Full wwPDB X-ray Structure Validation Report ⓘ

Jul 25, 2017 – 06:55 AM EDT

PDB ID	:	5UED
Title	:	RNA primer-template complex with guanosine dinucleotide ligand G(5')pp(5')G
Authors	:	Zhang, W.; Tam, C.P.; Szostak, J.W.
Deposited on	:	unknown
Resolution	:	1.50 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
A user guide is available at
http://wwpdb.org/validation/2016/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:

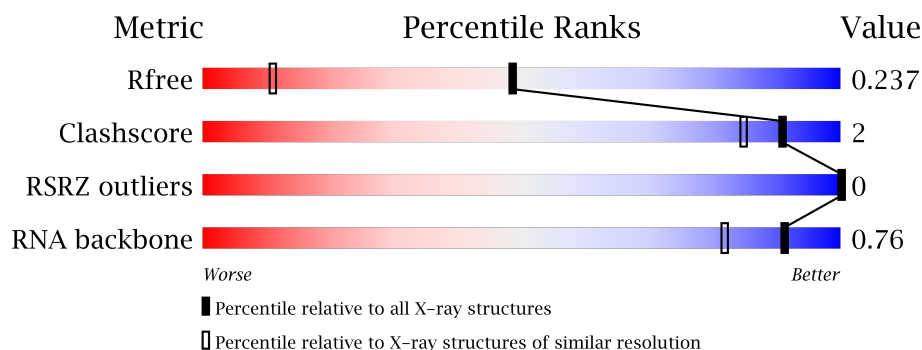|		
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20029824

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 1.50 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		0.237
Clashscore		2
RSRZ outliers		0
RNA backbone		0.76

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	2279 (1.50-1.50)
Clashscore	112137	2503 (1.50-1.50)
RSRZ outliers	101464	2305 (1.50-1.50)
RNA backbone	2435	1043 (2.60-0.62)

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.

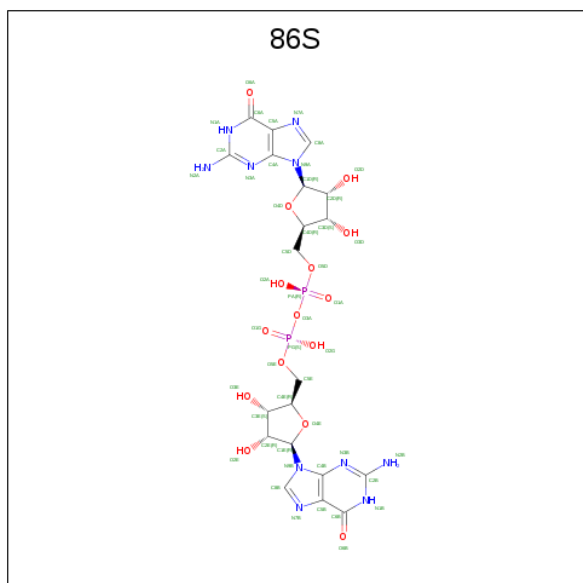| Mol	Chain	Length	Quality of chain
1	A	14	86% ▬▬▬▬▬▬▬▬▬▬▬ 14%
1	B	14	64% ▬▬▬▬▬▬▬ 36%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 787 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 RNA chain called RNA (5'-R(*(LCC)P*(LCC)P*(LCC)P*GP*AP*CP*UP *UP*AP*AP*GP*UP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	14	Total	C	N	O	P	0	0	0
			298	138	51	96	13			
1	B	14	Total	C	N	O	P	0	0	0
			298	138	51	96	13			

- Molecule 2 is [[(2 {R},3 {S},4 {R},5 {R})-5-(2-azanyl-6-oxidanylidene-1 {H}-purin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl] [(2 {R},3 {S},4 {R},5 {R})-5-(2-azanyl-6-oxidanylidene-1 {H}-purin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methyl hydrogen phosphate (three-letter code: 86S) (formula: $C_{20}H_{26}N_{10}O_{15}P_2$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			47	20	10	15	2		
2	B	1	Total	C	N	O	P	0	0
			47	20	10	15	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	57	Total 57	O 57	0	0
3	B	40	Total 40	O 40	0	0

3 Residue-property plots ⓘ

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.
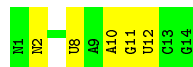
• Molecule 1: RNA (5'-R(*(LCC)P*(LCC)P*(LCC)P*GP*AP*CP*UP*UP*AP*AP*GP*UP*CP*G)-3')

Chain A:

