wwPDB X-ray Structure Validation Summary Report (i)

Oct 5, 2023 – 03:35 AM EDT

PDB ID	:	6VF4
Title	:	DNA Polymerase Mu, 8-oxorGTP:At Reaction State Ternary Complex, 50 mM Mn2+ (30 min)
Authors	:	Jamsen, J.A.; Wilson, S.H.
Deposited on	:	2020-01-03
Resolution	:	1.75 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	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
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)	:	2.35.1

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 1.75 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 3425 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 protein called DNA-directed DNA/RNA polymerase mu.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	325	2644	1686	474	473	11	0	20	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	GLY	-	expression tag	UNP Q9NP87
A	128	SER	-	expression tag	UNP Q9NP87
A	129	ALA	-	expression tag	UNP Q9NP87
A	130	ALA	-	expression tag	UNP Q9NP87
A	131	ALA	-	expression tag	UNP Q9NP87
A	?	-	PRO	deletion	UNP Q9NP87
A	?	-	GLY	deletion	UNP Q9NP87
A	?	-	ALA	deletion	UNP Q9NP87
A	?	-	ALA	deletion	UNP Q9NP87
A	?	-	VAL	deletion	UNP Q9NP87
A	?	-	GLY	deletion	UNP Q9NP87
A	?	-	GLY	deletion	UNP Q9NP87
A	?	-	SER	deletion	UNP Q9NP87
A	?	-	THR	deletion	UNP Q9NP87
A	?	-	ARG	deletion	UNP Q9NP87
A	?	-	PRO	deletion	UNP Q9NP87
A	?	-	CYS	deletion	UNP Q9NP87
A	410	GLY	PRO	conflict	UNP Q9NP87

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	T	9	182	87	36	51	8	0	0	0

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*GP*TP*AP*(8GM))-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	5	Total	C	N	O	P	0	2	0
			124	59	25	35	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	4	Total	C	N	O	P	19	2	0
			124	57	24	37	6			

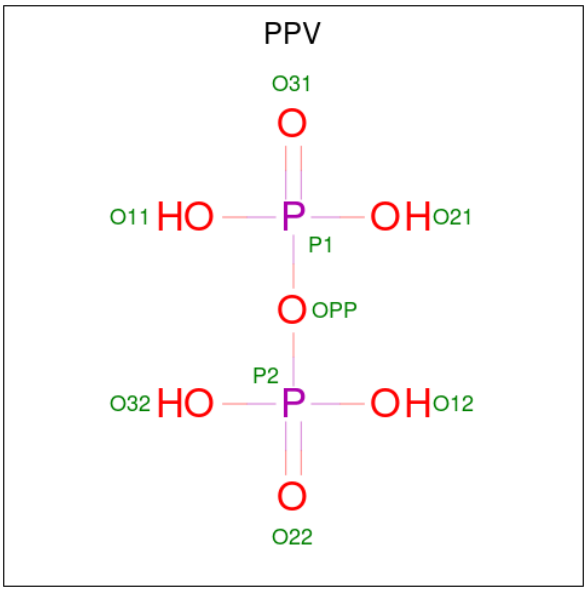
- Molecule 5 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	Mn	0	0
			4	4		
5	T	1	Total	Mn	0	0
			1	1		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

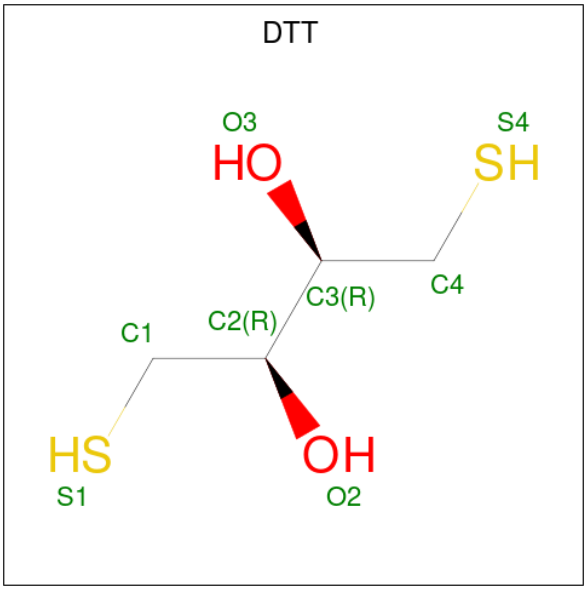
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Na	0	0
			1	1		

- Molecule 7 is PYROPHOSPHATE (three-letter code: PPV) (formula: $H_4O_7P_2$) (labeled as "Ligand of Interest" by depositor).



