

Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	1B60
Title	:	3,N4-ETHENO-2'-DEOXYCYTIDINE OPPOSITE CYTIDINE IN AN
		11-MER DUPLEX, SOLUTION STRUCTURE FROM NMR AND MOLEC-
		ULAR DYNAMICS
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Deposited on	:	1999-01-20

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.

SOFTWARE-VERSIONS INFOmissingINFO

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	Percentile Ranks	Value
Clashscore		1
	Worse	Better
	Percentile relative to all structures	
	Percentile relative to all NMR structures	
	Whole archive NMB archive	

Metric	$egin{array}{c} { m Whole \ archive}\ (\#{ m Entries}) \end{array}$	$f NMR ext{ archive } \ (\#Entries)$			
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	11	91%	9%
2	В	11	91%	9%



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 2 unique types of molecules in this entry. The entry contains 694 atoms, of which 250 are hydrogens and 0 are deuteriums.

• Molecule 1 is a DNA chain called DNA (5'-D(*CP*GP*TP*AP*CP*(EDC)P*CP*AP*TP* GP*C)-3').

Mol	Chain	Residues		Atoms					
1	Δ	11	Total	С	Η	Ν	0	Р	0
1	1 A	11	345	107	125	39	64	10	0

• Molecule 2 is a DNA chain called DNA (5'-D(*GP*CP*AP*TP*GP*CP*GP*TP*AP*CP*G)-3').

Mol	Chain	Residues	Atoms						Trace
0	D	11	Total	С	Η	Ν	0	Р	0
	D		349	107	125	43	64	10	U



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: DNA (5'-D(*CP*GP*TP*AP*CP*(EDC)P*CP*AP*TP*GP*C)-3')

Chain A:	91%	9%
C1 13 13 13 13 13 13 13 13 13 13 13 13 13		
• Molecule	e 2: DNA (5'-D(*GP*CP*AP*TP*GP*CP*GP*TP*AP*CP	⊇*G)-3')
Chain B:	91%	9%
61 C C C C C C C C C C C C C C C C C C C		



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *RESTRAINED MOLECULAR DYNAMICS SIMULATIONS*.

Of the 1 calculated structures, 1 were deposited, based on the following criterion: SEE DE-TAILS.

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

Software name	Classification	Version
X-PLOR	refinement	3.851
Felix	structure solution	
X-PLOR	structure solution	

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: EDC

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	Bo	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	$\#Z{>}5$	RMSZ	#Z>5	
1	А	2.25	10/221~(~4.5%)	2.08	10/336~(~3.0%)	
2	В	2.18	11/251~(~4.4%)	2.10	14/386 ($3.6%$)	
All	All	2.22	21/472 ($4.4%$)	2.09	24/722 ($3.3%$)	

All bond outliers are	listed below.	They are sorted	according to the Z-score.
min bond buildib are	instea serow.	They are borted	according to the 2 beere.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	8	DA	C6-N6	11.62	1.43	1.33
1	А	4	DA	C6-N6	11.61	1.43	1.33
2	В	9	DA	C6-N6	11.59	1.43	1.33
2	В	3	DA	C6-N6	11.58	1.43	1.33
1	А	5	DC	C4-N4	10.60	1.43	1.33
1	А	11	DC	C4-N4	10.57	1.43	1.33
2	В	2	DC	C4-N4	10.57	1.43	1.33
2	В	10	DC	C4-N4	10.54	1.43	1.33
1	А	1	DC	C4-N4	10.47	1.43	1.33
1	А	7	DC	C4-N4	10.43	1.43	1.33
2	В	6	DC	C4-N4	9.78	1.42	1.33
2	В	11	DG	C2-N2	8.36	1.43	1.34
1	А	10	DG	C2-N2	8.33	1.42	1.34
2	В	5	DG	C2-N2	8.19	1.42	1.34
2	В	7	DG	C2-N2	8.18	1.42	1.34
1	А	2	DG	C2-N2	7.97	1.42	1.34
2	В	1	DG	C2-N2	7.89	1.42	1.34
2	В	8	DT	C5-C7	6.08	1.53	1.50
2	В	4	DT	C5-C7	5.97	1.53	1.50
1	А	9	DT	C5-C7	5.73	1.53	1.50
1	А	3	DT	C5-C7	5.64	1.53	1.50

All angle outliers are listed below. They are sorted according to the Z-score.



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	11	DC	O4'-C1'-N1	10.31	115.22	108.00
2	В	7	DG	N7-C8-N9	6.71	116.45	113.10
2	В	7	DG	O4'-C1'-C2'	-6.57	100.65	105.90
1	А	10	DG	N7-C8-N9	6.50	116.35	113.10
1	А	2	DG	N7-C8-N9	6.47	116.33	113.10
2	В	1	DG	N7-C8-N9	6.37	116.28	113.10
2	В	6	DC	O4'-C1'-N1	6.27	112.39	108.00
2	В	7	DG	C8-N9-C4	-6.25	103.90	106.40
2	В	4	DT	C6-C5-C7	-6.23	119.16	122.90
2	В	11	DG	N7-C8-N9	6.20	116.20	113.10
2	В	5	DG	N7-C8-N9	6.15	116.17	113.10
1	А	3	DT	C6-C5-C7	-6.04	119.28	122.90
1	А	9	DT	C6-C5-C7	-6.00	119.30	122.90
2	В	1	DG	C8-N9-C4	-5.89	104.05	106.40
1	А	10	DG	C8-N9-C4	-5.66	104.14	106.40
2	В	3	DA	N7-C8-N9	5.48	116.54	113.80
1	А	5	DC	N1-C2-O2	5.42	122.15	118.90
2	В	9	DA	N7-C8-N9	5.39	116.50	113.80
1	А	2	DG	C8-N9-C4	-5.33	104.27	106.40
2	В	11	DG	C8-N9-C4	-5.25	104.30	106.40
1	А	8	DA	N7-C8-N9	5.23	116.42	113.80
2	В	2	DC	N1-C2-O2	5.21	122.03	118.90
2	В	8	DT	C6-C5-C7	-5.15	119.81	122.90
1	А	4	DA	N7-C8-N9	5.09	116.35	113.80

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	220	125	125	1
2	В	224	125	125	1
All	All	444	250	250	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 1.



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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:4:DA:C2	2:B:9:DA:C2	0.51	2.98

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)

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	Type	Chain	Res	Tiple	Bond lengths		
					Counts	RMSZ	#Z>2
1	EDC	А	6	1	18,23,24	1.42	1 (5%)

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	$\begin{array}{c c c c c c c c c c c c c c c c c c c $		
	туре	Ullaili	nes	LIIIK	Counts	RMSZ	#Z>2
1	EDC	А	6	1	22,33,36	1.12	3 (13%)

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	EDC	А	6	1	-	0,7,21,22	0,2,3,3

All bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	6	EDC	C8-N3	5.58	1.33	1.38

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	6	EDC	O4'-C1'-N1	2.87	112.99	107.86
1	А	6	EDC	C2'-C1'-N1	2.19	118.81	113.77
1	А	6	EDC	C7-N4-C4	2.10	101.56	104.34

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

