wwPDB X-ray Structure Validation Summary Report (i)

Feb 4, 2024 – 01:16 AM EST

PDB ID	:	1O0K
Title	:	Structure of the First Parallel DNA Quadruplex-drug Complex
Authors	:	Clark, G.R.; Pytel, P.D.; Squire, C.J.; Neidle, S.
Deposited on	:	2003-02-22
Resolution	:	1.17 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 (i)) were used in the production of this report:

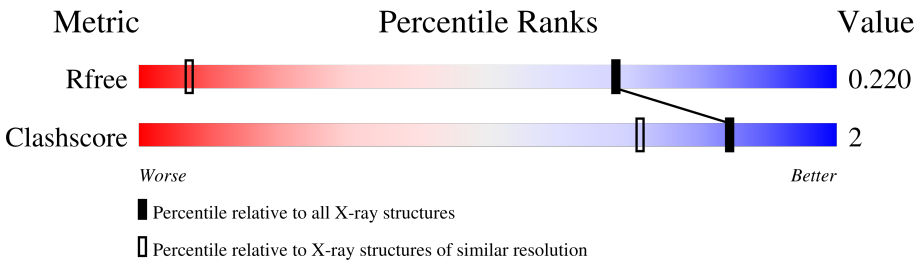
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 1.17 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}	130704	1123 (1.20-1.16)
Clashscore	141614	1182 (1.20-1.16)

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%

Mol	Chain	Length	Quality of chain
1	A	6	17% 83%
1	B	6	50% 50%
1	C	6	17% 83%
1	D	6	33% 67%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 718 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.

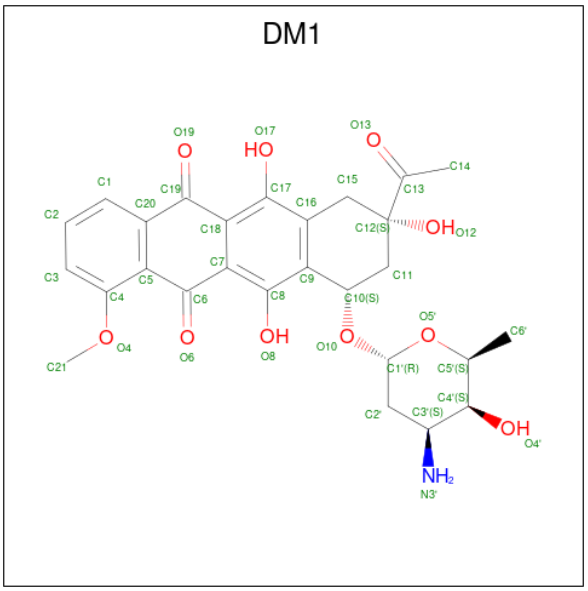
- Molecule 1 is a DNA chain called 5'-D(*TP*GP*GP*GP*GP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	6	109	50	22	32	5	0	0	0
1	B	6	93	40	20	28	5	0	0	1
1	C	6	125	60	24	36	5	0	0	0
1	D	6	107	49	22	31	5	0	0	0

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
2	A	2	2	2	0	0
2	C	1	1	1	0	0

- Molecule 3 is DAUNOMYCIN (three-letter code: DM1) (formula: $C_{27}H_{29}NO_{10}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C N O 38 27 1 10	0	0
3	C	1	Total C N O 38 27 1 10	0	0
3	D	1	Total C N O 38 27 1 10	0	0

- Molecule 4 is water.

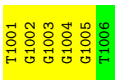
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	40	Total O 40 40	0	0
4	B	39	Total O 39 39	0	0
4	C	49	Total O 49 49	0	0
4	D	39	Total O 39 39	0	0

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. 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.

