



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:21 AM GMT

PDB ID : 3OTI
Title : Crystal Structure of CalG3, Calicheamicin Glycostyltransferase, TDP and calicheamicin T0 bound form
Authors : Chang, A.; Singh, S.; Bingman, C.A.; Thorson, J.S.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG); Enzyme Discovery for Natural Product Biosynthesis (NatPro)
Deposited on : 2010-09-11
Resolution : 1.60 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

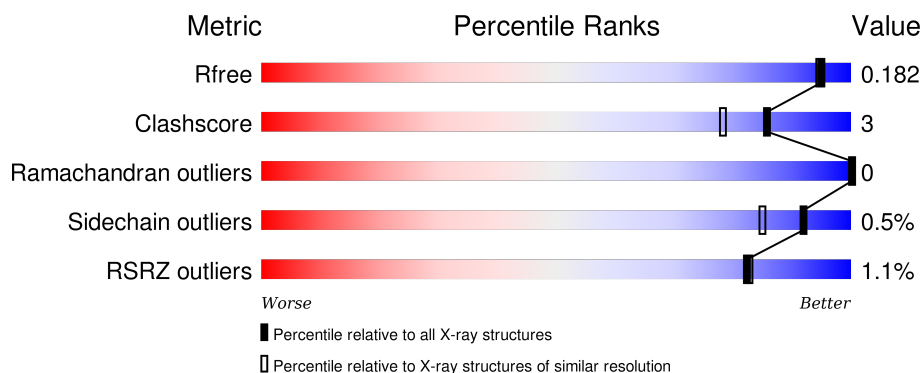
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (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 $\leq 5\%$. 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	398	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 10px; left: 0; width: 100%;"></div> <div style="position: absolute; left: 0; top: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 89%, yellow 89%, yellow 95%, green 95%, green 100%);"></div> <div style="position: absolute; right: 0; top: 0; width: 5%; height: 100%; background: grey;"></div> </div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 89% 6% 5% </div> </div>
1	B	398	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 10px; left: 0; width: 100%;"></div> <div style="position: absolute; left: 0; top: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 89%, yellow 89%, yellow 95%, green 95%, green 100%);"></div> <div style="position: absolute; right: 0; top: 0; width: 5%; height: 100%; background: grey;"></div> </div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 89% 6% 5% </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6936 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 CalG3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	7	0
			2932	1854	525	544	9			
1	B	379	Total	C	N	O	S	0	7	0
			2935	1856	528	542	9			

There are 46 discrepancies between the modelled and reference sequences:

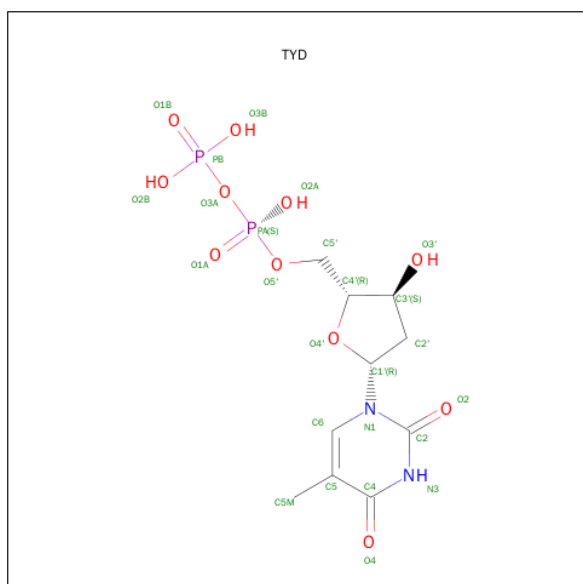
Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	GLY	-	EXPRESSION TAG	UNP Q8KND7
A	-20	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-19	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-18	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-17	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-16	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-15	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-14	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-13	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-12	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-11	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-10	SER	-	EXPRESSION TAG	UNP Q8KND7
A	-9	SER	-	EXPRESSION TAG	UNP Q8KND7
A	-8	GLY	-	EXPRESSION TAG	UNP Q8KND7
A	-7	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-6	ILE	-	EXPRESSION TAG	UNP Q8KND7
A	-5	GLU	-	EXPRESSION TAG	UNP Q8KND7
A	-4	GLY	-	EXPRESSION TAG	UNP Q8KND7
A	-3	ARG	-	EXPRESSION TAG	UNP Q8KND7
A	-2	HIS	-	EXPRESSION TAG	UNP Q8KND7
A	-1	MET	-	EXPRESSION TAG	UNP Q8KND7
A	0	ARG	-	EXPRESSION TAG	UNP Q8KND7
A	1	VAL	-	EXPRESSION TAG	UNP Q8KND7
B	-21	GLY	-	EXPRESSION TAG	UNP Q8KND7
B	-20	HIS	-	EXPRESSION TAG	UNP Q8KND7

