



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 12:29 PM BST

PDB ID : 1Q0T  
Title : Ternary Structure of T4DAM with AdoHcy and DNA  
Authors : Yang, Z.; Horton, J.R.; Zhou, L.; Zhang, X.J.; Dong, A.; Zhang, X.; Schlagman, S.L.; Kossykh, V.; Hattman, S.; Cheng, X.  
Deposited on : 2003-07-17  
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

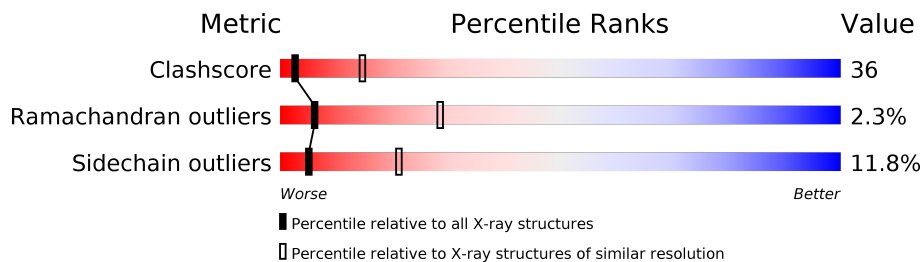
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)

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  $\geq 3$ , 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	C	12	42% 42% 17%
1	D	12	8% 83% 8%
2	A	259	42% 41% 10% 7%
2	B	259	37% 49% 7% 7%

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
3	IOD	C	2	-	-	X	-

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
3	IOD	D	1	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4538 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(\*AP\*CP\*AP\*GP\*GP\*AP\*TP\*CP\*CP\*TP\*GP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	C	12	Total 243	C 117	N 45	O 70	P 11	0	0	0
1	D	12	Total 243	C 117	N 45	O 70	P 11	0	0	0

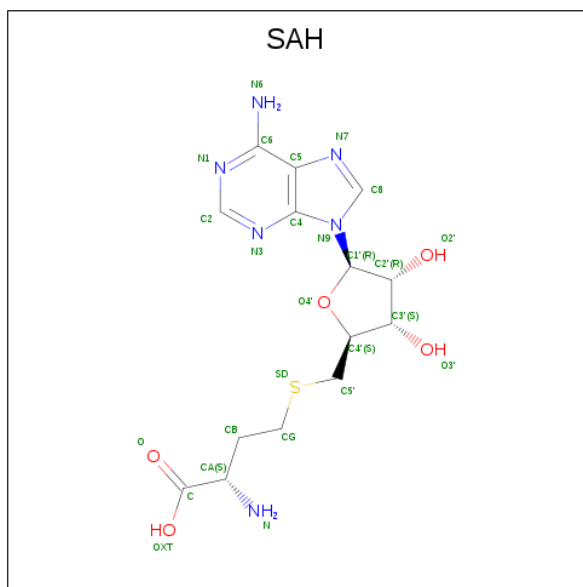
- Molecule 2 is a protein called DNA adenine methylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	241	Total 1999	C 1293	N 335	O 366	S 5	0	0	0
2	B	241	Total 1999	C 1293	N 335	O 366	S 5	0	0	0

- Molecule 3 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total 1 I 1	0	0
3	C	1	Total 1 I 1	0	0

- Molecule 4 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C<sub>14</sub>H<sub>20</sub>N<sub>6</sub>O<sub>5</sub>S).



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

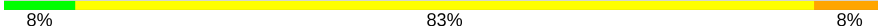
Note EDS was not executed.

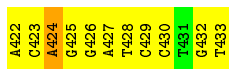
- Molecule 1: 5'-D(\*AP\*CP\*AP\*GP\*GP\*AP\*TP\*CP\*CP\*TP\*GP\*T)-3'

Chain C: 



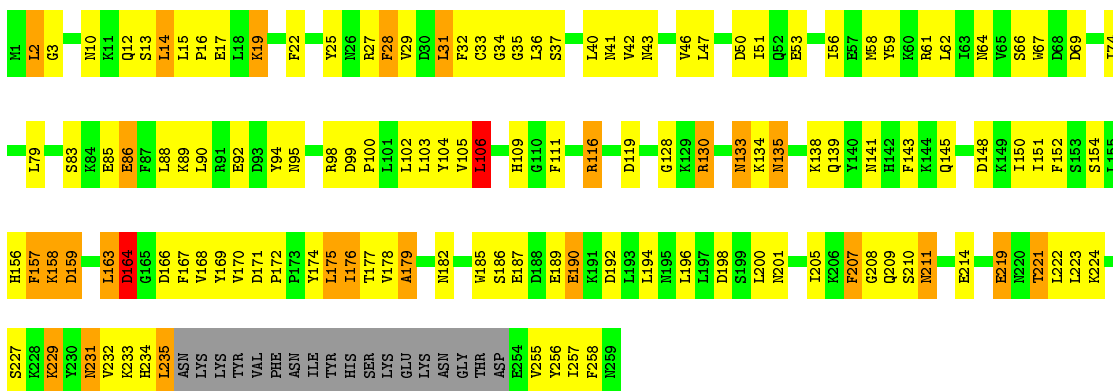
- Molecule 1: 5'-D(\*AP\*CP\*AP\*GP\*GP\*AP\*TP\*CP\*CP\*TP\*GP\*T)-3'

Chain D: 



