Full wwPDB X-ray Structure Validation Report (i)

Nov 12, 2017 – 06:20 AM EST

PDB ID	:	4O5W
Title	:	O6-carboxymethylguanine in DNA forms a sequence context dependent wobble base pair structure with thymine
Authors	:	Zhang, F.; Tsunoda, M.; Suzuki, K.; Kikuchi, Y.; Wilkinson, O.; Millington, C.L.; Margison, G.P.; Williams, D.M.; Takenaka, A.
Deposited on	:	unknown
Resolution	:	1.60 Å(reported)

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

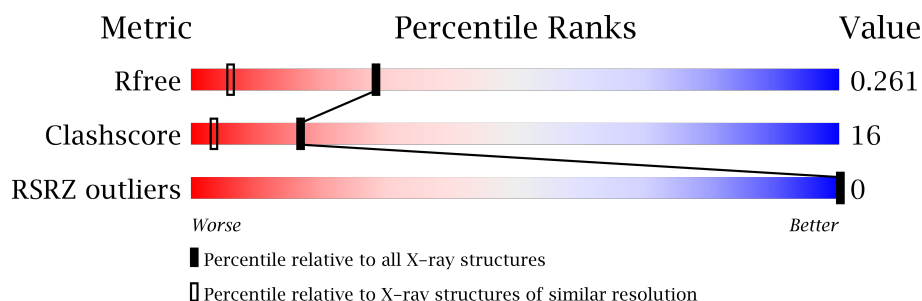|		
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

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 1.60 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	Percentile Ranks	Value
Rfree		0.261
Clashscore		16
RSRZ outliers		0

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2696 (1.60-1.60)
Clashscore	112137	2967 (1.60-1.60)
RSRZ outliers	101464	2714 (1.60-1.60)

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 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.

Mol	Chain	Length	Quality of chain
1	A	12	83% 17%
1	B	12	17% 67% 17%

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
2	HT	A	101	-	-	X	X
3	MG	A	103	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 640 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(*CP*GP*CP*(C6G)P*AP*AP*TP*TP*TP*GP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	12	Total	C	N	O	P	0	0	0
			248	119	45	73	11			
1	B	12	Total	C	N	O	P	0	0	0
			248	119	45	73	11			

- Molecule 2 is 2'-(4-HYDROXYPHENYL)-5-(4-METHYL-1-PIPERAZINYL)-2,5'-BI-BENZ IMIDAZOLE (three-letter code: HT) (formula: $C_{25}H_{24}N_6O$).
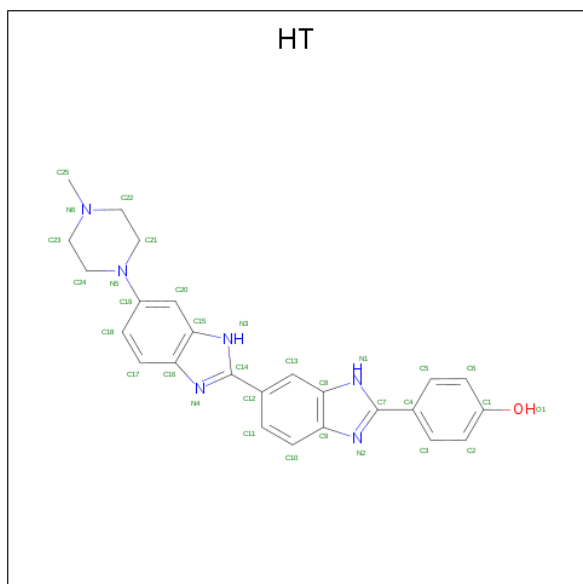
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			32	25	6	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Mg 2	0	0

- Molecule 4 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Sr 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	48	Total 48	O 48	0	0
5	B	61	Total 61	O 61	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 the various outlier classes 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.

