



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 16, 2023 – 10:13 PM EDT

PDB ID : 2B8T  
Title : Crystal structure of Thymidine Kinase from *U.urealyticum* in complex with thymidine  
Authors : Kosinska, U.; Carnrot, C.; Eriksson, S.; Wang, L.; Eklund, H.  
Deposited on : 2005-10-10  
Resolution : 2.00 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

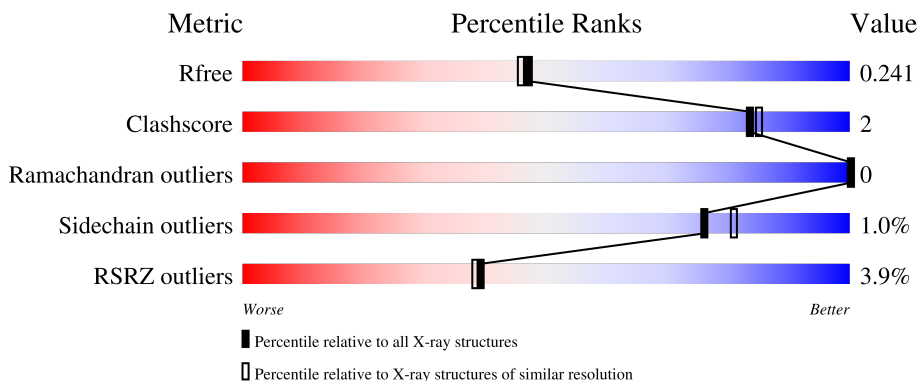
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	223	 3% 89% 8%
1	B	223	 4% 76% 8% 15%
1	C	223	 1% 83% 7% 11%
1	D	223	 6% 87% 9%

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	TRS	D	5006	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6690 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 Thymidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	206	Total 1650	C 1055	N 281	O 307	S 7	0	0	0
1	B	189	Total 1516	C 979	N 251	O 279	S 7	0	0	0
1	C	199	Total 1591	C 1021	N 267	O 296	S 7	0	0	0
1	D	204	Total 1623	C 1038	N 276	O 302	S 7	0	0	0

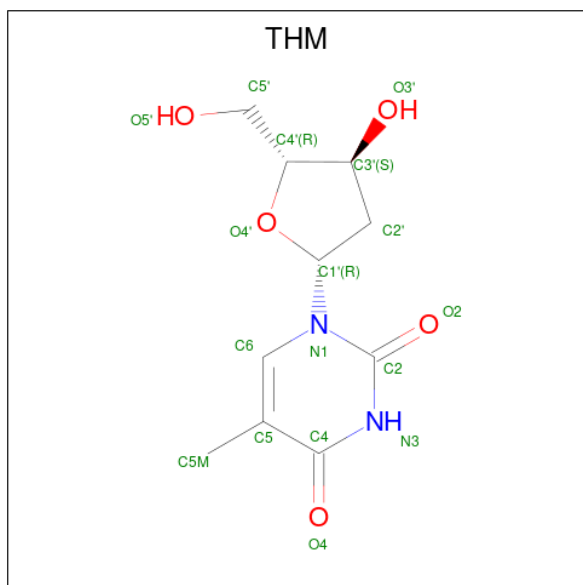
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	PHE	LEU	engineered mutation	UNP Q9PPP5
B	16	PHE	LEU	engineered mutation	UNP Q9PPP5
C	16	PHE	LEU	engineered mutation	UNP Q9PPP5
D	16	PHE	LEU	engineered mutation	UNP Q9PPP5

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

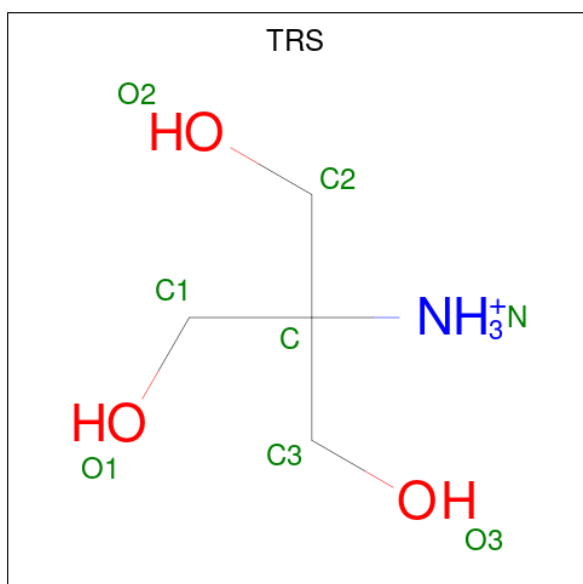
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0

