



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 8, 2024 – 07:27 am GMT

PDB ID : 6G7Z  
Title : Lariat-capping ribozyme with a shortened DP2 stem loop  
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Deposited on : 2018-04-06  
Resolution : 3.34 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.4, CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

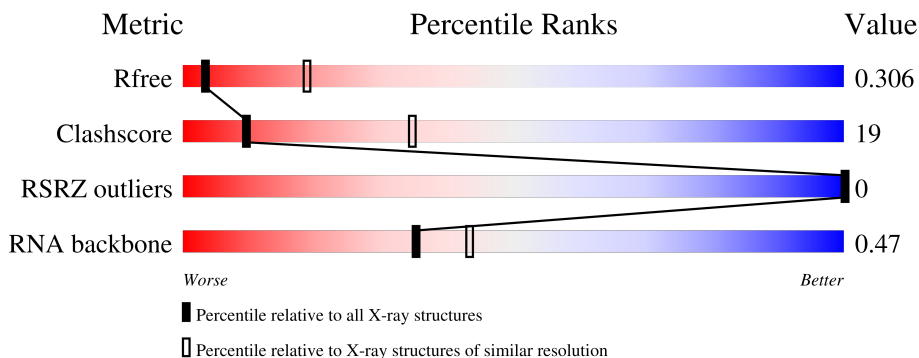
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.34 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))
$R_{free}$	130704	1060 (3.38-3.30)
Clashscore	141614	1111 (3.38-3.30)
RSRZ outliers	127900	1028 (3.38-3.30)
RNA backbone	3102	1129 (3.78-2.90)

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 of 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  $\leq 5\%$ . 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	132	
2	B	54	

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
4	MES	B	201	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3995 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 Lariat-capping ribozyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	132	2816	1259	507	919	131	0	0	0

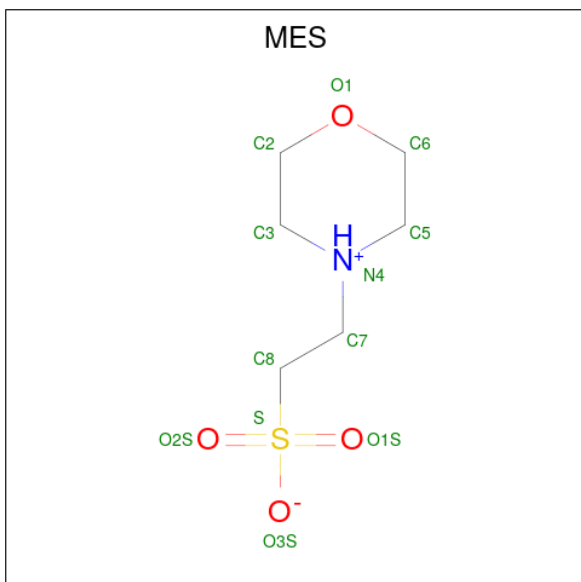
- Molecule 2 is a RNA chain called Lariat-capping ribozyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	54	1154	515	209	376	54	0	0	0

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

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

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	B	1	12	6	1	4	1	0	0

- Molecule 5 is water.

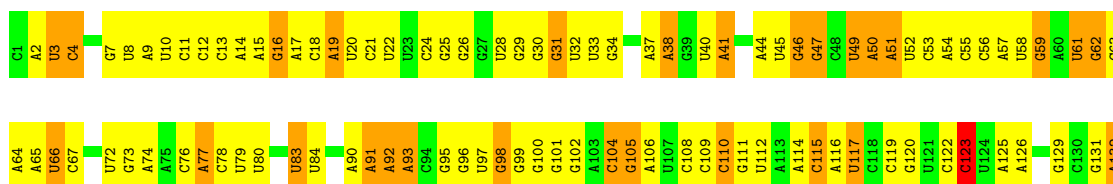
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	11	Total	O	0	0
			11	11		

### 3 Residue-property plots [i](#)

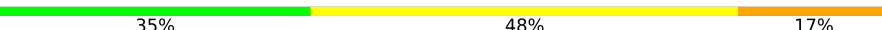
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Lariat-capping ribozyme

