wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 12:46 AM GMT

PDB ID	:	2BH2
Title	:	CRYSTAL STRUCTURE OF E. COLI 5-METHYLURIDINE METHYLTRANSFERASE RUMA IN COMPLEX WITH RIBOSOMAL RNA SUBSTRATE AND S-ADENOSYLHOMOCYSTEINE.
Authors	:	Lee, T.T.; Agarwalla, S.; Stroud, R.M.
Deposited on	:	2005-01-06
Resolution	:	2.15 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

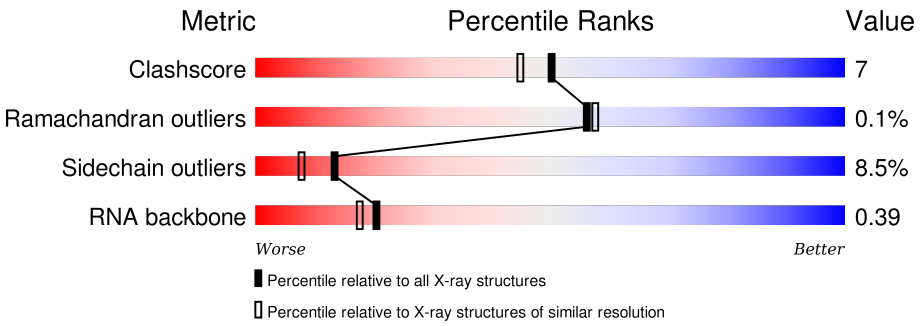
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.15 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	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RNA backbone	2183	1077 (2.80-1.52)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	433	74% 19% • •
1	B	433	76% 17% • •
2	C	37	30% 35% 11% 5% 19%
2	D	37	38% 22% 16% 5% 19%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8156 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.

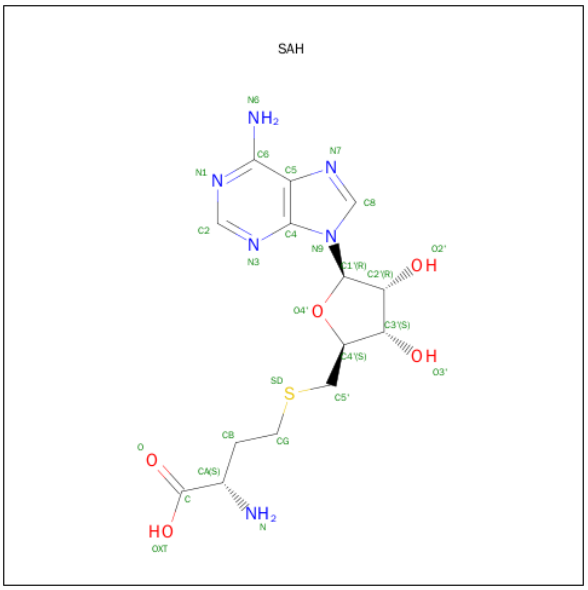
- Molecule 1 is a protein called 23S RRNA (URACIL-5-)-METHYLTRANSFERASE RUMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	418	3245	2039	586	602	18	0	0	0
1	B	416	3229	2029	583	599	18	0	0	0

- Molecule 2 is a RNA chain called 23S RIBOSOMAL RNA 1932-1968.

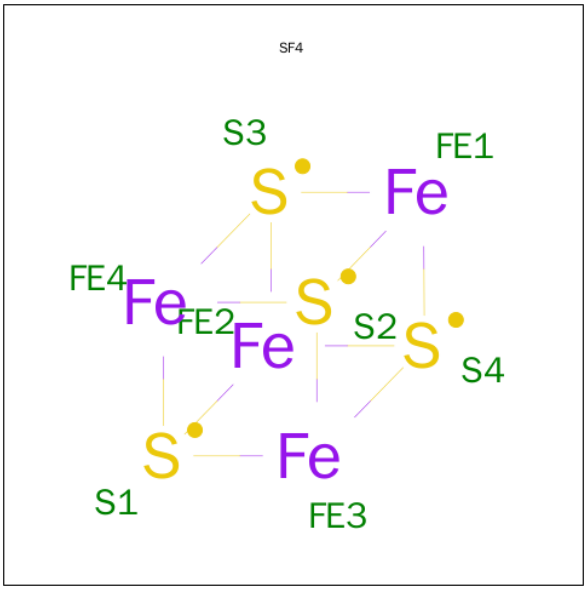
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	F	N	O	P			
2	C	30	637	286	1	112	209	29	0	0	0
2	D	30	637	286	1	112	209	29	0	0	0

