



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:05 PM UTC

PDB ID : 3B39 / pdb_00003b39
Title : Structure of the DnaG primase catalytic domain bound to ssDNA
Authors : Corn, J.E.; Pelton, J.G.; Berger, J.M.
Deposited on : 2007-10-19
Resolution : 2.35 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

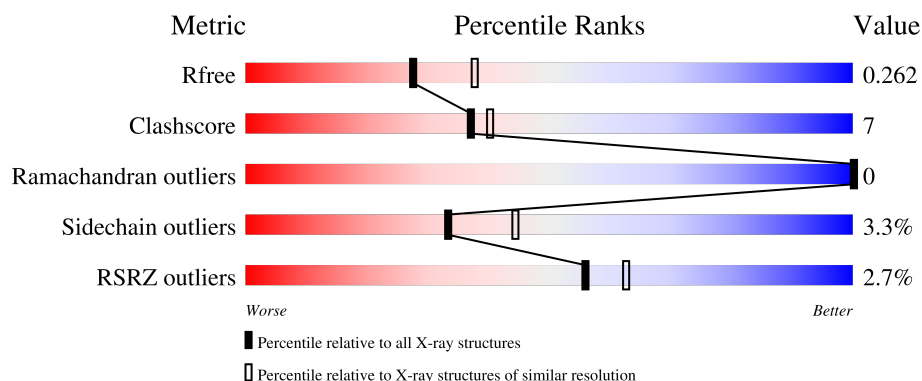
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	C	15	7% 20% 20% 60%
1	D	15	7% 53% 47%
2	A	322	3% 80% 17% ..
2	B	322	% 78% 18% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5354 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 DNA (5'-D(*DCP*DAP*DAP*DAP*DGP*DCP*DCP*DAP*DAP*DAP*DAP*DGP*DGP*DAP*DC)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	6	Total	C	N	O	P	0	0	0
			108	49	23	30	6			
1	D	8	Total	C	N	O	P	0	0	0
			132	59	28	37	8			

- Molecule 2 is a protein called DNA primase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	317	Total	C	N	O	S	0	0	0
			2511	1577	451	471	12			
2	B	310	Total	C	N	O	S	0	0	0
			2457	1542	444	459	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	108	SER	-	expression tag	UNP P0ABS5
A	109	ASN	-	expression tag	UNP P0ABS5
A	110	ALA	-	expression tag	UNP P0ABS5
A	320	CYS	ARG	engineered mutation	UNP P0ABS5
B	108	SER	-	expression tag	UNP P0ABS5
B	109	ASN	-	expression tag	UNP P0ABS5
B	110	ALA	-	expression tag	UNP P0ABS5
B	320	CYS	ARG	engineered mutation	UNP P0ABS5

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	8	Total	O	0	0
			8	8		

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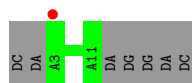
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	9	Total 9	O 9	0	0
3	A	62	Total 62	O 62	0	0
3	B	67	Total 67	O 67	0	0

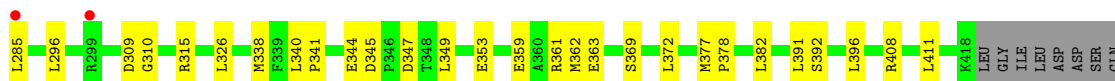
- Molecule 1: DNA (5'-D(*DCP*DAP*DAP*DAP*DGP*DCP*DCP*DAP*DAP*DAP*DAP*DGP*DGP*DAP*DC)-3')



- Molecule 1: DNA (5'-D(*DCP*DAP*DAP*DAP*DGP*DCP*DCP*DAP*DAP*DAP*DAP*DGP*DGP*DAP*DC)-3')



SER	Value
M109	0.00
Q112	0.00
R113	0.00
Q114	0.00
Y117	0.00
Q118	0.00
L123	0.00
V135	0.00
A136	0.00
T137	0.00
Q141	0.00
R146	0.00
V152	0.00
F172	0.00
T190	0.00
M191	0.00
D192	0.00
Q193	0.00
G194	0.00
R195	0.00
S196	0.00
R203	0.00
R214	0.00
V222	0.00
M225	0.00
D226	0.00
T227	0.00
P228	0.00
K229	0.00
Y230	0.00
S233	0.00
T236	0.00
F239	0.00
H240	0.00
R243	0.00
Q244	0.00
L245	0.00
T246	0.00
R260	0.00
S284	0.00



LEU
GLU
ARG

4 Data and refinement statistics

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α , β , γ	136.83Å 136.83Å 71.07Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 2.35 40.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	94.6 (40.00-2.35) 94.6 (40.00-2.35)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.3.0021	Depositor
R, R_{free}	0.212 , 0.254 0.216 , 0.262	Depositor DCC
R_{free} test set	1519 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.032 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5354	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% 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](#)

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	0.40	0/121	1.13	0/185
1	D	0.30	0/147	0.85	0/222
2	A	0.69	1/2560 (0.0%)	0.82	0/3463
2	B	0.68	0/2507	0.83	0/3392
All	All	0.67	1/5335 (0.0%)	0.83	0/7262

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	181	SER	C-N	-6.13	1.24	1.33

There are no bond angle outliers.

