В	12	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Dog	Total models with violations		
IVIOI	Unam		nes	Chirality	Geometry	
3	А	HNB	125	1	-	



### 2 Ensemble composition and analysis (i)

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.



# 3 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 785 atoms, of which 288 are hydrogens and 0 are deuteriums.

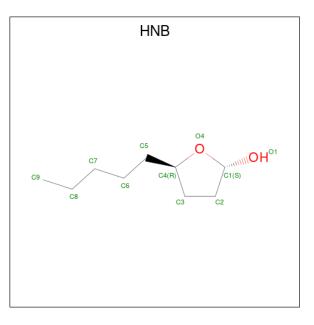
• Molecule 1 is a DNA chain called 5'-D(\*DGP\*DCP\*DTP\*DAP\*DGP\*DCP\*DGP\*DAP\*D GP\*DTP\*DCP\*DC)-3'.

Mol	Chain	Residues	Atoms						Trace
1	Δ	19	Total	С	Η	Ν	Ο	Р	0
	A	12	378	116	135	46	70	11	0

• Molecule 2 is a DNA chain called 5'-D(\*DGP\*DGP\*DAP\*DCP\*DTP\*DCP\*DGP\*DCP\*D TP\*DAP\*DGP\*DC)-3'.

Mol	Chain	Residues	Atoms					Trace	
0	D	19	Total	С	Η	Ν	Ο	Р	0
	D	12	379	116	136	46	70	11	U

• Molecule 3 is (2S,5R)-5-pentyltetrahydrofuran-2-ol (three-letter code: HNB) (formula:  $C_9H_{18}O_2$ ).



Mol	Chain	Residues	Atoms			
2	Λ	1	Total	С	Η	0
5	A	1	28	9	17	2



## 4 Residue-property plots (i)

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: 5'-D(\*DGP\*DCP\*DTP\*DAP\*DGP\*DCP\*DGP\*DAP\*DGP\*DTP\*DCP\*DC)-3

Chain A:	100%	I.
G1 C2 C2 C2 C5 C5 C5 C3 C3 C11 C11 C12 C12 C12		
• Molecule 2: 5',	-D(*DGP*DGP*DAP*DCP*DTP*DCP*DGP*DCP*D1	'P*DAP*DGP*DC)-3
Chain B:	100%	
613 614 614 717 717 717 718 619 619 619 721 721 721 721 721 722 623 623		



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

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

Of the 10 calculated structures, 1 were deposited, based on the following criterion: *back calculated data agree with experimental NOESY spectrum*.

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

Software name	Classification	Version
Amber	refinement	7.0

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: HNB

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
All	All	11	17	0	-

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is -.

There are no clashes.

### 6.3 Torsion angles (i)

#### 6.3.1 Protein backbone (i)

There are no protein molecules in this entry.

#### 6.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

#### 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 monosaccharides in this entry.

### 6.6 Ligand geometry (i)

1 ligand 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	Type	Chain	Chain Res			nd lengt	
		Ullalli	nes		Counts	RMSZ	#Z>2
3	HNB	А	125	1	11,11,11	0.57	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.

Mal	Turne	Chain	Dec	Link	Bond anglesCountsRMSZ#Z>2		
WIOI	rybe	Ullaili	nes		Counts	RMSZ	#Z>2
3	HNB	А	125	1	10,13,13	1.03	1 (10%)

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
3	HNB	А	125	1	2,2,2,2	$0,\!5,\!14,\!14$	0,1,1,1



There are no bond-length outliers.

All angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	125	HNB	C5-C4-C3	2.22	118.98	114.32

All chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms
3	А	125	HNB	C1
3	А	125	HNB	C4

There are no torsion outliers.

There are no ring outliers.

### 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

