



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 20, 2018 – 09:14 am GMT

PDB ID : 1A5T
Title : CRYSTAL STRUCTURE OF THE DELTA PRIME SUBUNIT OF THE CLAMP-LOADER COMPLEX OF ESCHERICHIA COLI DNA POLYMERASE III
Authors : Guenther, B.; Onrust, R.; Sali, A.; O'Donnell, M.; Kuriyan, J.
Deposited on : 1998-02-18
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

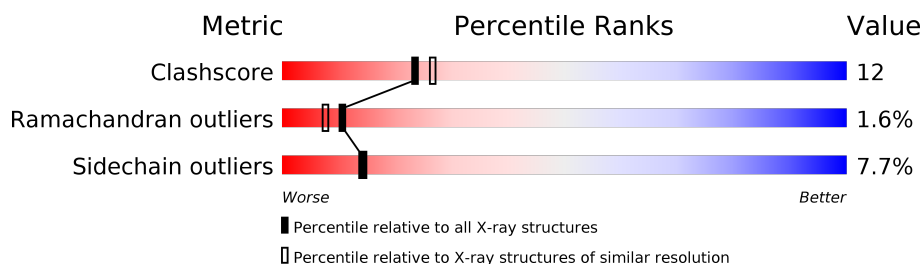
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	122078	5026 (2.20-2.20)
Ramachandran outliers	120005	4951 (2.20-2.20)
Sidechain outliers	119972	4952 (2.20-2.20)

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 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	334	 73% 21% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3669 atoms, of which 954 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 DELTA PRIME.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	324	Total	C	H	N	O	S	0	0	0
			3062	1600	550	448	451	13			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

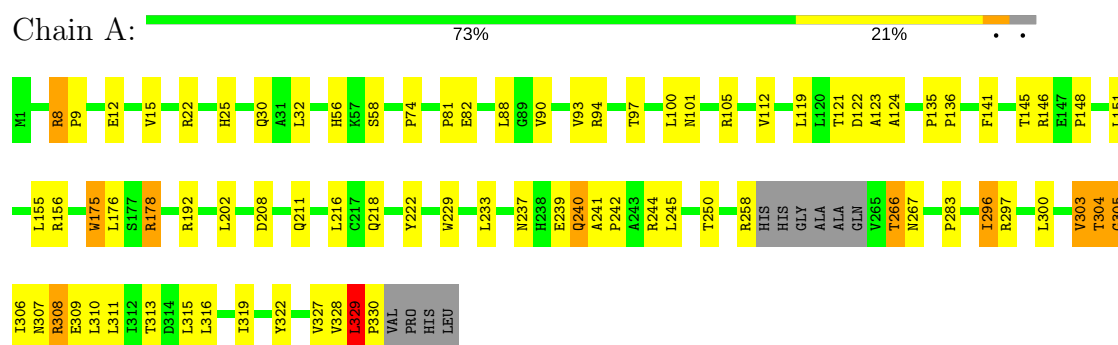
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	202	Total	H	O	0	0
			606	404	202		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 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 ($RSRZ > 2$). 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.

Note EDS was not executed.

• Molecule 1: DELTA PRIME



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	98.90Å 104.00Å 75.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20	Depositor
% Data completeness (in resolution range)	88.0 (30.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.205 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3669	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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: 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	0.55	0/2571	0.76	1/3507 (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
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	329	LEU	N-CA-C	5.71	126.42	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	222	TYR	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	2512	550	2510	61	0
2	A	1	0	0	0	0
3	A	202	404	0	6	0
All	All	2715	954	2510	61	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 12.