• Molecule 1: RNA (5'-R(*(LCC)P*(LCC)P*(LCC)P*GP*AP*CP*UP*UP*AP*AP*GP*UP*CP*G)-3')

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α, β, γ	43.91Å 43.91Å 85.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.50 28.47 – 1.50	Depositor EDS
% Data completeness (in resolution range)	94.5 (50.00-1.50) 94.6 (28.47-1.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.08 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.210 , 0.232 0.218 , 0.237	Depositor DCC
R_{free} test set	795 reflections (5.58%)	DCC
Wilson B-factor (Å^2)	15.7	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 45.1	EDS
L-test for twinning[2]	$< |L| > = 0.52, < L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	787	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.22% 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: 86S, LCC

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	1.10	2/262 (0.8%)	1.33	1/406 (0.2%)
1	B	1.19	3/262 (1.1%)	1.18	1/406 (0.2%)
All	All	1.14	5/524 (1.0%)	1.26	2/812 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	7	U	P-OP2	-6.23	1.38	1.49
1	B	10	A	O3'-P	5.76	1.68	1.61
1	B	12	U	O3'-P	-5.35	1.54	1.61
1	B	8	U	O3'-P	-5.21	1.54	1.61
1	A	7	U	O3'-P	-5.16	1.54	1.61

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	11	G	O5'-P-OP2	-12.73	94.25	105.70
1	A	11	G	O5'-P-OP2	-11.78	95.10	105.70

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	298	0	158	0	0
1	B	298	0	158	1	0
2	A	47	0	0	0	0
2	B	47	0	0	1	0
3	A	57	0	0	0	0
3	B	40	0	0	0	0
All	All	787	0	316	2	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 2.

All (2) 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:B:101:86S:C8B	2:B:101:86S:O1G	2.45	0.65
1:B:2:LCC:H41	1:B:2:LCC:H5M1	1.69	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	10/14 (71%)	0	0
1	B	10/14 (71%)	0	0
All	All	20/28 (71%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

6 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	LCC	A	1	1	16,21,25	2.24	6 (37%)	20,33,40	1.86	5 (25%)
1	LCC	A	2	1	16,24,25	2.87	8 (50%)	19,37,40	1.44	4 (21%)
1	LCC	A	3	1	16,24,25	2.58	6 (37%)	19,37,40	1.67	5 (26%)
1	LCC	B	1	1	16,21,25	2.62	7 (43%)	20,33,40	2.16	7 (35%)
1	LCC	B	2	1	16,24,25	3.79	10 (62%)	19,37,40	1.86	3 (15%)
1	LCC	B	3	1	16,24,25	1.96	6 (37%)	19,37,40	1.71	4 (21%)

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	LCC	A	1	1	-	0/3/32/36	0/1/3/3
1	LCC	A	2	1	-	0/4/35/36	0/1/3/3
1	LCC	A	3	1	-	0/4/35/36	0/1/3/3
1	LCC	B	1	1	-	0/3/32/36	0/1/3/3
1	LCC	B	2	1	-	0/4/35/36	0/1/3/3
1	LCC	B	3	1	-	0/4/35/36	0/1/3/3

