



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2026 – 04:59 AM EDT

PDB ID : 3NWS / pdb_00003nws
Title : Crystal structure of the N-terminal domain of the yeast telomere-binding and telomerase regulatory protein Cdc13
Authors : Mitchell, M.T.; Smith, J.S.; Mason, M.; Harper, S.; Speicher, D.W.; Johnson, F.B.; Skordalakes, E.
Deposited on : 2010-07-10
Resolution : 2.50 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	:	FAILED
Xtriage (Phenix)	:	2.0
EDS	:	FAILED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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 2.50 Å.

There are no overall percentile quality scores available for this entry.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6406 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 Cell division control protein 13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	0	0	0
			1595	1023	266	300	6			
1	B	195	Total	C	N	O	S	0	0	0
			1595	1023	266	300	6			
1	C	195	Total	C	N	O	S	0	0	0
			1595	1023	266	300	6			
1	D	195	Total	C	N	O	S	0	0	0
			1595	1023	266	300	6			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLY	-	expression tag	UNP P32797
A	10	HIS	-	expression tag	UNP P32797
A	11	MET	-	expression tag	UNP P32797
A	12	MET	-	expression tag	UNP P32797
B	9	GLY	-	expression tag	UNP P32797
B	10	HIS	-	expression tag	UNP P32797
B	11	MET	-	expression tag	UNP P32797
B	12	MET	-	expression tag	UNP P32797
C	9	GLY	-	expression tag	UNP P32797
C	10	HIS	-	expression tag	UNP P32797
C	11	MET	-	expression tag	UNP P32797
C	12	MET	-	expression tag	UNP P32797
D	9	GLY	-	expression tag	UNP P32797
D	10	HIS	-	expression tag	UNP P32797
D	11	MET	-	expression tag	UNP P32797
D	12	MET	-	expression tag	UNP P32797

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total 5	O 5	0	0
2	B	7	Total 7	O 7	0	0
2	C	6	Total 6	O 6	0	0
2	D	8	Total 8	O 8	0	0

SEQUENCE-PLOTS INFOmissingINFO

3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.96Å 66.87Å 68.14Å 116.22° 90.29° 94.72°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	92.9 (20.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.245 , 0.288	Depositor
Wilson B-factor (Å ²)	57.3	Xtriage
Anisotropy	0.294	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.014 for -h,-l,-k	Xtriage
Total number of atoms	6406	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.11% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 Protein, DNA and RNA chains [i](#)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates [i](#)

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5.4 Ligands [i](#)

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5.5 Other polymers [i](#)

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