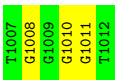
- Molecule 1: 5'-D(*TP*GP*GP*GP*GP*T)-3'

Chain A:



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

Chain B:

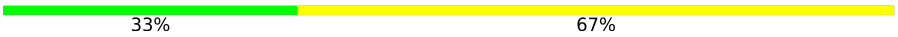


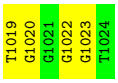
- Molecule 1: 5'-D(*TP*GP*GP*GP*GP*T)-3'

Chain C:

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

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	53.00Å 47.07Å 31.86Å 90.00° 119.80° 90.00°	Depositor
Resolution (Å)	10.00 – 1.17 27.65 – 1.17	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.17) 93.2 (27.65-1.17)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.79 (at 1.17Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	(Not available) , (Not available) 0.181 , 0.220	Depositor DCC
R_{free} test set	1101 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	10.3	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 53.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	718	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.61% 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.

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: DM1, NA

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	1.93	2/122 (1.6%)	2.75	11/189 (5.8%)
1	B	1.47	0/104	2.13	6/162 (3.7%)
1	C	1.91	3/140 (2.1%)	2.71	11/216 (5.1%)
1	D	1.46	0/120	2.26	12/186 (6.5%)
All	All	1.72	5/486 (1.0%)	2.50	40/753 (5.3%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1014	DG	C2'-C1'	10.75	1.63	1.52
1	A	1002	DG	C2'-C1'	8.43	1.60	1.52
1	C	1014	DG	O4'-C1'	-8.09	1.32	1.42
1	C	1015	DG	O4'-C1'	6.14	1.49	1.42
1	A	1002	DG	O4'-C1'	-5.97	1.35	1.42

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	1014	DG	O4'-C1'-N9	17.18	120.02	108.00
1	A	1002	DG	O4'-C1'-N9	15.36	118.75	108.00
1	C	1017	DG	O4'-C1'-N9	-13.04	98.87	108.00
1	C	1015	DG	O4'-C1'-N9	-10.41	100.71	108.00
1	A	1004	DG	OP1-P-OP2	-10.20	104.30	119.60

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	109	0	57	0	0
1	B	93	0	44	0	0
1	C	125	0	70	0	0
1	D	107	0	53	0	0
2	A	2	0	0	0	0
2	C	1	0	0	0	0
3	B	38	0	28	2	0
3	C	38	0	28	0	0
3	D	38	0	28	0	0
4	A	40	0	0	0	0
4	B	39	0	0	0	0
4	C	49	0	0	0	0
4	D	39	0	0	0	0
All	All	718	0	308	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)
3:B:25:DM1:C14	3:B:25:DM1:C13	1.76	1.58
3:B:25:DM1:C14	3:B:25:DM1:C12	2.62	0.77

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 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
3	DM1	B	25	-	40,42,42	2.77	19 (47%)	54,66,66	1.92	15 (27%)
3	DM1	C	27	-	40,42,42	2.69	20 (50%)	54,66,66	1.48	10 (18%)
3	DM1	D	26	-	40,42,42	1.57	7 (17%)	54,66,66	1.16	5 (9%)

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
3	DM1	B	25	-	-	0/12/58/58	0/5/5/5
3	DM1	C	27	-	-	0/12/58/58	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DM1	D	26	-	-	0/12/58/58	0/5/5/5

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	25	DM1	C14-C13	10.29	1.76	1.50
3	C	27	DM1	C15-C16	7.63	1.61	1.51
3	C	27	DM1	C11-C12	-6.03	1.42	1.53
3	C	27	DM1	O10-C10	5.04	1.53	1.44
3	B	25	DM1	C6'-C5'	4.88	1.63	1.51

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	25	DM1	C14-C13-C12	-5.81	108.35	118.92
3	B	25	DM1	O5'-C1'-C2'	3.51	116.16	110.87
3	C	27	DM1	C15-C16-C17	-3.46	112.80	119.23
3	B	25	DM1	O13-C13-C14	-3.43	114.67	121.35
3	D	26	DM1	O4-C4-C5	3.42	120.61	115.85

There are no chirality outliers.

There are no torsion outliers.

