wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID	:	4U9M
Title	:	Structure of the DNA duplex d(ATTAAT)2 with Hoogsteen hydrogen bonds
Authors	:	Acosta-Reyes, F.J.; Alechaga, E.; Subirana, J.A.; Campos, J.L.
Deposited on	:	2014-08-06
Resolution	:	3.13 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
http://wwpdb.org/validation/2016/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:

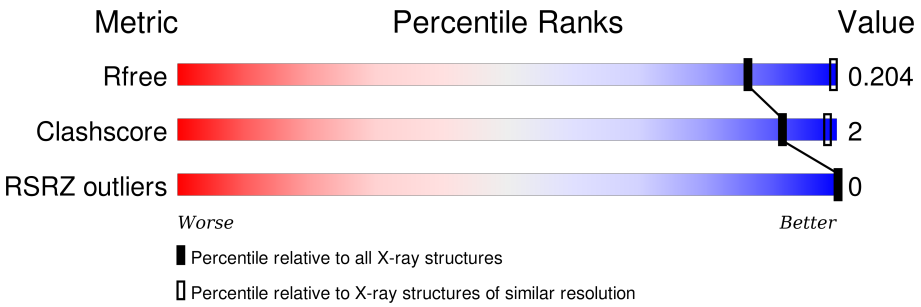
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 3.13 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.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1095 (3.18-3.10)
Clashscore	102246	1202 (3.18-3.10)
RSRZ outliers	91569	1097 (3.18-3.10)

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. 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	Quality of chain
1	A	6	100%
1	B	6	100%
1	C	6	100%
1	D	6	50% 50%
1	E	6	100%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 600 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.

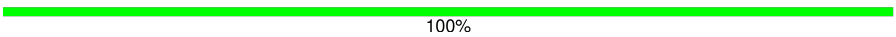
- Molecule 1 is a DNA chain called DNA (5'-D(*AP*TP*TP*AP*AP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	6	120	60	21	34	5	0	0	0
1	B	6	120	60	21	34	5	0	0	0
1	C	6	120	60	21	34	5	0	0	0
1	D	6	120	60	21	34	5	0	0	0
1	E	6	120	60	21	34	5	0	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 errors 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(*AP*TP*TP*AP*AP*T)-3')

Chain A: 

There are no outlier residues recorded for this chain.

- Molecule 1: DNA (5'-D(*AP*TP*TP*AP*AP*T)-3')

Chain B:

There are no outlier residues recorded for this chain.

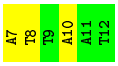
- Molecule 1: DNA (5'-D(*AP*TP*TP*AP*AP*T)-3')

Chain C:

There are no outlier residues recorded for this chain.

- Molecule 1: DNA (5'-D(*AP*TP*TP*AP*AP*T)-3')

Chain D:



- Molecule 1: DNA (5'-D(*AP*TP*TP*AP*AP*T)-3')

Chain E:

There are no outlier residues recorded for this chain.

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	24.76Å 42.90Å 99.42Å 90.00° 90.04° 90.00°	Depositor
Resolution (Å)	33.14 – 3.13 33.14 – 3.13	Depositor EDS
% Data completeness (in resolution range)	99.3 (33.14-3.13) 98.3 (33.14-3.13)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.146 , 0.200 0.147 , 0.204	Depositor DCC
R_{free} test set	107 reflections (6.05%)	DCC
Wilson B-factor (Å^2)	152.8	Xtriage
Anisotropy	0.298	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 114.7	EDS
Estimated twinning fraction	0.184 for H, K, L 0.156 for 1/2H+1/2K, -3/2H+1/2K, L 0.147 for 1/2H-1/2K, 3/2H+1/2K, L 0.168 for -H, -K, L 0.185 for -1/2H+1/2K, -3/2H-1/2K, L 0.159 for -1/2H-1/2K, 3/2H-1/2K, L 0.088 for -1/2*h-1/2*k,-3/2*h+1/2*k,-l 0.095 for -1/2*h+1/2*k,3/2*h+1/2*k,-l 0.091 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.061 for 1/2*h+1/2*k,3/2*h-1/2*k,-l 0.126 for h,-k,-l	Xtriage
Reported twinning fraction	0.184 for H, K, L 0.156 for 1/2H+1/2K, -3/2H+1/2K, L 0.147 for 1/2H-1/2K, 3/2H+1/2K, L 0.168 for -H, -K, L 0.185 for -1/2H+1/2K, -3/2H-1/2K, L 0.159 for -1/2H-1/2K, 3/2H-1/2K, L	Depositor
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	1 of 1885 reflections (0.053%)	Xtriage
F_o,F_c correlation	0.99	EDS
Total number of atoms	600	wwPDB-VP

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[1] Intensities estimated from amplitudes.

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

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Property	Value	Source
Average B, all atoms ($Å^2$)	144.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.02 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.5514e-04.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.57	0/134	0.90	0/205
1	B	0.62	0/134	0.91	0/205
1	C	0.63	0/134	0.83	0/205
1	D	0.59	0/134	0.86	0/205
1	E	0.51	0/134	0.87	0/205
All	All	0.59	0/670	0.88	0/1025

There are no bond length outliers.

There are no bond angle outliers.

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	120	0	71	0	0
1	B	120	0	71	0	0
1	C	120	0	71	0	0
1	D	120	0	71	2	0
1	E	120	0	71	0	0
All	All	600	0	355	2	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 2.

All (2) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:10:DA:H2'	1:D:10:DA:N3	2.33	0.43
1:D:7:DA:H2"	1:D:8:DT:O5'	2.19	0.43

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)

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, 95th 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>2			OWAB(Å^2)	Q<0.9
1	A	6/6 (100%)	-0.85	0	100	100	127, 151, 153, 154	0
1	B	6/6 (100%)	-0.53	0	100	100	139, 147, 150, 169	0
1	C	6/6 (100%)	-0.43	0	100	100	139, 150, 151, 156	0
1	D	6/6 (100%)	-0.79	0	100	100	122, 137, 141, 146	0
1	E	6/6 (100%)	-0.66	0	100	100	126, 135, 148, 151	0
All	All	30/30 (100%)	-0.65	0	100	100	122, 146, 154, 169	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 carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.