



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 26, 2024 – 07:07 PM EDT

PDB ID : 1MHT
Title : COVALENT TERNARY STRUCTURE OF HHAI METHYLTRANSFERASE, DNA AND S-ADENOSYL-L-HOMOCYSTEINE
Authors : Cheng, X.
Deposited on : 1994-12-08
Resolution : 2.60 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

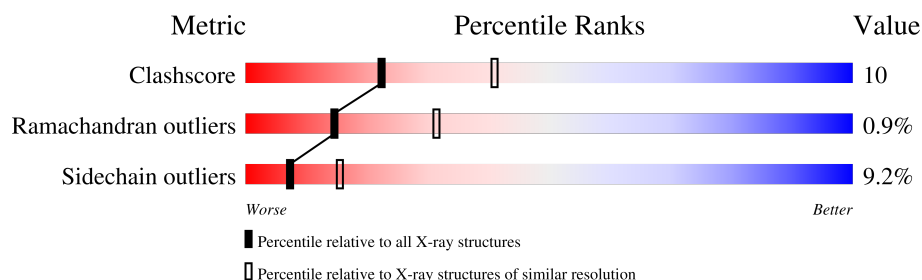
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)

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	B	12	
2	C	13	
3	A	327	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	C36	B	407	X	-	-	-
2	C36	C	427	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3144 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 DNA (5'-D(P*GP*AP*TP*AP*GP*(C36)P*GP*CP*TP*AP*TP*C)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	12	Total	C	F	N	O	P	0	0	0
			247	117	1	45	72	12			

- Molecule 2 is a DNA chain called DNA (5'-D(*TP*GP*AP*TP*AP*GP*(C36)P*GP*CP*TP*AP*TP*C)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	13	Total	C	F	N	O	P	0	0	0
			265	128	1	47	77	12			

- Molecule 3 is a protein called PROTEIN (HHAI METHYLTRANSFERASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	327	Total	C	N	O	S	0	0	0
			2606	1662	444	487	13			

- Molecule 4 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).




Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

3 Residue-property plots

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.

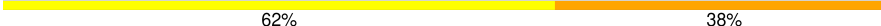
Note EDS was not executed.

- Molecule 1: DNA (5'-D(P*GP*AP*TP*AP*GP*(C36)P*GP*CP*TP*AP*TP*C)-3')

Chain B: 

G402
A403
T404
A405
G406
C407
G408
C409
T410
A411
T412
C413

- Molecule 2: DNA (5'-D(*TP*GP*AP*TP*AP*GP*(C36)P*GP*CP*TP*AP*TP*C)-3')

Chain C: 

T421
G422
A423
T424
A425
G426
C427
G428
C429
T430
A431
T432
C433

- Molecule 3: PROTEIN (HHA1 METHYLTRANSFERASE)

Chain A: 

M1
F14
I15
R25
L26
A27
L28
E29
C35
G36
V37
V41
V48
F53
D60
I61
T62
T68
I69
H72
P80
G81
Q82
F93
E94
D95
S96
R97
F101
I104
A105
R106
K111
F117
H127
M131
T132
K137
M140
M141

A149
L155
R163
Y167
H168
I169
C170
D174
L175
T190
K193
D194
V202
E203
H204
L205
V206
I207
L212
I219
T223
P224
K225
T226
V227
R228
T231
V232
G235
G236
Q237
G238
E239
R240
S243
T244
R245
T250
L251
G256
G257
T258
F259
A260
K261

V267
T271
R272
H275
P276
R277
E278
C279
V282
H283
Q297
Q301
S305
N309
Y327

4 Data and refinement statistics

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

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	99.86Å 99.86Å 325.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.60)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.174 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3144	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: C36, SAH

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	B	2.38	13/253 (5.1%)	3.29	51/386 (13.2%)
2	C	2.79	15/272 (5.5%)	3.55	52/416 (12.5%)
3	A	0.52	0/2661	0.72	1/3586 (0.0%)
All	All	1.16	28/3186 (0.9%)	1.61	104/4388 (2.4%)

