



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:41 PM GMT

PDB ID : 3RMD
Title : Crystal Structure of a replicative DNA polymerase bound to DNA containing
Thymine Glycol
Authors : Aller, P.; Duclos, S.; Wallace, S.S.; Doublié, S.
Deposited on : 2011-04-20
Resolution : 2.98 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

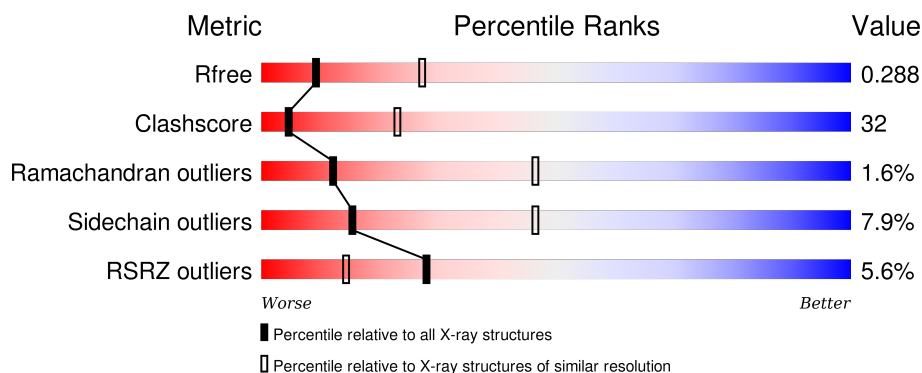
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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.





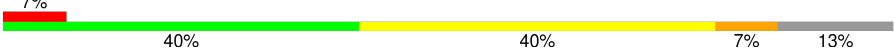


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1992 (3.00-2.96)
Clashscore	102246	2349 (3.00-2.96)
Ramachandran outliers	100387	2274 (3.00-2.96)
Sidechain outliers	100360	2277 (3.00-2.96)
RSRZ outliers	91569	2007 (3.00-2.96)

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 $\leq 5\%$. 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	906	<div> <div>6%</div> <div>56%</div> <div>40%</div> <div>.</div> </div>
1	B	906	<div> <div>7%</div> <div>58%</div> <div>37%</div> <div>5%</div> </div>
1	C	906	<div> <div>5%</div> <div>49%</div> <div>45%</div> <div>6%</div> <div>.</div> </div>
1	D	906	<div> <div>5%</div> <div>40%</div> <div>52%</div> <div>7%</div> <div>.</div> </div>
2	E	18	<div> <div>6%</div> <div>22%</div> <div>50%</div> <div>28%</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	18	
2	I	18	
2	K	18	
3	F	15	
3	H	15	
3	J	15	
3	L	15	

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	DTP	B	907	-	-	-	X
4	DTP	J	2	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 31870 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	902	Total	C	N	O	S	0	0	0
			7284	4679	1208	1365	32			
1	B	902	Total	C	N	O	S	0	0	0
			7315	4695	1216	1371	33			
1	C	901	Total	C	N	O	S	0	0	0
			7312	4695	1212	1372	33			
1	D	897	Total	C	N	O	S	3	0	0
			7165	4599	1184	1350	32			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	222	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
A	327	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
A	904	HIS	-	EXPRESSION TAG	UNP Q38087
A	905	HIS	-	EXPRESSION TAG	UNP Q38087
A	906	HIS	-	EXPRESSION TAG	UNP Q38087
B	222	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
B	327	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
B	904	HIS	-	EXPRESSION TAG	UNP Q38087
B	905	HIS	-	EXPRESSION TAG	UNP Q38087
B	906	HIS	-	EXPRESSION TAG	UNP Q38087
C	222	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
C	327	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
C	904	HIS	-	EXPRESSION TAG	UNP Q38087
C	905	HIS	-	EXPRESSION TAG	UNP Q38087
C	906	HIS	-	EXPRESSION TAG	UNP Q38087
D	222	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
D	327	ALA	ASP	ENGINEERED MUTATION	UNP Q38087
D	904	HIS	-	EXPRESSION TAG	UNP Q38087
D	905	HIS	-	EXPRESSION TAG	UNP Q38087
D	906	HIS	-	EXPRESSION TAG	UNP Q38087

