

wwPDB X-ray Structure Validation Summary Report (i)

May 27, 2020 – 12:36 am BST

PDB ID : 1D81

Title : THE CONFORMATIONAL VARIABILITY OF AN ADENOSINE. INOSINE

BASE-PAIR IN A SYNTHETIC DNA DODECAMER

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 $Deposited \ on \quad : \quad 1992-07-07$

Resolution : 2.50 Å(reported)

This is a wwPDB X-ray 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/XrayValidationReportHelp 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

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

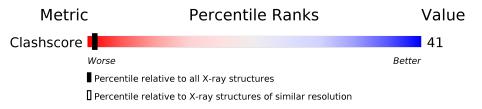
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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.



Motric	Whole archive	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
Clashscore	141614	5346 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain				
1	A	12	8% 50% 42%				
1	В	12	25%		75%		



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 559 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	12	Total	С	N	О	Р	0	0	0
1	$\begin{array}{c c} 1 & A & \end{array}$	12	244	117	47	69	11	U	U	0
1	D	12	Total	С	N	О	Р	0	0	0
	Б	12	244	117	47	69	11			U

• Molecule 2 is water.

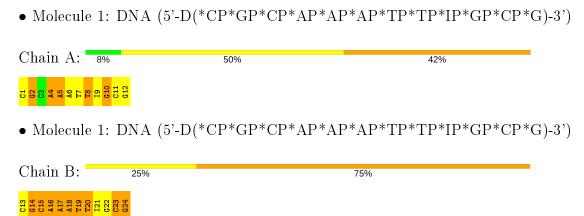
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	33	Total O 33 33	0	0
2	В	38	Total O 38 38	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	25.16Å 41.06Å 65.45Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	7.00 - 2.50	Depositor	
% Data completeness	(Not available) (7.00-2.50)	Depositor	
(in resolution range)	(1101 available) (1.00 2.00)	Depositor	
R_{merge}	0.09	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	NUCLSQ	Depositor	
R, R_{free}	0.158 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	559	wwPDB-VP	
Average B, all atoms (Å ²)	32.0	wwPDB-VP	



5 Model quality (i)

5.1 Standard geometry (i)

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 root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bon	d lengths	Bond angles		
Wioi Chain	RMSZ	# Z > 5	RMSZ	# Z >5		
1	A	1.53	0/249	3.08	43/380 (11.3%)	
1	В	1.49	$1/249 \ (0.4\%)$	2.92	43/380 (11.3%)	
All	All	1.51	$1/498 \ (0.2\%)$	3.00	86/760 (11.3%)	

All (1) bond length outliers are listed below:

Mol	Chain	${f Res}$	\mathbf{Type}	${f Atoms}$	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$oxed{Ideal(A)}$	
1	В	15	DC	O4'-C1'	5.99	1.49	1.42	

The worst 5 of 86 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	В	22	DG	P-O3'-C3'	13.67	136.11	119.70
1	A	2	DG	O4'-C1'-N9	11.28	115.89	108.00
1	A	10	DG	O4'-C1'-N9	11.08	115.75	108.00
1	A	5	DA	O4'-C1'-N9	10.20	115.14	108.00
1	A	5	DA	C4'-C3'-C2'	-9.44	94.61	103.10

There are no chirality outliers.

There are no planarity outliers.

5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	244	0	135	14	0
1	В	244	0	135	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	33	0	0	3	0
2	В	38	0	0	1	0
All	All	559	0	270	30	0

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 41.

The worst 5 of 30 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{c} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:B:24:DG:H5'	1:B:24:DG:C8	1.72	1.24
1:B:23:DC:H2"	1:B:24:DG:C5'	1.71	1.20
1:B:23:DC:C2'	1:B:24:DG:H5"	1.83	1.08
1:A:5:DA:O5'	1:A:5:DA:H2'	1.64	0.97
1:B:23:DC:H2"	1:B:24:DG:H5"	0.99	0.97

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.



5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