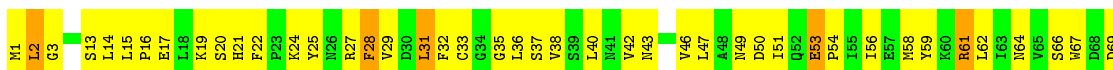
- Molecule 2: DNA adenine methylase

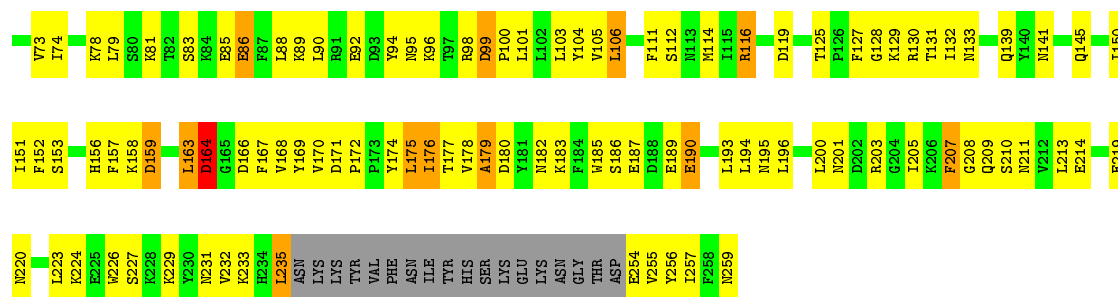
Chain A: 



- Molecule 2: DNA adenine methylase

Chain B: 





## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	39.70Å 109.70Å 73.60Å 90.00° 104.20° 90.00°	Depositor
Resolution (Å)	20.00 – 3.10	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-3.10)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.238 , 0.293	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4538	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	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: SAH, IOD

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	C	0.74	0/272	1.45	5/418 (1.2%)
1	D	0.70	0/272	0.87	0/418
2	A	0.45	0/2046	0.65	0/2756
2	B	0.42	0/2046	0.63	0/2756
All	All	0.48	0/4636	0.74	5/6348 (0.1%)

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	C	0	5
1	D	0	1
All	All	0	6

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	405	DG	N9-C1'-C2'	7.85	127.52	112.60
1	C	408	DT	O4'-C1'-N1	6.32	112.42	108.00
1	C	406	DG	N9-C1'-C2'	6.11	124.21	112.60
1	C	408	DT	O3'-P-O5'	5.91	115.23	104.00
1	C	410	DC	N1-C1'-C2'	5.47	122.99	112.60

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	404	DA	Sidechain
1	C	406	DG	Sidechain
1	C	407	DA	Sidechain
1	C	409	DC	Sidechain
1	C	410	DC	Sidechain
1	D	424	DA	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	C	243	0	137	30	0
1	D	243	0	137	15	0
2	A	1999	0	1997	141	0
2	B	1999	0	1997	137	0
3	C	1	0	0	2	0
3	D	1	0	0	2	0
4	A	26	0	19	4	0
4	B	26	0	19	2	0
All	All	4538	0	4306	320	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 36.

