



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 07:56 PM EDT

PDB ID : 4F50 / pdb_00004f50
Title : Y-family DNA polymerase chimera Dbh-Dbh-Dpo4
Authors : Pata, J.D.; Wilson, R.C.
Deposited on : 2012-05-11
Resolution : 2.21 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

<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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

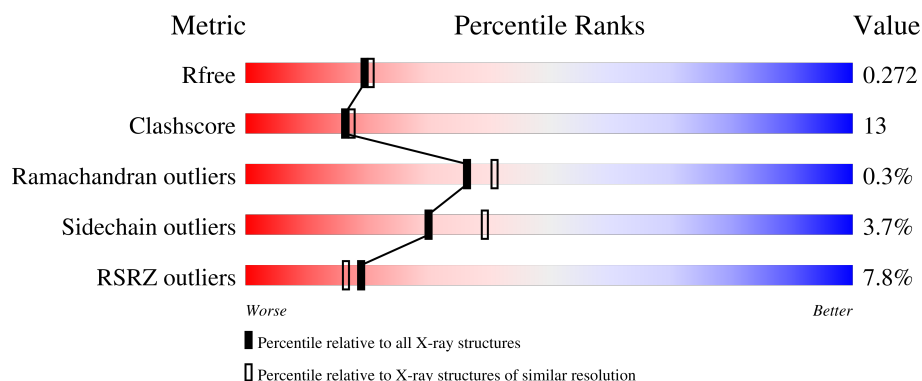
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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}	180053	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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 $\leq 5\%$. 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	361	
2	P	11	
3	T	14	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3234 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 IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	337	Total	C	N	O	S	0	1	0
			2693	1730	464	492	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	354	GLY	-	expression tag	UNP Q97W02
A	355	GLY	-	expression tag	UNP Q97W02
A	356	HIS	-	expression tag	UNP Q97W02
A	357	HIS	-	expression tag	UNP Q97W02
A	358	HIS	-	expression tag	UNP Q97W02
A	359	HIS	-	expression tag	UNP Q97W02
A	360	HIS	-	expression tag	UNP Q97W02
A	361	HIS	-	expression tag	UNP Q97W02

- Molecule 2 is a DNA chain called DNA (5'-D(*GP*GP*GP*AP*AP*GP*CP*CP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	11	Total	C	N	O	P	0	0	0
			228	107	49	62	10			

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*CP*GP*CP*CP*T*GP*GP*CP*TP*TP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	13	Total	C	N	O	P	0	0	0
			238	112	40	74	12			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ca 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	57	Total O 57 57	0	0
5	P	4	Total O 4 4	0	0
5	T	13	Total O 13 13	0	0

- Molecule 1: DNA polymerase IV



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	124.48Å 124.48Å 70.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.47 – 2.21 28.47 – 2.21	Depositor EDS
% Data completeness (in resolution range)	97.4 (28.47-2.21) 97.4 (28.47-2.21)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.22Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.212 , 0.269 0.220 , 0.272	Depositor DCC
R_{free} test set	1367 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 80.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3234	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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, 0.333 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: CA

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	0.54	0/2735	0.91	0/3681
2	P	0.29	0/257	0.80	0/396
3	T	0.32	0/262	1.10	1/397 (0.3%)
All	All	0.51	0/3254	0.92	1/4474 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	3	DG	C4'-C3'-O3'	-5.50	101.75	110.00

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	2693	0	2830	76	0
2	P	228	0	123	1	0
3	T	238	0	133	6	0
4	A	1	0	0	0	0
5	A	57	0	0	7	1
5	P	4	0	0	0	0
5	T	13	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3234	0	3086	81	1

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 13.

