



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 20, 2016 – 08:29 PM EDT

PDB ID : 1T3W
Title : Crystal Structure of the E.coli DnaG C-terminal domain (residues 434 to 581)
Authors : Oakley, A.J.; Loscha, K.V.; Schaeffer, P.M.; Liepinsh, E.; Wilce, M.C.J.; Otting, G.; Dixon, N.E.
Deposited on : 2004-04-28
Resolution : 2.80 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

<http://wwpdb.org/validation/2016/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
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

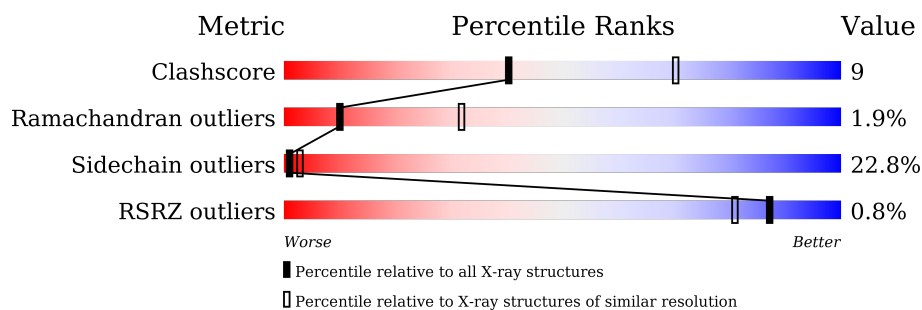
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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.

Mol	Chain	Length	Quality of chain
1	A	148	
1	B	148	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACY	B	582	-	-	-	X

2 Entry composition [i](#)

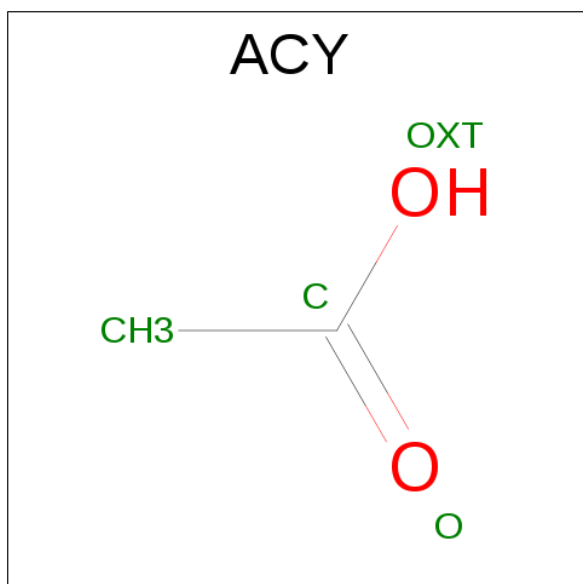
There are 3 unique types of molecules in this entry. The entry contains 2170 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 primase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	134	Total	C	N	O	S	Se	0	0	0
			1072	671	187	210	1	3			
1	B	135	Total	C	N	O	S	Se	0	1	0
			1089	682	190	212	1	4			

- Molecule 2 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	O	0	0
			3	3		

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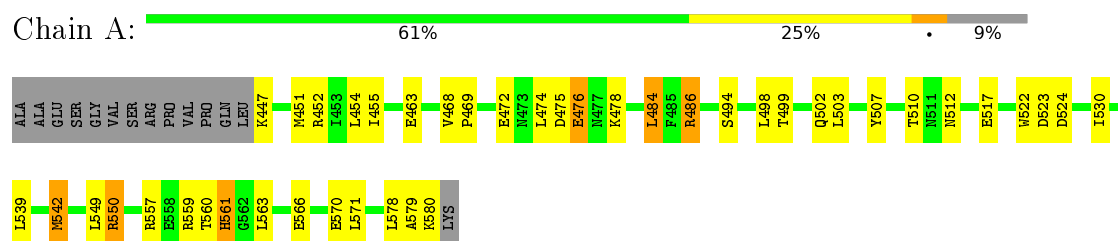
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	O	0	0
			2	2		

