

wwPDB X-ray Structure Validation Summary Report (i)

Dec 11, 2023 – 10:19 AM EST

PDB ID : 8TDT

Title : Sequence specific (AATT) orientation of DAPI molecules at a unique minor

groove binding site (position2) within a self-assembled 3D DNA lattice (4x6)

Authors: Simmons, C.R.; MacCulloch, T.; Stephanopoulos, N.; Yan, H.

Deposited on : 2023-07-04

Resolution : 3.01 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 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:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS: 2.36

buster-report : 1.1.7 (2018)

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

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

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

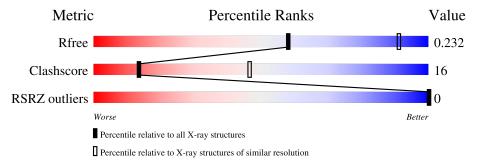
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.01 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.



Matria	Whole archive	Similar resolution			
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(\AA))$			
R_{free}	130704	2092 (3.00-3.00)			
Clashscore	141614	2416 (3.00-3.00)			
RSRZ outliers	127900	1990 (3.00-3.00)			

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 of 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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quali	ty of chain	
1	A	21	33%	62%	5%
2	В	6	50%	50%	
3	С	8	38%	62%	
4	D	7	57%	14%	29%



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 885 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(*GP*AP*GP*CP*AP*GP*AP*CP*CP*TP* GP*AP*CP*GP*AP*AP*AP*AP*TP*TP*A)-3').

ľ	Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
	1	A	21	Total 433	C 206	N 88	O 119	P 20	0	0	0

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

\mathbf{Mol}	Chain	Residues	\mathbf{Atoms}			ZeroOcc	AltConf	Trace		
2	В	6	Total 120	C 57	N 21	O 36	P 6	0	0	0

• Molecule 3 is a DNA chain called DNA (5'-D(*TP*CP*TP*AP*AP*TP*T)-3').

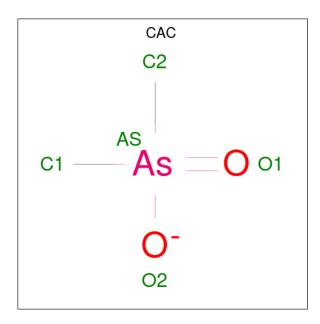
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	C	Q	Total	С	N	О	Р	0	0	0
3		8	158	79	23	49	7	0	U	U

• Molecule 4 is a DNA chain called DNA (5'-D(P*GP*GP*TP*CP*TP*GP*C)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
4	D	7	Total 144	C 68	N 25	O 44	P 7	0	0	0

• Molecule 5 is CACODYLATE ION (three-letter code: CAC) (formula: C₂H₆AsO₂).





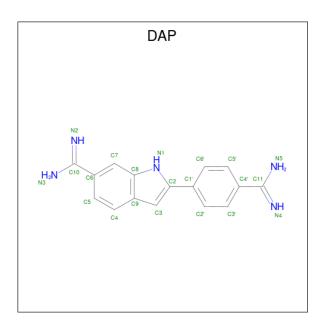
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total As 1 1	0	0
5	A	1	Total As 1 1	0	0
5	A	1	Total As 1 1	0	0
5	D	1	Total As 1 1	0	0

• Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Mg 1 1	0	0
6	В	1	Total Mg 1 1	0	0

• Molecule 7 is 6-AMIDINE-2-(4-AMIDINO-PHENYL)INDOLE (three-letter code: DAP) (formula: $C_{16}H_{15}N_5$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	С	1	Total 21	C 16	N 5	0	0

• Molecule 8 is water.