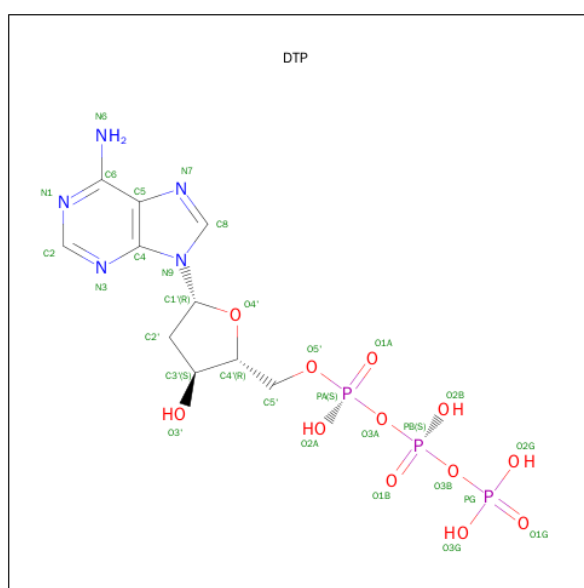
- Molecule 2 is a DNA chain called DNA (5'-D(*CP*GP*TP*(CTG)P*G*AP*AP*TP*GP*AP*CP*AP*GP*CP*CP*GP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	13	Total	C	N	O	P	0	0	0
			265	126	54	73	12			
2	G	18	Total	C	N	O	P	0	0	0
			370	175	71	107	17			
2	I	18	Total	C	N	O	P	0	0	0
			370	175	71	107	17			
2	K	18	Total	C	N	O	P	0	0	0
			370	175	71	107	17			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	13	Total	C	N	O	P	0	0	0
			262	126	45	79	12			
3	H	15	Total	C	N	O	P	0	0	0
			304	146	55	89	14			
3	J	15	Total	C	N	O	P	0	0	0
			304	146	55	89	14			
3	L	15	Total	C	N	O	P	0	0	0
			301	143	55	89	14			

- Molecule 4 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃).