Chain A: 



- Molecule 2: Lariat-capping ribozyme

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.95Å 88.79Å 110.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.40 – 3.34 44.40 – 3.34	Depositor EDS
% Data completeness (in resolution range)	92.7 (44.40-3.34) 92.7 (44.40-3.34)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.33 (at 3.32Å)	Xtrriage
Refinement program	REFMAC 1.11rc1_2513, PHENIX 1.11rc1_2513	Depositor
R, $R_{free}$	0.235 , 0.304 0.244 , 0.306	Depositor DCC
$R_{free}$ test set	418 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	87.9	Xtrriage
Anisotropy	0.101	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.18 , 11.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.22$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3995	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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: MES, MG

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	0.31	0/3150	0.94	6/4909 (0.1%)
2	B	0.27	0/1289	0.79	0/2005
All	All	0.30	0/4439	0.90	6/6914 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123	C	C2-N1-C1'	6.97	126.46	118.80
1	A	123	C	N1-C2-O2	5.95	122.47	118.90
1	A	83	U	N1-C2-O2	5.66	126.76	122.80
1	A	123	C	C6-N1-C1'	-5.49	114.21	120.80
1	A	83	U	C2-N1-C1'	5.42	124.20	117.70
1	A	83	U	N3-C2-O2	-5.12	118.62	122.20

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	2816	0	1423	84	0
2	B	1154	0	585	29	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	12	0	12	0	0
5	A	11	0	0	0	0
All	All	3995	0	2020	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 19.