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



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

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
4	A	1	8	4	4	0	0
			Total	Fe	S		
4	B	1	8	4	4	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	143	143	143	0	0
			Total	O		
5	B	142	142	142	0	0
			Total	O		
5	C	23	23	23	0	0
			Total	O		
5	D	32	32	32	0	0

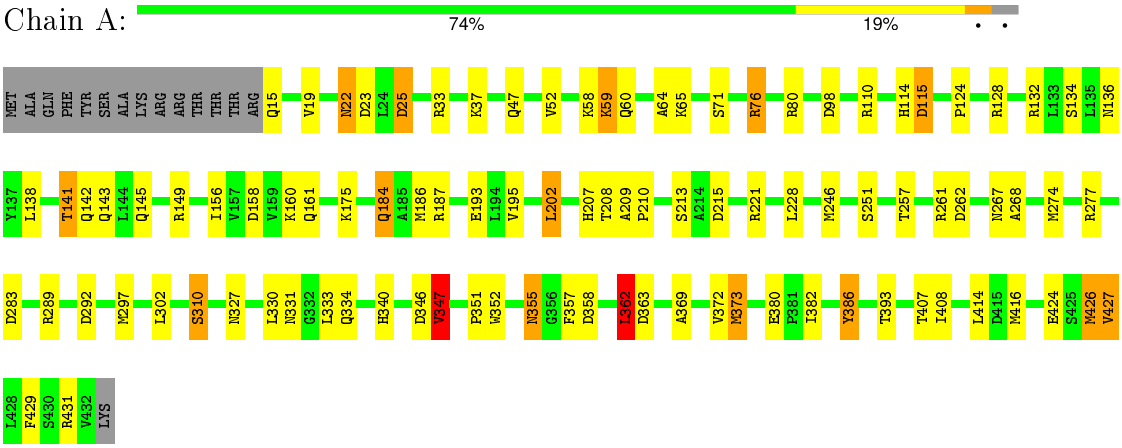
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

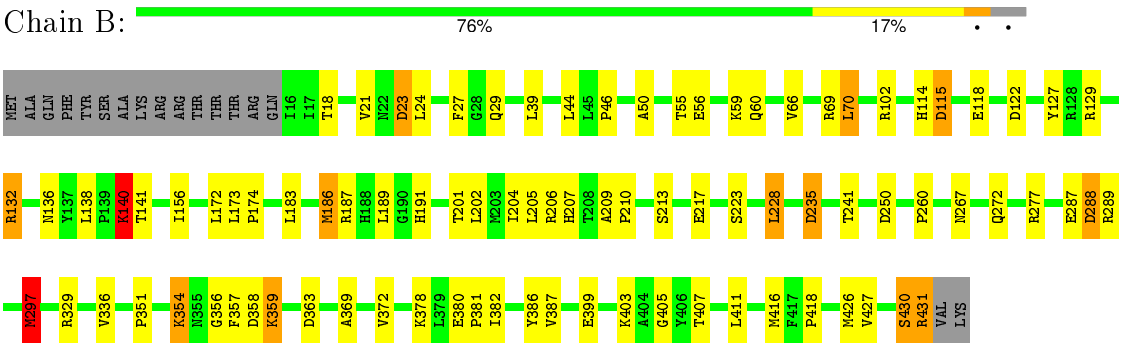
- Molecule 1: 23S RRNA (URACIL-5-)-METHYLTRANSFERASE RUMA