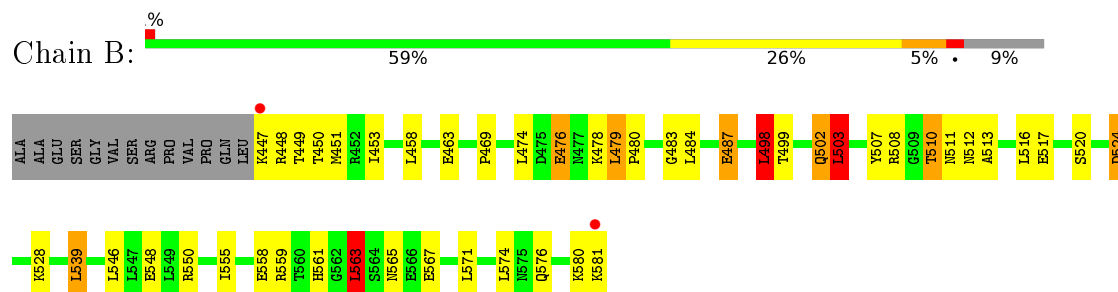
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

• Molecule 1: DNA primase



• Molecule 1: DNA primase



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	142.24Å 142.24Å 192.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 71.12 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.6 (50.00-2.80) 97.6 (71.12-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.269 , 0.308 0.263 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	71.2	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.007 for -1/2*h+1/2*k-1/2*l,1/2*h-1/2*k-1/2*l,-h-k 0.022 for -1/2*h-1/2*k+1/2*l,-1/2*h-1/2*k-1/2*l,h-k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2170	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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: ACY

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	0.63	1/1084 (0.1%)	0.87	2/1464 (0.1%)
1	B	0.55	0/1101	0.86	4/1485 (0.3%)
All	All	0.59	1/2185 (0.0%)	0.86	6/2949 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	542	MSE	SE-CE	-5.66	1.62	1.95

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	498	LEU	CA-CB-CG	6.36	129.92	115.30
1	A	524	ASP	CB-CG-OD2	6.28	123.95	118.30
1	A	523	ASP	CB-CG-OD2	5.70	123.43	118.30
1	B	503	LEU	CA-CB-CG	5.38	127.68	115.30
1	B	563	LEU	CA-CB-CG	5.29	127.46	115.30
1	B	524	ASP	CB-CG-OD2	5.06	122.85	118.30

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	1072	0	1078	18	0
1	B	1089	0	1099	26	0
2	B	4	0	3	1	0
3	A	3	0	0	0	0
3	B	2	0	0	0	0
All	All	2170	0	2180	38	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 9.

All (38) 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:B:565:ASN:OD1	2:B:582:ACY:H1	1.52	1.08
1:B:510:THR:HG22	1:B:512:ASN:H	1.35	0.89
1:B:487:GLU:OE1	1:B:507:TYR:OH	2.02	0.78
1:B:507:TYR:O	1:B:510:THR:HB	1.88	0.72
1:A:550:ARG:HD3	1:A:570:GLU:OE1	1.92	0.70
1:A:560:THR:O	1:A:561:HIS:CB	2.42	0.66
1:B:499:THR:HG23	1:B:502:GLN:HE21	1.61	0.66
1:B:499:THR:H	1:B:502:GLN:HG3	1.61	0.65
1:A:542:MSE:HG2	1:B:451:MSE:HE2	1.82	0.60
1:B:476:GLU:HG2	1:B:483:GLY:HA2	1.86	0.58
1:B:451:MSE:HE3	1:B:479:LEU:HD21	1.88	0.56
1:B:499:THR:HG23	1:B:502:GLN:NE2	2.20	0.55
1:A:542:MSE:HG2	1:B:451:MSE:CE	2.36	0.54
1:B:510:THR:HG22	1:B:512:ASN:N	2.16	0.53
1:A:476:GLU:HG3	1:A:486:ARG:NH1	2.25	0.52
1:A:539:LEU:HD13	1:B:469:PRO:HD3	1.92	0.52
1:B:498:LEU:HD12	1:B:499:THR:N	2.25	0.52
1:B:517:GLU:O	1:B:520:SER:HB3	2.10	0.51
1:B:563:LEU:HG	1:B:567:GLU:HB3	1.94	0.50
1:A:560:THR:O	1:A:561:HIS:HB2	2.11	0.49
1:A:499:THR:H	1:A:502:GLN:HE21	1.59	0.49
1:B:563:LEU:HB2	1:B:567:GLU:OE1	2.14	0.48
1:B:498:LEU:HD12	1:B:499:THR:O	2.14	0.47
1:B:498:LEU:HD11	1:B:503:LEU:N	2.30	0.46
1:B:479:LEU:HA	1:B:480:PRO:HD2	1.67	0.46
1:A:507:TYR:HA	1:A:512:ASN:HD22	1.82	0.45
1:A:454:LEU:CD2	1:B:539:LEU:HD13	2.47	0.45
1:A:468:VAL:HG12	1:A:469:PRO:O	2.17	0.44
1:A:455:ILE:HD13	1:A:484:LEU:HD13	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:507:TYR:O	1:B:513:ALA:HB2	2.19	0.43
1:B:449:THR:HG22	1:B:451:MSE:H	1.83	0.43
1:A:560:THR:O	1:A:560:THR:OG1	2.34	0.42
1:A:474:LEU:HD22	1:B:546:LEU:HD13	2.01	0.42
1:B:498:LEU:HD11	1:B:503:LEU:CA	2.50	0.41
1:A:560:THR:O	1:A:561:HIS:HB3	2.19	0.41
1:A:498:LEU:HD22	1:A:502:GLN:HB3	2.04	0.40
1:A:452:ARG:HD3	1:A:522:TRP:NE1	2.36	0.40
1:A:454:LEU:HD21	1:B:539:LEU:HD13	2.03	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	132/148 (89%)	126 (96%)	3 (2%)	3 (2%)	8	26
1	B	134/148 (90%)	120 (90%)	12 (9%)	2 (2%)	13	40
All	All	266/296 (90%)	246 (92%)	15 (6%)	5 (2%)	10	32