All (320) 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:D:423:DC:H5	3:D:1:IOD:I	1.94	1.21
2:B:83:SER:HB2	2:B:86:GLU:HG3	1.28	1.12
2:A:83:SER:HB2	2:A:86:GLU:HG3	1.35	1.08
1:C:403:DC:H5	3:C:2:IOD:I	2.08	1.07
1:D:423:DC:C5	3:D:1:IOD:I	2.78	1.06
2:A:50:ASP:HB3	2:A:56:ILE:HD11	1.40	1.04
2:A:15:LEU:HG	2:A:19:LYS:HD2	1.38	1.02
2:B:50:ASP:HB3	2:B:56:ILE:HD11	1.48	0.96
2:A:83:SER:HB2	2:A:86:GLU:CG	1.96	0.95
1:C:402:DA:H2''	1:C:403:DC:O5'	1.66	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:83:SER:HB2	2:B:86:GLU:CG	1.96	0.94
2:B:21:HIS:NE2	2:B:233:LYS:HE2	1.83	0.94
2:B:61:ARG:HH11	2:B:61:ARG:HG3	1.32	0.93
2:A:135:ASN:HD22	2:A:135:ASN:H	1.08	0.93
2:A:53:GLU:HG2	2:A:154:SER:CB	2.01	0.91
2:A:170:VAL:HG22	2:A:172:PRO:HD3	1.51	0.91
2:B:170:VAL:HG22	2:B:172:PRO:HD3	1.51	0.91
1:C:404:DA:H2''	1:C:405:DG:H5'	1.56	0.88
2:A:53:GLU:HG2	2:A:154:SER:HB2	1.58	0.85
2:A:141:ASN:O	2:A:145:GLN:HG2	1.78	0.84
1:C:403:DC:C5	3:C:2:IOD:I	2.99	0.82
2:A:14:LEU:HD12	2:A:14:LEU:H	1.44	0.81
2:A:135:ASN:N	2:A:135:ASN:HD22	1.80	0.79
2:B:19:LYS:HA	2:B:22:PHE:CD2	2.20	0.77
2:A:25:TYR:CE1	2:A:28:PHE:HB2	2.21	0.76
2:B:25:TYR:CE1	2:B:28:PHE:HB2	2.21	0.76
2:B:226:TRP:HA	2:B:229:LYS:HE3	1.67	0.76
2:A:232:VAL:HG12	2:A:257:ILE:HG12	1.68	0.76
2:B:232:VAL:HG12	2:B:257:ILE:HG12	1.67	0.76
2:B:141:ASN:O	2:B:145:GLN:HG2	1.86	0.75
2:A:135:ASN:H	2:A:135:ASN:ND2	1.84	0.74
2:B:169:TYR:HE2	2:B:171:ASP:HB2	1.54	0.72
1:C:408:DT:H2''	1:C:409:DC:O5'	1.88	0.72
2:A:85:GLU:OE2	2:A:85:GLU:HA	1.88	0.72
2:B:51:ILE:HB	4:B:301:SAH:C2	2.20	0.72
2:A:15:LEU:CG	2:A:19:LYS:HD2	2.20	0.71
2:A:164:ASP:OD2	2:A:164:ASP:N	2.23	0.71
2:A:17:GLU:OE2	2:A:235:LEU:HB3	1.91	0.71
2:B:21:HIS:CD2	2:B:233:LYS:HE2	2.27	0.70
2:B:15:LEU:HB3	2:B:16:PRO:HD3	1.75	0.69
2:A:33:CYS:HB2	2:A:36:LEU:HD23	1.74	0.69
1:C:412:DG:H2''	1:C:413:DT:C5'	2.24	0.68
2:B:14:LEU:HD12	2:B:14:LEU:H	1.57	0.68
1:C:407:DA:H2''	1:C:408:DT:C5'	2.23	0.68
2:B:61:ARG:NH1	2:B:61:ARG:HG3	2.03	0.68
2:A:35:GLY:O	2:A:36:LEU:HB2	1.95	0.67
2:B:33:CYS:HB2	2:B:36:LEU:HD23	1.76	0.67
2:B:209:GLN:HE21	2:B:210:SER:N	1.93	0.67
1:C:403:DC:H2''	1:C:404:DA:O5'	1.92	0.67
2:B:186:SER:OG	2:B:189:GLU:HG2	1.95	0.66
1:C:411:DT:OP2	2:A:133:ASN:HB2	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:226:TRP:O	2:B:229:LYS:HG3	1.94	0.66
2:B:32:PHE:CE1	2:B:170:VAL:HG23	2.31	0.66
2:A:32:PHE:CE1	2:A:170:VAL:HG23	2.31	0.66
1:D:425:DG:H1'	1:D:426:DG:C8	2.32	0.65
1:D:423:DC:H2''	1:D:424:DA:C8	2.32	0.65
2:B:29:VAL:CG1	2:B:168:VAL:HG22	2.28	0.64
2:A:29:VAL:CG1	2:A:168:VAL:HG22	2.28	0.64
2:A:14:LEU:N	2:A:14:LEU:HD12	2.13	0.63
2:A:190:GLU:O	2:A:194:LEU:HG	1.98	0.63
2:A:209:GLN:NE2	2:A:210:SER:O	2.31	0.63
2:A:135:ASN:N	2:A:135:ASN:ND2	2.41	0.63
2:A:169:TYR:HE2	2:A:171:ASP:HB2	1.63	0.63
2:B:94:TYR:CE1	2:B:103:LEU:HB2	2.34	0.63
2:A:25:TYR:HE1	2:A:28:PHE:HB2	1.63	0.62
2:A:15:LEU:HB3	2:A:16:PRO:HD3	1.80	0.62
2:B:163:LEU:O	2:B:164:ASP:O	2.18	0.62
2:B:235:LEU:H	2:B:235:LEU:HD12	1.65	0.62
2:B:209:GLN:HB3	2:B:257:ILE:O	2.00	0.61
2:A:158:LYS:HG2	2:A:159:ASP:N	2.15	0.61
1:C:407:DA:H2''	1:C:408:DT:H5'	1.83	0.60
2:A:74:ILE:HG23	2:A:79:LEU:HB2	1.83	0.60
2:A:163:LEU:O	2:A:164:ASP:O	2.20	0.60
1:C:406:DG:H2''	1:C:407:DA:O5'	2.02	0.60
2:A:61:ARG:HG3	2:A:61:ARG:HH11	1.66	0.59
2:B:227:SER:HB3	2:B:257:ILE:HD13	1.83	0.59
2:B:40:LEU:HD23	2:B:150:ILE:HD11	1.85	0.59
2:B:90:LEU:O	2:B:90:LEU:HD12	2.02	0.59