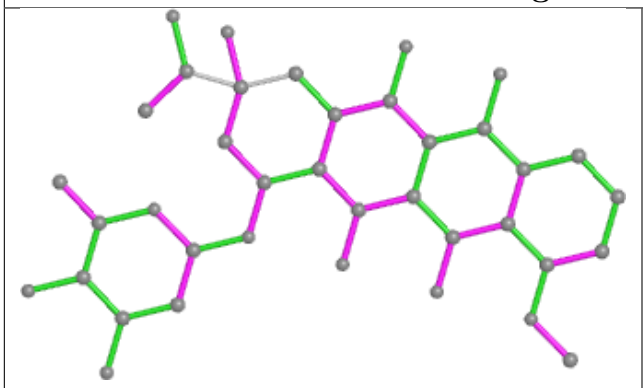
There are no ring outliers.

1 monomer is involved in 2 short contacts:

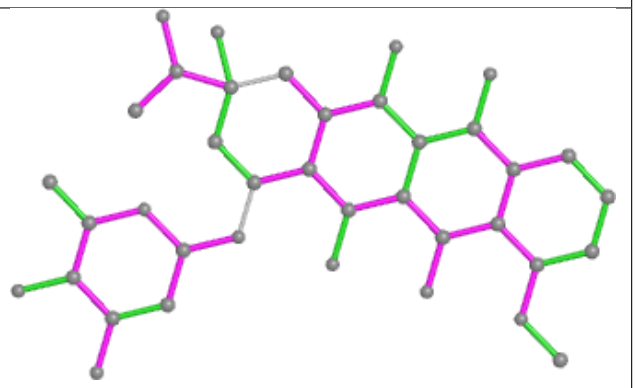
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	25	DM1	2	0

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.

