



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 30, 2024 – 06:44 PM EST

PDB ID : 1HUZ
Title : CRYSTAL STRUCTURE OF DNA POLYMERASE COMPLEXED WITH
DNA AND CR-PCP
Authors : Arndt, J.W.; Gong, W.; Zhong, X.; Showalter, A.K.; Liu, J.; Lin, Z.; Paxson,
C.; Tsai, M.-D.; Chan, M.K.
Deposited on : 2001-01-04
Resolution : 2.60 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

<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>.

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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

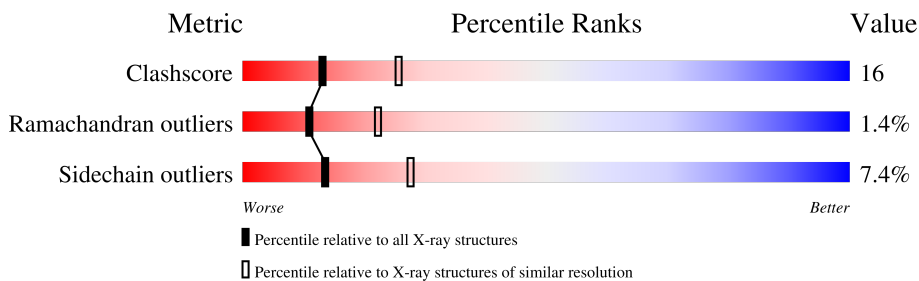
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	11	
1	T	11	
2	D	8	
2	P	8	
3	A	335	
3	B	335	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MDN	A	338	-	X	-	-
5	MDN	B	338	-	X	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5994 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 DNA chain called 5'-D(*AP*AP*TP*AP*GP*GP*CP*GP*TP*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	8	Total	C	N	O	P	0	0	0
			167	78	33	48	8			
1	C	8	Total	C	N	O	P	0	0	0
			167	78	33	48	8			

- Molecule 2 is a DNA chain called 5'-D(P*CP*GP*AP*CP*GP*CP*CP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	8	Total	C	N	O	P	0	0	0
			161	76	29	48	8			
2	D	8	Total	C	N	O	P	0	0	0
			161	76	29	48	8			

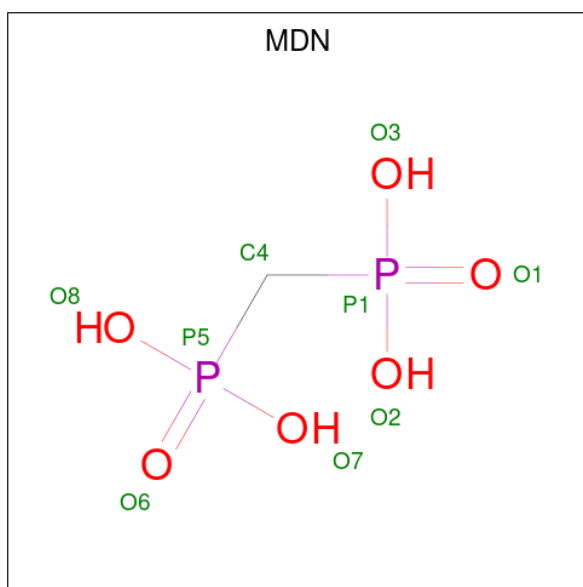
- Molecule 3 is a protein called DNA POLYMERASE BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	325	Total	C	N	O	S	0	0	0
			2598	1639	457	493	9			
3	B	325	Total	C	N	O	S	0	0	0
			2598	1639	457	493	9			

- Molecule 4 is CHROMIUM ION (three-letter code: CR) (formula: Cr).

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

- Molecule 5 is METHYLENEDIPHOSPHONIC ACID (three-letter code: MDN) (formula: CH₆O₆P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	P	0	0
			9	1	6	2		
5	B	1	Total	C	O	P	0	0
			9	1	6	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	T	6	Total	O	0	0
			6	6		
6	P	3	Total	O	0	0
			3	3		
6	C	5	Total	O	0	0
			5	5		
6	D	6	Total	O	0	0
			6	6		
6	A	41	Total	O	0	0
			41	41		
6	B	61	Total	O	0	0
			61	61		

3 Residue-property plots

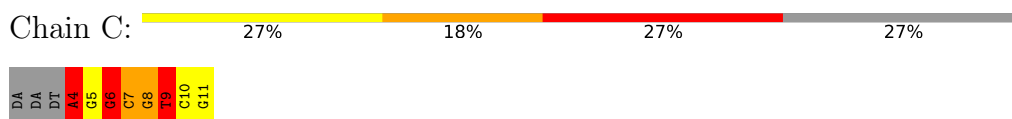
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