2:A:186:SER:OG	2:A:189:GLU:HG2	2.02	0.59
2:A:83:SER:HB2	2:A:86:GLU:HG2	1.84	0.59
2:B:190:GLU:O	2:B:194:LEU:HG	2.02	0.59
2:A:209:GLN:HE21	2:A:210:SER:N	2.01	0.58
1:C:404:DA:H2'	1:C:405:DG:C8	2.39	0.58
2:B:35:GLY:O	2:B:36:LEU:HB2	2.02	0.58
2:B:47:LEU:HD12	2:B:151:ILE:O	2.02	0.58
1:D:429:DC:H2''	1:D:430:DC:H5'	1.86	0.58
2:B:74:ILE:HG23	2:B:79:LEU:HB2	1.85	0.58
2:B:127:PHE:CE2	2:B:129:LYS:HA	2.38	0.58
2:A:19:LYS:HA	2:A:22:PHE:CD2	2.39	0.57
2:A:94:TYR:O	2:A:98:ARG:HD3	2.05	0.57
1:D:433:DT:H6	1:D:433:DT:H5'	1.68	0.57
2:B:169:TYR:CE2	2:B:171:ASP:HB2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:169:TYR:C	2:A:169:TYR:CD2	2.77	0.56
2:A:3:GLY:HA2	2:A:37:SER:HA	1.87	0.56
2:B:17:GLU:OE2	2:B:235:LEU:HB3	2.05	0.56
2:B:3:GLY:HA2	2:B:37:SER:HA	1.87	0.56
2:B:58:MET:HA	2:B:100:PRO:HB3	1.87	0.56
1:C:412:DG:H2''	1:C:413:DT:H5'	1.87	0.56
2:A:58:MET:HA	2:A:100:PRO:HB3	1.86	0.56
2:A:50:ASP:CB	2:A:56:ILE:HD11	2.25	0.56
1:C:404:DA:H2''	1:C:405:DG:C5'	2.34	0.56
2:B:170:VAL:CG2	2:B:172:PRO:HD3	2.29	0.56
2:B:209:GLN:NE2	2:B:210:SER:O	2.38	0.56
1:C:412:DG:H2''	1:C:413:DT:O5'	2.06	0.56
1:C:402:DA:H2''	1:C:403:DC:C5'	2.35	0.55
2:B:27:ARG:NH2	2:B:163:LEU:H	2.05	0.55
2:B:178:VAL:O	2:B:179:ALA:HB2	2.05	0.55
2:B:17:GLU:OE1	2:B:233:LYS:HE3	2.06	0.55
1:C:409:DC:H2''	1:C:410:DC:C5'	2.36	0.55
2:B:169:TYR:C	2:B:169:TYR:CD2	2.80	0.55
2:B:116:ARG:HG3	2:B:125:THR:OG1	2.07	0.55
2:B:175:LEU:HD12	2:B:190:GLU:HG3	1.88	0.55
2:A:2:LEU:HD22	2:A:139:GLN:HG2	1.87	0.54
2:A:175:LEU:HD12	2:A:190:GLU:HG3	1.90	0.54
2:B:214:GLU:HA	2:B:219:GLU:HA	1.88	0.54
2:A:134:LYS:O	2:A:138:LYS:HG3	2.06	0.54
1:C:409:DC:H2''	1:C:410:DC:H5'	1.89	0.54
2:B:158:LYS:HE2	2:B:159:ASP:OD1	2.07	0.54
2:A:14:LEU:CD1	2:A:14:LEU:H	2.19	0.54
1:D:427:DA:H1'	1:D:428:DT:H5''	1.88	0.54
2:A:66:SER:O	2:A:69:ASP:HB2	2.08	0.54
2:A:62:LEU:HD11	2:A:104:TYR:CE1	2.42	0.54
2:A:10:ASN:CG	2:A:12:GLN:HG3	2.29	0.54
2:A:214:GLU:HA	2:A:219:GLU:HA	1.89	0.54
2:A:28:PHE:HB3	2:A:46:VAL:HG22	1.90	0.54
2:A:111:PHE:HA	2:A:128:GLY:HA2	1.91	0.53
2:B:25:TYR:HE1	2:B:28:PHE:HB2	1.70	0.53
2:A:31:LEU:CD2	2:A:157:PHE:HB2	2.38	0.53
2:A:50:ASP:OD2	4:A:300:SAH:O2'	2.26	0.53
2:A:99:ASP:HB3	2:A:102:LEU:HD12	1.90	0.53
1:D:423:DC:H5'	1:D:423:DC:H6	1.74	0.53
2:B:50:ASP:CB	2:B:56:ILE:HD11	2.31	0.53
2:B:2:LEU:HD22	2:B:139:GLN:HG2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:235:LEU:HD12	2:B:235:LEU:N	2.24	0.52
2:A:27:ARG:NH2	2:A:163:LEU:H	2.07	0.52
2:A:13:SER:O	2:A:16:PRO:HD2	2.10	0.52
1:C:407:DA:H2''	1:C:408:DT:O5'	2.10	0.52
2:B:213:LEU:CD1	2:B:255:VAL:HG11	2.40	0.52
1:C:406:DG:H2''	1:C:407:DA:C5'	2.39	0.52
2:A:233:LYS:O	2:A:255:VAL:HA	2.10	0.52
1:C:408:DT:H4'	1:C:409:DC:OP1	2.10	0.52
2:B:209:GLN:NE2	2:B:210:SER:N	2.57	0.52
2:B:92:GLU:O	2:B:96:LYS:HG2	2.10	0.51
2:B:53:GLU:HB2	2:B:54:PRO:HD3	1.90	0.51
1:D:425:DG:H4'	1:D:426:DG:OP1	2.10	0.51
2:B:29:VAL:HG11	2:B:168:VAL:HG22	1.91	0.51
2:B:223:LEU:HD23	2:B:223:LEU:O	2.10	0.51
2:B:233:LYS:O	2:B:255:VAL:HA	2.11	0.51
2:A:32:PHE:CD1	2:A:170:VAL:HG23	2.45	0.51
2:A:223:LEU:O	2:A:223:LEU:HD23	2.10	0.51
2:A:150:ILE:HG21	2:A:152:PHE:CE2	2.46	0.51
2:A:116:ARG:HG3	2:A:116:ARG:NH1	2.24	0.51
2:B:166:ASP:OD1	2:B:166:ASP:N	2.43	0.51
2:A:40:LEU:HD23	2:A:150:ILE:HD11	1.92	0.51
2:B:111:PHE:O	2:B:112:SER:HB2	2.12	0.51
2:B:14:LEU:HD12	2:B:14:LEU:N	2.25	0.50
2:B:167:PHE:HZ	2:B:256:TYR:OH	1.94	0.50
2:B:66:SER:O	2:B:69:ASP:HB2	2.11	0.50
