



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 13, 2019 – 09:57 PM EDT

PDB ID : 2C7P
Title : HhaI DNA methyltransferase complex with oligonucleotide containing 2-aminopurine opposite to the target base (GCGC:GMPC) and SAH
Authors : Neely, R.K.; Daujotyte, D.; Grazulis, S.; Magennis, S.W.; Dryden, D.T.F.; Klimasauskas, S.; Jones, A.C.
Deposited on : 2005-11-25
Resolution : 1.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.3.2

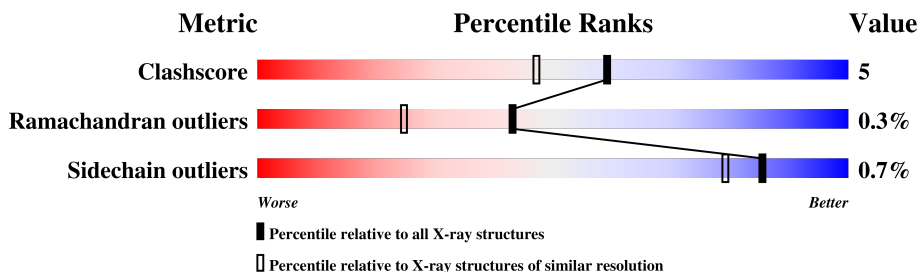
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	122126	4167 (1.70-1.70)
Ramachandran outliers	120053	4100 (1.70-1.70)
Sidechain outliers	120020	4100 (1.70-1.70)

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. 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	A	327	88% 12%
2	C	12	67% 33%
3	D	12	67% 25% 8%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 3485 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 MODIFICATION METHYLASE HHAI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	2	0
			2621	1670	447	491	13			

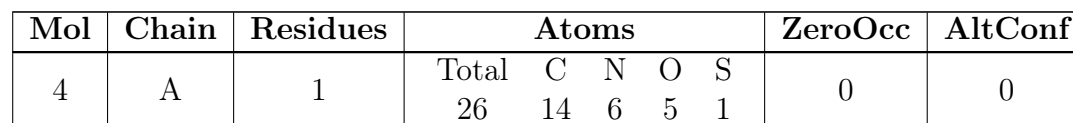
- Molecule 2 is a DNA chain called 5'-D(*G*GP*AP*TP*GP*(5CM*2PR)*CP*TP*GP*AP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	P	0	0	0
			250	118	48	72	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	12	Total	C	N	O	P	0	0	0
			244	115	44	73	12			

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



-
- Diagram illustrating the Lewis structure of the sulfate ion (SO_4^{2-}). The central sulfur atom (S) is bonded to four oxygen atoms (O). The top and bottom oxygen atoms are double-bonded to sulfur, while the left and right oxygen atoms are single-bonded. Each single-bonded oxygen atom carries a negative charge (O^-). The sulfur atom has a formal charge of +6, indicated by a green 'S' with a '+' sign. The oxygen atoms are labeled O1, O2, O3, and O4 in green. The overall charge is -2, indicated by a green '2-'.

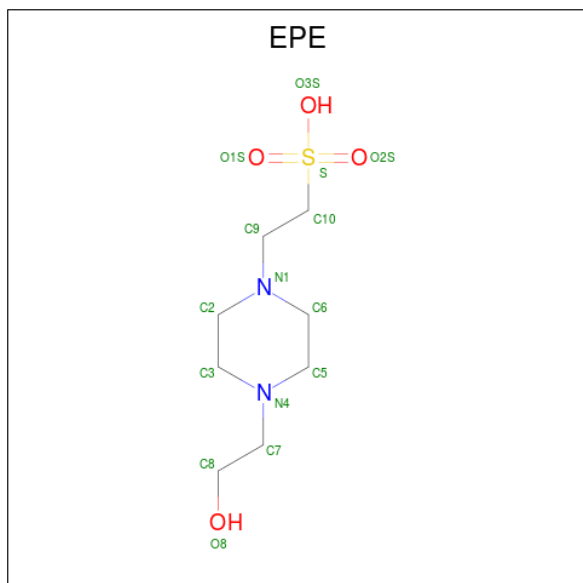
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 5	O 4	S 1	0	0
5	A	1	Total 5	O 4	S 1	0	0
5	A	1	Total 5	O 4	S 1	0	0



Continued from previous page...