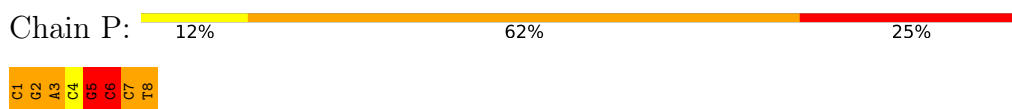
- Molecule 1: 5'-D(*AP*AP*TP*AP*GP*GP*CP*GP*TP*CP*G)-3'



- Molecule 1: 5'-D(*AP*AP*TP*AP*GP*GP*CP*GP*TP*CP*G)-3'



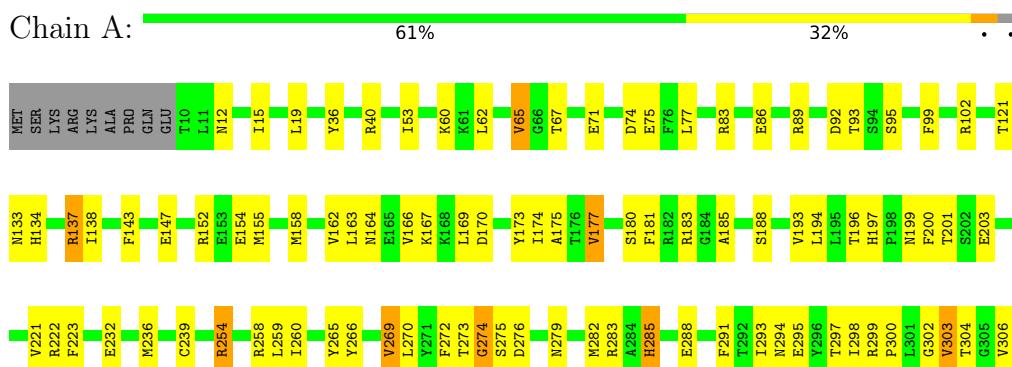
- Molecule 2: 5'-D(P*CP*GP*AP*CP*GP*CP*CP*T)-3'



- Molecule 2: 5'-D(P*CP*GP*AP*CP*GP*CP*CP*T)-3'



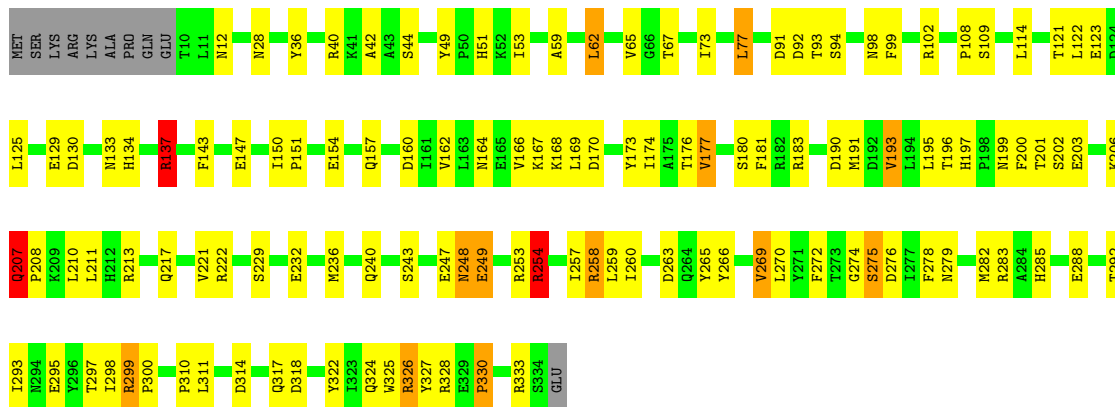
- Molecule 3: DNA POLYMERASE BETA





- Molecule 3: DNA POLYMERASE BETA

Chain B: 60% 33%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.78Å 56.13Å 85.41Å 90.00° 106.94° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.60)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.224 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5994	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

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: MDN, CR

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	C	3.77	27/187 (14.4%)	3.66	51/287 (17.8%)
1	T	3.72	29/187 (15.5%)	3.66	47/287 (16.4%)
2	D	5.04	35/179 (19.6%)	4.58	70/273 (25.6%)
2	P	5.20	46/179 (25.7%)	4.23	57/273 (20.9%)
3	A	0.70	1/2645 (0.0%)	0.80	0/3562
3	B	0.64	0/2645	0.83	7/3562 (0.2%)
All	All	1.68	138/6022 (2.3%)	1.67	232/8244 (2.8%)