All (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)
1:A:116:A:H4'	1:A:117:U:H5'	1.62	0.79
1:A:101:G:H1	1:A:108:C:H42	1.28	0.78
1:A:117:U:O2'	1:A:131:G:N2	2.21	0.73
1:A:98:G:H5''	1:A:99:G:H5'	1.73	0.70
1:A:93:A:OP2	1:A:129:G:O2'	2.09	0.70
1:A:56:C:H2'	1:A:57:A:C8	2.31	0.66
1:A:104:C:O2'	1:A:105:G:O5'	2.15	0.65
1:A:56:C:H2'	1:A:57:A:H8	1.62	0.64
1:A:132:A:H8	2:B:171:A:H62	1.46	0.63
2:B:149:G:H1	2:B:159:U:H3	1.45	0.63
1:A:100:G:H1	1:A:109:C:H42	1.46	0.62
1:A:100:G:H2'	1:A:101:G:H8	1.64	0.62
1:A:8:U:H2'	1:A:9:A:H8	1.64	0.62
1:A:40:U:H2'	1:A:41:A:C8	2.37	0.59
1:A:58:U:H2'	1:A:59:G:C8	2.37	0.59
1:A:92:A:N1	1:A:122:C:O2'	2.28	0.59
1:A:45:U:H2'	1:A:46:G:C8	2.37	0.59
1:A:33:U:H2'	1:A:34:G:C8	2.38	0.59
2:B:187:G:H2'	2:B:188:A:H8	1.67	0.58
1:A:16:G:N2	1:A:31:G:H22	2.01	0.58
1:A:132:A:N7	2:B:190:G:H1'	2.19	0.58
1:A:50:A:H2'	1:A:51:A:C8	2.39	0.57
1:A:32:U:H2'	1:A:33:U:O4'	2.06	0.56
1:A:18:C:H2'	1:A:19:A:O4'	2.05	0.56
1:A:92:A:N6	1:A:123:C:OP1	2.39	0.56
1:A:90:A:H4'	1:A:91:A:C8	2.41	0.55
2:B:141:A:N3	2:B:142:C:N4	2.53	0.55
1:A:49:U:H2'	1:A:50:A:H3'	1.87	0.55
1:A:99:G:H2'	1:A:100:G:C8	2.42	0.55
1:A:29:G:O2'	2:B:182:G:O2'	2.26	0.54
2:B:187:G:H2'	2:B:188:A:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:G:H2'	1:A:101:G:C8	2.43	0.53
1:A:28:U:H2'	1:A:29:G:C8	2.44	0.53
2:B:182:G:N2	2:B:185:A:OP2	2.31	0.53
2:B:184:A:H2'	2:B:185:A:C8	2.44	0.53
1:A:44:A:H2'	1:A:45:U:O4'	2.09	0.53
1:A:119:C:H2'	1:A:120:G:C8	2.44	0.53
2:B:147:C:H2'	2:B:148:U:C6	2.44	0.53
1:A:16:G:H22	1:A:31:G:H1	1.57	0.52
1:A:115:C:H3'	1:A:116:A:C8	2.45	0.51
1:A:115:C:H3'	1:A:116:A:H8	1.74	0.51
1:A:132:A:O4'	2:B:171:A:N6	2.42	0.51
2:B:188:A:H2'	2:B:189:A:C8	2.45	0.51
2:B:183:A:H8	2:B:183:A:OP1	1.93	0.51
1:A:76:C:H2'	1:A:77:A:C8	2.46	0.50
2:B:141:A:H1'	2:B:142:C:H5	1.76	0.49
1:A:66:U:H2'	1:A:67:C:C6	2.47	0.49
1:A:20:U:H2'	1:A:21:C:C6	2.48	0.49
1:A:22:U:O2'	1:A:25:G:O6	2.28	0.49
2:B:166:A:H2'	2:B:167:A:C8	2.47	0.49
1:A:47:G:H1	1:A:55:C:H42	1.61	0.49
1:A:104:C:HO2'	1:A:105:G:P	2.36	0.48
1:A:53:C:H2'	1:A:54:A:O4'	2.13	0.48
2:B:160:G:H2'	2:B:161:U:O4'	2.14	0.48
1:A:16:G:N2	1:A:31:G:H1	2.11	0.48
1:A:50:A:O2'	1:A:51:A:OP1	2.23	0.47
1:A:105:G:H2'	1:A:106:A:C8	2.50	0.47
1:A:132:A:H8	2:B:171:A:N6	2.11	0.47
2:B:168:U:H4'	2:B:169:G:C5'	2.44	0.47
1:A:8:U:H2'	1:A:9:A:C8	2.49	0.46
1:A:38:A:H61	1:A:64:A:H2'	1.79	0.46
1:A:72:U:O2'	2:B:142:C:H5''	2.15	0.46
2:B:180:C:H42	2:B:187:G:H1	1.63	0.46
1:A:91:A:O2'	1:A:92:A:H3'	2.15	0.46
2:B:148:U:H2'	2:B:149:G:H8	1.81	0.46
2:B:157:G:H2'	2:B:158:G:O4'	2.15	0.46
1:A:51:A:H2'	1:A:52:U:C6	2.51	0.46
1:A:52:U:H2'	1:A:53:C:C6	2.51	0.46
1:A:109:C:H2'	1:A:110:C:O4'	2.16	0.46
2:B:163:U:H2'	2:B:164:U:C6	2.52	0.45
1:A:132:A:H2'	1:A:132:A:N3	2.32	0.45
1:A:99:G:H2'	1:A:100:G:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:188:A:H2'	2:B:189:A:H8	1.81	0.44
2:B:179:U:H2'	2:B:180:C:C6	2.52	0.44
1:A:54:A:H2'	1:A:55:C:O4'	2.18	0.44
1:A:61:U:H2'	1:A:62:G:C8	2.53	0.44
1:A:91:A:HO2'	1:A:92:A:H3'	1.83	0.44
1:A:46:G:H2'	1:A:47:G:H8	1.83	0.44
1:A:15:A:H2'	1:A:16:G:O4'	2.18	0.44
1:A:13:C:H2'	1:A:14:A:C8	2.53	0.43
1:A:66:U:H2'	1:A:67:C:H6	1.84	0.43
2:B:180:C:H2'	2:B:181:C:C6	2.54	0.43
1:A:16:G:C2	1:A:17:A:C5	3.07	0.43
1:A:119:C:H2'	1:A:120:G:H8	1.84	0.43
1:A:104:C:O2'	1:A:106:A:OP2	2.36	0.42
1:A:46:G:H2'	1:A:47:G:C8	2.54	0.42
1:A:78:C:H2'	1:A:79:U:C6	2.55	0.42
1:A:14:A:H2'	1:A:15:A:O4'	2.20	0.42
1:A:63:C:H2'	1:A:64:A:O4'	2.19	0.42
1:A:125:A:H2	2:B:145:C:HO2'	1.66	0.42
1:A:54:A:H1'	1:A:105:G:N2	2.35	0.41
1:A:28:U:H2'	1:A:29:G:H8	1.84	0.41
1:A:30:G:O3'	2:B:186:G:N2	2.52	0.41
1:A:3:U:O2'	1:A:4:C:OP2	2.28	0.41
1:A:7:G:N3	1:A:40:U:H4'	2.36	0.41
1:A:96:G:O2'	1:A:114:A:N1	2.41	0.41
1:A:100:G:N2	1:A:110:C:C2	2.89	0.41
1:A:21:C:H2'	1:A:22:U:O4'	2.21	0.41
2:B:180:C:O2'	2:B:181:C:H5'	2.20	0.41
1:A:125:A:H2'	1:A:126:A:O4'	2.21	0.40
1:A:73:G:H2'	1:A:74:A:H8	1.86	0.40
1:A:73:G:H2'	1:A:74:A:C8	2.56	0.40
1:A:111:G:H2'	1:A:112:U:O4'	2.22	0.40
1:A:16:G:H22	1:A:31:G:N2	2.19	0.40
1:A:97:U:H2'	1:A:98:G:C8	2.57	0.40