- Molecule 3 is THYMIDINE (three-letter code: THM) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>2</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	Total	C	N	O	0	0
			17	10	2	5		
3	B	1	Total	C	N	O	0	0
			17	10	2	5		
3	C	1	Total	C	N	O	0	0
			17	10	2	5		
3	D	1	Total	C	N	O	0	0
			17	10	2	5		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $C_4H_{12}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	N	O	0	0
			8	4	1	3		

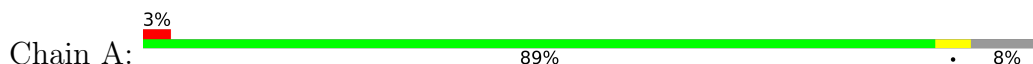
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	62	Total	O	0	0
			62	62		
5	B	40	Total	O	0	0
			40	40		
5	C	73	Total	O	0	0
			73	73		
5	D	55	Total	O	0	0
			55	55		

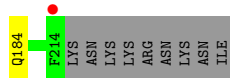
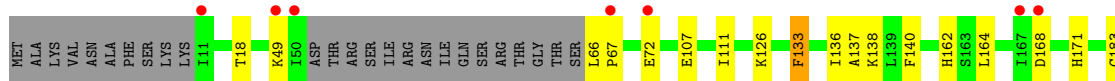
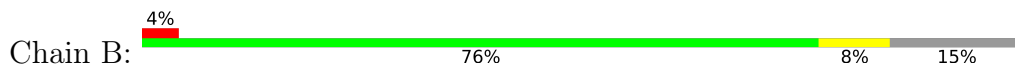
### 3 Residue-property plots [i](#)

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.

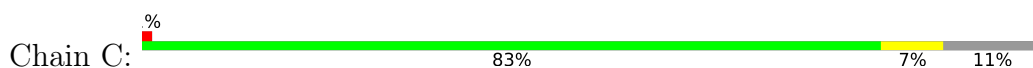
- Molecule 1: Thymidine kinase



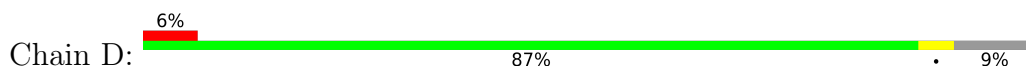
- Molecule 1: Thymidine kinase



- Molecule 1: Thymidine kinase



- Molecule 1: Thymidine kinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.16Å 115.65Å 64.47Å 90.00° 101.02° 90.00°	Depositor
Resolution (Å)	26.95 – 2.00 26.92 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (26.95-2.00) 98.3 (26.92-2.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.04 (at 1.99Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.195 , 0.235 0.210 , 0.241	Depositor DCC
$R_{free}$ test set	2769 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.3	Xtrriage
Anisotropy	0.423	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 40.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6690	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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: ZN, THM, TRS

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	0.42	0/1686	0.51	0/2276
1	B	0.39	0/1551	0.49	0/2094
1	C	0.41	0/1626	0.51	0/2193
1	D	0.40	0/1658	0.51	0/2237
All	All	0.40	0/6521	0.51	0/8800

There are no bond length outliers.

There are no bond angle outliers.

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	1650	0	1633	5	0
1	B	1516	0	1495	10	0
1	C	1591	0	1571	10	0
1	D	1623	0	1592	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	17	0	14	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	14	0	0
3	C	17	0	14	0	0
3	D	17	0	14	0	0
4	D	8	0	12	6	0
5	A	62	0	0	0	0
5	B	40	0	0	0	0
5	C	73	0	0	0	0
5	D	55	0	0	0	0
All	All	6690	0	6359	31	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 (31) 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:25:LYS:H	4:D:5006:TRS:H31	1.11	1.13
1:D:25:LYS:N	4:D:5006:TRS:H31	1.94	0.81
1:D:25:LYS:H	4:D:5006:TRS:C3	1.91	0.81
1:C:125:ASP:HA	1:C:136:ILE:HG21	1.77	0.66
1:B:66:LEU:N	1:B:67:PRO:HD3	2.08	0.66
1:B:133:PHE:O	1:B:136:ILE:HG13	2.00	0.61
1:C:86:PHE:CZ	1:C:90:THR:HB	2.35	0.61
1:B:66:LEU:N	1:B:67:PRO:CD	2.64	0.60
1:B:164:LEU:HD11	1:B:171:HIS:HD2	1.71	0.54
1:D:26:THR:H	4:D:5006:TRS:H11	1.71	0.54
1:C:124:LEU:O	1:C:136:ILE:HG13	2.10	0.51
1:D:24:GLY:H	4:D:5006:TRS:H22	1.76	0.50
1:C:98:VAL:HG13	1:C:136:ILE:HD11	1.93	0.50
1:B:107:GLU:O	1:B:111:ILE:HG12	2.13	0.49
1:B:49:LYS:HG3	1:B:72:GLU:HG2	1.93	0.48
1:B:136:ILE:HD12	1:B:137:ALA:N	2.28	0.48
1:A:132:PRO:HB3	1:C:141:THR:HG21	1.95	0.48
1:C:30:ILE:HG12	1:C:66:LEU:HG	1.97	0.47
1:C:45:VAL:HG21	1:C:66:LEU:HD22	1.97	0.46
1:D:110:ASN:HD21	1:D:142:TYR:HB3	1.81	0.46
1:B:126:LYS:HE3	1:B:162:HIS:CE1	2.52	0.45
1:A:125:ASP:O	1:A:136:ILE:HD11	2.18	0.43
1:A:129:LYS:HE3	1:A:178:ILE:CD1	2.49	0.43
1:A:82:MET:HG2	1:C:213:PHE:CD2	2.54	0.42
1:D:24:GLY:N	4:D:5006:TRS:H31	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:LEU:HD11	1:D:171:HIS:CD2	2.54	0.42
1:B:18:THR:HG21	1:B:140:PHE:CZ	2.55	0.42
1:D:48:PRO:O	1:D:49:LYS:HB2	2.20	0.42
1:C:98:VAL:HG12	1:C:123:GLY:HA3	2.01	0.42
1:A:140:PHE:CG	1:C:140:PHE:HB3	2.55	0.42
1:B:183:CYS:SG	1:B:184:GLN:N	2.93	0.41