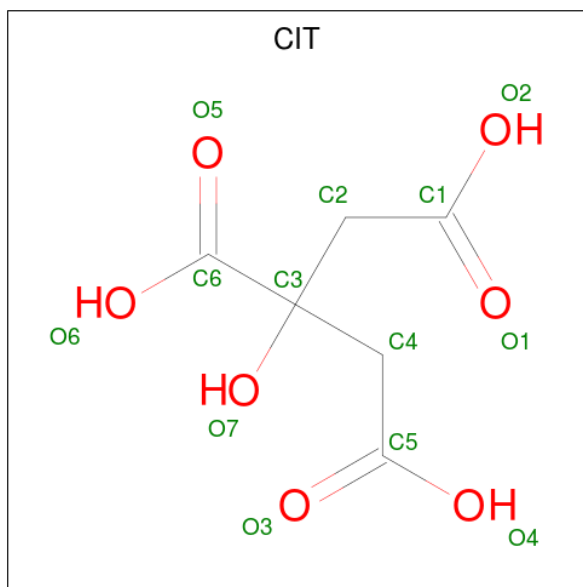
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 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
6	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 7 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 8 is water.

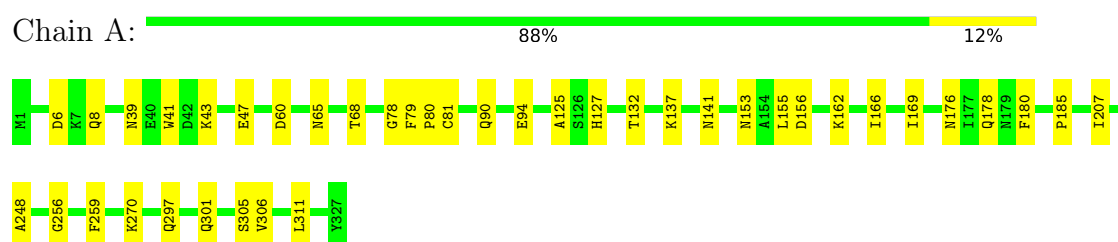
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	238	Total	O	0	0
			238	238		
8	C	34	Total	O	0	0
			34	34		
8	D	19	Total	O	0	0
			19	19		

3 Residue-property plots [i](#)

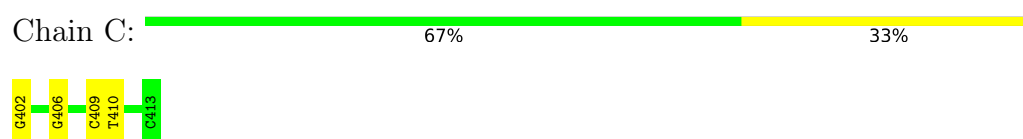
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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.

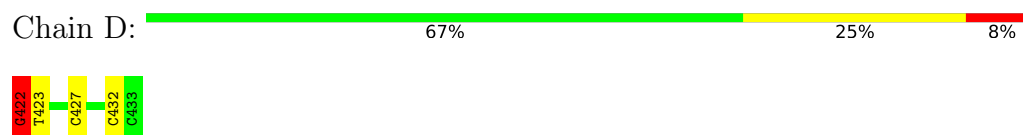
- Molecule 1: MODIFICATION METHYLASE HHAI



- Molecule 2: 5'-D(*G*GP*AP*TP*GP*(5CM*2PR)*CP*TP*GP*AP*C)-3'



- Molecule 3: 5'-D(*G*TP*CP*AP*GP*CP*GP*CP*AP*TP*CP*C)-3'



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	94.84Å 94.84Å 313.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	56.66 – 1.70	Depositor
% Data completeness (in resolution range)	99.6 (56.66-1.70)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.196 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3485	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2PR, SAH, SO4, CIT, 5CM, EPE

