



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 03:42 PM GMT

PDB ID : 2D34
Title : FORMALDEHYDE CROSS-LINKS DAUNORUBICIN AND DNA EFFICIENTLY: HPLC AND X-RAY DIFFRACTION STUDIES
Authors : Wang, A.H.-J.; Gao, Y.-G.; Liaw, Y.-C.; Li, Y.-K.
Deposited on : 1991-05-23
Resolution : 1.40 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

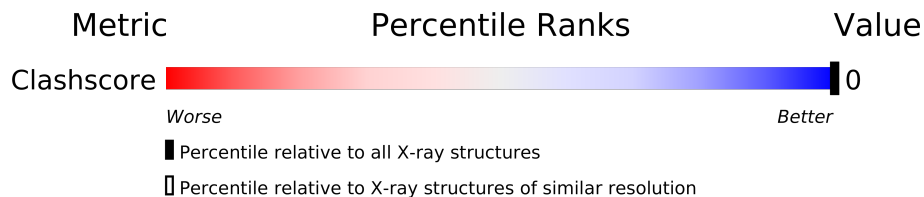
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.40 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))
Clashscore	79885	1246 (1.42-1.38)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	6	

2 Entry composition i

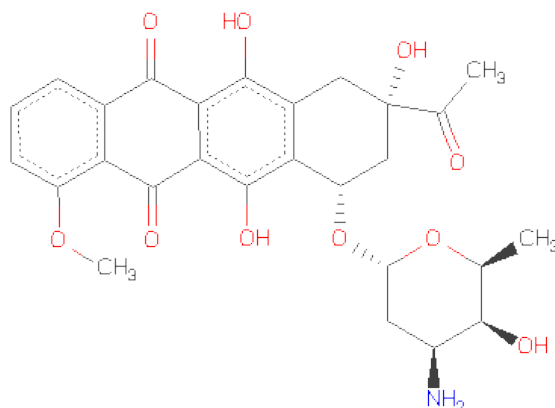
There are 4 unique types of molecules in this entry. The entry contains 225 atoms, of which 0 are hydrogen and 0 are deuterium.

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(*CP*GP*TP*(A35)P*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	6	Total	C	N	O	P	0	0	0
			122	59	24	34	5			

- Molecule 2 is DAUNOMYCIN (three-letter code: DM1) (formula: C₂₇H₂₉NO₁₀).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			38	27	1	10		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	64	Total 64	O 64	0	0

3 Residue-property plots

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.

Note EDS was not executed.

- Molecule 1: 5'-D(*CP*GP*TP*(A35)P*CP*G)-3'

Chain A:  

C1	C2	T3	A4	C5	G6
----	----	----	----	----	----

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	28.02Å 28.02Å 52.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.40	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	NUCLSQ	Depositor
R, R_{free}	0.178 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	225	wwPDB-VP
Average B, all atoms (Å ²)	19.0	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: DM1, MG, A40

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	2.08	4/109 (3.7%)	3.28	18/164 (11.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	5	DC	P-O5'	6.73	1.66	1.59
1	A	1	DC	C4'-O4'	-5.64	1.39	1.45
1	A	5	DC	N3-C4	5.29	1.37	1.33
1	A	3	DT	C4'-O4'	-5.00	1.40	1.45

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	DC	O4'-C1'-N1	17.22	120.06	108.00
1	A	1	DC	P-O3'-C3'	10.91	132.79	119.70
1	A	2	DG	O4'-C1'-N9	9.88	114.91	108.00
1	A	3	DT	C2-N3-C4	-9.27	121.64	127.20
1	A	3	DT	O5'-P-OP2	8.23	120.58	110.70
1	A	6	DG	C5-C6-O6	-8.11	123.73	128.60
1	A	3	DT	N3-C4-C5	8.03	120.02	115.20
1	A	6	DG	C5-C6-N1	6.81	114.91	111.50
1	A	2	DG	C5-C6-N1	6.53	114.77	111.50
1	A	3	DT	N1-C2-N3	6.32	118.39	114.60
1	A	5	DC	OP2-P-O3'	-6.20	91.56	105.20
1	A	3	DT	N1-C2-O2	-6.18	118.16	123.10
1	A	3	DT	OP1-P-OP2	-6.02	110.57	119.60
1	A	6	DG	O5'-P-OP2	5.70	117.54	110.70
1	A	2	DG	N3-C2-N2	-5.67	115.93	119.90
1	A	2	DG	C3'-C2'-C1'	-5.36	96.07	102.50
1	A	2	DG	P-O3'-C3'	5.32	126.09	119.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	DC	P-O3'-C3'	5.01	125.71	119.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	122	0	71	0	0
2	A	38	0	27	0	0
3	A	1	0	0	0	0
4	A	64	0	0	0	2
All	All	225	0	98	0	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 0.