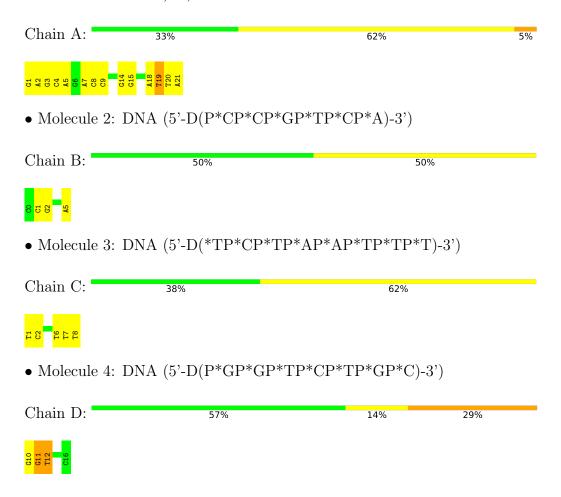
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	2	Total O 2 2	0	0
8	В	1	Total O 1 1	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

• Molecule 1: DNA (5'-D(*GP*AP*GP*CP*AP*GP*AP*CP*CP*TP*GP*AP*CP*GP*AP*AP*AP*AP*TP*A)-3')





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants	68.49Å 68.49Å 56.75Å	Donositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.00 - 3.01	Depositor
resolution (A)	41.00 - 3.01	EDS
% Data completeness	92.7 (41.00-3.01)	Depositor
(in resolution range)	93.0 (41.00-3.01)	EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.39 (at 3.01Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.199 , 0.231	Depositor
it, it free	0.199 , 0.232	DCC
R_{free} test set	284 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	89.6	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.23 \; , 50.2$	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
	0.025 for -h,-k,l	
Estimated twinning fraction	0.041 for h,-h-k,-l	Xtriage
	0.047 for -k,-h,-l	
F_o, F_c correlation	0.96	EDS
Total number of atoms	885	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.02% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, DAP, CAC

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).

Mal	Clasia.	Bon	nd lengths	Bond angles		
IVIOI	Mol Chain		# Z > 5	RMSZ	# Z >5	
1	A	1.16	1/488 (0.2%)	1.04	0/752	
2	В	1.37	1/133 (0.8%)	1.27	0/202	
3	С	1.41	2/175 (1.1%)	1.34	$2/268 \; (0.7\%)$	
4	D	1.07	0/160	1.21	3/245 (1.2%)	
All	All	1.22	4/956 (0.4%)	1.16	5/1467 (0.3%)	

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\text{\AA})$
3	С	7	DT	C2-O2	9.74	1.30	1.22
2	В	5	DA	C3'-O3'	-5.72	1.36	1.44
1	A	19	DT	C3'-O3'	-5.42	1.36	1.44
3	С	8	DT	C3'-O3'	-5.28	1.37	1.44

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\mathbf{Ideal}(^o)$
3	С	7	DT	N3-C4-O4	6.26	123.66	119.90
4	D	10	DG	O4'-C4'-C3'	-6.23	102.01	104.50
3	С	7	DT	C5-C4-O4	-5.86	120.80	124.90
4	D	12	DT	O5'-P-OP2	-5.41	100.83	105.70
4	D	11	DG	O4'-C4'-C3'	-5.37	102.35	104.50

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	433	0	236	14	0
2	В	120	0	68	3	0
3	С	158	0	95	4	0
4	D	144	0	80	1	0
5	A	3	0	0	1	0
5	D	1	0	0	0	0
6	A	1	0	0	0	0
6	В	1	0	0	0	0
7	С	21	0	12	2	0
8	A	2	0	0	0	0
8	В	1	0	0	0	0
All	All	885	0	491	22	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 16.