All (81) 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:280:ARG:NH2	5:A:536:HOH:O	1.88	0.86
3:T:1:DC:O3'	5:T:110:HOH:O	1.99	0.74
3:T:1:DC:N3	5:T:101:HOH:O	2.22	0.72
3:T:6:DT:OP2	5:T:107:HOH:O	2.09	0.70
1:A:253:LYS:NZ	5:A:557:HOH:O	2.24	0.69
1:A:290:VAL:HG22	1:A:333:ARG:HB2	1.74	0.69
1:A:303:PHE:HZ	1:A:315:GLU:HG2	1.58	0.69
1:A:181:ILE:HD12	1:A:184:ILE:HD12	1.77	0.67
3:T:8:DG:OP1	5:T:113:HOH:O	2.13	0.66
1:A:166:VAL:N	5:A:539:HOH:O	2.05	0.66
1:A:124:GLU:OE1	1:A:127:ARG:NH1	2.29	0.65
1:A:285:ILE:HG22	1:A:303:PHE:HE2	1.62	0.64
1:A:20:ASN:HB3	1:A:22:GLN:HE22	1.63	0.63
1:A:305:HIS:ND1	1:A:306:GLY:O	2.30	0.63
1:A:195:LEU:HD22	1:A:200:ILE:HD12	1.83	0.61
1:A:20:ASN:HB3	1:A:22:GLN:NE2	2.16	0.60
1:A:231:GLN:HG3	1:A:233:LYS:HG3	1.83	0.60
1:A:96:ALA:HB2	1:A:109:LEU:HD23	1.83	0.59
1:A:248:ARG:HB3	5:A:546:HOH:O	2.00	0.59
1:A:303:PHE:CZ	1:A:315:GLU:HG2	2.37	0.58
1:A:342:ILE:O	5:A:503:HOH:O	2.17	0.58
1:A:191:LEU:HG	2:P:8:DC:OP1	2.05	0.57
1:A:115:VAL:HG11	1:A:122:GLY:HA2	1.86	0.56
1:A:327:ASP:OD2	1:A:329:ARG:NH2	2.38	0.56
1:A:1:MET:HE1	1:A:237:PRO:HA	1.87	0.55
1:A:251:THR:HA	1:A:333:ARG:HG2	1.89	0.55
1:A:1:MET:HE1	1:A:238:VAL:H	1.71	0.54
1:A:252:MET:HA	1:A:265:TYR:CE1	2.43	0.54
1:A:62:ILE:HA	1:A:65:MET:HE2	1.89	0.54
1:A:255:ASN:ND2	1:A:292:GLU:OE1	2.42	0.53
1:A:299:ARG:HB3	1:A:319:LEU:HD22	1.91	0.53
1:A:115:VAL:O	1:A:118:ASN:ND2	2.42	0.53
1:A:271:GLU:OE2	1:A:313:TYR:OH	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:TYR:OH	1:A:307:ILE:O	2.28	0.52
1:A:4:ILE:HD13	1:A:126:ALA:HB2	1.92	0.51
3:T:1:DC:OP1	3:T:1:DC:H4'	2.10	0.51
1:A:59:MET:HA	3:T:1:DC:H2''	1.93	0.51
1:A:184:ILE:HD11	1:A:203:LEU:HB2	1.92	0.50
1:A:2:ILE:H	1:A:112:THR:CG2	2.24	0.50
1:A:248:ARG:HH12	1:A:250:VAL:HA	1.76	0.50
1:A:312:ALA:O	1:A:316:SER:N	2.44	0.49
1:A:76:MET:HE3	1:A:78:LYS:HB2	1.93	0.49
1:A:299:ARG:HG2	1:A:323:ILE:HG12	1.95	0.49
1:A:253:LYS:HG2	1:A:265:TYR:OH	2.13	0.49
1:A:2:ILE:H	1:A:112:THR:HG23	1.79	0.48
1:A:191:LEU:HA	1:A:194:ARG:HG2	1.94	0.48
1:A:212:ASN:O	1:A:216:LYS:HG2	2.14	0.48
1:A:269:ALA:C	1:A:271:GLU:H	2.22	0.48
1:A:214:LEU:O	1:A:218:THR:HG22	2.14	0.48
1:A:285:ILE:HG22	1:A:303:PHE:CE2	2.46	0.47
1:A:193:ARG:HE	1:A:193:ARG:HB2	1.54	0.47
1:A:187:ILE:HG23	1:A:191:LEU:HD12	1.97	0.47
1:A:290:VAL:CG2	1:A:333:ARG:HB2	2.45	0.46
1:A:170:THR:O	5:A:505:HOH:O	2.21	0.46
1:A:182:ASP:O	5:A:517:HOH:O	2.21	0.45
1:A:120:GLU:OE2	1:A:168:ARG:NH1	2.34	0.45
1:A:130:LYS:NZ	1:A:141:VAL:O	2.49	0.45
1:A:277:LEU:HD11	1:A:341:PHE:HE1	1.81	0.45
1:A:284:ALA:HB2	1:A:340:LYS:HZ3	1.82	0.45
1:A:200:ILE:HG23	1:A:205:ASP:HB2	1.98	0.45
1:A:77:ARG:O	1:A:80:ILE:HG22	2.18	0.44
1:A:147:PRO:HG2	1:A:172:VAL:HG21	2.00	0.44
1:A:286:HIS:NE2	1:A:300:GLY:HA3	2.33	0.43
1:A:200:ILE:HD13	1:A:206:ILE:HD13	2.01	0.42
1:A:283:LYS:NZ	1:A:342:ILE:HD11	2.34	0.42
1:A:281:ILE:HA	1:A:282:PRO:HD3	1.76	0.42
1:A:187:ILE:HA	1:A:191:LEU:HD11	2.02	0.42
1:A:252:MET:C	1:A:332:ARG:HH12	2.26	0.41
1:A:1:MET:HA	1:A:112:THR:CG2	2.50	0.41
1:A:155:ILE:HB	1:A:167:ILE:HD11	2.02	0.41
1:A:220:LYS:HG3	1:A:221:ALA:H	1.86	0.41
1:A:267:PHE:CD2	1:A:313:TYR:HD1	2.38	0.41
1:A:249[A]:ILE:HA	1:A:335:GLY:HA3	2.03	0.41
1:A:252:MET:HG2	1:A:265:TYR:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:PRO:HB2	1:A:71:ALA:HA	2.03	0.41
1:A:100:GLU:HB2	1:A:239:GLU:O	2.20	0.40
1:A:160:LYS:HA	1:A:161:PRO:HA	1.78	0.40
1:A:290:VAL:HG12	1:A:296:ILE:HD12	2.04	0.40
1:A:299:ARG:HD3	1:A:299:ARG:HA	1.85	0.40
1:A:263:LYS:HG2	1:A:317:VAL:HG12	2.02	0.40
1:A:318:LYS:O	1:A:321:GLN:HB2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:501:HOH:O	5:A:508:HOH:O[7_554]	1.93	0.27

