



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4BPX / pdb_00004bpx
Title : Crystal structure of human primase in complex with the primase- binding motif of DNA polymerase alpha
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Deposited on : 2013-05-28
Resolution : 3.40 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

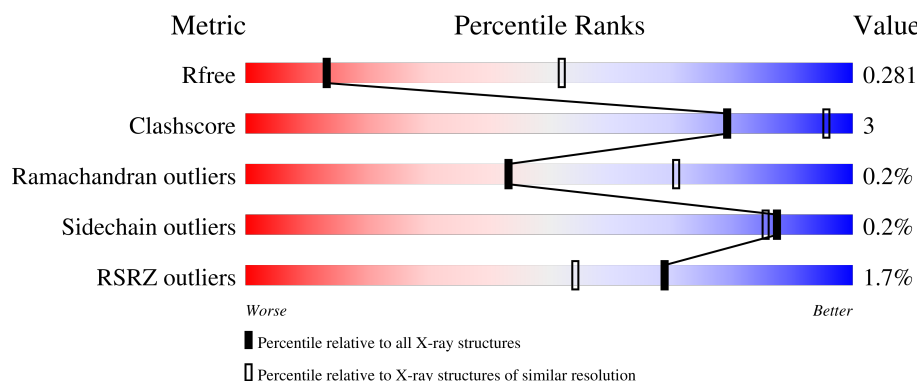
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	423	
1	C	423	
2	B	269	
2	D	269	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19218 atoms, of which 9629 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 PRIMASE SMALL SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	381	Total	C	H	N	O	S	0	2	0
			6392	2059	3190	558	572	13			
1	C	372	Total	C	H	N	O	S	0	0	0
			6195	2002	3086	537	557	13			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P49642
A	-1	THR	-	expression tag	UNP P49642
A	0	SER	-	expression tag	UNP P49642
A	72	ALA	LYS	engineered mutation	UNP P49642
A	73	ALA	MET	engineered mutation	UNP P49642
C	-2	GLY	-	expression tag	UNP P49642
C	-1	THR	-	expression tag	UNP P49642
C	0	SER	-	expression tag	UNP P49642
C	72	ALA	LYS	engineered mutation	UNP P49642
C	73	ALA	MET	engineered mutation	UNP P49642

- Molecule 2 is a protein called DNA POLYMERASE ALPHA CATALYTIC SUBUNIT, DNA PRIMASE LARGE SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	181	Total	C	H	N	O	S	0	0	0
			3056	970	1553	258	273	2			
2	D	213	Total	C	H	N	O	S	0	0	0
			3573	1142	1800	300	329	2			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1444	MET	-	expression tag	UNP P09884

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Chain	Residue	Modelled	Actual	Comment	Reference
B	4	THR	-	linker	UNP P49643
B	5	GLY	-	linker	UNP P49643
B	6	SER	-	linker	UNP P49643
B	7	THR	-	linker	UNP P49643
B	8	GLY	-	linker	UNP P49643
B	9	SER	-	linker	UNP P49643
B	10	THR	-	linker	UNP P49643
B	11	GLY	-	linker	UNP P49643
B	12	SER	-	linker	UNP P49643
B	13	THR	-	linker	UNP P49643
B	14	GLY	-	linker	UNP P49643
B	15	SER	-	linker	UNP P49643
B	16	THR	-	linker	UNP P49643
B	17	GLY	-	linker	UNP P49643
B	18	SER	-	linker	UNP P49643
D	1444	MET	-	expression tag	UNP P09884
D	4	THR	-	linker	UNP P49643
D	5	GLY	-	linker	UNP P49643
D	6	SER	-	linker	UNP P49643
D	7	THR	-	linker	UNP P49643
D	8	GLY	-	linker	UNP P49643
D	9	SER	-	linker	UNP P49643
D	10	THR	-	linker	UNP P49643
D	11	GLY	-	linker	UNP P49643
D	12	SER	-	linker	UNP P49643
D	13	THR	-	linker	UNP P49643
D	14	GLY	-	linker	UNP P49643
D	15	SER	-	linker	UNP P49643
D	16	THR	-	linker	UNP P49643
D	17	GLY	-	linker	UNP P49643
D	18	SER	-	linker	UNP P49643