All (61) 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:250:THR:HG22	1:A:267:ASN:HD21	1.30	0.93
1:A:145:THR:HG21	1:A:151:LEU:HD21	1.55	0.88
1:A:74:PRO:HB2	1:A:105:ARG:HD2	1.64	0.77
1:A:74:PRO:CB	1:A:105:ARG:HD2	2.21	0.70
1:A:329:LEU:N	1:A:330:PRO:HD2	2.08	0.68
1:A:250:THR:HG22	1:A:267:ASN:ND2	2.07	0.67
1:A:239:GLU:HA	1:A:308:ARG:HH21	1.61	0.66
1:A:175:TRP:CD1	1:A:176:LEU:N	2.66	0.63
1:A:305:GLY:O	1:A:307:ASN:N	2.32	0.63
1:A:100:LEU:HD11	1:A:112:VAL:HG21	1.82	0.61
1:A:303:VAL:O	1:A:305:GLY:N	2.33	0.61
1:A:239:GLU:HA	1:A:308:ARG:NH2	2.16	0.60
1:A:145:THR:CG2	1:A:151:LEU:HD21	2.32	0.58
1:A:74:PRO:HB3	1:A:105:ARG:HH11	1.67	0.57
1:A:74:PRO:HB3	1:A:105:ARG:NH1	2.19	0.57
1:A:74:PRO:HB2	1:A:105:ARG:CD	2.36	0.54
1:A:211:GLN:HG2	3:A:764:HOH:O	2.08	0.54
1:A:245:LEU:HD11	1:A:296:ILE:HG22	1.90	0.53
1:A:319:ILE:HA	1:A:322:TYR:CD2	2.44	0.53
1:A:135:PRO:HB2	3:A:791:HOH:O	2.07	0.53
1:A:328:VAL:C	1:A:330:PRO:HD2	2.29	0.52
1:A:327:VAL:HB	3:A:687:HOH:O	2.10	0.52
1:A:240:GLN:HA	1:A:240:GLN:HE21	1.74	0.51
1:A:297:ARG:NH2	3:A:781:HOH:O	2.44	0.50
1:A:94:ARG:HA	1:A:97:THR:OG1	2.11	0.50
1:A:30:GLN:HG3	1:A:148:PRO:HD3	1.95	0.48
1:A:329:LEU:O	1:A:330:PRO:C	2.52	0.48
1:A:239:GLU:OE1	1:A:239:GLU:HA	2.13	0.48
1:A:233:LEU:HD22	1:A:313:THR:HG22	1.95	0.47
1:A:12:GLU:HA	1:A:15:VAL:HG12	1.97	0.47
1:A:178:ARG:HA	1:A:178:ARG:HH11	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:TRP:O	1:A:316:LEU:HD22	2.14	0.47
1:A:8:ARG:HB3	1:A:9:PRO:HD3	1.97	0.47
1:A:304:THR:O	1:A:305:GLY:C	2.53	0.47
1:A:266:THR:HG23	3:A:654:HOH:O	2.16	0.46
1:A:93:VAL:HG21	1:A:124:ALA:HB1	1.96	0.46
1:A:175:TRP:HD1	1:A:176:LEU:HG	1.82	0.45
1:A:82:GLU:H	1:A:82:GLU:CD	2.20	0.45
1:A:90:VAL:CG2	1:A:123:ALA:HB3	2.46	0.45
1:A:175:TRP:CD1	1:A:176:LEU:HG	2.51	0.45
1:A:240:GLN:O	1:A:244:ARG:HG3	2.17	0.45
1:A:241:ALA:HB3	1:A:242:PRO:HD3	1.99	0.45
1:A:303:VAL:O	1:A:304:THR:C	2.55	0.45
1:A:81:PRO:HG3	1:A:119:LEU:HD13	1.98	0.45
1:A:309:GLU:O	1:A:313:THR:HG23	2.17	0.44
1:A:121:THR:HG22	1:A:122:ASP:N	2.32	0.44
1:A:25:HIS:O	1:A:141:PHE:HD1	2.02	0.43
1:A:296:ILE:HA	1:A:296:ILE:HD12	1.79	0.43
1:A:192:ARG:HB3	1:A:266:THR:HB	2.01	0.43
1:A:22:ARG:HH11	1:A:22:ARG:HG3	1.84	0.42
1:A:245:LEU:CD1	1:A:296:ILE:HG22	2.49	0.42
1:A:148:PRO:O	1:A:156:ARG:HD2	2.18	0.42
1:A:311:LEU:HA	1:A:311:LEU:HD23	1.84	0.42
1:A:146:ARG:NH2	3:A:692:HOH:O	2.52	0.42
1:A:12:GLU:OE1	1:A:56:HIS:ND1	2.53	0.42
1:A:300:LEU:HA	1:A:300:LEU:HD23	1.88	0.42
1:A:135:PRO:HA	1:A:136:PRO:HD3	1.99	0.41
1:A:22:ARG:CG	1:A:22:ARG:HH11	2.34	0.40
1:A:305:GLY:C	1:A:307:ASN:N	2.75	0.40
1:A:237:ASN:OD1	1:A:308:ARG:HD3	2.22	0.40
1:A:90:VAL:HG21	1:A:123:ALA:HB3	2.03	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
1	A	320/334 (96%)	305 (95%)	10 (3%)	5 (2%)	11 8

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	ASP
1	A	304	THR
1	A	306	ILE
1	A	303	VAL
1	A	305	GLY

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	259/270 (96%)	239 (92%)	20 (8%)	14 14

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	32	LEU
1	A	58	SER
1	A	88	LEU
1	A	101	ASN
1	A	155	LEU
1	A	175	TRP
1	A	178	ARG
1	A	202	LEU
1	A	216	LEU
1	A	218	GLN
1	A	240	GLN
1	A	258	ARG
1	A	266	THR

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Mol	Chain	Res	Type
1	A	283	PRO
1	A	296	ILE
1	A	308	ARG
1	A	310	LEU
1	A	315	LEU
1	A	329	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	61	HIS
1	A	101	ASN
1	A	184	GLN
1	A	218	GLN
1	A	240	GLN
1	A	279	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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

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

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.