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

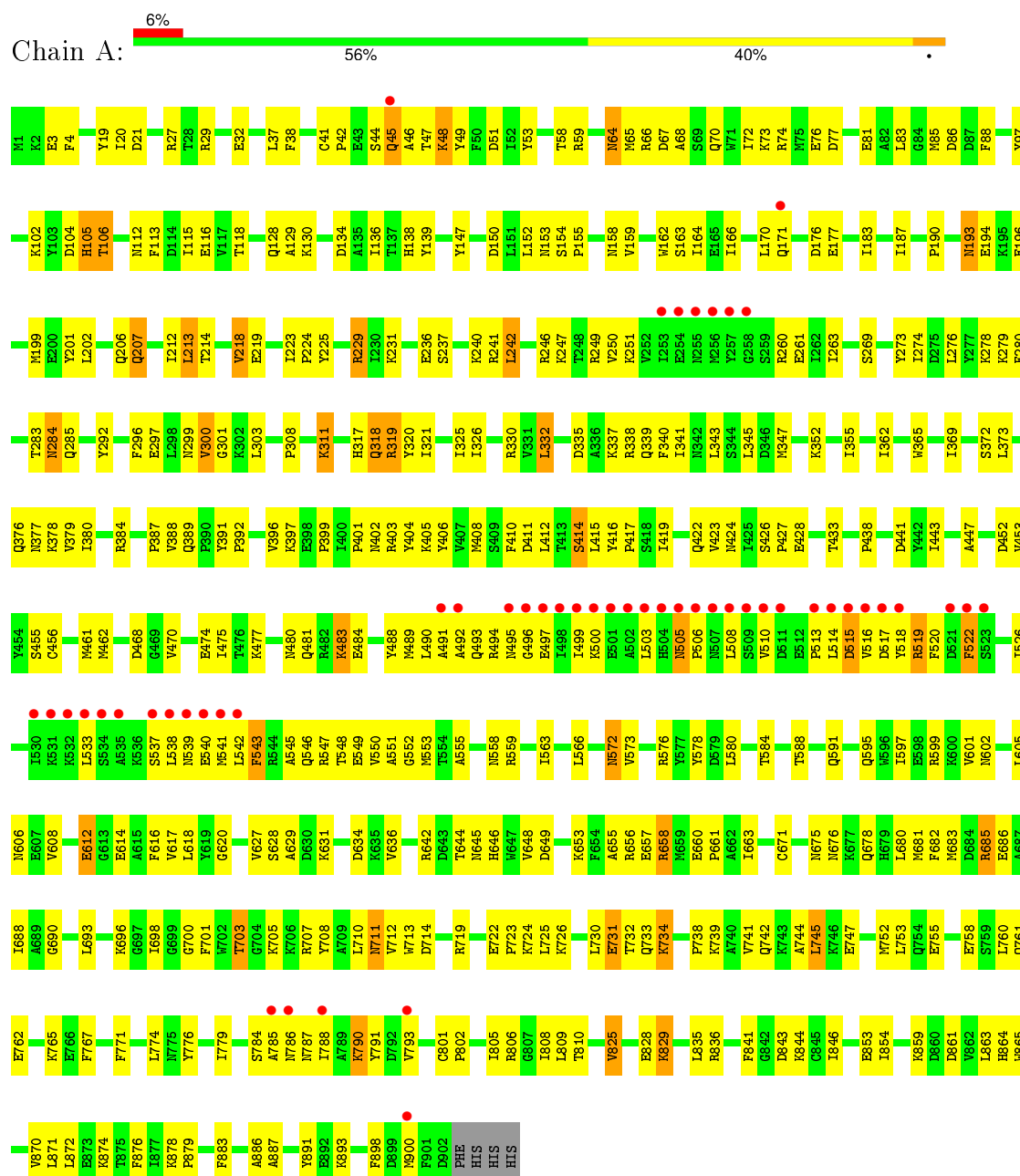
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	59	Total	O	0	0
			59	59		
5	B	50	Total	O	0	0
			50	50		
5	C	40	Total	O	0	0
			40	40		
5	D	27	Total	O	0	0
			27	27		
5	E	1	Total	O	0	0
			1	1		
5	F	1	Total	O	0	0
			1	1		
5	G	2	Total	O	0	0
			2	2		
5	H	1	Total	O	0	0
			1	1		
5	I	3	Total	O	0	0
			3	3		
5	J	2	Total	O	0	0
			2	2		
5	K	1	Total	O	0	0
			1	1		
5	L	1	Total	O	0	0
			1	1		

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 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 ($\text{RSRZ} > 2$). 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.