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	C	108	0	55	4	0
1	D	132	0	66	0	0
2	A	2511	0	2470	37	0
2	B	2457	0	2414	34	0
3	A	62	0	0	0	0
3	B	67	0	0	0	0
3	C	8	0	0	0	0
3	D	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5354	0	5005	72	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 7.

All (72) 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:B:310:GLY:O	2:B:315:ARG:NH1	1.91	1.02
2:A:236:THR:HG22	2:A:238:ILE:H	1.27	0.99
2:A:246:TYR:HB2	2:A:285:LEU:HD21	1.71	0.72
2:A:345:ASP:OD1	2:A:348:THR:HG23	1.94	0.67
2:A:236:THR:HG22	2:A:238:ILE:N	2.07	0.67
2:A:396:LEU:O	2:A:400:SER:OG	2.15	0.65
2:A:222:VAL:HG21	2:A:226:ASP:O	2.00	0.62
2:A:340:LEU:HD22	2:A:349:LEU:HD12	1.82	0.62
2:A:236:THR:CG2	2:A:237:ASP:N	2.64	0.61
2:B:114:GLN:HE21	2:B:118:GLN:HE21	1.48	0.60
2:A:359:GLU:HA	2:A:362:MET:HE3	1.84	0.59
2:A:360:ALA:O	2:A:363:GLU:HG2	2.03	0.57
2:A:353:GLU:HB3	2:A:357:ALA:HB3	1.86	0.56
2:B:377:MET:HE1	2:B:382:LEU:HD11	1.88	0.56
2:A:305:ILE:HD12	2:A:305:ILE:N	2.21	0.55
1:C:6:DC:H2''	2:B:109:ASN:HB2	1.91	0.53
2:B:190:THR:OG1	2:B:196:SER:OG	2.26	0.53
2:B:359:GLU:HA	2:B:362:MET:HE3	1.91	0.53
2:B:236:THR:O	2:B:239:PHE:O	2.26	0.53
1:C:2:DA:H2'	1:C:3:DA:C8	2.45	0.52
2:B:117:TYR:CE1	2:B:214:ARG:HD2	2.44	0.52
1:C:6:DC:C2'	2:B:109:ASN:HB2	2.41	0.51
2:B:372:LEU:CD2	2:B:411:LEU:HD22	2.40	0.50
1:C:2:DA:H2''	1:C:3:DA:O5'	2.11	0.50
2:A:112:GLN:O	2:A:116:LEU:HD13	2.11	0.50
2:A:148:LEU:HD11	2:A:268:MET:HE1	1.94	0.49
2:B:114:GLN:HE21	2:B:118:GLN:NE2	2.09	0.49
2:A:414:GLU:O	2:A:418:LYS:HG2	2.13	0.49
2:B:341:PRO:HG2	2:B:344:GLU:HG3	1.95	0.49
2:A:191:ASN:O	2:A:192:ASP:HB2	2.14	0.47
2:A:116:LEU:O	2:A:120:MET:HG2	2.14	0.47
2:B:227:THR:HA	2:B:228:PRO:C	2.39	0.47
2:B:349:LEU:O	2:B:353:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:372:LEU:HD22	2:B:411:LEU:HD22	1.98	0.45
2:A:338:MET:HE3	2:A:361:ARG:HB3	1.99	0.45
2:B:191:ASN:HB3	2:B:193:GLN:H	1.82	0.44
2:B:260:ARG:NH1	2:B:363:GLU:OE2	2.48	0.44
2:B:229:LYS:CG	2:B:230:TYR:CD2	3.00	0.44
2:B:245:LEU:HD23	2:B:284:SER:HA	1.99	0.44
2:A:146:ARG:O	2:A:351:ARG:NH2	2.50	0.44
2:A:408:ARG:HH12	2:B:408:ARG:HH22	1.64	0.44
2:B:137:THR:O	2:B:141:GLN:HG3	2.17	0.44
2:B:377:MET:HB2	2:B:378:PRO:HD3	1.98	0.44
2:A:191:ASN:HB3	2:A:195:ARG:HA	1.99	0.44
2:A:246:TYR:CB	2:A:285:LEU:HD21	2.45	0.44
2:A:326:LEU:HB2	2:A:327:PRO:HD3	2.00	0.44
2:A:142:TYR:OH	2:A:221:ARG:NH1	2.51	0.43
2:B:229:LYS:HG2	2:B:230:TYR:N	2.33	0.43
2:B:340:LEU:HD13	2:B:345:ASP:HA	2.01	0.43
2:A:142:TYR:OH	2:A:221:ARG:CZ	2.66	0.43
2:A:203:ARG:NH1	2:A:222:VAL:HG13	2.34	0.43
2:B:203:ARG:NH1	2:B:222:VAL:HG13	2.33	0.43
2:A:227:THR:OG1	2:A:228:PRO:HA	2.19	0.43
2:A:236:THR:HG22	2:A:237:ASP:N	2.33	0.42
2:B:246:TYR:HB2	2:B:285:LEU:HD21	2.01	0.42
2:A:235:GLU:OE2	2:A:241:LYS:HG3	2.20	0.42
2:A:123:LEU:HD23	2:A:187:MET:HG3	2.02	0.42
2:A:192:ASP:H	2:A:195:ARG:HA	1.84	0.42
2:B:338:MET:HE3	2:B:361:ARG:HG2	2.02	0.42
2:A:216:ILE:O	2:A:239:PHE:HB2	2.19	0.42
2:A:311:ASP:OD2	2:A:313:ALA:HB3	2.19	0.42
2:A:377:MET:N	2:A:378:PRO:HD2	2.34	0.42
2:A:308:TYR:O	2:A:339:PHE:HA	2.19	0.42
2:B:369:SER:OG	2:B:411:LEU:HD23	2.20	0.41
2:B:146:ARG:NH2	2:B:347:ASP:OD2	2.51	0.41
2:B:240:HIS:HB3	2:B:243:ARG:HH11	1.85	0.41
2:A:123:LEU:CD2	2:A:187:MET:HG3	2.51	0.41
2:B:123:LEU:HD23	2:B:172:PHE:CE1	2.56	0.41
2:B:191:ASN:HB2	2:B:195:ARG:H	1.86	0.40
2:A:397:PRO:O	2:A:401:GLN:HG3	2.21	0.40
2:B:382:LEU:HD21	2:B:391:LEU:HD22	2.04	0.40
2:B:392:SER:O	2:B:396:LEU:HD12	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
2	A	313/322 (97%)	306 (98%)	7 (2%)	0	100	100
2	B	308/322 (96%)	298 (97%)	10 (3%)	0	100	100
All	All	621/644 (96%)	604 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	A	265/269 (98%)	255 (96%)	10 (4%)	29	39
2	B	258/269 (96%)	251 (97%)	7 (3%)	39	52
All	All	523/538 (97%)	506 (97%)	17 (3%)	33	44