1:C:406:DG:H2'	1:C:407:DA:C8	2.45	0.50
2:A:99:ASP:C	2:A:99:ASP:OD1	2.48	0.50
2:B:156:HIS:CD2	2:B:158:LYS:H	2.29	0.50
1:D:432:DG:H1'	1:D:433:DT:H5''	1.93	0.50
2:A:235:LEU:HD12	2:A:235:LEU:H	1.76	0.50
2:A:227:SER:HB3	2:A:257:ILE:HD13	1.93	0.50
1:C:406:DG:OP1	2:B:133:ASN:HB2	2.11	0.50
2:A:167:PHE:HZ	2:A:256:TYR:OH	1.94	0.50
2:B:38:VAL:O	2:B:42:VAL:HG13	2.11	0.50
2:A:178:VAL:O	2:A:179:ALA:HB2	2.11	0.50
2:A:95:ASN:O	2:A:98:ARG:NE	2.43	0.50
2:B:176:ILE:HG13	2:B:176:ILE:O	2.11	0.50
2:A:156:HIS:CD2	2:A:158:LYS:H	2.30	0.50
2:B:112:SER:HA	2:B:130:ARG:NH1	2.26	0.50
2:A:169:TYR:CE2	2:A:171:ASP:HB2	2.44	0.50
1:D:422:DA:H2''	1:D:423:DC:H5'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:14:LEU:O	2:B:15:LEU:C	2.50	0.49
2:A:179:ALA:N	2:A:182:ASN:HD22	2.10	0.49
2:B:33:CYS:HG	2:B:49:ASN:C	2.16	0.49
2:A:207:PHE:CD2	2:A:207:PHE:C	2.85	0.49
2:B:196:LEU:O	2:B:196:LEU:HD12	2.13	0.49
2:A:233:LYS:HD3	2:A:234:HIS:H	1.78	0.49
2:B:207:PHE:CD2	2:B:207:PHE:C	2.86	0.49
2:B:56:ILE:O	2:B:59:TYR:HB2	2.13	0.49
2:A:130:ARG:HG3	2:A:130:ARG:HH11	1.76	0.49
2:A:14:LEU:O	2:A:15:LEU:C	2.51	0.49
2:A:166:ASP:N	2:A:166:ASP:OD1	2.44	0.48
2:A:47:LEU:HD12	2:A:151:ILE:O	2.13	0.48
2:A:67:TRP:CE3	2:A:67:TRP:HA	2.48	0.48
2:A:51:ILE:HB	4:A:300:SAH:C2	2.42	0.48
2:A:221:THR:HG22	2:A:222:LEU:N	2.29	0.48
2:B:29:VAL:HG12	2:B:167:PHE:O	2.13	0.48
2:B:99:ASP:OD1	2:B:99:ASP:C	2.52	0.48
2:A:85:GLU:OE2	2:A:88:LEU:HD12	2.13	0.48
2:A:85:GLU:OE2	2:A:85:GLU:CA	2.59	0.48
2:B:233:LYS:HD3	2:B:235:LEU:HG	1.94	0.48
2:B:83:SER:HB2	2:B:86:GLU:HG2	1.91	0.48
2:A:89:LYS:HA	2:A:92:GLU:HB2	1.96	0.48
2:B:177:THR:O	2:B:182:ASN:ND2	2.47	0.48
2:B:131:THR:HG23	2:B:132:ILE:N	2.28	0.47
2:B:180:ASP:O	2:B:183:LYS:HG2	2.14	0.47
2:A:31:LEU:HB3	2:A:32:PHE:CD1	2.50	0.47
2:B:193:LEU:O	2:B:196:LEU:HB3	2.13	0.47
2:B:33:CYS:HB2	2:B:36:LEU:CD2	2.42	0.47
2:A:169:TYR:CD2	2:A:170:VAL:N	2.83	0.47
2:B:179:ALA:N	2:B:182:ASN:HD22	2.12	0.47
2:A:10:ASN:OD1	2:A:12:GLN:HG3	2.15	0.47
2:A:61:ARG:HG3	2:A:61:ARG:NH1	2.28	0.47
2:B:159:ASP:OD1	2:B:159:ASP:N	2.47	0.47
2:A:29:VAL:HG11	2:A:168:VAL:HG22	1.96	0.47
2:B:200:LEU:O	2:B:205:ILE:HB	2.15	0.47
1:D:422:DA:H2''	1:D:423:DC:C5'	2.44	0.47
1:C:410:DC:OP1	2:A:130:ARG:NH2	2.49	0.46
2:B:32:PHE:CD1	2:B:170:VAL:HG23	2.50	0.46
2:B:67:TRP:CE3	2:B:67:TRP:HA	2.51	0.46
2:B:195:ASN:HD22	2:B:195:ASN:N	2.13	0.46
2:B:62:LEU:HD11	2:B:104:TYR:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95:ASN:O	2:B:98:ARG:NE	2.45	0.46
2:A:209:GLN:HB3	2:A:257:ILE:O	2.16	0.46
2:B:235:LEU:HD12	2:B:254:GLU:O	2.15	0.46
1:C:406:DG:H2'	1:C:407:DA:H8	1.80	0.46
2:B:201:ASN:HD22	2:B:259:ASN:HD22	1.65	0.45
2:A:208:GLY:CA	2:A:256:TYR:CE1	2.99	0.45
2:A:209:GLN:O	2:A:256:TYR:HA	2.17	0.45
2:A:105:VAL:O	2:A:109:HIS:HD2	2.00	0.45
2:A:33:CYS:HB2	2:A:36:LEU:CD2	2.43	0.45
2:B:40:LEU:HD23	2:B:150:ILE:CD1	2.45	0.45
2:A:35:GLY:N	4:A:300:SAH:O	2.47	0.45
2:B:169:TYR:CD2	2:B:170:VAL:N	2.85	0.45
2:B:170:VAL:HG12	2:B:208:GLY:O	2.17	0.45
2:A:27:ARG:NH2	2:A:166:ASP:OD2	2.35	0.45
2:A:256:TYR:CE2	2:A:258:PHE:HB3	2.52	0.45
2:A:56:ILE:O	2:A:59:TYR:HB2	2.17	0.45
2:A:79:LEU:HD11	2:A:90:LEU:HD22	1.99	0.45
2:B:73:VAL:HG11	2:B:105:VAL:HG21	1.98	0.44
1:C:409:DC:H2''	1:C:410:DC:O5'	2.17	0.44
2:B:33:CYS:SG	2:B:49:ASN:O	2.74	0.44
2:A:40:LEU:HD23	2:A:150:ILE:CD1	2.48	0.44
2:A:85:GLU:O	2:A:88:LEU:HB2	2.17	0.44
2:B:111:PHE:HA	2:B:128:GLY:HA2	1.99	0.44
2:A:198:ASP:O	2:A:201:ASN:HB3	2.18	0.44