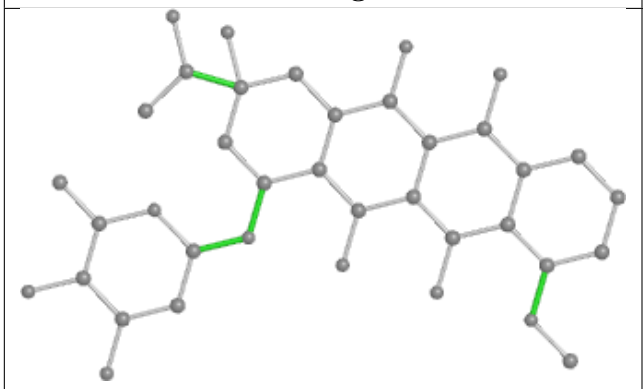
Ligand DM1 B 25



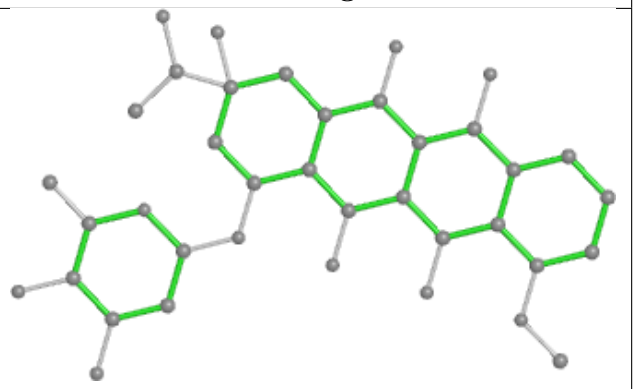
Bond lengths



Bond angles

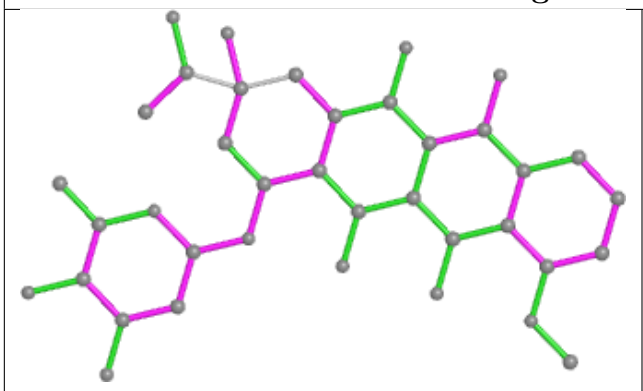


Torsions

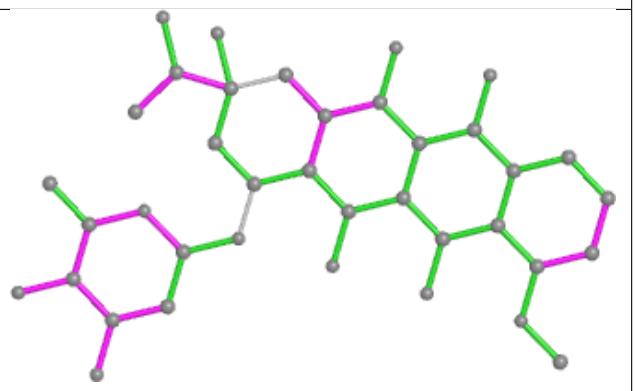


Rings

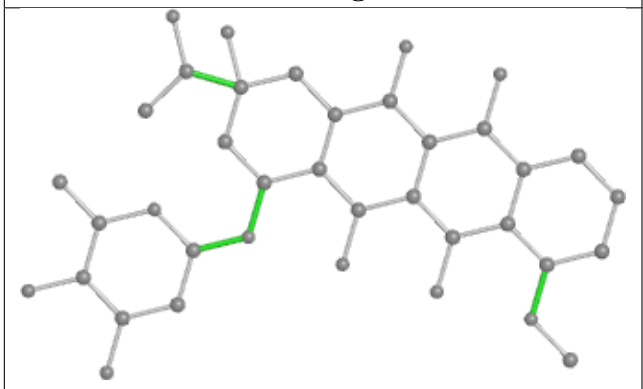
Ligand DM1 C 27



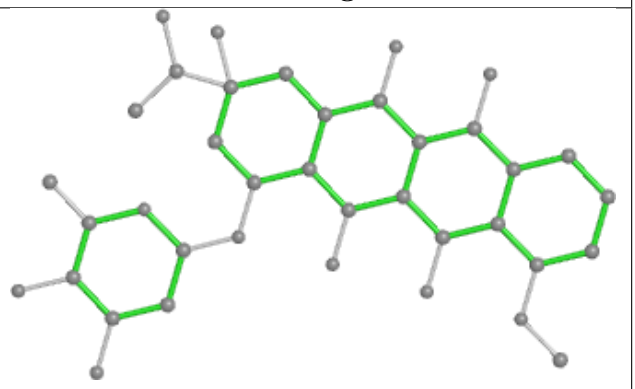
Bond lengths



Bond angles