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	204/223 (92%)	200 (98%)	4 (2%)	0	100	100
1	B	185/223 (83%)	182 (98%)	3 (2%)	0	100	100
1	C	195/223 (87%)	191 (98%)	4 (2%)	0	100	100
1	D	200/223 (90%)	197 (98%)	3 (2%)	0	100	100
All	All	784/892 (88%)	770 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	181/196 (92%)	180 (99%)	1 (1%)	86	90
1	B	165/196 (84%)	162 (98%)	3 (2%)	59	63
1	C	174/196 (89%)	172 (99%)	2 (1%)	73	78
1	D	176/196 (90%)	175 (99%)	1 (1%)	86	90
All	All	696/784 (89%)	689 (99%)	7 (1%)	76	81

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	PHE
1	B	133	PHE
1	B	138	LYS
1	B	168	ASP
1	C	133	PHE
1	C	196	LYS
1	D	133	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	A	171	HIS
1	A	195	HIS
1	B	115	ASN
1	B	171	HIS
1	B	195	HIS
1	C	115	ASN
1	D	110	ASN
1	D	115	ASN

### 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 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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
3	THM	D	7970	-	18,18,18	1.48	4 (22%)	26,26,26	2.04	6 (23%)
4	TRS	D	5006	-	7,7,7	0.60	0	9,9,9	0.54	0
3	THM	B	5970	-	18,18,18	1.48	4 (22%)	26,26,26	2.08	8 (30%)
3	THM	C	6970	-	18,18,18	1.43	4 (22%)	26,26,26	2.07	6 (23%)
3	THM	A	4970	-	18,18,18	1.53	5 (27%)	26,26,26	2.01	6 (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
3	THM	D	7970	-	-	0/6/18/18	0/2/2/2
4	TRS	D	5006	-	-	3/9/9/9	-
3	THM	B	5970	-	-	2/6/18/18	0/2/2/2
3	THM	C	6970	-	-	0/6/18/18	0/2/2/2
3	THM	A	4970	-	-	2/6/18/18	0/2/2/2

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	4970	THM	C6-C5	3.28	1.40	1.34
3	C	6970	THM	C6-C5	3.25	1.39	1.34
3	D	7970	THM	C6-C5	3.14	1.39	1.34
3	B	5970	THM	C4-C5	2.91	1.49	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	4970	THM	C4-C5	2.84	1.49	1.44
3	B	5970	THM	C6-C5	2.81	1.39	1.34
3	D	7970	THM	C4-C5	2.63	1.49	1.44
3	A	4970	THM	C4-N3	-2.61	1.34	1.38
3	C	6970	THM	C4-C5	2.60	1.49	1.44
3	D	7970	THM	C4-N3	-2.48	1.34	1.38
3	B	5970	THM	C2-N1	2.39	1.42	1.38
3	D	7970	THM	C2-N1	2.36	1.42	1.38
3	C	6970	THM	C2-N1	2.34	1.42	1.38
3	B	5970	THM	C4-N3	-2.30	1.34	1.38
3	C	6970	THM	C4-N3	-2.22	1.34	1.38
3	A	4970	THM	C2-N1	2.20	1.42	1.38
3	A	4970	THM	C2-N3	-2.08	1.34	1.38