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	0.34	0/2676	0.59	1/3606 (0.0%)
2	C	0.63	1/233 (0.4%)	0.86	0/354
3	D	0.61	1/272 (0.4%)	0.86	0/415
All	All	0.40	2/3181 (0.1%)	0.65	1/4375 (0.0%)

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
3	D	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	422	DG	OP3-P	-6.80	1.52	1.61
2	C	402	DG	OP3-P	-6.65	1.53	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	78	GLY	N-CA-C	-6.21	97.58	113.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	422	DG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
3	D	432	DC	Sidechain

5.2 Too-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 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	2621	0	2598	28	0
2	C	250	0	137	2	0
3	D	244	0	135	4	0
4	A	26	0	19	1	0
5	A	25	0	0	0	0
6	A	15	0	17	0	0
7	A	13	0	5	2	0
8	A	238	0	0	2	1
8	C	34	0	0	0	0
8	D	19	0	0	0	0
All	All	3485	0	2911	31	1

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 5.

The worst 5 of 31 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)
2:C:409:DC:H2''	2:C:410:DT:H71	1.72	0.72
1:A:125:ALA:HB2	1:A:166:ILE:HD12	1.75	0.68
1:A:127:HIS:HD2	1:A:132:THR:OG1	1.78	0.67
1:A:256:GLY:HA3	2:C:406:DG:O6	1.96	0.65
1:A:81:CYS:SG	3:D:427:DC:C6	2.90	0.57

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
8:A:2037:HOH:O	8:A:2143:HOH:O[3_455]	0.28	1.92

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	
1	A	327/327 (100%)	318 (97%)	8 (2%)	1 (0%)	43	25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	ASP

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	
1	A	285/283 (101%)	283 (99%)	2 (1%)	85	79

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	TRP
1	A	305	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	141	ASN
1	A	268	ASN
1	A	176	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	123	ASN
1	A	181	GLN

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	5CM	C	407	3,2	14,21,22	1.18	3 (21%)	19,30,33	2.53	5 (26%)
2	2PR	C	408	2	16,23,24	1.12	2 (12%)	17,33,36	1.63	2 (11%)

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	C	407	3,2	-	0/3/21/22	0/2/2/2
2	2PR	C	408	2	-	0/3/21/22	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	408	2PR	C6-N1	3.18	1.39	1.32
2	C	407	5CM	C5-C4	2.36	1.44	1.41
2	C	407	5CM	C4-N3	2.26	1.38	1.35
2	C	408	2PR	C8-N7	-2.13	1.30	1.34
2	C	407	5CM	O5'-C5'	-2.10	1.41	1.44

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	407	5CM	C2-N3-C4	9.52	126.78	115.92
2	C	408	2PR	C6-N1-C2	5.21	125.07	116.31
2	C	407	5CM	C5-C4-N3	-3.26	116.09	121.25
2	C	408	2PR	C2-N3-C4	-3.04	111.88	115.36
2	C	407	5CM	C5A-C5-C4	-2.44	119.24	121.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 ligands 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	$\# Z > 2$
4	SAH	A	1328	-	20,28,28	1.19	2 (10%)	19,40,40	0.96	1 (5%)
5	SO4	A	1329	-	4,4,4	1.92	2 (50%)	6,6,6	0.89	0
5	SO4	A	1330	-	4,4,4	1.93	2 (50%)	6,6,6	0.87	0
5	SO4	A	1331	-	4,4,4	1.94	2 (50%)	6,6,6	0.87	0
5	SO4	A	1332	-	4,4,4	1.91	2 (50%)	6,6,6	0.87	0
5	SO4	A	1333	-	4,4,4	1.90	2 (50%)	6,6,6	0.88	0
6	EPE	A	1334	-	15,15,15	1.20	1 (6%)	18,20,20	0.94	0
7	CIT	A	1335	-	3,12,12	1.46	1 (33%)	3,17,17	1.92	1 (33%)