Chain A:



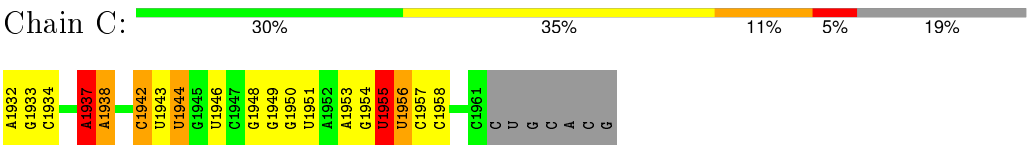
- Molecule 1: 23S RRNA (URACIL-5-)-METHYLTRANSFERASE RUMA

Chain B:



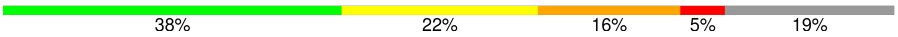
- Molecule 2: 23S RIBOSOMAL RNA 1932-1968

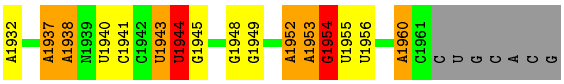
Chain C:



- Molecule 2: 23S RIBOSOMAL RNA 1932-1968

Chain D:


38%
22%
16%
5%
19%


A1932
A1937
A1938
N1939
U1940
C1941
C1942
U1943
U1944
G1945
G1948
G1949
A1952
A1953
G1954
U1955
U1956
A1960
C1961
C
U
G
C
A
C
G

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	190.06Å 63.54Å 112.02Å 90.00° 125.15° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15	Depositor
% Data completeness (in resolution range)	99.6 (50.00-2.15)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.174 , 0.229	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8156	wwPDB-VP
Average B, all atoms (Å^2)	48.0	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: SF4, SAH, FMU

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	0.92	6/3306 (0.2%)	1.01	21/4480 (0.5%)
1	B	0.93	2/3290 (0.1%)	0.99	11/4458 (0.2%)
2	C	1.47	1/687 (0.1%)	2.13	30/1069 (2.8%)
2	D	1.51	1/687 (0.1%)	2.12	26/1069 (2.4%)
All	All	1.04	10/7970 (0.1%)	1.30	88/11076 (0.8%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	297	MET	SD-CE	-9.35	1.25	1.77
1	A	373	MET	SD-CE	-6.65	1.40	1.77
1	B	359	LYS	CE-NZ	-6.16	1.33	1.49
1	A	268	ALA	CA-CB	6.03	1.65	1.52
1	A	347	VAL	CB-CG2	-5.81	1.40	1.52

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1956	U	O4'-C1'-N1	12.80	118.44	108.20
2	D	1944	U	O4'-C1'-N1	10.84	116.88	108.20
2	D	1932	A	O4'-C1'-N9	10.82	116.85	108.20
2	D	1952	A	P-O3'-C3'	10.41	132.19	119.70
2	C	1956	U	O4'-C1'-N1	10.34	116.47	108.20

There are no chirality outliers.

There are no planarity outliers.

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	A	3245	0	3268	45	0
1	B	3229	0	3251	54	0
2	C	637	0	326	7	0
2	D	637	0	326	4	0
3	A	26	0	19	0	0
3	B	26	0	19	0	0
4	A	8	0	0	0	0
4	B	8	0	0	0	0
5	A	143	0	0	9	0
5	B	142	0	0	5	0
5	C	23	0	0	2	0
5	D	32	0	0	0	0
All	All	8156	0	7209	105	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 7.