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2	LCC	C5M-C5	-6.90	1.37	1.51
1	A	1	LCC	C5M-C5	-6.71	1.37	1.51
1	B	2	LCC	O4'-C4'	-6.24	1.37	1.45
1	B	2	LCC	O5'-C5'	-5.84	1.36	1.44
1	A	2	LCC	O5'-C5'	-5.83	1.36	1.44
1	B	1	LCC	C5M-C5	-5.75	1.39	1.51
1	B	2	LCC	O4'-C1'	-5.68	1.34	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2	LCC	C5M-C5	-5.45	1.40	1.51
1	B	1	LCC	O4'-C1'	-5.32	1.34	1.42
1	A	3	LCC	C2'-C3'	-4.65	1.41	1.53
1	A	2	LCC	O4'-C1'	-4.46	1.36	1.42
1	B	2	LCC	C2'-C3'	-4.25	1.42	1.53
1	B	3	LCC	C5M-C5	-4.23	1.42	1.51
1	B	2	LCC	C2-N3	-4.04	1.30	1.38
1	B	2	LCC	C4-N3	-3.99	1.29	1.35
1	B	1	LCC	O4'-C4'	-3.70	1.40	1.45
1	B	2	LCC	C5-C4	-3.39	1.36	1.41
1	A	2	LCC	C4'-C3'	-3.19	1.49	1.53
1	A	3	LCC	C5M-C5	-3.17	1.44	1.51
1	B	1	LCC	C2-N3	-2.88	1.32	1.38
1	A	1	LCC	C4'-C3'	-2.85	1.50	1.53
1	B	1	LCC	C4'-C3'	-2.82	1.50	1.53
1	A	2	LCC	C2-N3	-2.75	1.32	1.38
1	A	2	LCC	C4-N3	-2.72	1.30	1.35
1	B	1	LCC	O2'-C6'	-2.63	1.39	1.44
1	A	1	LCC	C2-N3	-2.52	1.33	1.38
1	A	3	LCC	C6-C5	-2.48	1.33	1.40
1	B	1	LCC	C5-C4	-2.41	1.37	1.41
1	A	1	LCC	O4'-C4'	-2.36	1.42	1.45
1	B	3	LCC	C2'-C3'	-2.33	1.47	1.53
1	B	2	LCC	C4'-C3'	-2.33	1.50	1.53
1	A	2	LCC	C5-C4	-2.31	1.37	1.41
1	B	3	LCC	C2-N3	-2.21	1.33	1.38
1	B	3	LCC	C4-N3	-2.09	1.31	1.35
1	A	1	LCC	O5'-C5'	-2.08	1.35	1.42
1	B	2	LCC	O2'-C6'	-2.07	1.40	1.44
1	A	2	LCC	O3'-C3'	-2.03	1.38	1.42
1	A	1	LCC	O4'-C1'	2.19	1.45	1.42
1	B	3	LCC	O3'-C3'	2.34	1.47	1.42
1	B	3	LCC	O4'-C4'	2.66	1.49	1.45
1	A	3	LCC	O4'-C1'	2.75	1.46	1.42
1	A	3	LCC	O2'-C6'	3.94	1.51	1.44
1	A	3	LCC	O5'-C5'	4.99	1.51	1.44

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2	LCC	C5-C6-N1	-5.07	116.66	122.15
1	A	3	LCC	C6'-O2'-C2'	-3.33	101.73	107.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2	LCC	O2'-C6'-C4'	-3.31	97.41	104.15
1	B	1	LCC	O4'-C4'-C3'	-3.10	99.28	101.83
1	B	1	LCC	C6'-C4'-C5'	-2.69	108.38	116.11
1	A	2	LCC	O2'-C6'-C4'	-2.68	98.68	104.15
1	A	3	LCC	O5'-C5'-C4'	-2.51	102.98	107.84
1	B	3	LCC	N4-C4-N3	-2.38	113.49	117.00
1	A	1	LCC	C5-C6-N1	-2.22	119.74	122.15
1	A	2	LCC	C5-C4-N3	-2.19	117.67	121.22
1	A	1	LCC	O2'-C6'-C4'	-2.16	99.74	104.15
1	B	1	LCC	C5-C6-N1	-2.15	119.82	122.15
1	B	3	LCC	C6'-O2'-C2'	-2.10	104.00	107.89
1	B	1	LCC	C5-C4-N3	-2.07	117.86	121.22
1	A	3	LCC	C4'-O4'-C1'	-2.07	104.08	107.84
1	A	2	LCC	O4'-C1'-N1	2.12	111.61	108.71
1	B	3	LCC	C5-C4-N3	2.38	125.07	121.22
1	A	3	LCC	C5M-C5-C6	2.58	123.82	118.67
1	A	3	LCC	C5-C4-N3	2.96	126.02	121.22
1	A	1	LCC	C5M-C5-C4	3.06	124.80	121.65
1	A	1	LCC	O4'-C1'-N1	3.53	113.54	108.71
1	A	2	LCC	N4-C4-N3	3.67	122.43	117.00
1	B	1	LCC	O4'-C4'-C5'	3.70	115.85	108.98
1	B	1	LCC	O4'-C1'-N1	4.36	114.68	108.71
1	B	3	LCC	C5M-C5-C4	4.50	126.28	121.65
1	B	2	LCC	O4'-C1'-N1	4.60	115.01	108.71
1	B	1	LCC	N4-C4-N3	4.83	124.14	117.00
1	A	1	LCC	N4-C4-N3	5.14	124.59	117.00

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	B	2	LCC	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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	#$|Z| > 2$
2	86S	A	101	-	42,52,52	1.83	11 (26%)	44,81,81	2.48	11 (25%)
2	86S	B	101	-	42,52,52	2.51	12 (28%)	44,81,81	2.10	12 (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
2	86S	A	101	-	-	0/18/58/58	0/6/6/6
2	86S	B	101	-	-	0/18/58/58	0/6/6/6