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	131/132 (99%)	40 (30%)	4 (3%)
2	B	52/54 (96%)	14 (26%)	0
All	All	183/186 (98%)	54 (29%)	4 (2%)

All (54) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	U
1	A	4	C
1	A	11	C
1	A	12	C
1	A	16	G
1	A	19	A
1	A	24	C
1	A	26	G
1	A	31	G
1	A	37	A
1	A	38	A
1	A	41	A
1	A	46	G
1	A	47	G
1	A	49	U
1	A	50	A
1	A	51	A
1	A	59	G
1	A	61	U
1	A	62	G
1	A	65	A
1	A	66	U
1	A	77	A
1	A	80	U
1	A	83	U
1	A	84	U
1	A	91	A
1	A	92	A

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Mol	Chain	Res	Type
1	A	93	A
1	A	95	G
1	A	98	G
1	A	102	G
1	A	104	C
1	A	105	G
1	A	110	C
1	A	115	C
1	A	117	U
1	A	123	C
1	A	132	A
2	B	141	A
2	B	153	C
2	B	162	G
2	B	164	U
2	B	168	U
2	B	169	G
2	B	170	A
2	B	171	A
2	B	172	C
2	B	175	U
2	B	181	C
2	B	186	G
2	B	189	A
2	B	190	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	3	U
1	A	10	U
1	A	50	A
1	A	104	C

#### 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

Of 3 ligands modelled in this entry, 2 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
4	MES	B	201	-	12,12,12	2.34	1 (8%)	14,16,16	2.24	6 (42%)

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	MES	B	201	-	-	0/6/14/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	201	MES	C8-S	-7.83	1.66	1.77

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	201	MES	C5-N4-C3	4.85	119.75	108.83
4	B	201	MES	C2-C3-N4	-3.04	105.49	110.10
4	B	201	MES	C7-N4-C3	2.66	118.04	111.23
4	B	201	MES	O3S-S-C8	2.56	109.91	105.77
4	B	201	MES	C6-C5-N4	-2.51	106.29	110.10
4	B	201	MES	C7-N4-C5	2.50	117.63	111.23

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	153:C	O3'	156:A	P	13.52

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	132/132 (100%)	-0.48	0 100 100	46, 69, 110, 140	0
2	B	54/54 (100%)	-0.44	0 100 100	60, 80, 117, 133	0
All	All	186/186 (100%)	-0.47	0 100 100	46, 73, 113, 140	0

There are no RSRZ outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	A	201	1/1	0.68	0.14	57,57,57,57	0
4	MES	B	201	12/12	0.80	0.48	76,85,92,95	12
3	MG	A	202	1/1	0.93	0.07	53,53,53,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.