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	B	1	1
2	C	1	1
All	All	2	2

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	428	DG	C6-N1	-10.65	1.32	1.39
2	C	424	DT	C5-C7	10.17	1.56	1.50
2	C	423	DA	N3-C4	9.11	1.40	1.34
1	B	412	DT	C5-C7	8.90	1.55	1.50
1	B	409	DC	C4'-O4'	-8.56	1.36	1.45

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	421	DT	O4'-C4'-C3'	-19.15	94.51	106.00
2	C	433	DC	O4'-C1'-C2'	-16.51	92.69	105.90
2	C	433	DC	O4'-C4'-C3'	-13.97	97.62	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	429	DC	N1-C2-O2	12.86	126.62	118.90
1	B	405	DA	O4'-C1'-C2'	-12.59	95.83	105.90

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	407	C36	C5
2	C	427	C36	C5

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	413	DC	Sidechain
2	C	430	DT	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	B	247	0	136	1	0
2	C	265	0	147	3	0
3	A	2606	0	2586	61	0
4	A	26	0	19	0	0
All	All	3144	0	2888	63	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 10.

The worst 5 of 63 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:A:202:VAL:HG13	3:A:205:LEU:HD12	1.56	0.86
3:A:275:HIS:HD2	3:A:277:ARG:H	1.31	0.79
3:A:309:ASN:HD22	3:A:309:ASN:H	1.31	0.76
3:A:275:HIS:CD2	3:A:277:ARG:H	2.06	0.74
3:A:309:ASN:HD22	3:A:309:ASN:N	1.87	0.70

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	325/327 (99%)	298 (92%)	24 (7%)	3 (1%)	14 31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	60	ASP
3	A	174	ASP
3	A	203	GLU

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	283/283 (100%)	257 (91%)	26 (9%)	7 15

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	175	LEU
3	A	227	VAL
3	A	282	VAL
3	A	212	LEU
3	A	231	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	275	HIS
3	A	309	ASN
3	A	127	HIS
3	A	141	ASN
3	A	204	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	C36	C	427	3,2	16,22,24	7.80	6 (37%)	17,33,37	6.46	3 (17%)
1	C36	B	407	1,2	14,21,24	3.24	5 (35%)	18,30,37	2.88	9 (50%)

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	C36	C	427	3,2	1/1/8/8	4/7/40/44	0/1/2/2
1	C36	B	407	1,2	1/1/8/8	2/7/37/44	0/1/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	427	C36	C-C5	-18.90	1.09	1.51
2	C	427	C36	C6-C5	-16.69	1.31	1.52
2	C	427	C36	C6-N1	-12.72	1.33	1.46
2	C	427	C36	F-C5	-12.57	1.19	1.42
1	B	407	C36	C6-N1	-8.71	1.36	1.46

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	427	C36	F-C5-C	-26.19	70.60	106.49
1	B	407	C36	O4'-C4'-C3'	-6.56	90.70	105.65
1	B	407	C36	F-C5-C6	5.12	115.88	108.59
1	B	407	C36	C2-N3-C4	4.94	125.10	119.32
1	B	407	C36	N4-C4-N3	3.76	123.43	118.39

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	407	C36	C5
2	C	427	C36	C5

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	427	C36	O4'-C1'-N1-C6
2	C	427	C36	C2'-C1'-N1-C6
2	C	427	C36	C2'-C1'-N1-C2
1	B	407	C36	O4'-C4'-C5'-O5'
2	C	427	C36	O4'-C1'-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z > 2$
4	SAH	A	328	-	23,28,28	1.31	5 (21%)	22,40,40	1.83	6 (27%)

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
4	SAH	A	328	-	-	3/11/31/31	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	328	SAH	C1'-N9	-3.08	1.42	1.49
4	A	328	SAH	C4-N3	2.75	1.39	1.35
4	A	328	SAH	C8-N7	-2.54	1.30	1.34
4	A	328	SAH	O-C	2.54	1.29	1.22
4	A	328	SAH	O4'-C4'	-2.38	1.39	1.45

