



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2026 – 07:38 AM EDT

PDB ID : 1DCT / pdb_00001dct
Title : DNA (CYTOSINE-5) METHYLASE FROM HAEIII COVALENTLY BOUND TO DNA
Authors : Reinisch, K.M.; Chen, L.; Verdine, G.L.; Lipscomb, W.N.
Deposited on : 1995-05-17
Resolution : 2.80 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

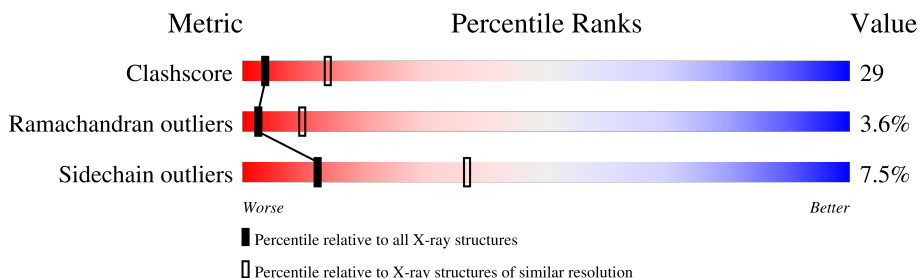
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	F	18	11% (red), 67% (yellow), 22% (orange)
1	G	18	22% (green), 56% (yellow), 11% (orange), 11% (grey)
2	M	18	17% (green), 56% (yellow), 28% (orange)
2	N	18	33% (green), 56% (yellow), 6% (orange), 6% (grey)
3	A	324	45% (green), 47% (yellow), 8% (orange)
3	B	324	45% (green), 45% (yellow), 9% (orange), . (red)

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	C49	F	10	X	-	-	-
1	C49	G	10	X	-	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6908 atoms, of which 268 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*CP*CP*AP*GP*CP*AP*GP*GP*(C49)P*CP*AP*CP*CP*AP*GP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	F	N	O				P
1	F	18	Total 367	C 174	F 1	N 73	O 102	P 17	0	0	0
1	G	16	Total 327	C 155	F 1	N 65	O 91	P 15	0	0	0

- Molecule 2 is a DNA chain called DNA (5'-D(*TP*CP*AP*CP*TP*GP*GP*TP*GP*GP*(C5M)P*CP*TP*GP*CP*TP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	M	18	Total 368	C 176	N 65	O 110	P 17	0	0	0
2	N	17	Total 346	C 166	N 60	O 104	P 16	0	0	0

- Molecule 3 is a protein called PROTEIN (MODIFICATION METHYLASE HAEIII).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	A	324	Total 2749	C 1680	H 134	N 455	O 468	S 12	0	0	0
3	B	324	Total 2749	C 1680	H 134	N 455	O 468	S 12	0	0	0

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Ca 1	0	0
4	B	1	Total 1	Ca 1	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.

Note EDS was not executed.

- Molecule 1: DNA (5'-D(*AP*CP*CP*AP*GP*CP*AP*GP*GP*(C49)P*CP*AP*CP*CP*AP*GP*TP*G)-3')

Chain F: 

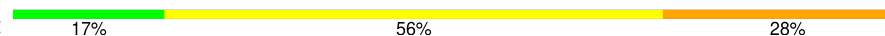


- Molecule 1: DNA (5'-D(*AP*CP*CP*AP*GP*CP*AP*GP*GP*(C49)P*CP*AP*CP*CP*AP*GP*TP*G)-3')

Chain G: 



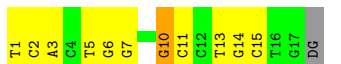
- Molecule 2: DNA (5'-D(*TP*CP*AP*CP*TP*GP*GP*TP*GP*GP*(C5M)P*CP*TP*GP*CP*TP*GP*G)-3')

Chain M: 



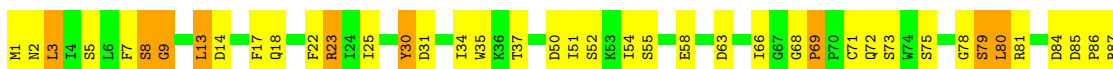
- Molecule 2: DNA (5'-D(*TP*CP*AP*CP*TP*GP*GP*TP*GP*GP*(C5M)P*CP*TP*GP*CP*TP*GP*G)-3')

Chain N: 



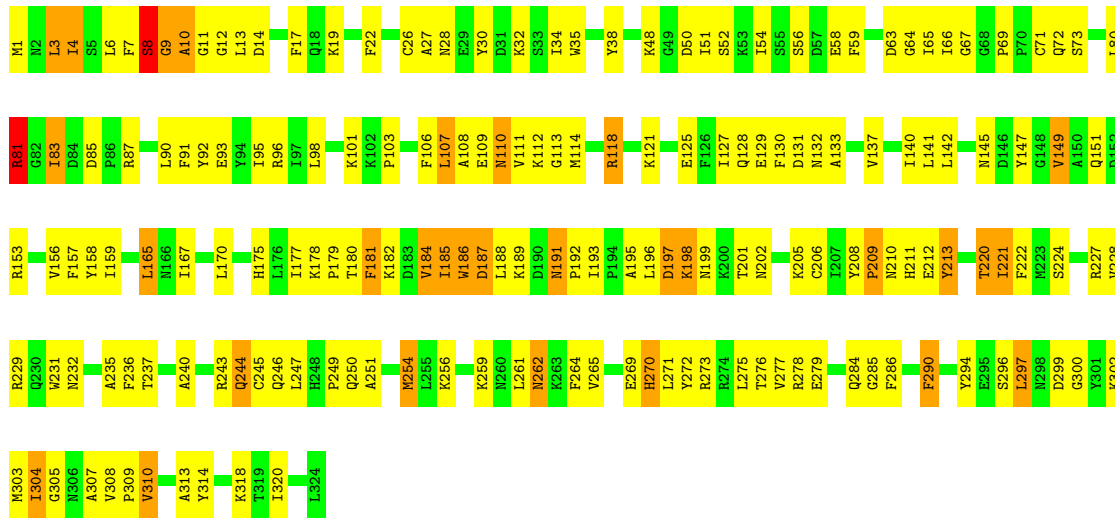
- Molecule 3: PROTEIN (MODIFICATION METHYLASE HAEIII)