• Molecule 1: DNA (5'-D(*CP*GP*CP*(C6G)P*AP*AP*TP*TP*TP*GP*CP*G)-3')

Chain A:
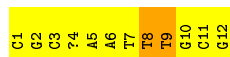
• Molecule 1: DNA (5'-D(*CP*GP*CP*(C6G)P*AP*AP*TP*TP*TP*GP*CP*G)-3')

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	25.86Å 40.29Å 65.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.29 – 1.60 17.14 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.1 (34.29-1.60) 99.2 (17.14-1.60)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.97 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.225 , 0.255 0.221 , 0.261	Depositor DCC
R_{free} test set	448 reflections (5.00%)	DCC
Wilson B-factor (Å^2)	24.8	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 42.2	EDS
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	640	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.55% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: SR, MG, HT, C6G

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	2.79	18/247 (7.3%)	2.59	23/377 (6.1%)
1	B	2.65	13/247 (5.3%)	2.51	19/377 (5.0%)
All	All	2.72	31/494 (6.3%)	2.55	42/754 (5.6%)

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	8	DT	N1-C6	10.43	1.45	1.38
1	A	7	DT	N1-C6	9.72	1.45	1.38
1	A	7	DT	C5-C6	-8.66	1.28	1.34
1	B	18	DA	N3-C4	-8.65	1.29	1.34
1	B	15	DC	C2-N3	-7.42	1.29	1.35
1	B	14	DG	N9-C4	7.33	1.43	1.38
1	B	23	DC	N3-C4	-7.30	1.28	1.33
1	B	15	DC	C3'-O3'	-7.24	1.34	1.44
1	A	5	DA	N9-C4	7.18	1.42	1.37
1	B	13	DC	N3-C4	-6.75	1.29	1.33
1	A	5	DA	N9-C8	-6.59	1.32	1.37
1	A	3	DC	C2'-C1'	-6.26	1.46	1.52
1	A	2	DG	N9-C8	6.22	1.42	1.37
1	B	14	DG	C3'-C2'	-6.22	1.44	1.52
1	A	12	DG	P-O5'	6.15	1.65	1.59
1	B	18	DA	N9-C4	6.09	1.41	1.37
1	A	5	DA	C5-C4	-6.08	1.34	1.38
1	A	12	DG	N7-C5	5.72	1.42	1.39
1	B	21	DT	C5-C6	-5.70	1.30	1.34
1	A	10	DG	C6-N1	-5.62	1.35	1.39
1	A	10	DG	P-O5'	5.60	1.65	1.59
1	B	22	DG	C4'-O4'	5.55	1.50	1.45
1	A	3	DC	O4'-C1'	5.47	1.48	1.42
1	B	14	DG	C5-C4	-5.45	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	11	DC	N1-C6	-5.37	1.33	1.37
1	A	12	DG	C5-C4	-5.37	1.34	1.38
1	B	19	DT	C3'-C2'	5.36	1.58	1.52
1	A	1	DC	C2-N3	-5.28	1.31	1.35
1	A	3	DC	P-O5'	5.25	1.65	1.59
1	A	12	DG	N3-C4	-5.01	1.31	1.35
1	B	22	DG	C3'-O3'	-5.01	1.37	1.44