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
1	C	0	5
1	T	0	4
2	D	0	8
2	P	0	6
All	All	0	23

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	1	DC	P-O5'	25.10	1.84	1.59
2	D	1	DC	P-O5'	25.03	1.84	1.59
2	P	3	DA	N9-C4	21.61	1.50	1.37
1	C	9	DT	C5-C7	19.53	1.61	1.50
2	P	8	DT	C4'-O4'	18.46	1.63	1.45

The worst 5 of 232 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	7	DC	O4'-C1'-N1	17.57	120.30	108.00
2	D	1	DC	O4'-C1'-N1	16.33	119.43	108.00
2	D	7	DC	P-O3'-C3'	15.26	138.01	119.70
2	P	7	DC	O4'-C4'-C3'	-14.81	97.11	106.00
2	P	1	DC	O4'-C4'-C3'	-14.01	97.59	106.00

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	P	1	DC	Sidechain
1	T	11	DG	Sidechain
1	T	5	DG	Sidechain
1	T	6	DG	Sidechain
1	T	8	DG	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	C	167	0	90	3	0
1	T	167	0	90	0	0
2	D	161	0	90	4	0
2	P	161	0	90	4	0
3	A	2598	0	2604	87	0
3	B	2598	0	2604	95	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	9	0	2	0	0
5	B	9	0	2	0	0
6	A	41	0	0	2	0
6	B	61	0	0	7	0
6	C	5	0	0	1	0
6	D	6	0	0	0	0
6	P	3	0	0	0	0
6	T	6	0	0	0	0
All	All	5994	0	5572	187	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 16.

The worst 5 of 187 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)
2:D:1:DC:O5'	2:D:1:DC:C5'	1.64	1.44
2:P:8:DT:O4'	2:P:8:DT:C4'	1.63	1.38
3:B:248:ASN:O	3:B:249:GLU:HG2	1.41	1.18
3:A:183:ARG:HD3	3:A:274:GLY:O	1.64	0.98
3:B:180:SER:HA	3:B:183:ARG:HG2	1.54	0.90

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	
3	A	323/335 (96%)	298 (92%)	21 (6%)	4 (1%)	13	27
3	B	323/335 (96%)	289 (90%)	29 (9%)	5 (2%)	10	21
All	All	646/670 (96%)	587 (91%)	50 (8%)	9 (1%)	11	22

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	303	VAL
3	B	248	ASN
3	B	274	GLY
3	A	274	GLY
3	A	275	SER

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	
3	A	283/296 (96%)	262 (93%)	21 (7%)	13	28
3	B	283/296 (96%)	262 (93%)	21 (7%)	13	28
All	All	566/592 (96%)	524 (93%)	42 (7%)	13	28

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	130	ASP
3	B	258	ARG
3	B	137	ARG
3	B	193	VAL
3	B	272	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	199	ASN
3	B	264	GLN
3	A	264	GLN
3	B	12	ASN
3	B	98	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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
5	MDN	A	338	4	6,8,8	2.97	4 (66%)	12,13,13	2.79	5 (41%)
5	MDN	B	338	4	6,8,8	3.10	4 (66%)	12,13,13	2.72	7 (58%)

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
5	MDN	A	338	4	-	4/6/6/6	-
5	MDN	B	338	4	-	5/6/6/6	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	338	MDN	P5-O6	4.28	1.59	1.50
5	B	338	MDN	P5-O7	-4.25	1.45	1.54
5	A	338	MDN	P5-O7	-4.06	1.45	1.54
5	B	338	MDN	P5-O6	3.80	1.58	1.50
5	B	338	MDN	P1-O2	3.53	1.63	1.54

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	338	MDN	O3-P1-C4	-6.35	90.99	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	338	MDN	O3-P1-C4	-6.21	91.34	106.40
5	A	338	MDN	O2-P1-O1	3.90	122.69	112.39
5	A	338	MDN	O2-P1-O3	-3.61	97.56	108.08
5	B	338	MDN	O2-P1-O1	3.47	121.57	112.39

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	338	MDN	P1-C4-P5-O8
5	B	338	MDN	P5-C4-P1-O3
5	B	338	MDN	P5-C4-P1-O1
5	B	338	MDN	P1-C4-P5-O6
5	B	338	MDN	P1-C4-P5-O8

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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.