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	116	LEU
2	A	123	LEU
2	A	181	SER
2	A	236	THR
2	A	259	ASN
2	A	296	LEU
2	A	311	ASP
2	A	382	LEU

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Mol	Chain	Res	Type
2	A	400	SER
2	A	427	LEU
2	B	135	VAL
2	B	152	VAL
2	B	233	SER
2	B	284	SER
2	B	296	LEU
2	B	309	ASP
2	B	326	LEU

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

Mol	Chain	Res	Type
2	A	252	GLN
2	A	401	GLN
2	B	114	GLN
2	B	141	GLN
2	B	167	ASN
2	B	178	ASN
2	B	191	ASN
2	B	232	ASN
2	B	253	GLN
2	B	334	GLN
2	B	413	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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 [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	C	6/15 (40%)	1.20	1 (16%) 4 4	65, 68, 76, 84	0
1	D	8/15 (53%)	1.06	1 (12%) 8 9	69, 75, 93, 97	0
2	A	317/322 (98%)	0.46	11 (3%) 47 53	38, 50, 64, 78	0
2	B	310/322 (96%)	0.31	4 (1%) 75 79	35, 47, 71, 78	0
All	All	641/674 (95%)	0.40	17 (2%) 56 63	35, 49, 70, 97	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	342	ASP	3.7
2	B	285	LEU	3.4
2	A	287	THR	3.2
2	B	225	ASN	2.9
2	A	427	LEU	2.8
2	B	112	GLN	2.8
2	A	285	LEU	2.8
2	A	226	ASP	2.8
2	A	191	ASN	2.6
2	A	110	ALA	2.5
2	A	381	ASP	2.5
1	D	3	DA	2.4
2	A	195	ARG	2.4
2	A	192	ASP	2.3
2	A	111	HIS	2.2
2	B	299	ARG	2.2
1	C	2	DA	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.