2:A:35:GLY:O	2:A:36:LEU:CB	2.65	0.44
2:B:156:HIS:O	2:B:158:LYS:N	2.51	0.44
2:B:29:VAL:O	2:B:29:VAL:HG13	2.17	0.44
1:C:412:DG:C2'	1:C:413:DT:O5'	2.66	0.44
1:D:425:DG:H1'	1:D:426:DG:N7	2.33	0.44
2:B:28:PHE:HB3	2:B:46:VAL:HG22	2.00	0.44
2:B:61:ARG:NH1	2:B:61:ARG:CG	2.70	0.44
2:B:13:SER:O	2:B:16:PRO:HD2	2.18	0.44
2:B:15:LEU:O	2:B:16:PRO:C	2.56	0.44
2:B:101:LEU:O	2:B:105:VAL:HG23	2.18	0.44
2:B:220:ASN:OD1	2:B:223:LEU:HB2	2.17	0.44
2:A:174:TYR:CE1	2:A:211:ASN:HA	2.53	0.43
2:A:176:ILE:HG13	2:A:176:ILE:O	2.17	0.43
2:A:42:VAL:O	2:A:43:ASN:C	2.56	0.43
2:B:85:GLU:O	2:B:88:LEU:HB2	2.18	0.43
2:A:111:PHE:HA	2:A:128:GLY:CA	2.48	0.43
2:B:49:ASN:HB2	2:B:153:SER:OG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:94:TYR:O	2:B:98:ARG:HD3	2.18	0.43
2:A:31:LEU:HD21	2:A:157:PHE:HB2	2.00	0.43
2:B:89:LYS:HA	2:B:92:GLU:HB2	2.01	0.43
2:B:187:GLU:O	2:B:190:GLU:HB2	2.18	0.43
1:C:409:DC:C2'	1:C:410:DC:O5'	2.67	0.43
2:A:170:VAL:CG2	2:A:172:PRO:HD3	2.35	0.43
2:A:33:CYS:O	2:A:34:GLY:C	2.56	0.43
2:A:15:LEU:O	2:A:16:PRO:C	2.56	0.42
2:B:94:TYR:CZ	2:B:103:LEU:HB2	2.54	0.42
2:A:31:LEU:HD23	2:A:157:PHE:HB2	2.01	0.42
2:A:62:LEU:HD23	2:A:62:LEU:HA	1.74	0.42
2:B:209:GLN:O	2:B:256:TYR:HA	2.19	0.42
2:A:231:ASN:N	2:A:231:ASN:OD1	2.52	0.42
2:B:112:SER:HB2	2:B:114:MET:HG2	2.01	0.42
2:B:203:ARG:C	2:B:205:ILE:H	2.23	0.42
2:A:156:HIS:O	2:A:158:LYS:N	2.52	0.42
2:A:42:VAL:O	2:A:42:VAL:HG23	2.19	0.42
1:D:429:DC:H1'	1:D:430:DC:H5''	2.00	0.42
2:B:29:VAL:HG13	2:B:168:VAL:HG13	2.02	0.42
2:B:150:ILE:HG21	2:B:152:PHE:CE2	2.55	0.42
2:B:17:GLU:OE1	2:B:233:LYS:CE	2.68	0.42
2:B:24:LYS:O	2:B:25:TYR:HB3	2.20	0.42
2:A:27:ARG:O	2:A:166:ASP:HB2	2.20	0.42
2:A:15:LEU:HD21	2:A:41:ASN:HB2	2.02	0.42
2:B:31:LEU:HB3	2:B:32:PHE:CD1	2.55	0.42
2:A:159:ASP:N	2:A:159:ASP:OD1	2.52	0.41
2:A:177:THR:O	2:A:182:ASN:ND2	2.53	0.41
2:A:53:GLU:HG2	2:A:154:SER:OG	2.19	0.41
2:A:106:LEU:HA	2:A:106:LEU:HD23	1.82	0.41
2:A:200:LEU:O	2:A:205:ILE:HB	2.20	0.41
2:B:156:HIS:HD2	2:B:158:LYS:H	1.67	0.41
2:B:209:GLN:HE21	2:B:209:GLN:C	2.24	0.41
2:A:224:LYS:O	2:A:227:SER:OG	2.38	0.41
2:A:229:LYS:CB	2:A:229:LYS:NZ	2.83	0.41
2:A:187:GLU:O	2:A:190:GLU:HB2	2.20	0.41
1:C:410:DC:H2''	1:C:411:DT:O5'	2.19	0.41
2:A:105:VAL:O	2:A:109:HIS:CD2	2.74	0.41
2:A:116:ARG:HH11	2:A:116:ARG:HG3	1.84	0.41
2:A:171:ASP:OD2	2:A:171:ASP:C	2.59	0.41
2:A:209:GLN:HE21	2:A:210:SER:C	2.22	0.41
2:A:235:LEU:HD12	2:A:235:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:407:DA:C2'	1:C:408:DT:O5'	2.68	0.41
2:A:100:PRO:O	2:A:103:LEU:N	2.53	0.41
2:A:29:VAL:HG13	2:A:168:VAL:HA	2.03	0.41
2:B:195:ASN:N	2:B:195:ASN:ND2	2.68	0.41
2:A:32:PHE:HD2	4:A:300:SAH:O4'	2.04	0.41
2:B:163:LEU:O	2:B:166:ASP:OD1	2.37	0.41
2:B:224:LYS:O	2:B:227:SER:OG	2.39	0.41
2:B:32:PHE:HD2	4:B:301:SAH:O4'	2.03	0.41
2:B:33:CYS:SG	2:B:50:ASP:HB2	2.61	0.41
2:A:170:VAL:HG12	2:A:208:GLY:O	2.21	0.41
2:B:15:LEU:HB3	2:B:16:PRO:CD	2.48	0.41
2:A:156:HIS:HD2	2:A:158:LYS:H	1.68	0.41
2:B:42:VAL:HG23	2:B:42:VAL:O	2.21	0.41
2:B:62:LEU:HD23	2:B:62:LEU:HA	1.83	0.41
2:A:233:LYS:HD3	2:A:234:HIS:N	2.36	0.40
2:B:14:LEU:CD1	2:B:14:LEU:H	2.31	0.40
2:B:17:GLU:OE1	2:B:233:LYS:NZ	2.51	0.40
1:D:432:DG:H2''	1:D:433:DT:C5'	2.50	0.40
2:A:62:LEU:HB3	2:A:143:PHE:CE2	2.56	0.40
2:A:196:LEU:O	2:A:196:LEU:HD12	2.21	0.40
2:B:53:GLU:CB	2:B:54:PRO:HD3	2.50	0.40
2:B:174:TYR:HB2	2:B:177:THR:HB	2.04	0.40
2:B:42:VAL:O	2:B:43:ASN:C	2.59	0.40