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	11	DC	O4'-C4'-C3'	-12.93	98.24	106.00
1	A	5	DA	N7-C8-N9	9.61	118.60	113.80
1	B	24	DG	O5'-P-OP2	-9.13	97.48	105.70
1	A	5	DA	C5-N7-C8	-8.74	99.53	103.90
1	A	11	DC	O4'-C1'-N1	-8.67	101.93	108.00
1	B	13	DC	C2-N3-C4	8.23	124.01	119.90
1	B	24	DG	OP1-P-OP2	8.06	131.70	119.60
1	A	9	DT	N3-C2-O2	7.92	127.05	122.30
1	B	14	DG	N3-C4-C5	7.78	132.49	128.60
1	A	3	DC	OP1-P-OP2	7.05	130.17	119.60
1	B	14	DG	N1-C2-N3	-6.98	119.71	123.90
1	B	13	DC	O4'-C1'-C2'	-6.94	100.35	105.90
1	A	2	DG	O4'-C1'-N9	-6.92	103.16	108.00
1	B	21	DT	C5-C6-N1	6.84	127.81	123.70
1	B	18	DA	O4'-C1'-C2'	-6.84	100.43	105.90
1	A	1	DC	C6-N1-C2	-6.83	117.57	120.30
1	B	20	DT	O4'-C1'-N1	-6.80	103.24	108.00
1	B	14	DG	C6-N1-C2	6.72	129.13	125.10
1	A	2	DG	C4-C5-N7	6.62	113.45	110.80
1	A	7	DT	C6-N1-C2	-6.55	118.03	121.30
1	B	23	DC	C2-N3-C4	6.54	123.17	119.90
1	A	10	DG	C3'-C2'-C1'	-6.51	94.69	102.50
1	A	5	DA	C8-N9-C4	-6.32	103.27	105.80
1	B	14	DG	C4-C5-N7	6.28	113.31	110.80
1	A	2	DG	OP1-P-OP2	5.90	128.45	119.60
1	A	6	DA	OP1-P-OP2	5.79	128.28	119.60
1	B	23	DC	OP1-P-OP2	5.75	128.23	119.60
1	B	21	DT	C4-C5-C7	5.74	122.44	119.00
1	A	2	DG	O5'-P-OP2	-5.64	100.62	105.70
1	A	7	DT	N1-C2-N3	5.62	117.97	114.60
1	B	23	DC	N3-C4-N4	5.48	121.84	118.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	3	DC	C5-C4-N4	-5.48	116.37	120.20
1	A	1	DC	N3-C4-C5	-5.42	119.73	121.90
1	A	8	DT	C6-N1-C2	-5.42	118.59	121.30
1	B	15	DC	C6-N1-C2	-5.32	118.17	120.30
1	A	2	DG	O4'-C4'-C3'	5.27	109.16	106.00
1	A	9	DT	C2-N3-C4	5.19	130.31	127.20
1	A	3	DC	C1'-O4'-C4'	-5.19	104.91	110.10
1	A	7	DT	C1'-O4'-C4'	-5.18	104.92	110.10
1	B	24	DG	C5-N7-C8	-5.17	101.72	104.30
1	B	19	DT	C2-N3-C4	5.14	130.29	127.20
1	B	19	DT	OP1-P-OP2	5.13	127.30	119.60

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	248	0	138	6	0
1	B	248	0	137	5	0
2	A	32	0	24	12	0
3	A	2	0	0	0	0
4	B	1	0	0	0	0
5	A	48	0	0	1	0
5	B	61	0	0	1	0
All	All	640	0	299	13	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 16.

All (13) 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:A:101:HT:H252	5:B:211:HOH:O	1.69	0.91
2:A:101:HT:H6	1:B:18:DA:N3	1.91	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:DT:H4'	2:A:101:HT:H2	1.59	0.85
1:A:9:DT:H4'	2:A:101:HT:C2	2.14	0.77
2:A:101:HT:C16	1:B:21:DT:H4'	2.29	0.61
1:A:9:DT:C4'	2:A:101:HT:C2	2.79	0.60
2:A:101:HT:C6	1:B:18:DA:N3	2.65	0.57
1:A:8:DT:H2"	1:A:9:DT:C6	2.48	0.49
2:A:101:HT:H5	1:B:18:DA:C2	2.47	0.48
2:A:101:HT:H10	5:A:226:HOH:O	2.13	0.48
2:A:101:HT:C17	1:B:21:DT:H4'	2.45	0.47
1:A:4:C6G:H21	2:A:101:HT:H222	1.83	0.42
1:A:8:DT:H4'	2:A:101:HT:N2	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

There are no protein molecules in this entry.

5.3.2 Protein sidechains ⓘ

There are no protein molecules in this entry.

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
1	C6G	A	4	1	18,28,29	1.98	4 (22%)	22,40,43	2.41	7 (31%)
1	C6G	B	16	1	18,28,29	1.54	4 (22%)	22,40,43	2.20	7 (31%)

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
1	C6G	A	4	1	-	0/6/26/27	0/3/3/3
1	C6G	B	16	1	-	0/6/26/27	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4	C6G	O5'-C5'	-3.72	1.39	1.44
1	B	16	C6G	C8-N7	-3.25	1.28	1.34
1	B	16	C6G	O6-CH3	-2.15	1.36	1.43
1	A	4	C6G	O6-CH3	-2.13	1.36	1.43
1	A	4	C6G	O4'-C4'	-2.09	1.40	1.45
1	B	16	C6G	C5-C4	-2.07	1.35	1.40
1	B	16	C6G	C4-N3	2.27	1.39	1.35
1	A	4	C6G	O6-C6	5.99	1.39	1.35