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0
3	C	1	Total Zn 1 1	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	120.68Å 70.70Å 127.16Å 90.00° 105.83° 90.00°	Depositor
Resolution (Å)	45.33 – 3.40 45.33 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.33-3.40) 99.8 (45.33-3.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 3.40Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.234 , 0.267 0.247 , 0.281	Depositor DCC
R_{free} test set	1487 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	171.8	Xtriage
Anisotropy	0.334	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 145.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19218	wwPDB-VP
Average B, all atoms (Å ²)	218.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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

5.1 Standard geometry

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

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	0.31	0/3297	0.70	0/4449
1	C	0.29	0/3190	0.67	0/4307
2	B	0.29	0/1524	0.69	0/2040
2	D	0.30	0/1803	0.71	0/2420
All	All	0.30	0/9814	0.69	0/13216

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	3202	3190	3167	23	0
1	C	3109	3086	3073	15	0
2	B	1503	1553	1550	5	0
2	D	1773	1800	1794	9	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
All	All	9589	9629	9584	51	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 (51) 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:160:SER:O	1:A:318:LYS:NZ	2.19	0.76
2:D:119:TRP:O	2:D:123:GLN:NE2	2.19	0.74
1:A:403:ASP:OD1	1:A:406:ARG:NH2	2.26	0.69
1:C:254:GLU:OE2	1:C:278:ARG:NH2	2.28	0.67
1:C:71:GLN:O	1:C:74:ASN:ND2	2.29	0.66
2:D:29:TYR:O	2:D:107:ARG:NH2	2.28	0.66
1:A:232:ASP:OD1	1:A:265:SER:OG	2.14	0.65
2:B:119:TRP:O	2:B:123:GLN:NE2	2.31	0.64
1:A:92:ASN:OD1	2:D:1448:GLU:N	2.32	0.62
2:B:99:ASP:OD1	2:B:131:ARG:NH2	2.38	0.57
2:D:68:GLU:O	2:D:72:SER:N	2.38	0.56
1:C:111:ASP:OD2	1:C:163:ARG:NH2	2.39	0.56
1:A:335:ASP:OD2	1:A:338:LYS:NZ	2.40	0.55
1:C:104:LYS:NZ	1:C:315:HIS:O	2.36	0.53
1:A:43:ARG:NH1	1:A:81:GLY:O	2.40	0.52
2:B:193:ASP:OD2	2:B:220:ASN:ND2	2.43	0.52
1:C:232:ASP:OD1	1:C:265:SER:OG	2.25	0.51
1:A:237:LYS:HA	1:A:240:TRP:CE2	2.46	0.50
1:C:329:ARG:NH1	1:C:344:PRO:O	2.45	0.50
2:D:99:ASP:OD1	2:D:131:ARG:NH2	2.46	0.49
1:C:121:CYS:SG	1:C:131:CYS:HB3	2.55	0.47
1:A:254:GLU:OE2	1:A:278[A]:ARG:NH2	2.47	0.47
1:C:152:PHE:O	1:C:155:ARG:NH1	2.47	0.47
1:C:128:CYS:SG	1:C:130:LYS:HB2	2.55	0.46
1:A:106:LEU:HB3	1:A:169:VAL:HB	1.96	0.46
1:A:234:LEU:O	1:A:268:ARG:NE	2.49	0.46
2:B:149:LEU:O	2:B:151:PHE:N	2.47	0.46
2:B:125:MET:SD	2:B:223:ARG:NE	2.90	0.46
1:A:112:MET:HE1	1:A:131:CYS:HB2	1.98	0.44
1:A:44:GLU:OE2	1:A:56:ARG:NE	2.44	0.44
1:A:396:GLU:O	1:A:400:GLU:N	2.44	0.44
1:A:302:PHE:CG	1:A:303:PRO:HD2	2.53	0.43
1:C:237:LYS:HA	1:C:240:TRP:CE2	2.52	0.43
2:D:41:GLU:OE2	2:D:97:ARG:NH2	2.47	0.43
2:D:94:GLU:HB2	2:D:95:PRO:HD3	2.01	0.42
1:A:389:ALA:N	1:A:390:PRO:HD2	2.34	0.42
1:A:29:TRP:HB2	1:A:399:LEU:HD21	2.02	0.42
1:A:112:MET:SD	1:A:135:MET:HG2	2.60	0.42
1:A:219:ILE:O	1:A:223:PHE:N	2.51	0.42
1:C:302:PHE:CG	1:C:303:PRO:HD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:389:ALA:N	1:C:390:PRO:HD2	2.36	0.41
2:D:45:LEU:HG	2:D:102:SER:HB3	2.01	0.41
2:D:247:GLN:N	2:D:248:PRO:HD2	2.36	0.41
1:C:9:LEU:N	1:C:10:PRO:HD2	2.35	0.41
1:C:344:PRO:HA	1:C:347:VAL:HG23	2.02	0.41
1:A:9:LEU:N	1:A:10:PRO:HD2	2.36	0.40
1:A:121:CYS:SG	1:A:131:CYS:HB3	2.61	0.40
1:A:23:TYR:CG	1:A:67:GLU:HG2	2.56	0.40
1:A:71:GLN:O	1:A:74:ASN:ND2	2.54	0.40
1:A:240:TRP:CD1	1:A:240:TRP:C	3.00	0.40
1:C:157:TRP:CD1	1:C:336:LEU:HD21	2.56	0.40