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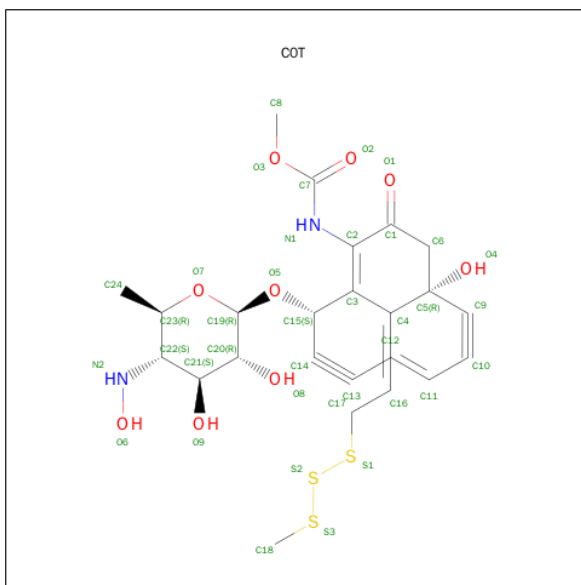
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-18	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-17	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-16	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-15	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-14	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-13	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-12	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-11	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-10	SER	-	EXPRESSION TAG	UNP Q8KND7
B	-9	SER	-	EXPRESSION TAG	UNP Q8KND7
B	-8	GLY	-	EXPRESSION TAG	UNP Q8KND7
B	-7	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-6	ILE	-	EXPRESSION TAG	UNP Q8KND7
B	-5	GLU	-	EXPRESSION TAG	UNP Q8KND7
B	-4	GLY	-	EXPRESSION TAG	UNP Q8KND7
B	-3	ARG	-	EXPRESSION TAG	UNP Q8KND7
B	-2	HIS	-	EXPRESSION TAG	UNP Q8KND7
B	-1	MET	-	EXPRESSION TAG	UNP Q8KND7
B	0	ARG	-	EXPRESSION TAG	UNP Q8KND7
B	1	VAL	-	EXPRESSION TAG	UNP Q8KND7

- Molecule 2 is THYMIDINE-5'-DIPHOSPHATE (three-letter code: TYD) (formula: $C_{10}H_{16}N_2O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
2	B	1	Total	C	N	O	P	0	0
			25	10	2	11	2		

- Molecule 3 is CALICHEAMICIN T0 (three-letter code: C0T) (formula: $C_{24}H_{28}N_2O_9S_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			38	24	2	9	3		
3	B	1	Total	C	N	O	S	0	0
			38	24	2	9	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	492	Total	O	0	0
			492	492		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	449	Total 449	O 449	0	0

- Molecule 1: CalG3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	45.57Å 135.09Å 62.09Å 90.00° 95.75° 90.00°	Depositor
Resolution (Å)	29.23 – 1.60 29.23 – 1.60	Depositor EDS
% Data completeness (in resolution range)	94.7 (29.23-1.60) 94.7 (29.23-1.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.75 (at 1.60Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.152 , 0.181 0.151 , 0.182	Depositor DCC
R_{free} test set	2000 reflections (2.19%)	DCC
Wilson B-factor (Å ²)	13.4	Xtriage
Anisotropy	0.362	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 96478 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6936	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TYD, C0T, CL

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	0.59	0/2997	0.70	0/4096
1	B	0.57	0/3000	0.66	0/4100
All	All	0.58	0/5997	0.68	0/8196

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

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	2932	0	2932	18	0
1	B	2935	0	2941	14	0
2	A	25	0	13	0	0
2	B	25	0	13	0	0
3	A	38	0	27	2	0
3	B	38	0	27	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	492	0	0	7	0
5	B	449	0	0	3	0
All	All	6936	0	5953	33	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 3.