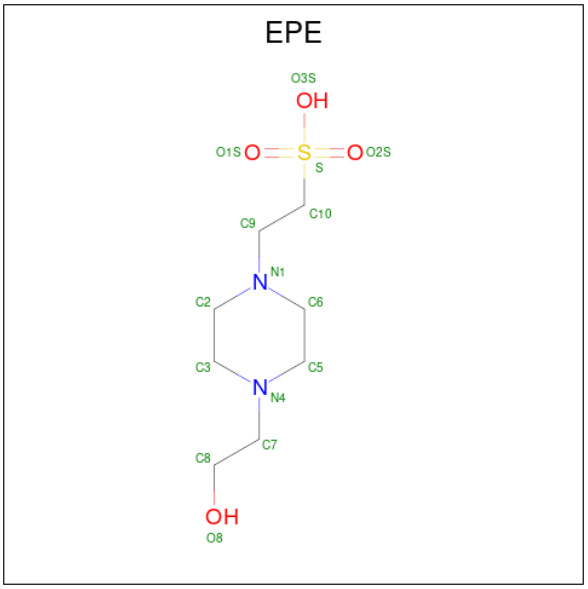
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total O P 9 7 2	0	1

- Molecule 8 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula: $C_4H_{10}O_2S_2$).



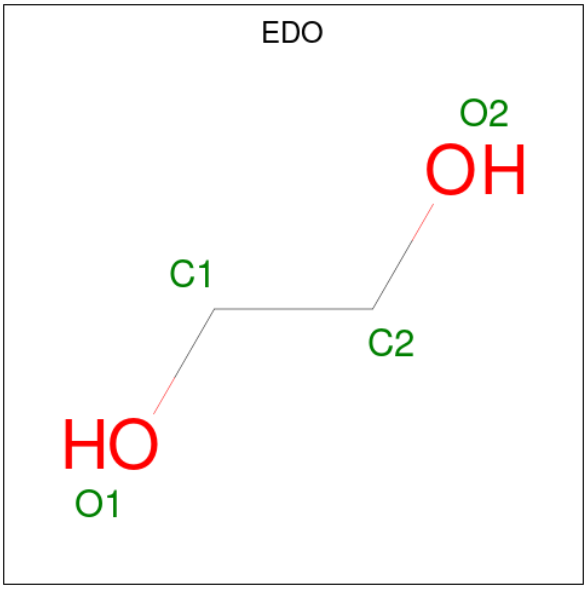
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total S 1 1	0	0

- Molecule 9 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



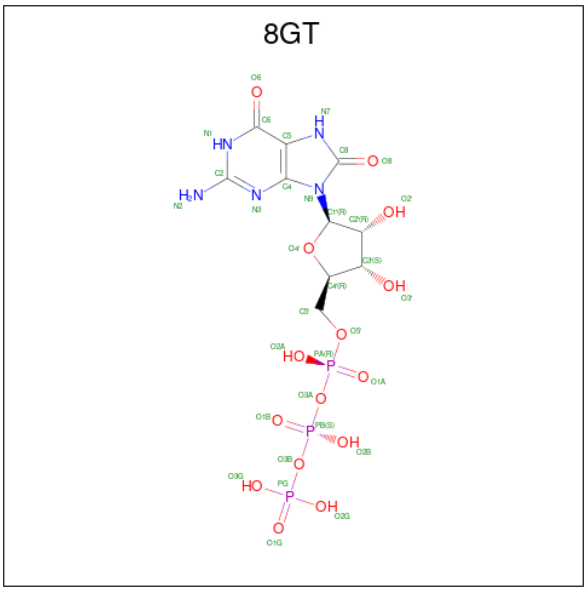
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total O S 4 3 1	0	0

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C O 3 2 1	0	0
10	A	1	Total C O 4 2 2	0	0
10	P	1	Total C O 4 2 2	0	0

- Molecule 11 is 8-OXO-GUANOSINE-5'-TRIPHOSPHATE (three-letter code: 8GT) (formula: $C_{10}H_{16}N_5O_{15}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	A	1	Total	C	N	O	P	0	1
			33	10	5	15	3		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	225	Total	O	0	15
			231	231		
12	T	26	Total	O	0	1
			27	27		
12	P	16	Total	O	0	0
			16	16		
12	D	12	Total	O	0	1
			13	13		