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	328	SAH	OXT-C-O	-3.73	115.61	124.08
4	A	328	SAH	C4'-O4'-C1'	-3.44	106.77	109.92
4	A	328	SAH	O4'-C1'-N9	-2.91	104.89	108.75
4	A	328	SAH	CB-CG-SD	-2.89	106.99	113.45
4	A	328	SAH	C4-C5-N7	2.77	112.27	109.34

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	328	SAH	OXT-C-CA-CB

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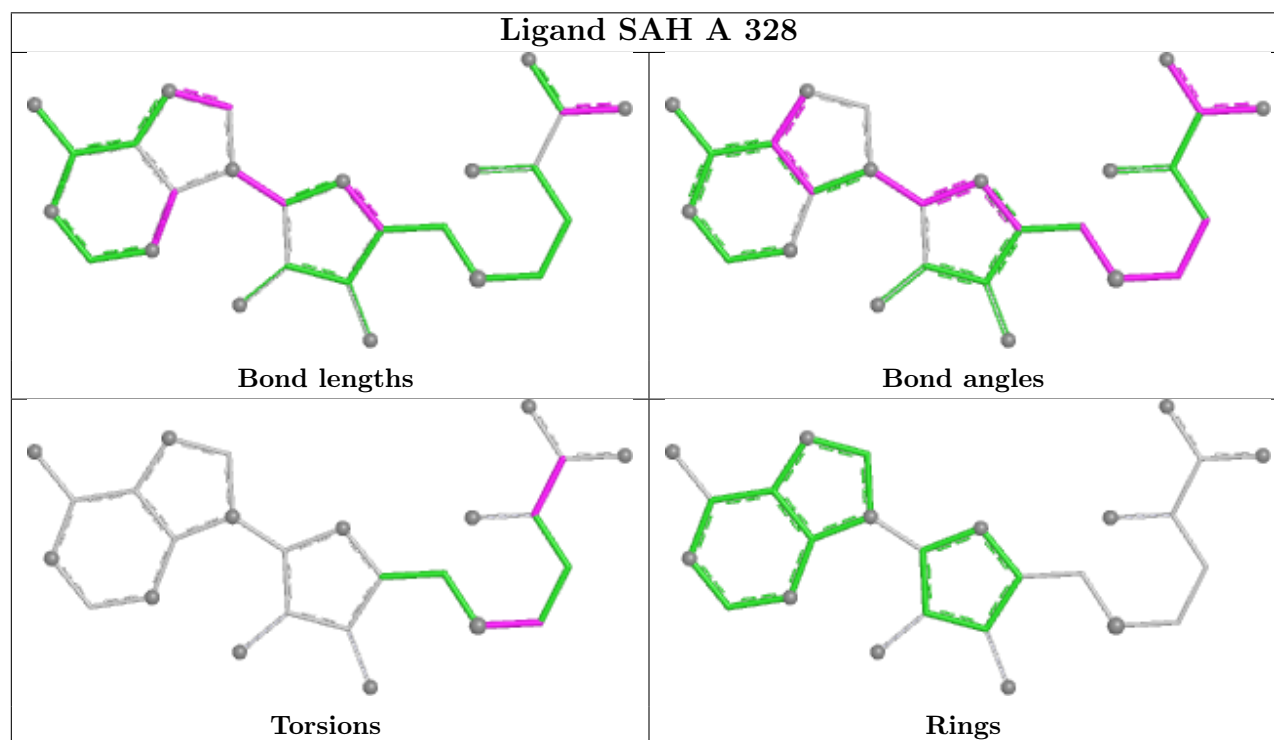
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Mol	Chain	Res	Type	Atoms
4	A	328	SAH	CB-CG-SD-C5'
4	A	328	SAH	OXT-C-CA-N

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 than 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.



5.7 Other polymers [i](#)

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 [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.