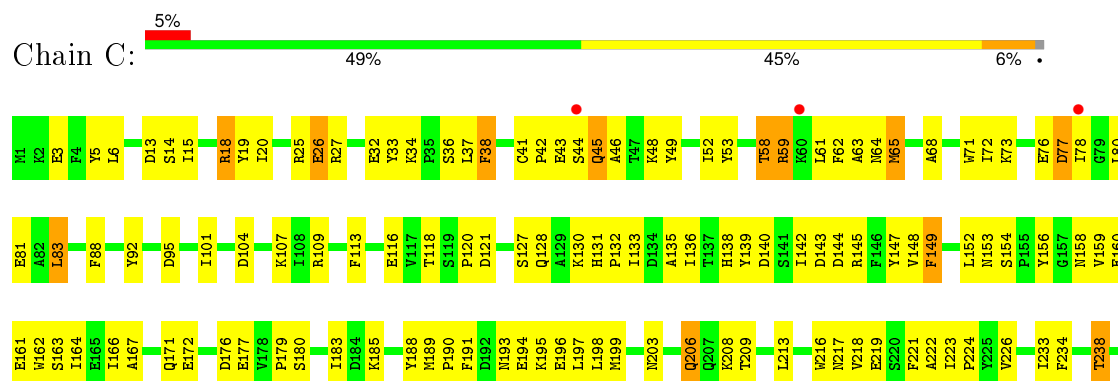
- Molecule 1: DNA polymerase

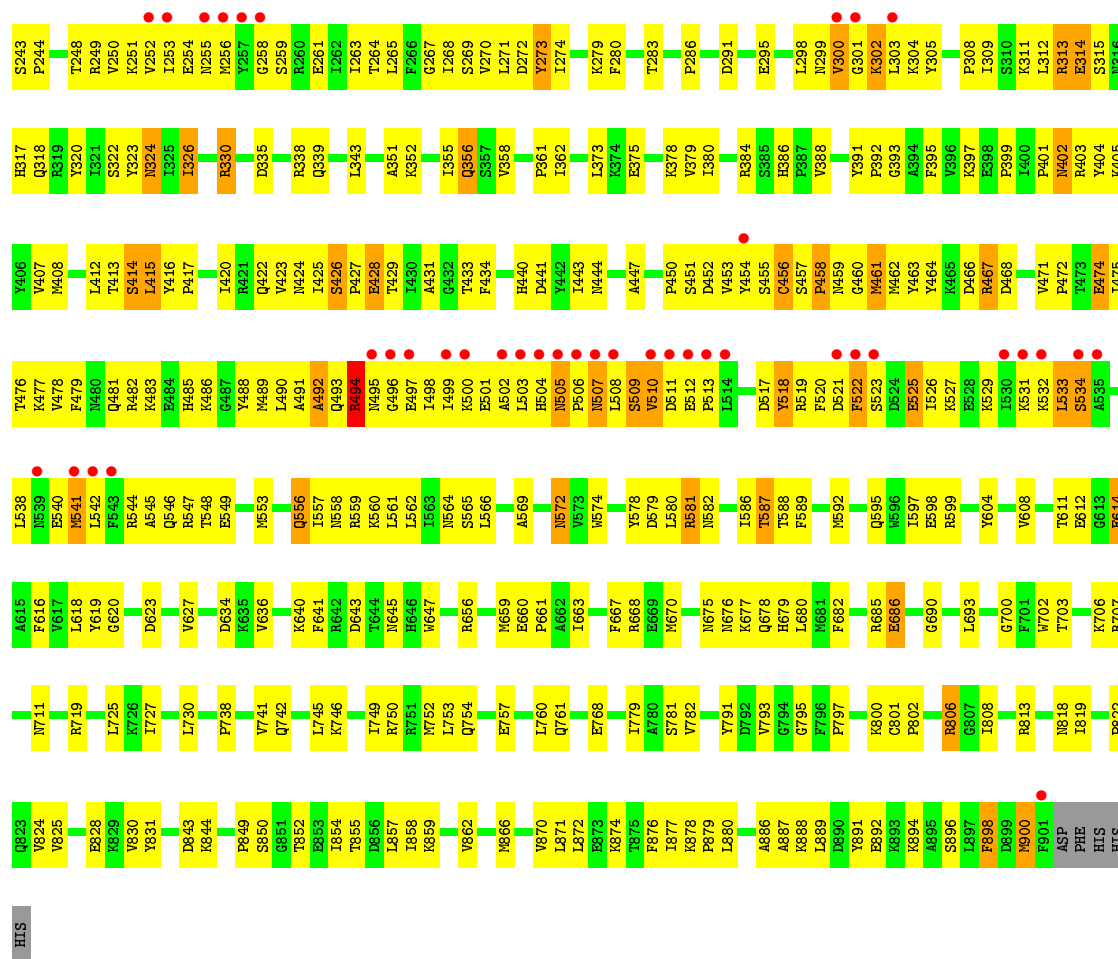


Chain B:

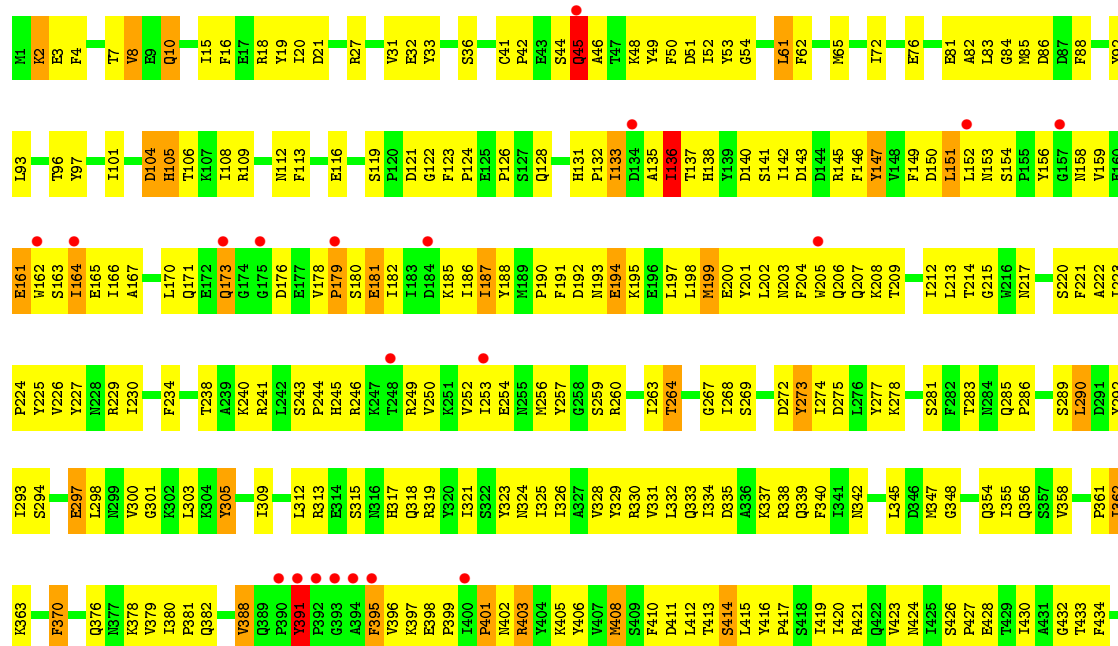


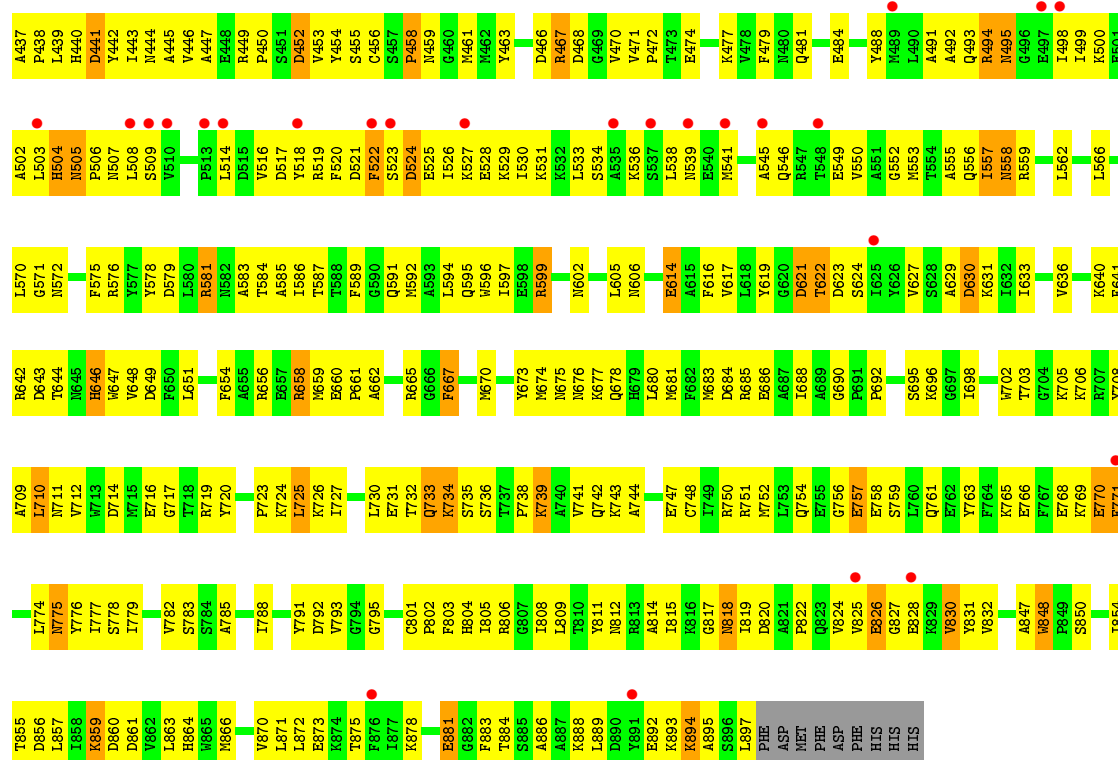
Chain C:



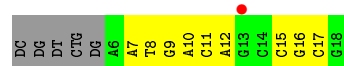


• Molecule 1: DNA polymerase





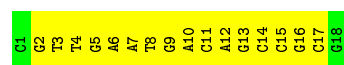
- Molecule 2: DNA (5'-D(*CP*GP*TP*(CTG)P*G*AP*AP*TP*GP*AP*CP*AP*GP*CP*CP*GP*CP*G)-3')



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



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



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

Chain K:  22% 78%



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

Chain F:  7% 40% 40% 7% 13%



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

Chain H:  47% 53%



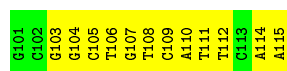
- Molecule 3: DNA (5'-D(*GP*CP*GP*GP*CP*TP*GP*TP*CP*AP*TP*TP*CP*AP*A)-3')

Chain J:  13% 87%



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

Chain L:  20% 80%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	132.84Å 123.03Å 168.78Å 90.00° 95.87° 90.00°	Depositor
Resolution (Å)	50.00 – 2.98 49.74 – 2.98	Depositor EDS
% Data completeness (in resolution range)	92.8 (50.00-2.98) 96.6 (49.74-2.98)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.96Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.220 , 0.275 0.235 , 0.288	Depositor DCC
R_{free} test set	10250 reflections (9.59%)	DCC
Wilson B-factor (Å ²)	56.6	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 70.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 211897 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	31870	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CTG, DTP

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	0.45	0/7462	0.64	0/10099
1	B	0.44	0/7494	0.63	0/10138
1	C	0.45	0/7491	0.64	0/10134
1	D	0.39	0/7343	0.63	2/9963 (0.0%)
2	E	0.33	0/298	0.68	0/458
2	G	0.40	0/390	0.78	0/598
2	I	0.55	0/390	0.78	0/598
2	K	0.30	0/390	0.65	0/598
3	F	0.57	1/292 (0.3%)	0.71	0/449
3	H	0.39	0/340	0.72	0/523
3	J	0.49	0/340	0.83	0/523
3	L	0.34	0/337	0.68	0/517
All	All	0.43	1/32567 (0.0%)	0.64	2/44598 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	G	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	113	DC	N1-C2	5.00	1.45	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	D	391	TYR	N-CA-CB	-6.65	98.62	110.60
1	D	391	TYR	CA-CB-CG	6.42	125.59	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	G	12	DA	Sidechain

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	7284	0	7114	388	0
1	B	7315	0	7162	349	0
1	C	7312	0	7157	510	0
1	D	7165	0	6893	607	0
2	E	265	0	146	17	0
2	G	370	0	205	20	0
2	I	370	0	205	29	0
2	K	370	0	205	23	0
3	F	262	0	149	9	0
3	H	304	0	171	10	0
3	J	304	0	171	17	0
3	L	301	0	162	20	0
4	B	30	0	12	3	0
4	J	30	0	12	2	0
5	A	59	0	0	8	0
5	B	50	0	0	3	0
5	C	40	0	0	6	0
5	D	27	0	0	3	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	2	0	0	0	0
5	H	1	0	0	0	0
5	I	3	0	0	1	0
5	J	2	0	0	0	0
5	K	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	1	0	0	0	0
All	All	31870	0	29764	1967	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 32.

The worst 5 of 1967 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:C:149:PHE:HB3	1:C:197:LEU:HD11	1.20	1.17
1:B:732:THR:HG23	1:B:733:GLN:HE21	0.98	1.13
1:C:424:ASN:HD22	1:C:677:LYS:HD3	1.01	1.10
1:D:214:THR:HG22	1:D:215:GLY:H	1.10	1.09
3:L:110:DA:H2''	3:L:111:DT:H5'	1.34	1.08

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	900/906 (99%)	824 (92%)	71 (8%)	5 (1%)	30	71
1	B	900/906 (99%)	822 (91%)	68 (8%)	10 (1%)	17	57
1	C	899/906 (99%)	803 (89%)	83 (9%)	13 (1%)	14	50
1	D	895/906 (99%)	764 (85%)	103 (12%)	28 (3%)	5	26
All	All	3594/3624 (99%)	3213 (89%)	325 (9%)	56 (2%)	12	46

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	300	VAL

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Mol	Chain	Res	Type
1	A	515	ASP
1	B	300	VAL
1	B	518	TYR
1	C	45	GLN