There are no clashes within the asymmetric unit.

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	Distance(Å)	Clash(Å)
4:A:64:HOH:O	4:A:65:HOH:O[4_454]	1.45	0.75
4:A:64:HOH:O	4:A:66:HOH:O[8_665]	1.46	0.74

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

There are no protein chains in this entry.

5.3.2 Protein sidechains ⓘ

There are no protein chains in this entry.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	A40	A	4	1,2	23,25,26	1.54	2 (8%)	33,36,39	2.48	6 (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	A40	A	4	1,2	-	0/8/23/24	0/1/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4	A40	P-O1P	5.84	1.53	1.46
1	A	4	A40	C5-C4	-2.17	1.35	1.40

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	A40	CH2-N2-C2	-11.03	110.54	123.04
1	A	4	A40	C2-N3-C4	-5.80	107.87	115.15

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	A40	C5-C4-N3	2.53	129.62	125.94
1	A	4	A40	C2-N1-C6	2.25	121.81	113.91
1	A	4	A40	N3-C4-N9	-2.16	123.74	126.91
1	A	4	A40	C8-N9-C1'	2.08	130.07	126.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DM1	A	7	1,3	42,42,42	1.99	16 (38%)	66,66,66	2.16	24 (36%)

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
2	DM1	A	7	1,3	-	0/12/58/58	0/1/5/5

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	7	DM1	C18-C7	4.04	1.50	1.41
2	A	7	DM1	O10-C10	3.73	1.51	1.44
2	A	7	DM1	C2-C3	3.26	1.46	1.39
2	A	7	DM1	C9-C10	3.24	1.57	1.51
2	A	7	DM1	C2'-C3'	3.12	1.54	1.52
2	A	7	DM1	O5'-C5'	2.91	1.51	1.44
2	A	7	DM1	C15-C16	-2.84	1.46	1.51
2	A	7	DM1	C20-C5	-2.80	1.36	1.41
2	A	7	DM1	C15-C12	2.80	1.58	1.53
2	A	7	DM1	O5'-C1'	2.75	1.49	1.42
2	A	7	DM1	O4-C4	-2.72	1.32	1.37
2	A	7	DM1	C3-C4	2.66	1.45	1.39
2	A	7	DM1	C3'-N3'	2.45	1.55	1.47
2	A	7	DM1	O4'-C4'	2.40	1.48	1.43
2	A	7	DM1	O4-C21	2.16	1.49	1.42
2	A	7	DM1	C11-C10	-2.10	1.48	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	7	DM1	C20-C5-C4	5.65	124.98	118.06
2	A	7	DM1	C5-C20-C19	4.52	127.35	120.77
2	A	7	DM1	O10-C10-C9	-4.45	97.18	107.73
2	A	7	DM1	C14-C13-C12	4.40	125.49	118.62
2	A	7	DM1	C4-C5-C6	-3.91	116.86	122.40
2	A	7	DM1	C1-C20-C19	-3.81	113.07	119.23
2	A	7	DM1	O6-C6-C7	-3.80	114.61	121.50
2	A	7	DM1	C21-O4-C4	3.27	122.42	117.59
2	A	7	DM1	O10-C1'-C2'	3.20	114.24	108.44
2	A	7	DM1	O6-C6-C5	3.01	126.96	121.50
2	A	7	DM1	C6'-C5'-C4'	2.84	117.67	113.06
2	A	7	DM1	C15-C16-C9	2.82	128.92	121.79
2	A	7	DM1	O13-C13-C14	-2.70	116.10	121.28
2	A	7	DM1	C8-C9-C16	2.69	125.45	119.69
2	A	7	DM1	C3-C4-C5	-2.64	115.40	120.34
2	A	7	DM1	C17-C18-C19	2.53	125.19	120.58
2	A	7	DM1	C17-C16-C9	-2.45	114.79	119.08
2	A	7	DM1	O5'-C5'-C4'	-2.45	105.39	109.53
2	A	7	DM1	C7-C18-C17	-2.40	115.77	119.67
2	A	7	DM1	C12-C11-C10	2.31	117.72	111.25
2	A	7	DM1	C18-C17-C16	2.30	125.94	121.55
2	A	7	DM1	O17-C17-C18	-2.21	115.90	120.95
2	A	7	DM1	C7-C8-C9	-2.08	117.15	121.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	7	DM1	O4-C4-C5	2.05	119.03	115.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.