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
2	A	237/259 (92%)	194 (82%)	37 (16%)	6 (2%)	<b>5</b>   <b>27</b>
2	B	237/259 (92%)	196 (83%)	36 (15%)	5 (2%)	<b>7</b>   <b>30</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	474/518 (92%)	390 (82%)	73 (15%)	11 (2%)	6	28

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	164	ASP
2	B	164	ASP
2	A	157	PHE
2	A	179	ALA
2	B	157	PHE
2	B	179	ALA
2	A	221	THR
2	B	106	LEU
2	A	106	LEU
2	A	176	ILE
2	B	176	ILE

### 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	
2	A	225/242 (93%)	197 (88%)	28 (12%)	4	19
2	B	225/242 (93%)	200 (89%)	25 (11%)	6	24
All	All	450/484 (93%)	397 (88%)	53 (12%)	5	21

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	2	LEU
2	A	14	LEU
2	A	19	LYS
2	A	28	PHE
2	A	31	LEU
2	A	64	ASN
2	A	86	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	A	106	LEU
2	A	116	ARG
2	A	119	ASP
2	A	130	ARG
2	A	133	ASN
2	A	135	ASN
2	A	148	ASP
2	A	158	LYS
2	A	159	ASP
2	A	163	LEU
2	A	164	ASP
2	A	175	LEU
2	A	185	TRP
2	A	190	GLU
2	A	192	ASP
2	A	207	PHE
2	A	211	ASN
2	A	219	GLU
2	A	229	LYS
2	A	231	ASN
2	A	235	LEU
2	B	1	MET
2	B	2	LEU
2	B	20	SER
2	B	28	PHE
2	B	31	LEU
2	B	53	GLU
2	B	61	ARG
2	B	64	ASN
2	B	78	LYS
2	B	81	LYS
2	B	86	GLU
2	B	99	ASP
2	B	106	LEU
2	B	116	ARG
2	B	119	ASP
2	B	159	ASP
2	B	163	LEU
2	B	164	ASP
2	B	175	LEU
2	B	185	TRP
2	B	190	GLU

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Mol	Chain	Res	Type
2	B	207	PHE
2	B	211	ASN
2	B	231	ASN
2	B	235	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	12	GLN
2	A	43	ASN
2	A	109	HIS
2	A	135	ASN
2	A	139	GLN
2	A	141	ASN
2	A	156	HIS
2	A	182	ASN
2	A	201	ASN
2	A	209	GLN
2	B	12	GLN
2	B	43	ASN
2	B	109	HIS
2	B	139	GLN
2	B	141	ASN
2	B	156	HIS
2	B	182	ASN
2	B	201	ASN
2	B	209	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](#)

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
4	SAH	A	300	-	21,28,28	0.68	0	20,40,40	1.20	2 (10%)
4	SAH	B	301	-	21,28,28	0.74	1 (4%)	20,40,40	1.06	2 (10%)

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	300	-	-	0/7/31/31	0/3/3/3
4	SAH	B	301	-	-	1/7/31/31	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	301	SAH	CA-N	-2.08	1.42	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	300	SAH	C5'-SD-CG	3.79	113.64	102.27
4	B	301	SAH	C4'-C5'-SD	-2.62	104.38	113.78
4	A	300	SAH	C5-C6-N6	2.22	123.72	120.35
4	B	301	SAH	C5-C6-N6	2.03	123.43	120.35

There are no chirality outliers.