All (33) 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:372:GLU:HG3	5:A:442:HOH:O	1.84	0.76
1:A:73:THR:CG2	5:A:625:HOH:O	2.42	0.67
1:A:273:THR:HG22	1:B:46:GLU:OE2	1.98	0.64
1:A:73:THR:HB	5:A:946:HOH:O	1.96	0.63
1:B:220:ILE:HG23	3:B:378:C0T:H8A	1.82	0.61
1:A:270:PRO:HB2	1:A:273:THR:HG23	1.83	0.61
1:A:73:THR:HG23	5:A:558:HOH:O	2.03	0.58
1:A:-2:HIS:HE1	5:A:818:HOH:O	1.88	0.56
3:B:378:C0T:H15	3:B:378:C0T:O2	2.05	0.56
1:A:7:PRO:HG2	1:A:54:TYR:CZ	2.42	0.54
1:B:7:PRO:HG3	1:B:54:TYR:CZ	2.46	0.50
1:B:-3:ARG:NH1	5:B:789:HOH:O	2.43	0.49
1:B:213:VAL:HG21	1:B:341:ILE:HD11	1.94	0.49
1:B:143:ARG:HD2	5:B:751:HOH:O	2.14	0.47
1:A:104[B]:VAL:HG13	1:A:128:ALA:HB2	1.97	0.47
1:A:216:THR:O	1:A:283:HIS:HA	2.15	0.46
3:A:378:C0T:O2	3:A:378:C0T:H15	2.17	0.45
1:B:205:PRO:HA	1:B:206:PRO:HD3	1.88	0.44
1:B:368:ARG:NH1	5:B:747:HOH:O	2.40	0.44
1:A:130:VAL:HB	1:A:131:PRO:HD2	1.98	0.44
1:A:94:ARG:HB3	1:A:95:PRO:HD3	1.99	0.44
1:B:130:VAL:HB	1:B:131:PRO:HD2	1.99	0.43
1:B:190[B]:ARG:CZ	1:B:358:VAL:O	2.66	0.43
1:B:178:LEU:HD23	1:B:321:ARG:HG3	2.00	0.43
1:B:178:LEU:HD11	1:B:294:ILE:HD11	2.01	0.42
1:A:220:ILE:HG23	3:A:378:C0T:H8A	2.02	0.42
1:B:227:ILE:O	1:B:230:VAL:HG22	2.19	0.42
1:A:40:ALA:HB3	1:A:47:VAL:HG21	2.02	0.42
1:A:-2:HIS:HD2	5:A:763:HOH:O	2.04	0.41
1:B:216:THR:O	1:B:283:HIS:HA	2.20	0.41
1:A:178:LEU:HD11	1:A:294:ILE:HD11	2.02	0.41
1:A:154:THR:HG23	5:A:942:HOH:O	2.21	0.40
1:A:116:GLN:HB2	1:A:136:ASN:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	384/398 (96%)	375 (98%)	9 (2%)	0	100	100
1	B	384/398 (96%)	376 (98%)	8 (2%)	0	100	100
All	All	768/796 (96%)	751 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	306/314 (98%)	305 (100%)	1 (0%)	94	90
1	B	306/314 (98%)	304 (99%)	2 (1%)	88	78
All	All	612/628 (98%)	609 (100%)	3 (0%)	92	85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	135	ARG
1	B	135	ARG
1	B	154	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-2	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	TYD	A	377	-	19,26,26	0.77	0	27,40,40	2.08	4 (14%)
3	C0T	A	378	-	29,40,40	2.44	13 (44%)	28,56,56	3.40	8 (28%)
2	TYD	B	377	-	19,26,26	0.86	0	27,40,40	2.34	3 (11%)
3	C0T	B	378	-	29,40,40	2.51	13 (44%)	28,56,56	3.38	7 (25%)

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	TYD	A	377	-	-	0/12/28/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	C0T	A	378	-	-	0/18/75/75	0/1/3/3
2	TYD	B	377	-	-	0/12/28/28	0/2/2/2
3	C0T	B	378	-	-	0/18/75/75	0/1/3/3

