

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID		
Title	:	A-DNA decamer GCGTA(UMS)ACGC with incorporated 2'-methylseleno-ur
		idine
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Deposited on	:	2002-08-01
$\operatorname{Resolution}$:	1.30 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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
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 1.30 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	Percent	tile Ranks	Value
Clashscore	[5
We	orse		Better
E F	Percentile relative to all X-ray stru	ictures	
0 F	Percentile relative to X-ray structu	ares of similar resolution	
Metric	Whole archive	Similar	resolution
I VIELCIC			0

Matria	Whole archive	Similar resolution		
Metric	$(\# {\it Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$		
Clashscore	141614	1101 (1.30-1.30)		

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	А	10	100%				
1	В	10	10% 90%				



1MA8

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 769 atoms, of which 222 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 5'-D(*GP*CP*GP*TP*AP*UMSP*AP*CP*GP*C)-3'.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace	
1	Δ	A 10	Total	С	Η	Ν	Ο	Р	Se	0	0	0
			314	97	111	38	58	9	1			
1	р	10	Total	С	Η	Ν	Ο	Р	Se	0	0	0
	ГВ	10	314	97	111	38	58	9	1	0	U	0

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	72	Total O 72 72	0	0
2	В	69	Total O 69 69	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 colorcoded 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.

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

Chain A:	100%
61 63 74 63 69 63 69 63 60 60 63 60 610	
• Molecule 1:	5'-D(*GP*CP*GP*TP*AP*UMSP*AP*CP*GP*C)-3'
Chain B: 10%	90%
11111111111111111111111111111111111111	



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	24.55Å 43.97 Å 45.34 Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	10.00 - 1.30	Depositor	
% Data completeness	(Not available) (10.00-1.30)	Depositor	
(in resolution range)	(1000 available) (10.00-1.50)	-	
R_{merge}	(Not available)	Depositor	
R _{sym}	0.05	Depositor	
Refinement program	SHELXL-97, CNS	Depositor	
R, R_{free}	0.149 , 0.173	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	769	wwPDB-VP	
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP	



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: UMS

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	Bo	nd lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	2.32	10/204~(4.9%)	2.37	15/313~(4.8%)	
1	В	2.71	15/204~(7.4%)	2.63	22/313~(7.0%)	
All	All	2.52	25/408~(6.1%)	2.51	37/626~(5.9%)	

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	${ m Observed}({ m \AA})$	Ideal(Å)
1	В	119	DG	C2'-C1'	-9.97	1.42	1.52
1	В	120	DC	C2'-C1'	-8.34	1.44	1.52
1	А	4	DT	C2'-C1'	-8.24	1.44	1.52
1	В	115	DA	C2'-C1'	-8.02	1.44	1.52
1	А	2	DC	N1-C6	-7.66	1.32	1.37

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	3	DG	O4'-C1'-N9	-9.31	101.48	108.00
1	В	120	DC	O4'-C1'-N1	-8.39	102.12	108.00
1	В	115	DA	O4'-C1'-N9	-8.13	102.31	108.00
1	А	9	DG	O4'-C1'-N9	-7.68	102.62	108.00
1	В	112	DC	C1'-O4'-C4'	-7.62	102.48	110.10

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	203	111	114	3	0
1	В	203	111	114	0	0
2	А	72	0	0	3	2
2	В	69	0	0	0	1
All	All	547	222	228	3	2

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.

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 5.

All (3) 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:A:6:UMS:SE2'	2:A:837:HOH:O	2.63	0.67
1:A:6:UMS:H1'	2:A:837:HOH:O	2.12	0.49
1:A:6:UMS:C1'	2:A:837:HOH:O	2.67	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:846:HOH:O	2:B:842:HOH:O[1_455]	1.95	0.25
2:A:752:HOH:O	2:A:808:HOH:O[3_655]	2.02	0.18

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)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	Turne	Chain	Res	Res Link	Bond lengths			Bond angles		
	Type	Cham	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	UMS	А	6	1	13,22,23	2.41	6 (46%)	11,31,34	1.98	4 (36%)
1	UMS	В	116	1	13,22,23	1.77	4 (30%)	11,31,34	2.08	2 (18%)

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	UMS	А	6	1	-	0/5/27/28	0/2/2/2
1	UMS	В	116	1	-	0/5/27/28	0/2/2/2

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(\operatorname{\AA})$
1	А	6	UMS	C2'- $C3$ '	-4.68	1.47	1.53
1	В	116	UMS	O5'-C5'	3.91	1.54	1.44
1	А	6	UMS	C4-N3	3.65	1.39	1.33
1	А	6	UMS	O5'-C5'	3.36	1.53	1.44
1	А	6	UMS	C5'-C4'	-3.04	1.42	1.51

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

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	116	UMS	C5-C4-N3	-4.85	112.64	123.31
1	В	116	UMS	O4'-C4'-C3'	-4.08	97.04	105.11
1	А	6	UMS	O3'-C3'-C2'	3.67	116.47	110.64
1	А	6	UMS	O4'-C4'-C3'	-3.65	97.90	105.11
1	А	6	UMS	C5-C4-N3	-3.13	116.42	123.31

There are no chirality outliers.



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There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	\mathbf{Res}	Type	Clashes	Symm-Clashes
1	А	6	UMS	3	0

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.