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	101	86S	C6B-C5B	-4.44	1.32	1.41
2	B	101	86S	C6A-C5A	-4.34	1.33	1.41
2	A	101	86S	O2E-C2E	-3.22	1.35	1.43
2	A	101	86S	C8B-N7B	-3.10	1.28	1.34
2	B	101	86S	C5A-C4A	-3.09	1.33	1.40
2	A	101	86S	C6B-C5B	-2.54	1.36	1.41
2	B	101	86S	C2E-C1E	-2.39	1.49	1.53
2	B	101	86S	PG-O1G	-2.27	1.42	1.50
2	A	101	86S	O6B-C6B	2.04	1.29	1.24
2	B	101	86S	PA-O1A	2.12	1.58	1.50
2	A	101	86S	O4E-C1E	2.25	1.44	1.41
2	A	101	86S	C2D-C1D	2.49	1.57	1.53
2	A	101	86S	O4D-C4D	2.56	1.50	1.45
2	B	101	86S	C2B-N1B	3.34	1.41	1.35
2	B	101	86S	C6B-N1B	3.35	1.39	1.33
2	A	101	86S	O3E-C3E	3.47	1.50	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	101	86S	C6B-N1B	3.67	1.39	1.33
2	A	101	86S	C2A-N1A	3.68	1.42	1.35
2	A	101	86S	C6A-N1A	4.24	1.40	1.33
2	B	101	86S	O4E-C4E	4.69	1.55	1.45
2	B	101	86S	C6A-N1A	4.76	1.41	1.33
2	B	101	86S	O4D-C1D	6.69	1.50	1.41
2	B	101	86S	O4E-C1E	7.63	1.51	1.41

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	101	86S	C5B-C6B-N1B	-6.14	114.74	123.48
2	A	101	86S	C5A-C6A-N1A	-6.05	114.86	123.48
2	A	101	86S	N3B-C2B-N1B	-5.20	119.87	127.46
2	A	101	86S	N3A-C2A-N1A	-5.14	119.96	127.46
2	B	101	86S	C5B-C6B-N1B	-4.76	116.70	123.48
2	B	101	86S	N3B-C2B-N1B	-4.44	120.98	127.46
2	B	101	86S	C4E-O4E-C1E	-4.00	105.51	109.77
2	B	101	86S	N3A-C2A-N1A	-3.84	121.86	127.46
2	A	101	86S	C6B-C5B-C4B	-2.91	117.95	120.84
2	B	101	86S	C5A-C6A-N1A	-2.84	119.45	123.48
2	A	101	86S	C6A-C5A-C4A	-2.72	118.14	120.84
2	B	101	86S	C4A-C5A-N7A	-2.14	107.34	109.41
2	A	101	86S	C4B-C5B-N7B	-2.14	107.34	109.41
2	B	101	86S	O4E-C4E-C3E	-2.13	100.94	105.17
2	B	101	86S	O2G-PG-O1G	2.32	124.30	112.28
2	B	101	86S	O5E-C5E-C4E	2.69	118.55	109.00
2	A	101	86S	N2B-C2B-N3B	2.69	122.72	117.75
2	A	101	86S	N2A-C2A-N3A	2.94	123.17	117.75
2	B	101	86S	C6B-N1B-C2B	3.15	120.59	116.06
2	B	101	86S	C2A-N3A-C4A	3.89	119.70	115.16
2	A	101	86S	C6A-N1A-C2A	5.55	124.05	116.06
2	B	101	86S	O4E-C4E-C5E	6.07	129.89	109.40
2	A	101	86S	C6B-N1B-C2B	6.70	125.70	116.06

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
2	B	101	86S	1	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	11/14 (78%)	-0.37	0	100	100	12, 15, 22, 23	0
1	B	11/14 (78%)	-0.32	0	100	100	14, 17, 19, 20	0
All	All	22/28 (78%)	-0.35	0	100	100	12, 16, 21, 23	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	LCC	A	2	22/23	0.96	0.07	-	11,12,16,20	0
1	LCC	B	2	22/23	0.94	0.10	-	20,24,28,29	0
1	LCC	B	1	19/23	0.87	0.12	-	23,30,37,43	0
1	LCC	A	3	22/23	0.98	0.07	-	11,13,14,16	0
1	LCC	B	3	22/23	0.94	0.08	-	16,20,24,27	0
1	LCC	A	1	19/23	0.95	0.08	-	12,13,17,18	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	86S	A	101	47/47	0.96	0.08	-	11,13,24,25	0
2	86S	B	101	47/47	0.87	0.15	-	21,29,70,88	0

6.5 Other polymers (i)

There are no such residues in this entry.