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	1328	-	-	1/7/31/31	0/3/3/3
6	EPE	A	1334	-	-	1/9/19/19	0/1/1/1
7	CIT	A	1335	-	-	0/6/16/16	-

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1328	SAH	C4-N3	3.30	1.40	1.35
5	A	1331	SO4	O1-S	3.27	1.62	1.45
5	A	1330	SO4	O1-S	3.26	1.62	1.45
5	A	1329	SO4	O1-S	3.26	1.62	1.45
5	A	1332	SO4	O1-S	3.20	1.62	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1335	CIT	C3-C2-C1	3.17	120.06	114.98
4	A	1328	SAH	C5-C6-N6	2.64	124.52	120.38

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1334	EPE	N4-C7-C8-O8
4	A	1328	SAH	CB-CG-SD-C5'

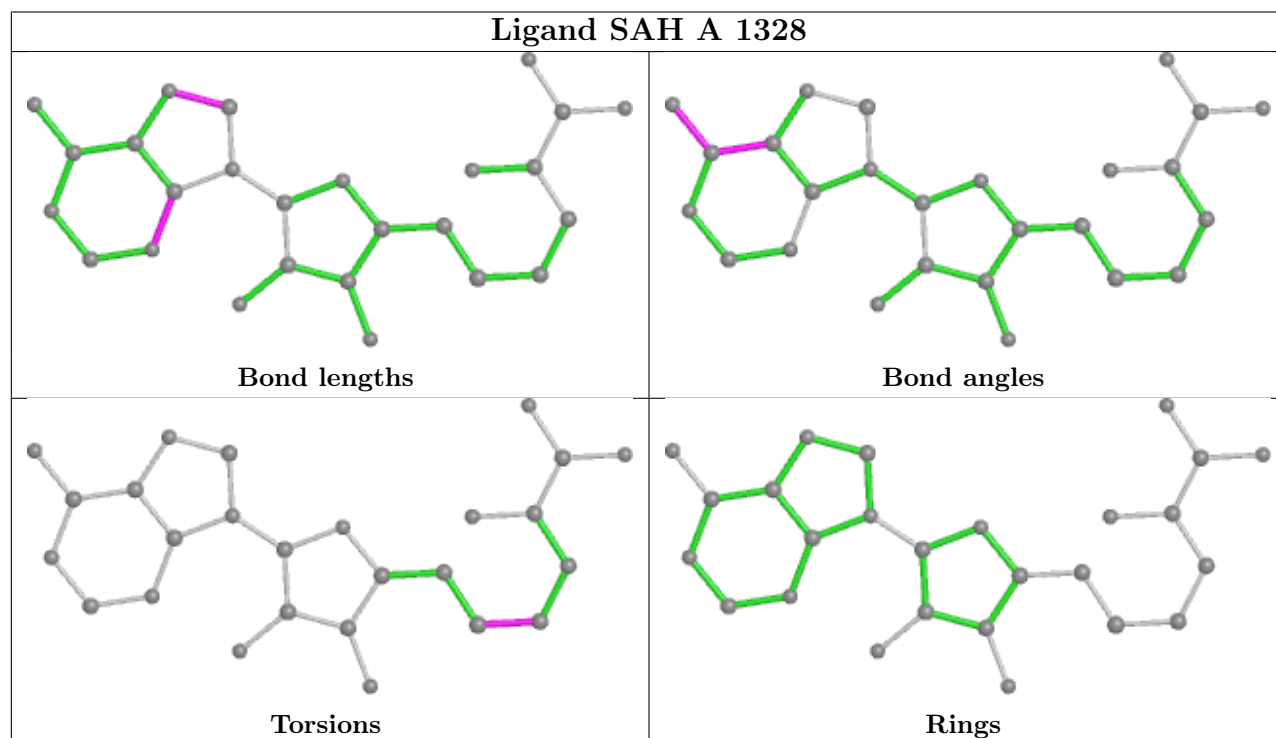
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1328	SAH	1	0
7	A	1335	CIT	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 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 [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.