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	6970	THM	N3-C2-N1	4.96	121.47	114.89
3	D	7970	THM	N3-C2-N1	4.88	121.36	114.89
3	C	6970	THM	C4-N3-C2	-4.85	121.08	127.35
3	A	4970	THM	N3-C2-N1	4.72	121.15	114.89
3	B	5970	THM	C4-N3-C2	-4.70	121.26	127.35
3	A	4970	THM	C4-N3-C2	-4.66	121.32	127.35
3	D	7970	THM	C4-N3-C2	-4.65	121.34	127.35
3	B	5970	THM	N3-C2-N1	4.42	120.75	114.89
3	B	5970	THM	C5-C4-N3	4.38	119.05	115.31
3	A	4970	THM	C5-C4-N3	4.32	119.00	115.31
3	C	6970	THM	C5-C4-N3	4.10	118.81	115.31
3	A	4970	THM	C5-C6-N1	-3.90	119.33	123.34
3	D	7970	THM	C5-C4-N3	3.82	118.57	115.31
3	D	7970	THM	O4-C4-C5	-3.46	120.89	124.90
3	C	6970	THM	O4-C4-C5	-3.37	120.99	124.90
3	D	7970	THM	C5-C6-N1	-3.34	119.90	123.34
3	C	6970	THM	C5-C6-N1	-3.32	119.92	123.34
3	B	5970	THM	C5-C6-N1	-3.31	119.93	123.34
3	B	5970	THM	O4-C4-C5	-3.25	121.13	124.90
3	A	4970	THM	O4-C4-C5	-3.04	121.38	124.90
3	D	7970	THM	O2-C2-N1	-2.91	118.92	122.79
3	B	5970	THM	O4'-C1'-N1	2.73	112.74	107.86
3	B	5970	THM	C5M-C5-C4	2.55	121.58	118.77
3	C	6970	THM	O2-C2-N1	-2.53	119.42	122.79
3	B	5970	THM	O2-C2-N1	-2.47	119.50	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	4970	THM	O2-C2-N1	-2.17	119.91	122.79

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	5970	THM	O4'-C4'-C5'-O5'
3	B	5970	THM	C3'-C4'-C5'-O5'
3	A	4970	THM	O4'-C4'-C5'-O5'
4	D	5006	TRS	N-C-C2-O2
3	A	4970	THM	C3'-C4'-C5'-O5'
4	D	5006	TRS	C1-C-C2-O2
4	D	5006	TRS	C3-C-C2-O2

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	5006	TRS	6	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

### 6.1 Protein, DNA and RNA chains

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	206/223 (92%)	0.04	7 (3%) 45 44	19, 30, 53, 78	0
1	B	189/223 (84%)	0.23	8 (4%) 36 35	22, 39, 62, 83	0
1	C	199/223 (89%)	-0.01	2 (1%) 82 81	17, 28, 52, 72	0
1	D	204/223 (91%)	0.23	14 (6%) 16 16	18, 33, 68, 93	0
All	All	798/892 (89%)	0.12	31 (3%) 39 38	17, 33, 62, 93	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	167	ILE	4.9
1	D	216	ASN	4.3
1	A	11	ILE	4.2
1	A	216	ASN	4.0
1	D	202	TYR	3.9
1	A	215	LYS	3.9
1	B	11	ILE	3.9
1	D	215	LYS	3.9
1	C	168	ASP	3.8
1	B	168	ASP	3.6
1	A	214	PHE	3.2
1	D	168	ASP	3.2
1	D	214	PHE	3.2
1	D	170	LYS	3.2
1	D	177	ASP	3.1
1	A	168	ASP	3.0
1	D	205	SER	3.0
1	D	212	LYS	2.9
1	B	50	ILE	2.9
1	D	203	LEU	2.9
1	A	84	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	54	SER	2.9
1	B	49	LYS	2.9
1	D	219	ARG	2.7
1	B	214	PHE	2.5
1	B	67	PRO	2.4
1	A	54	SER	2.3
1	B	167	ILE	2.3
1	C	95	ILE	2.1
1	B	72	GLU	2.0
1	D	93	ILE	2.0

## 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
4	TRS	D	5006	8/8	0.70	0.32	29,29,32,33	0
3	THM	D	7970	17/17	0.92	0.10	35,36,38,39	0
3	THM	B	5970	17/17	0.94	0.10	29,30,32,33	0
3	THM	C	6970	17/17	0.95	0.10	23,24,26,28	0
3	THM	A	4970	17/17	0.96	0.07	23,24,26,31	0
2	ZN	B	2218	1/1	0.98	0.09	37,37,37,37	0
2	ZN	D	4218	1/1	0.99	0.06	32,32,32,32	0
2	ZN	A	1218	1/1	0.99	0.06	33,33,33,33	0
2	ZN	C	3218	1/1	1.00	0.06	29,29,29,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.