Chain A: 





● Molecule 3: PROTEIN (MODIFICATION METHYLASE HAEIII)



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.57Å 108.04Å 155.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.226 , 0.326	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	6908	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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: 5CM, CA, C49

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	F	0.74	0/388	1.50	3/594 (0.5%)
1	G	0.74	0/343	1.43	2/525 (0.4%)
2	M	0.78	0/388	1.60	6/596 (1.0%)
2	N	0.80	0/363	1.59	3/557 (0.5%)
3	A	0.64	0/2681	1.10	17/3615 (0.5%)
3	B	0.62	0/2681	1.19	20/3615 (0.6%)
All	All	0.66	0/6844	1.25	51/9502 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	1	2
1	G	1	0
2	M	0	1
3	A	0	1
3	B	0	1
All	All	2	5

There are no bond length outliers.

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	178	LYS	CA-C-N	10.01	132.35	119.84
3	B	178	LYS	C-N-CA	10.01	132.35	119.84
3	B	170	LEU	CA-C-N	9.60	130.27	120.38
3	B	170	LEU	C-N-CA	9.60	130.27	120.38
3	B	307	ALA	N-CA-C	8.94	121.41	110.41

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	10	C49	C1'
1	G	10	C49	C1'

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	147	TYR	Sidechain
3	B	38	TYR	Sidechain
1	F	1	DA	Sidechain
1	F	17	DT	Sidechain
2	M	17	DG	Sidechain

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	F	367	0	200	18	0
1	G	327	0	178	10	0
2	M	368	0	207	14	0
2	N	346	0	196	6	0
3	A	2615	134	2606	165	0
3	B	2615	134	2606	169	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
All	All	6640	268	5993	364	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 29.

The worst 5 of 364 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:F:4:DA:H2''	1:F:5:DG:C8	2.04	0.93
3:A:202:ASN:HB3	3:A:205:LYS:HB3	1.51	0.92
3:B:240:ALA:HB1	3:B:302:LYS:HA	1.52	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:212:GLU:HG3	3:B:297:LEU:HD21	1.55	0.87
3:B:153:ARG:HG3	3:B:237:THR:HG23	1.60	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	322/324 (99%)	273 (85%)	39 (12%)	10 (3%)	3 12
3	B	322/324 (99%)	283 (88%)	26 (8%)	13 (4%)	2 8
All	All	644/648 (99%)	556 (86%)	65 (10%)	23 (4%)	2 10

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	9	GLY
3	A	80	LEU
3	A	241	SER
3	B	9	GLY
3	B	186	TRP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	281/281 (100%)	261 (93%)	20 (7%)	13	39
3	B	281/281 (100%)	259 (92%)	22 (8%)	11	35
All	All	562/562 (100%)	520 (92%)	42 (8%)	12	37

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	121	LYS
3	B	221	ILE
3	B	149	VAL
3	B	181	PHE
3	B	244	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	239	GLN
3	B	262	ASN
3	A	244	GLN
3	A	262	ASN
3	A	284	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	5CM	M	11	2,1	18,21,22	0.66	0	24,30,33	0.79	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	5CM	N	11	2,1	18,21,22	0.52	0	24,30,33	0.80	1 (4%)
1	C49	G	10	3,1	17,22,24	2.60	5 (29%)	17,33,38	4.28	7 (41%)
1	C49	F	10	3,1	17,22,24	2.66	6 (35%)	17,33,38	4.54	6 (35%)

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	5CM	M	11	2,1	-	4/7/21/22	0/2/2/2
2	5CM	N	11	2,1	-	4/7/21/22	0/2/2/2
1	C49	G	10	3,1	1/1/8/10	6/7/40/46	0/2/2/2
1	C49	F	10	3,1	1/1/8/10	6/7/40/46	0/2/2/2

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	10	C49	C6-C5	-7.67	1.42	1.52
1	G	10	C49	C6-C5	-7.04	1.43	1.52
1	G	10	C49	F-C5	-5.36	1.32	1.42
1	F	10	C49	F-C5	-4.89	1.33	1.42
1	F	10	C49	CM5-C5	-3.43	1.43	1.51

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	10	C49	O4'-C1'-N1	15.48	127.58	108.39
1	G	10	C49	O4'-C1'-N1	14.90	126.86	108.39
1	F	10	C49	C2'-C1'-N1	5.59	122.24	115.59
1	G	10	C49	C4'-O4'-C1'	-5.18	97.21	109.51
1	F	10	C49	C4'-O4'-C1'	-5.12	97.34	109.51

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	10	C49	C1'
1	G	10	C49	C1'

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	F	10	C49	O4'-C1'-N1-C2
1	F	10	C49	O4'-C1'-N1-C6
1	G	10	C49	O4'-C1'-N1-C2
1	G	10	C49	O4'-C1'-N1-C6
1	F	10	C49	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	10	C49	4	0
1	F	10	C49	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.