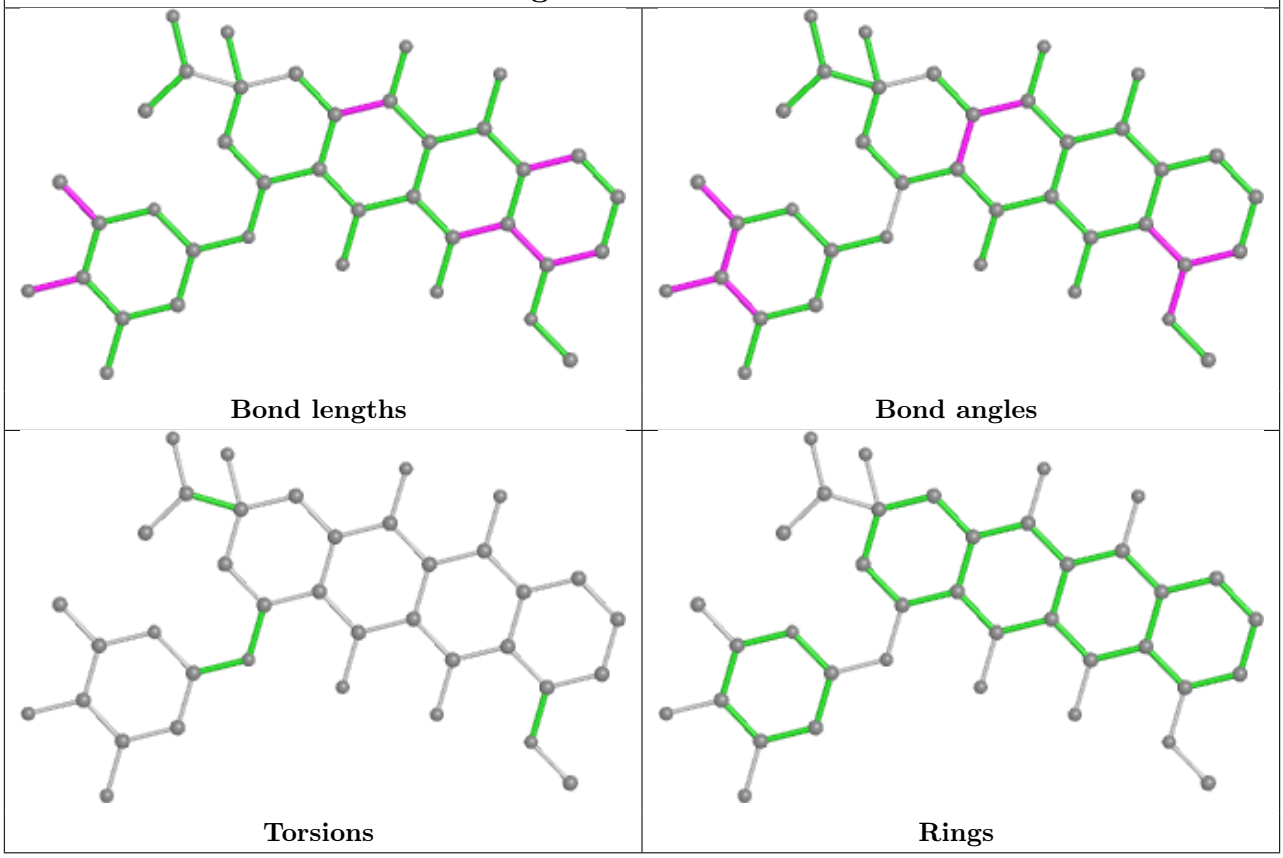


Torsions



Rings

Ligand DM1 D 26



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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

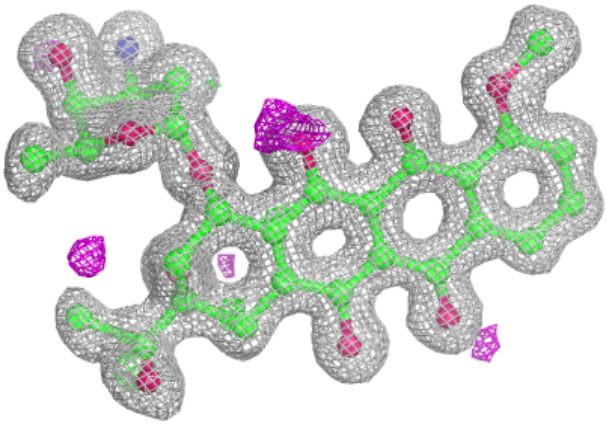
6.4 Ligands (i)

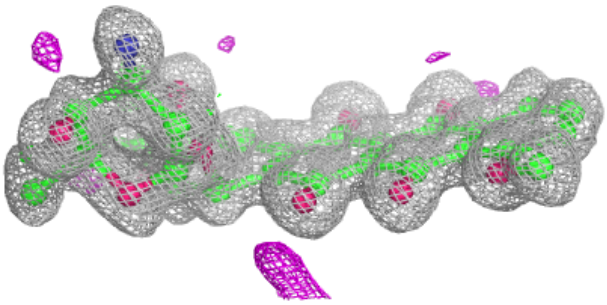
Unable to reproduce the depositors R factor - this section is therefore empty.