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	333/361 (92%)	310 (93%)	22 (7%)	1 (0%)	36 41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	270	ILE

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	295/314 (94%)	284 (96%)	11 (4%)	30	39

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	45	THR
1	A	114	LYS
1	A	170	THR
1	A	173	GLN
1	A	193	ARG
1	A	215	GLU
1	A	250	VAL
1	A	302	THR
1	A	303	PHE
1	A	311	THR

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

Mol	Chain	Res	Type
1	A	286	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

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	337/361 (93%)	0.56	28 (8%) 17 15	31, 80, 137, 176	1 (0%)
2	P	11/11 (100%)	-0.35	0 100 100	60, 68, 83, 87	0
3	T	13/14 (92%)	-0.18	0 100 100	64, 70, 94, 128	0
All	All	361/386 (93%)	0.51	28 (7%) 19 16	31, 78, 133, 176	1 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	ALA	4.9
1	A	342	ILE	4.4
1	A	303	PHE	4.1
1	A	270	ILE	3.7
1	A	305	HIS	3.5
1	A	307	ILE	3.4
1	A	308	SER	3.4
1	A	177	ASN	3.4
1	A	135	GLU	3.3
1	A	275	TYR	3.0
1	A	180	ASP	3.0
1	A	293	ASP	2.7
1	A	131	GLN	2.7
1	A	311	THR	2.7
1	A	302	THR	2.6
1	A	170	THR	2.6
1	A	217	ILE	2.6
1	A	250	VAL	2.4
1	A	259	LEU	2.2
1	A	34	SER	2.2
1	A	304	PRO	2.2
1	A	313	TYR	2.1
1	A	62	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	97	ASP	2.1
1	A	227	LEU	2.1
1	A	193	ARG	2.1
1	A	271	GLU	2.0
1	A	113	ASN	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 oligosaccharides 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, 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	B-factors(Å ²)	Q<0.9
4	CA	A	401	1/1	0.76	0.17	115,115,115,115	0

6.5 Other polymers [i](#)

There are no such residues in this entry.