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	377/423 (89%)	362 (96%)	15 (4%)	0	100	100
1	C	366/423 (86%)	351 (96%)	15 (4%)	0	100	100
2	B	171/269 (64%)	161 (94%)	9 (5%)	1 (1%)	21	50
2	D	203/269 (76%)	192 (95%)	10 (5%)	1 (0%)	24	54
All	All	1117/1384 (81%)	1066 (95%)	49 (4%)	2 (0%)	43	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	155	SER
2	D	62	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	
1	A	356/393 (91%)	356 (100%)	0	100	100
1	C	345/393 (88%)	344 (100%)	1 (0%)	86	84
2	B	166/240 (69%)	165 (99%)	1 (1%)	78	80
2	D	196/240 (82%)	196 (100%)	0	100	100
All	All	1063/1266 (84%)	1061 (100%)	2 (0%)	87	85

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	148	GLN
1	C	62	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	102	GLN
1	A	166	HIS
1	A	263	HIS
1	A	280	GLN
1	C	58	GLN
1	C	102	GLN
1	C	263	HIS
1	C	341	GLN
1	C	397	HIS
2	D	103	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 2 ligands modelled in this entry, 2 are 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 [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	381/423 (90%)	-0.44	4 (1%) 79 66	68, 158, 216, 264	1 (0%)
1	C	372/423 (87%)	-0.41	8 (2%) 62 47	156, 247, 313, 337	0
2	B	181/269 (67%)	-0.21	3 (1%) 69 54	142, 282, 332, 352	0
2	D	213/269 (79%)	-0.26	4 (1%) 66 51	153, 228, 279, 300	0
All	All	1147/1384 (82%)	-0.36	19 (1%) 69 54	68, 215, 315, 352	1 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	132	PHE	4.1
1	C	96	LEU	3.6
1	C	266	LEU	3.2
1	C	157	TRP	2.7
2	D	39	LEU	2.6
1	C	139	ILE	2.5
1	A	229	VAL	2.4
1	C	310	SER	2.4
1	C	301	CYS	2.4
2	D	53	LEU	2.4
1	C	290	PRO	2.4
2	D	66	GLY	2.3
2	B	110	TYR	2.3
2	D	47	ILE	2.3
1	C	109	ASP	2.1
1	A	321	PHE	2.1
1	A	385	LYS	2.1
1	A	290	PRO	2.1
2	B	109	ALA	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($\text{\AA}^2$)	Q<0.9
3	ZN	A	430	1/1	0.99	0.05	137,137,137,137	0
3	ZN	C	430	1/1	1.00	0.03	203,203,203,203	0

6.5 Other polymers [i](#)

There are no such residues in this entry.