Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 11:56 AM GMT

PDB ID	:	3QER
Title	:	RB69 DNA Polymerase (L561A/S565G/Y567A) Ternary Complex with dATP Opposite Difluorotoluene Nucleoside
Authors	:	Xia, S.; Konigsberg, W.H.; Wang, J.
Deposited on	:	2011-01-20
Resolution	:	1.96 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

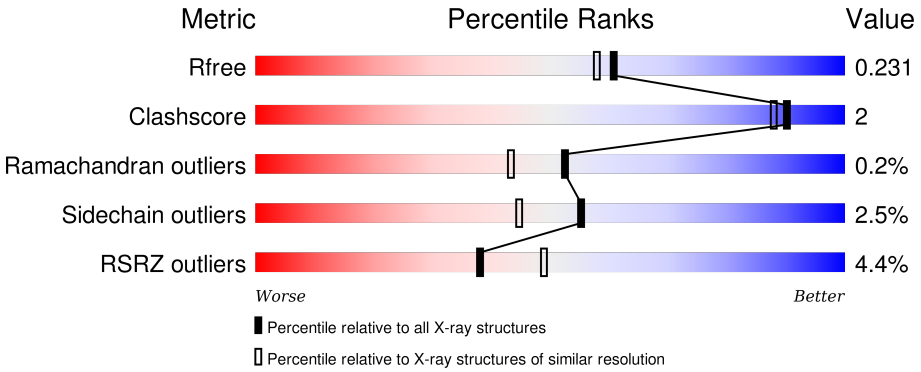
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	903	4% 92% 7%
2	T	18	11% 78% 22%
3	P	13	8% 77% 15% 8%

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
5	CA	A	905	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8995 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 DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	903	Total	C	N	O	S	0	7	0
			7402	4758	1233	1378	33			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	222	ALA	ASP	CONFLICT	UNP Q38087
A	327	ALA	ASP	CONFLICT	UNP Q38087
A	561	ALA	LEU	ENGINEERED MUTATION	UNP Q38087
A	565	GLY	SER	ENGINEERED MUTATION	UNP Q38087
A	567	ALA	TYR	ENGINEERED MUTATION	UNP Q38087

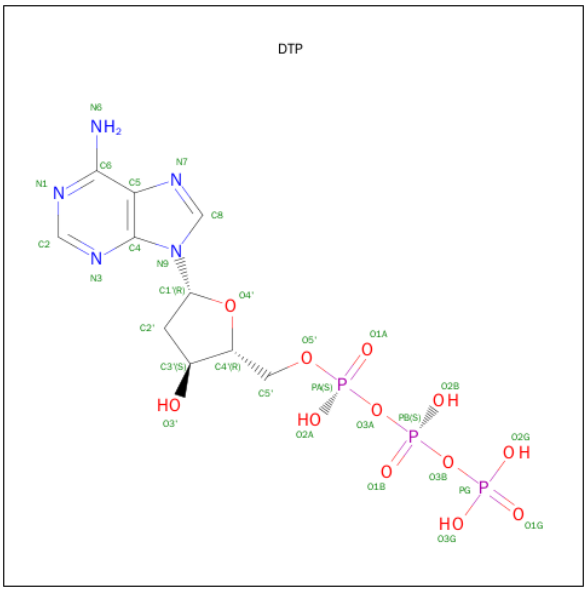
- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*CP*GP*(DFT)P*GP*TP*AP*AP*G P*CP*AP*GP*TP*CP*CP*GP*CP*G)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	T	18	Total	C	F	N	O	P	0	0	0
			370	177	2	66	107	18			

- Molecule 3 is a DNA chain called DNA (5'-D(*GP*CP*GP*GP*AP*CP*TP*GP*CP*TP* TP*AP*(DOC))-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	13	Total	C	N	O	P	0	0	0
			262	126	48	76	12			

- Molecule 4 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	Ca	0	0
			4	4		

- Molecule 6 is water.