The worst 5 of 22 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)
1:A:7:DA:H2"	1:A:8:DC:H5'	1.74	0.69
2:B:1:DC:H2'	2:B:2:DG:C8	2.29	0.68
2:B:1:DC:H2"	2:B:2:DG:H5'	1.76	0.68
3:C:1:DT:H2"	3:C:2:DC:O5'	1.97	0.64
1:A:2:DA:H2'	1:A:3:DG:C8	2.33	0.62

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 4 are modelled with single atom and 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or 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 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

	Mol Type		Chain	Res	Link	Bo	Bond lengths			ond ang	gles
1	Mol T	туре	Chain	nes	LINK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
	7	DAP	С	101	-	21,23,23	2.75	7 (33%)	19,33,33	2.79	10 (52%)

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
7	DAP	С	101	-	-	0/8/12/12	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$Ideal(\AA)$
7	С	101	DAP	C6-C10	6.03	1.58	1.47
7	С	101	DAP	C4'-C11	5.81	1.58	1.47
7	С	101	DAP	C10-N3	5.30	1.47	1.33
7	С	101	DAP	C11-N5	5.26	1.47	1.33
7	С	101	DAP	C6'-C5'	3.43	1.43	1.36

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
7	С	101	DAP	C4'-C11-N5	5.26	125.98	118.05
7	С	101	DAP	C7-C6-C10	4.61	128.06	120.29
7	С	101	DAP	C3-C9-C8	4.48	110.18	106.27
7	С	101	DAP	C5-C6-C7	-4.14	114.30	119.23
7	С	101	DAP	C4-C9-C8	-3.66	114.63	119.91

There are no chirality outliers.

There are no torsion outliers.

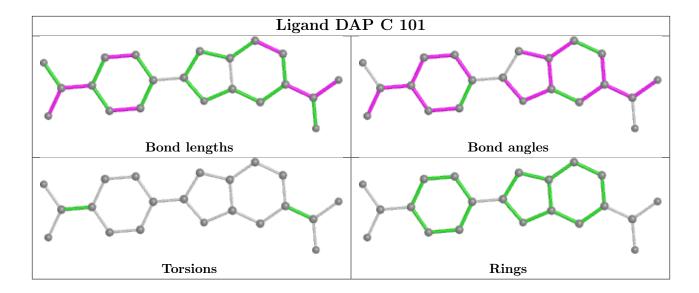
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	С	101	DAP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<rsrz></rsrz>	$\#\text{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	21/21 (100%)	-1.11	0 100 100	72, 86, 113, 119	0
2	В	6/6 (100%)	-0.92	0 100 100	61, 72, 77, 81	0
3	С	8/8 (100%)	-1.00	0 100 100	59, 92, 111, 112	0
4	D	7/7 (100%)	-1.02	0 100 100	61, 85, 127, 131	0
All	All	42/42 (100%)	-1.05	0 100 100	59, 85, 119, 131	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	CAC	A	103	1/5	0.28	0.12	205,205,205,205	0
5	CAC	A	101	1/5	0.56	0.14	185,185,185,185	0
6	MG	A	104	1/1	0.62	0.13	75,75,75,75	0
7	DAP	С	101	21/21	0.80	0.27	56,71,86,97	0

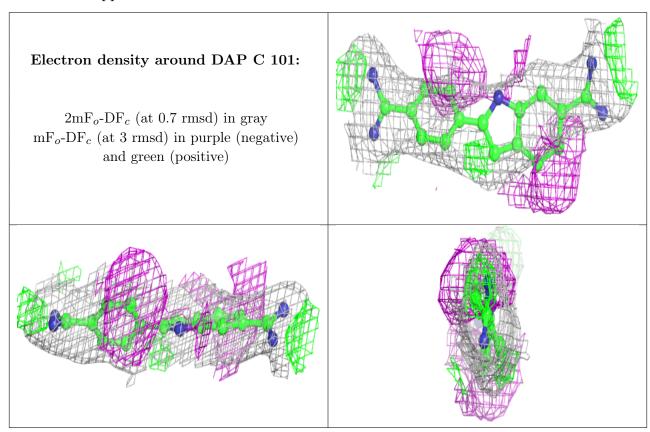
Continued on next page...



Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
5	CAC	D	101	1/5	0.87	0.17	144,144,144,144	0
5	CAC	A	102	1/5	0.93	0.09	135,135,135,135	0
6	MG	В	101	1/1	0.94	0.21	66,66,66,66	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers (i)

There are no such residues in this entry.