All (1) torsion outliers are listed below:

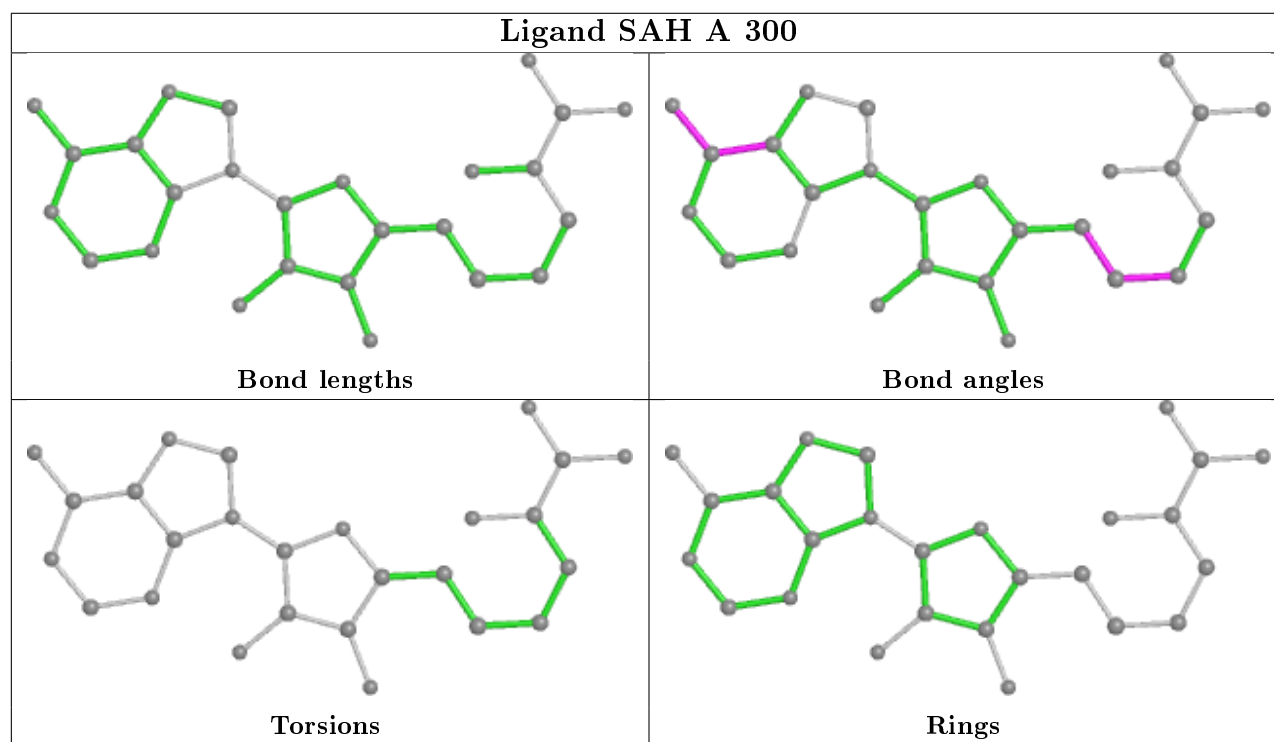
Mol	Chain	Res	Type	Atoms
4	B	301	SAH	CB-CG-SD-C5'

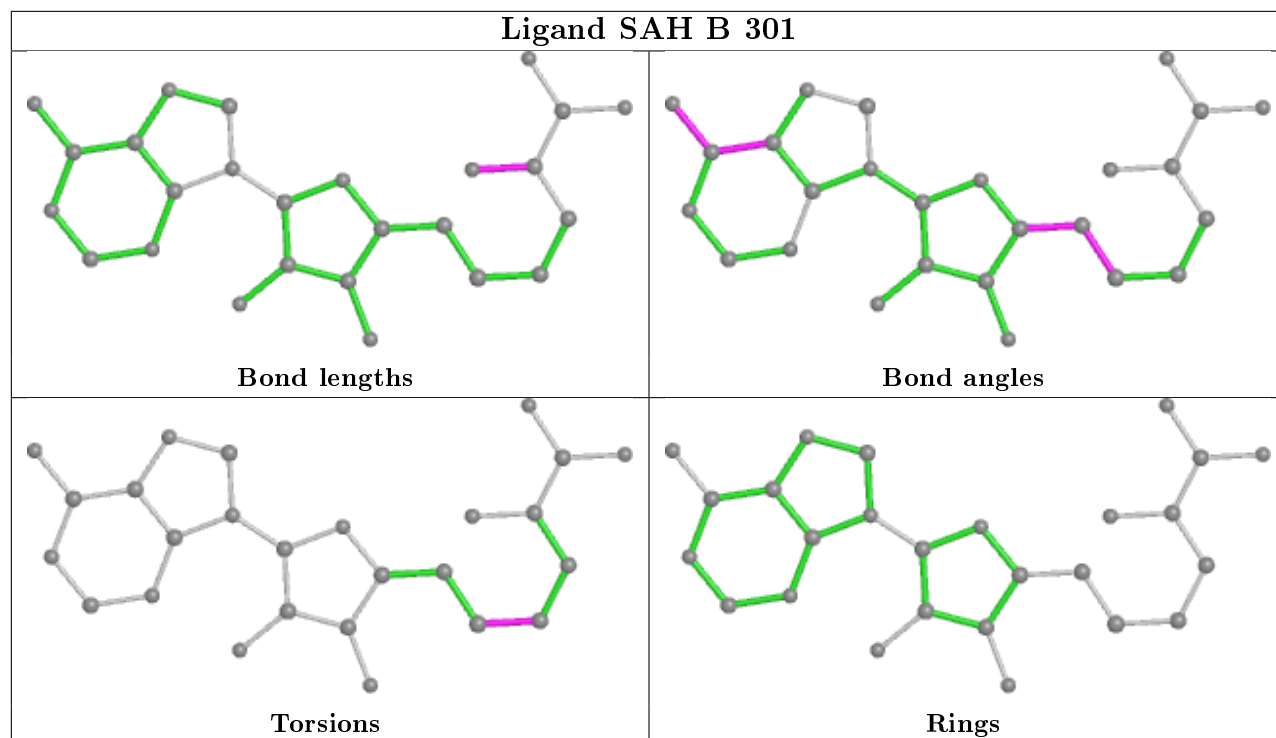
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	300	SAH	4	0
4	B	301	SAH	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

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.