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	781/803 (97%)	726 (93%)	55 (7%)	19	54
1	B	788/803 (98%)	732 (93%)	56 (7%)	18	53
1	C	788/803 (98%)	726 (92%)	62 (8%)	15	46
1	D	758/803 (94%)	684 (90%)	74 (10%)	10	35
All	All	3115/3212 (97%)	2868 (92%)	247 (8%)	15	46

5 of 247 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	18	ARG
1	C	408	MET
1	D	646	HIS
1	C	58	THR
1	C	203	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	40	HIS
1	C	402	ASN
1	D	675	ASN
1	C	131	HIS
1	C	255	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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$
2	CTG	G	4	3,2	16,23,24	0.75	0	17,35,38	0.80	1 (5%)
2	CTG	I	4	3,2	16,23,24	0.93	1 (6%)	17,35,38	0.75	1 (5%)
2	CTG	K	4	2	16,23,24	0.83	1 (6%)	17,35,38	0.63	0

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	CTG	G	4	3,2	-	0/7/45/46	0/2/2/2
2	CTG	I	4	3,2	-	0/7/45/46	0/2/2/2
2	CTG	K	4	2	-	0/7/45/46	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	4	CTG	C1'-N1	2.26	1.48	1.45
2	I	4	CTG	C1'-N1	2.77	1.49	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	4	CTG	N3-C2-N1	-2.80	114.02	116.82
2	G	4	CTG	N3-C2-N1	-2.32	114.50	116.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	4	CTG	1	0
2	I	4	CTG	2	0
2	K	4	CTG	2	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$
4	DTP	B	907	-	24,32,32	0.69	0	32,50,50	0.99	1 (3%)
4	DTP	J	2	-	24,32,32	0.75	0	32,50,50	0.88	2 (6%)

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	B	907	-	-	0/18/34/34	0/3/3/3
4	DTP	J	2	-	-	0/18/34/34	0/3/3/3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	J	2	DTP	O3A-PA-O5'	2.34	109.14	102.94
4	J	2	DTP	O2G-PG-O1G	2.68	119.22	110.58
4	B	907	DTP	O2G-PG-O1G	2.73	119.38	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	907	DTP	3	0
4	J	2	DTP	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	902/906 (99%)	0.38	53 (5%)	26	13	23, 52, 158, 200	0
1	B	902/906 (99%)	0.38	66 (7%)	18	9	27, 53, 146, 170	0
1	C	901/906 (99%)	0.34	43 (4%)	34	19	21, 55, 145, 173	0
1	D	897/906 (99%)	0.43	45 (5%)	32	17	37, 70, 126, 170	1 (0%)
2	E	13/18 (72%)	0.67	1 (7%)	16	8	69, 110, 130, 135	0
2	G	17/18 (94%)	0.20	0	100	100	52, 72, 106, 106	0
2	I	17/18 (94%)	-0.09	0	100	100	36, 53, 88, 96	0
2	K	17/18 (94%)	0.44	0	100	100	39, 105, 142, 145	0
3	F	13/15 (86%)	1.00	1 (7%)	16	8	94, 121, 139, 140	0
3	H	15/15 (100%)	0.12	0	100	100	45, 79, 149, 150	0
3	J	15/15 (100%)	-0.22	0	100	100	36, 63, 121, 124	0
3	L	15/15 (100%)	0.20	0	100	100	82, 116, 141, 145	0
All	All	3724/3756 (99%)	0.38	209 (5%)	28	14	21, 57, 140, 200	1 (0%)

The worst 5 of 209 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	535	ALA	10.7
1	D	394	ALA	9.3
1	B	545	ALA	9.3
1	A	498	ILE	8.7
1	B	499	ILE	8.0

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, 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	CTG	I	4	22/23	0.88	0.21	-	79,88,93,95	0
2	CTG	G	4	22/23	0.94	0.19	-	71,76,79,80	0
2	CTG	K	4	22/23	0.81	0.24	-	134,145,148,148	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
4	DTP	B	907	30/30	0.75	0.29	3.56	133,137,151,151	0
4	DTP	J	2	30/30	0.72	0.29	2.17	140,147,166,166	0

6.5 Other polymers [i](#)

There are no such residues in this entry.