The worst 5 of 105 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:1937:A:N6	5:C:2003:HOH:O	2.01	0.94
1:B:217:GLU:HG2	5:B:2064:HOH:O	1.70	0.91
1:B:288:ASP:OD2	1:B:359:LYS:HE3	1.73	0.88
1:B:288:ASP:OD2	1:B:359:LYS:CE	2.23	0.86
2:C:1955:U:OP2	2:C:1956:U:H5	1.66	0.78

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	
1	A	416/433 (96%)	404 (97%)	12 (3%)	0	100	100
1	B	414/433 (96%)	400 (97%)	13 (3%)	1 (0%)	52	51
All	All	830/866 (96%)	804 (97%)	25 (3%)	1 (0%)	56	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	140	LYS

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	352/365 (96%)	319 (91%)	33 (9%)	11	5
1	B	350/365 (96%)	323 (92%)	27 (8%)	16	10
All	All	702/730 (96%)	642 (92%)	60 (8%)	13	8

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	362	LEU
1	B	18	THR
1	B	382	ILE
1	A	386	TYR
1	B	39	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	331	ASN
1	A	340	HIS

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Mol	Chain	Res	Type
1	B	142	GLN
1	A	207	HIS
1	B	34	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	30/37 (81%)	4 (13%)	1 (3%)
2	D	29/37 (78%)	8 (27%)	5 (17%)
All	All	59/74 (79%)	12 (20%)	6 (10%)

5 of 12 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	1937	A
2	C	1938	A
2	C	1944	U
2	C	1955	U
2	D	1937	A

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	D	1943	U
2	D	1953	A
2	D	1944	U
2	D	1937	A
2	D	1952	A

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

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	FMU	C	1939	1,2	15,23,24	1.14	2 (13%)	21,35,38	1.98	5 (23%)
2	FMU	D	1939	1,2	15,23,24	1.28	2 (13%)	21,35,38	1.68	5 (23%)

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	FMU	C	1939	1,2	-	0/7/44/45	0/2/2/2
2	FMU	D	1939	1,2	-	0/7/44/45	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1939	FMU	C2-N3	-3.20	1.32	1.38
2	D	1939	FMU	C2-N3	-2.84	1.32	1.38
2	D	1939	FMU	C4-N3	-2.03	1.34	1.37
2	C	1939	FMU	C6-N1	2.06	1.48	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1939	FMU	O2-C2-N1	-2.69	119.78	123.30
2	D	1939	FMU	O2-C2-N3	-2.68	116.23	121.48
2	D	1939	FMU	C4-N3-C2	-2.62	122.13	126.84
2	D	1939	FMU	O4-C4-N3	-2.45	116.37	120.50
2	C	1939	FMU	C4'-O4'-C1'	-2.18	104.72	109.52

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)

4 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	$\#\|Z\| > 2$
3	SAH	A	500	-	20,28,28	1.31	2 (10%)	19,40,40	3.43	6 (31%)
4	SF4	A	501	1	0,12,12	0.00	-	0,24,24	0.00	-
3	SAH	B	500	-	20,28,28	1.03	1 (5%)	19,40,40	2.86	3 (15%)
4	SF4	B	501	1	0,12,12	0.00	-	0,24,24	0.00	-

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
3	SAH	A	500	-	-	0/7/31/31	0/3/3/3
4	SF4	A	501	1	-	0/0/48/48	0/6/5/5
3	SAH	B	500	-	-	0/7/31/31	0/3/3/3
4	SF4	B	501	1	-	0/0/48/48	0/6/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	500	SAH	C5-N7	-2.93	1.29	1.39
3	A	500	SAH	C2-N1	2.55	1.38	1.33
3	A	500	SAH	C2-N3	4.61	1.40	1.32

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	500	SAH	N3-C2-N1	-13.40	118.63	128.89
3	B	500	SAH	N3-C2-N1	-11.53	120.07	128.89
3	A	500	SAH	C4-C5-N7	-3.14	106.59	109.48
3	A	500	SAH	C1'-N9-C4	-2.46	123.23	126.94
3	A	500	SAH	C2'-C1'-N9	-2.40	110.63	114.29

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 will therefore be empty.

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

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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