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	476	GLU
1	A	579	ALA
1	B	498	LEU
1	A	561	HIS
1	B	511	ASN

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	120/128 (94%)	98 (82%)	22 (18%)	2	6
1	B	122/128 (95%)	89 (73%)	33 (27%)	0	1
All	All	242/256 (94%)	187 (77%)	55 (23%)	1	3

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	447	LYS
1	A	451	MSE
1	A	463	GLU
1	A	472	GLU
1	A	475	ASP
1	A	478	LYS
1	A	484	LEU
1	A	486	ARG
1	A	494	SER
1	A	503	LEU
1	A	510	THR
1	A	517	GLU
1	A	530	ILE
1	A	549	LEU
1	A	550	ARG
1	A	557	ARG
1	A	559	ARG
1	A	563	LEU
1	A	566	GLU
1	A	571	LEU
1	A	578	LEU
1	A	580	LYS
1	B	447	LYS
1	B	448	ARG
1	B	450	THR
1	B	453	ILE
1	B	458	LEU

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Mol	Chain	Res	Type
1	B	463	GLU
1	B	474	LEU
1	B	476	GLU
1	B	478	LYS
1	B	479	LEU
1	B	484	LEU
1	B	487	GLU
1	B	498	LEU
1	B	502	GLN
1	B	503	LEU
1	B	508	ARG
1	B	510	THR
1	B	516	LEU
1	B	524	ASP
1	B	528	LYS
1	B	539	LEU
1	B	548	GLU
1	B	550	ARG
1	B	555	ILE
1	B	558	GLU
1	B	559	ARG
1	B	561	HIS
1	B	563	LEU
1	B	571	LEU
1	B	574	LEU
1	B	576	GLN
1	B	580	LYS
1	B	581	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	473	ASN
1	A	502	GLN
1	B	460	GLN
1	B	502	GLN
1	B	561	HIS

5.3.3 RNA ⓘ

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	$\# Z > 2$
2	ACY	B	582	-	0,3,3	0.00	-	0,3,3	0.00	-

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
2	ACY	B	582	-	-	0/0/0/0	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	582	ACY	1	0

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	A	131/148 (88%)	0.05	0 100 100	45, 60, 76, 91	0
1	B	132/148 (89%)	0.28	2 (1%) 76 68	44, 63, 97, 112	0
All	All	263/296 (88%)	0.17	2 (0%) 87 81	44, 62, 92, 112	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	581	LYS	4.2
1	B	447	LYS	3.4

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	ACY	B	582	4/4	0.97	0.32	3.34	52,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.