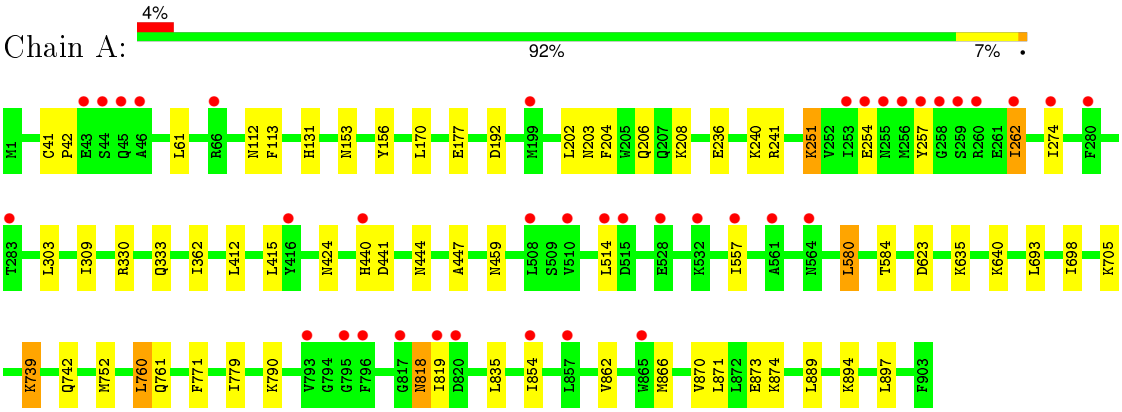
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	832	Total	O	0	16
			848	848		
6	T	59	Total	O	0	0
			59	59		
6	P	20	Total	O	0	0
			20	20		

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 errors 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.

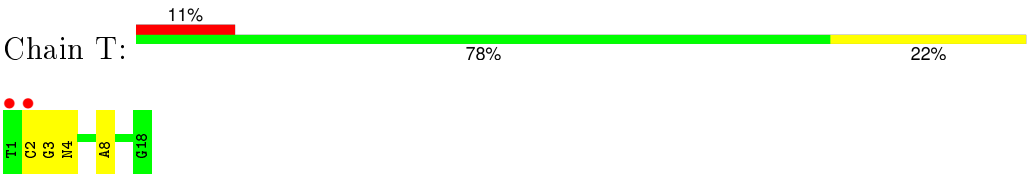
• Molecule 1: DNA polymerase

Chain A:



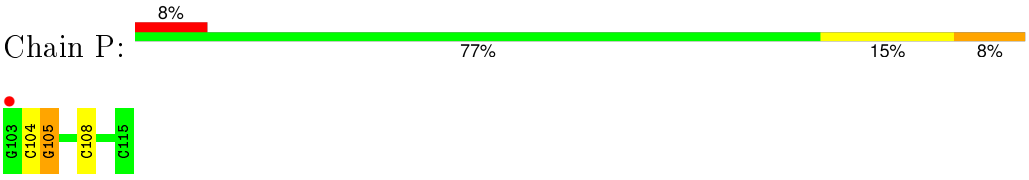
• Molecule 2: DNA (5'-D(P*TP*CP*GP*(DFT)P*GP*TP*AP*AP*GP*CP*AP*GP*TP*CP*CP*GP*CP*G)-3')

Chain T:



• Molecule 3: DNA (5'-D(*GP*CP*GP*GP*AP*CP*TP*GP*CP*TP*TP*AP*(DOC))-3')

Chain P:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	78.27Å 118.70Å 130.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.96 46.18 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.3 (50.00-1.96) 99.3 (46.18-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.44 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.178 , 0.217 0.198 , 0.231	Depositor DCC
R_{free} test set	4383 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	28.3	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 45.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 87511 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8995	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: DFT, CA, DTP, DOC

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	0.40	0/7608	0.50	0/10278
2	T	0.71	0/391	1.18	0/599
3	P	0.70	0/273	1.32	2/420 (0.5%)
All	All	0.43	0/8272	0.61	2/11297 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	108	DC	O4'-C1'-N1	6.72	112.70	108.00
3	P	105	DG	P-O3'-C3'	6.12	127.04	119.70