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	C6G	CH3-O6-C6	-6.15	109.40	117.50
1	A	4	C6G	N3-C2-N1	-3.80	121.90	127.46
1	B	16	C6G	CH3-O6-C6	-3.73	112.59	117.50
1	A	4	C6G	C6-C5-C4	-2.62	114.73	117.26
1	B	16	C6G	C2-N3-C4	-2.39	112.36	115.16
1	B	16	C6G	N3-C2-N1	-2.27	124.14	127.46
1	A	4	C6G	C2-N3-C4	-2.11	112.70	115.16
1	A	4	C6G	O6-C6-C5	2.48	118.99	115.14
1	B	16	C6G	O4'-C1'-N9	2.89	112.64	107.78
1	B	16	C6G	C4-C5-N7	2.93	112.24	109.41
1	A	4	C6G	C4-C5-N7	3.69	112.98	109.41
1	B	16	C6G	O6-C6-C5	4.04	121.41	115.14
1	A	4	C6G	C2-N1-C6	5.01	123.42	116.18
1	B	16	C6G	C2-N1-C6	5.44	124.04	116.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	4	C6G	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	#$|Z| > 2$
2	HT	A	101	-	37,37,37	1.91	11 (29%)	38,54,54	2.54	18 (47%)

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	HT	A	101	-	-	0/12/22/22	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	101	HT	C12-C14	-2.69	1.41	1.48
2	A	101	HT	C8-N1	-2.63	1.30	1.39
2	A	101	HT	C10-C11	2.20	1.41	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	101	HT	C16-C15	2.26	1.49	1.42
2	A	101	HT	C24-N5	2.63	1.50	1.46
2	A	101	HT	C14-N4	2.74	1.39	1.35
2	A	101	HT	O1-C1	2.81	1.43	1.37
2	A	101	HT	C21-N5	3.41	1.51	1.46
2	A	101	HT	C19-N5	3.61	1.48	1.38
2	A	101	HT	C7-N1	3.88	1.40	1.35
2	A	101	HT	C3-C2	4.13	1.46	1.38

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	101	HT	C6-C1-C2	-5.96	109.01	119.74
2	A	101	HT	C5-C4-C3	-3.65	110.35	117.59
2	A	101	HT	C18-C19-N5	-3.28	116.78	121.39
2	A	101	HT	C23-C24-N5	-2.96	104.84	110.68
2	A	101	HT	C24-N5-C19	2.17	124.24	118.21
2	A	101	HT	C20-C15-N3	2.19	137.10	130.75
2	A	101	HT	C19-C20-C15	2.21	122.10	120.86
2	A	101	HT	C20-C19-N5	2.33	124.76	121.95
2	A	101	HT	C12-C14-N3	2.37	126.69	123.51
2	A	101	HT	C10-C9-N2	2.51	138.05	130.78
2	A	101	HT	O1-C1-C2	2.68	127.58	120.04
2	A	101	HT	C2-C3-C4	2.68	124.99	121.10
2	A	101	HT	C6-C5-C4	2.79	125.15	121.10
2	A	101	HT	C21-C22-N6	3.23	114.50	110.79
2	A	101	HT	C3-C2-C1	3.26	123.58	119.88
2	A	101	HT	C4-C7-N2	3.49	128.19	123.51
2	A	101	HT	C3-C4-C7	5.29	129.53	120.79
2	A	101	HT	C5-C6-C1	6.08	126.78	119.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	101	HT	12	0

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)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	11/12 (91%)	0.08	0	100	100	21, 26, 35, 35	0
1	B	11/12 (91%)	-0.06	0	100	100	24, 26, 32, 32	0
All	All	22/24 (91%)	0.01	0	100	100	21, 26, 32, 35	0

There are no RSRZ outliers to report.

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	C6G	B	16	26/27	0.88	0.12	-	20,27,32,36	0
1	C6G	A	4	26/27	0.87	0.13	-	22,28,35,38	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	HT	A	101	32/32	0.70	0.27	6.61	33,47,71,71	0
3	MG	A	103	1/1	0.92	0.22	5.17	31,31,31,31	1
4	SR	B	101	1/1	0.99	0.03	-	27,27,27,27	1
3	MG	A	102	1/1	0.98	0.04	-	29,29,29,29	0

6.5 Other polymers (i)

There are no such residues in this entry.