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	60.09Å 68.76Å 110.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.48 – 1.75	Depositor
% Data completeness (in resolution range)	99.7 (32.48-1.75)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.69 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.168 , 0.192	Depositor
Wilson B-factor (Å^2)	26.7	Xtriage
Anisotropy	0.318	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3425	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

4 Model quality

4.1 Standard geometry

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles

4.3.1 Protein backbone

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains

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

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

Of 13 ligands modelled in this entry, 6 are monoatomic and 1 is modelled with single atom - leaving 6 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
10	EDO	P	101	-	3,3,3	0.42	0	2,2,2	0.43	0
9	EPE	A	508	-	0,3,15	-	-	0,3,20	-	-
10	EDO	A	510	-	3,3,3	0.43	0	2,2,2	0.30	0
7	PPV	A	506[B]	5	6,8,8	0.77	0	13,13,13	1.54	1 (7%)
11	8GT	A	511[A]	5	31,35,35	1.47	4 (12%)	45,56,56	3.01	9 (20%)
10	EDO	A	509	-	2,2,3	0.48	0	1,1,2	0.33	0

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
10	EDO	P	101	-	-	0/1/1/1	-
7	PPV	A	506[B]	5	-	0/6/6/6	-
11	8GT	A	511[A]	5	-	7/22/38/38	0/3/3/3
10	EDO	A	510	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	511[A]	8GT	O4'-C1'	-5.39	1.29	1.42
11	A	511[A]	8GT	C8-N7	-3.15	1.32	1.38
11	A	511[A]	8GT	C2'-C1'	2.76	1.62	1.53
11	A	511[A]	8GT	PA-O1A	2.07	1.58	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	511[A]	8GT	C2'-C1'-N9	-16.98	93.38	115.94
11	A	511[A]	8GT	O4'-C1'-N9	7.02	119.13	108.72
7	A	506[B]	PPV	P2-OPP-P1	-3.93	119.33	132.83
11	A	511[A]	8GT	N7-C8-N9	3.44	110.67	106.58
11	A	511[A]	8GT	O4'-C4'-C3'	-3.04	99.11	105.11

There are no chirality outliers.

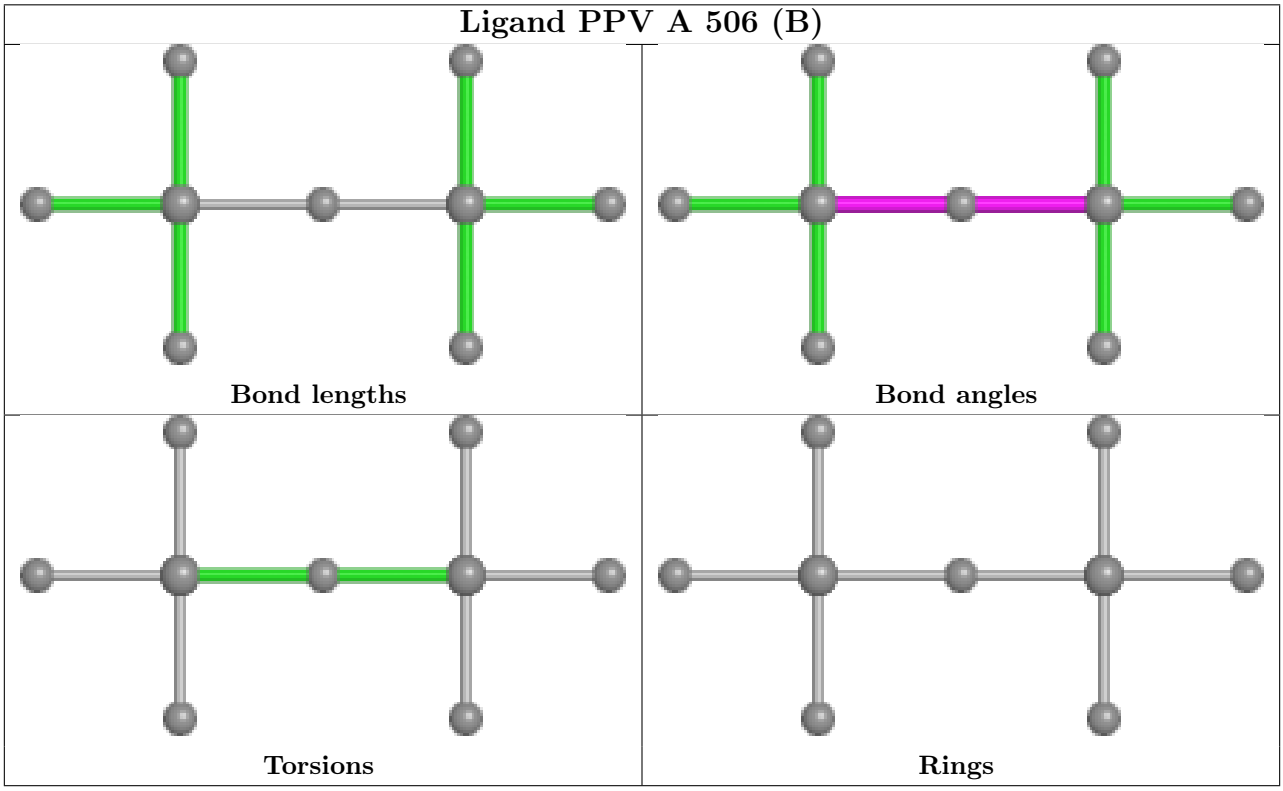
5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	511[A]	8GT	PB-O3B-PG-O3G
11	A	511[A]	8GT	PA-O3A-PB-O1B
11	A	511[A]	8GT	O4'-C1'-N9-C8
11	A	511[A]	8GT	C2'-C1'-N9-C8
11	A	511[A]	8GT	PB-O3B-PG-O1G