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	7402	0	7315	33	0
2	T	370	0	203	4	0
3	P	262	0	148	1	0
4	A	30	0	12	1	0
5	A	4	0	0	0	0
6	A	848	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	P	20	0	0	0	0
6	T	59	0	0	0	0
All	All	8995	0	7678	36	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 (36) 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:459:ASN:HD22	1:A:584[A]:THR:HG23	1.38	0.89
1:A:557[A]:ILE:CG2	1:A:557[A]:ILE:CG1	2.52	0.87
1:A:580:LEU:O	1:A:584[A]:THR:HG22	1.93	0.68
1:A:779:ILE:O	1:A:871:LEU:HD21	1.97	0.65
1:A:251:LYS:HB3	1:A:262:ILE:HG23	1.79	0.64
1:A:170:LEU:HA	1:A:177:GLU:HG3	1.81	0.63
1:A:870:VAL:HG13	1:A:874:LYS:HD3	1.82	0.60
1:A:459:ASN:ND2	1:A:584[A]:THR:HG23	2.14	0.60
1:A:415:LEU:HD22	1:A:623:ASP:HB3	1.85	0.58
1:A:202:LEU:O	1:A:206:GLN:HG2	2.03	0.58
1:A:862:VAL:O	1:A:866:MET:HG3	2.04	0.57
1:A:873:GLU:HG3	6:A:1515:HOH:O	2.05	0.57
1:A:771:PHE:HZ	1:A:871:LEU:HD22	1.69	0.57
1:A:131:HIS:HD2	1:A:156:TYR:OH	1.92	0.52
1:A:330:ARG:HA	1:A:333:GLN:HE21	1.76	0.50
1:A:206:GLN:NE2	1:A:241:ARG:HE	2.10	0.50
4:A:904:DTP:N1	2:T:4:DFT:H3	2.26	0.50
1:A:739:LYS:HE3	1:A:742:GLN:OE1	2.13	0.49
1:A:203:ASN:ND2	1:A:241:ARG:HH22	2.10	0.49
1:A:818:ASN:HD22	1:A:819:ILE:N	2.12	0.48
1:A:854:ILE:HD13	1:A:862:VAL:HG21	1.97	0.47
1:A:698:ILE:HG21	1:A:889:LEU:HD11	1.98	0.46
1:A:112[A]:ASN:ND2	6:A:941:HOH:O	2.49	0.46
1:A:153:ASN:HB2	1:A:192:ASP:O	2.17	0.44
1:A:752:MET:HG3	1:A:760:LEU:HG	1.99	0.43
1:A:761:GLN:NE2	6:A:1261:HOH:O	2.47	0.43
1:A:362:ILE:HD12	2:T:3:DG:H2"	2.00	0.43
1:A:41:CYS:HB2	1:A:42:PRO:HD2	2.00	0.42
1:A:204:PHE:CE1	1:A:208:LYS:HD2	2.55	0.42
1:A:441:ASP:HB3	1:A:447:ALA:HB2	2.02	0.42
1:A:440:HIS:CE1	1:A:444:ASN:ND2	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:LEU:HD13	1:A:415:LEU:HD13	2.02	0.41
3:P:104:DC:H2"	3:P:105:DG:C8	2.56	0.41
1:A:236:GLU:HG2	1:A:240[A]:LYS:HE3	2.02	0.41
2:T:2:DC:H5"	2:T:3:DG:C8	2.56	0.41
1:A:705:LYS:HD3	2:T:8:DA:H5"	2.03	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	909/903 (101%)	891 (98%)	16 (2%)	2 (0%)	52 43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	254	GLU
1	A	424	ASN

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	803/797 (101%)	783 (98%)	20 (2%)	55 45

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	LEU
1	A	113	PHE
1	A	251	LYS
1	A	257	TYR
1	A	262	ILE
1	A	274	ILE
1	A	303	LEU
1	A	309	ILE
1	A	514	LEU
1	A	580	LEU
1	A	635	LYS
1	A	640	LYS
1	A	693	LEU
1	A	739	LYS
1	A	760	LEU
1	A	790	LYS
1	A	818	ASN
1	A	835	LEU
1	A	894	LYS
1	A	897	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	HIS
1	A	203	ASN
1	A	206	GLN
1	A	255	ASN
1	A	333	GLN
1	A	339	GLN
1	A	354	GLN
1	A	440	HIS
1	A	444	ASN
1	A	459	ASN
1	A	761	GLN
1	A	818	ASN
1	A	823	GLN