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	378	C0T	C7-N1	-5.54	1.27	1.37
3	B	378	C0T	C7-N1	-4.92	1.28	1.37
3	A	378	C0T	C18-S3	-4.37	1.74	1.80
3	A	378	C0T	C2-N1	-4.20	1.31	1.41
3	B	378	C0T	C10-C9	-4.18	1.14	1.19
3	B	378	C0T	C13-C14	-4.02	1.12	1.19
3	B	378	C0T	C2-N1	-3.48	1.33	1.41
3	B	378	C0T	C18-S3	-3.40	1.75	1.80
3	A	378	C0T	O2-C7	-3.38	1.15	1.21
3	A	378	C0T	C13-C14	-3.20	1.14	1.19
3	A	378	C0T	O3-C8	-3.14	1.37	1.45
3	B	378	C0T	O6-N2	-2.97	1.22	1.44
3	B	378	C0T	O3-C8	-2.97	1.38	1.45
3	A	378	C0T	O6-N2	-2.89	1.22	1.44
3	B	378	C0T	O1-C1	-2.81	1.16	1.23
3	A	378	C0T	C10-C9	-2.81	1.15	1.19
3	B	378	C0T	O2-C7	-2.78	1.16	1.21
3	B	378	C0T	C15-C3	-2.50	1.48	1.51
3	B	378	C0T	S1-S2	-2.42	2.00	2.04
3	A	378	C0T	O1-C1	-2.27	1.18	1.23
3	A	378	C0T	O7-C23	-2.13	1.39	1.44
3	A	378	C0T	C12-C13	-2.09	1.39	1.42
3	B	378	C0T	O9-C21	-2.05	1.38	1.43
3	A	378	C0T	C6-C1	-2.04	1.47	1.51
3	A	378	C0T	O3-C7	4.53	1.40	1.34
3	B	378	C0T	O3-C7	5.63	1.42	1.34

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	378	C0T	O3-C7-O2	-9.44	112.39	124.70
3	B	378	C0T	O3-C7-O2	-9.25	112.64	124.70
2	B	377	TYD	C5-C4-N3	-5.97	118.49	125.14
2	A	377	TYD	C5-C4-N3	-5.42	119.11	125.14
3	B	378	C0T	O1-C1-C6	-2.43	116.06	120.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	378	C0T	C21-C22-C23	-2.36	105.68	110.35
3	B	378	C0T	O5-C19-O7	-2.05	105.49	110.68
3	A	378	C0T	O5-C19-O7	-2.05	105.50	110.68
2	A	377	TYD	O3B-PB-O2B	2.04	115.14	107.38
2	A	377	TYD	O3A-PA-O5'	2.04	108.35	102.94
2	B	377	TYD	O3A-PA-O5'	2.13	108.58	102.94
3	A	378	C0T	C6-C1-C2	2.17	120.76	115.83
3	A	378	C0T	C17-C16-C4	2.67	130.08	126.48
3	B	378	C0T	C6-C1-C2	2.76	122.08	115.83
3	B	378	C0T	C19-C20-C21	3.32	116.52	109.97
3	A	378	C0T	C19-C20-C21	3.38	116.63	109.97
3	A	378	C0T	C2-N1-C7	4.54	134.86	122.76
3	B	378	C0T	C2-N1-C7	5.04	136.21	122.76
2	A	377	TYD	C4-N3-C2	7.61	121.83	115.25
2	B	377	TYD	C4-N3-C2	9.06	123.08	115.25
3	B	378	C0T	O3-C7-N1	12.34	120.35	109.06
3	A	378	C0T	O3-C7-N1	12.74	120.71	109.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	378	C0T	2	0
3	B	378	C0T	2	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	379/398 (95%)	-0.26	5 (1%) 79 79	7, 14, 30, 65	1 (0%)
1	B	379/398 (95%)	-0.27	3 (0%) 87 87	7, 15, 31, 54	0
All	All	758/796 (95%)	-0.27	8 (1%) 82 83	7, 14, 31, 65	1 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-3	ARG	5.3
1	B	-3	ARG	4.4
1	A	73	THR	3.2
1	B	261	ARG	3.1
1	A	211	PRO	2.9
1	A	261	ARG	2.5
1	B	344	GLU	2.3
1	A	-2	HIS	2.2

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 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
3	C0T	A	378	38/38	0.96	0.07	-0.04	8,17,25,29	0
3	C0T	B	378	38/38	0.96	0.07	-0.07	8,16,26,27	0
2	TYD	B	377	25/25	0.99	0.05	-0.82	8,10,13,14	0
2	TYD	A	377	25/25	0.99	0.06	-0.83	7,9,12,14	0
4	CL	B	379	1/1	0.99	0.03	-3.00	14,14,14,14	0
4	CL	A	379	1/1	0.99	0.02	-3.59	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.