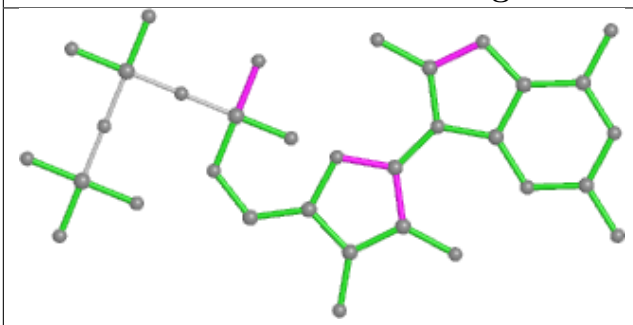
There are no ring outliers.

No monomer is involved in short contacts.

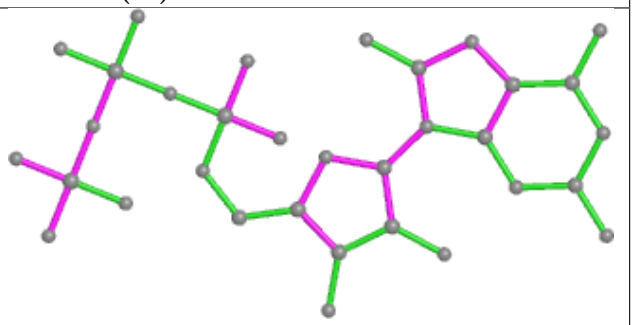
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



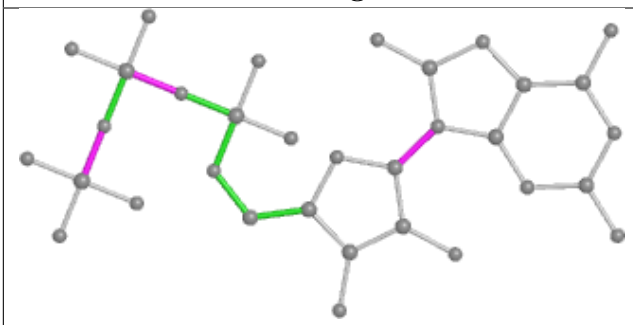
Ligand 8GT A 511 (A)



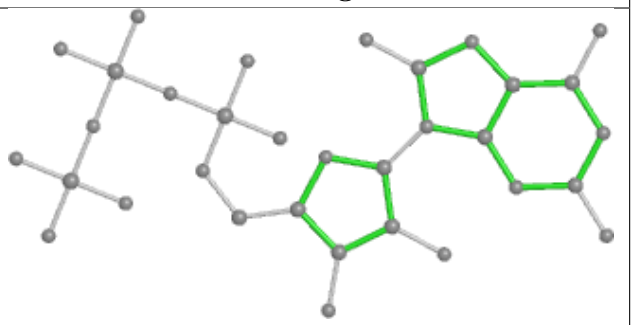
Bond lengths



Bond angles



Torsions



Rings

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.