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	$\#\|Z\| > 2$
3	DOC	P	115	3,2	11,19,20	0.54	0	14,26,29	1.43	1 (7%)
2	DFT	T	4	2	17,21,22	2.88	2 (11%)	23,30,33	2.05	6 (26%)

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	DOC	P	115	3,2	-	0/3/18/19	0/2/2/2
2	DFT	T	4	2	-	0/7/21/22	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	4	DFT	C1-C2	6.82	1.49	1.38
2	T	4	DFT	C5-C4	9.35	1.48	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	T	4	DFT	C5M-C5-C4	-4.42	119.14	121.68
2	T	4	DFT	C2'-C1'-C1	-4.01	108.99	114.79
2	T	4	DFT	C3-C2-C1	-3.26	120.31	123.78
2	T	4	DFT	O5'-C5'-C4'	-2.24	100.93	109.12
2	T	4	DFT	C6-C1-C2	2.41	119.42	116.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	115	DOC	C2-N3-C4	3.68	120.80	115.61
2	T	4	DFT	C6-C5-C4	5.04	119.65	115.93

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	T	4	DFT	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 4 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	DTP	A	904	5	24,32,32	0.98	1 (4%)	32,50,50	1.81	3 (9%)

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	DTP	A	904	5	-	0/18/34/34	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	904	DTP	C5-C4	3.23	1.47	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	904	DTP	N3-C2-N1	-7.61	123.07	128.89
4	A	904	DTP	C2'-C1'-N9	-3.11	106.59	114.16
4	A	904	DTP	C4-C5-N7	-2.62	107.07	109.48

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
4	A	904	DTP	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	903/903 (100%)	0.33	38 (4%) 40 51	9, 17, 32, 82	0
2	T	17/18 (94%)	0.71	2 (11%) 6 10	4, 17, 72, 93	0
3	P	12/13 (92%)	0.84	1 (8%) 14 22	7, 38, 76, 76	0
All	All	932/934 (99%)	0.34	41 (4%) 38 49	4, 17, 34, 93	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	257	TYR	13.0
1	A	256	MET	9.1
2	T	1	DT	9.1
1	A	255	ASN	8.4
1	A	258	GLY	8.0
1	A	44	SER	6.0
1	A	259	SER	5.7
1	A	254	GLU	4.8
1	A	819	ILE	4.7
1	A	557[B]	ILE	4.5
1	A	817	GLY	4.0
2	T	2	DC	3.4
1	A	46	ALA	3.2
1	A	45	GLN	3.2
1	A	253	ILE	3.1
1	A	561	ALA	3.1
1	A	510	VAL	3.1
1	A	508	LEU	3.0
1	A	515	ASP	2.8
1	A	795	GLY	2.8
1	A	857	LEU	2.8
1	A	260	ARG	2.7
1	A	66	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	820	ASP	2.5
1	A	796	PHE	2.5
1	A	262	ILE	2.4
1	A	564[A]	ASN	2.4
1	A	283	THR	2.4
1	A	793	VAL	2.4
1	A	199	MET	2.4
1	A	865	TRP	2.3
1	A	416	TYR	2.3
1	A	854	ILE	2.3
1	A	274	ILE	2.2
1	A	43	GLU	2.1
1	A	440	HIS	2.1
1	A	532	LYS	2.1
1	A	280	PHE	2.1
3	P	103	DG	2.1
1	A	528	GLU	2.0
1	A	514	LEU	2.0

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, 95^{th} 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	DFT	T	4	20/21	0.96	0.13	-	4,10,14,19	0
3	DOC	P	115	18/19	0.98	0.11	-	3,7,9,11	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, 95^{th} 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
5	CA	A	905	1/1	0.99	0.23	3.32	21,21,21,21	0
4	DTP	A	904	30/30	0.98	0.12	-1.50	2,4,6,6	0
5	CA	A	907	1/1	0.95	0.08	-1.75	43,43,43,43	0
5	CA	A	908	1/1	0.98	0.05	-	43,43,43,43	0
5	CA	A	906	1/1	0.91	0.19	-	43,43,43,43	0

6.5 Other polymers (i)

There are no such residues in this entry.