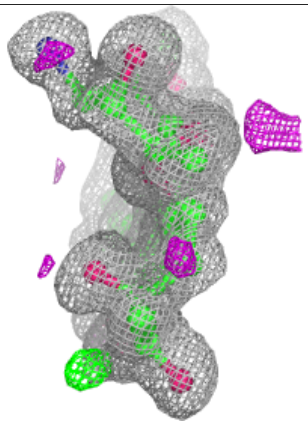
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DM1 B 25:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

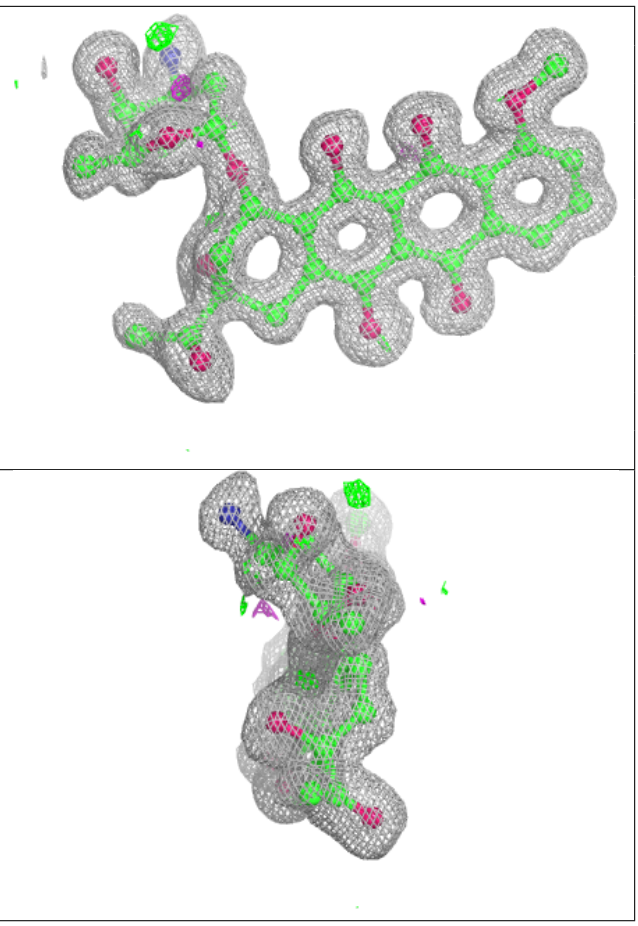






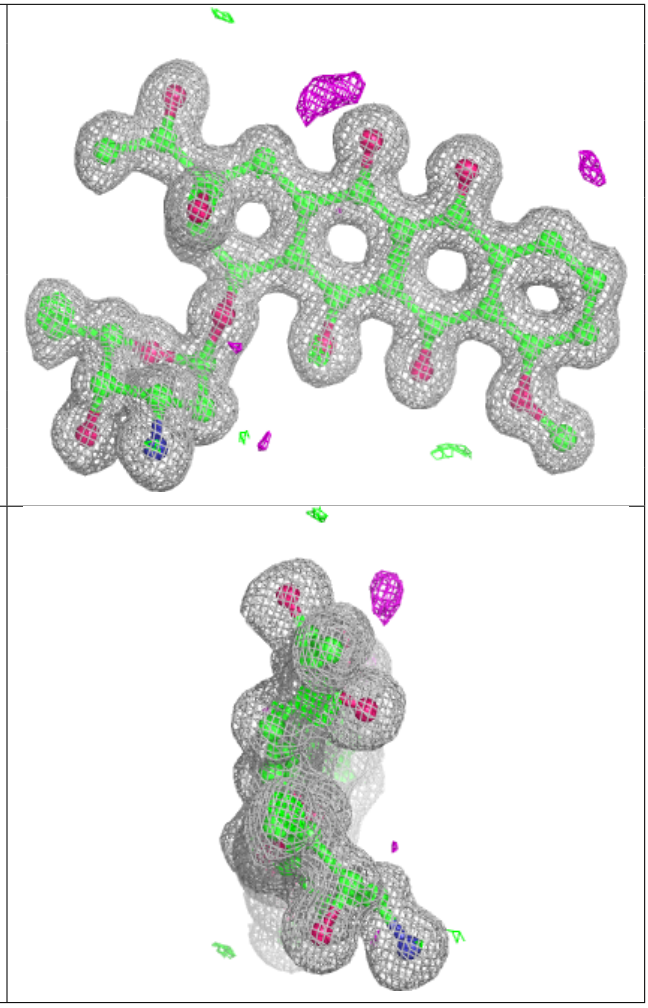
Electron density around DM1 C 27:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around DM1 D 26:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.