

Full wwPDB X-ray Structure Validation Report (i)

Oct 4, 2023 – 10:04 PM EDT

PDB ID : 6UCR

Title : Structure of ClpC1-NTD L92S L96P

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Deposited on : 2019-09-17

Resolution : 2.30 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 (i) 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 (i)) were used in the production of this report:

MolProbity : FAILED

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : FAILED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.30 Å.

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

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1299 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 Negative regulator of genetic competence ClpC/mecB.

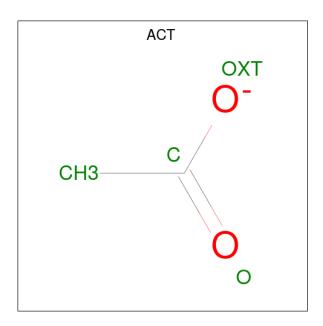
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	154	Total 1193	C 750	N 223	O 219	S 1	0	0	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue Modelled A		Actual	Comment	Reference	
A	92	SER	LEU	engineered mutation	UNP A0A0U0SI28	
A	96	PRO	LEU	engineered mutation	UNP A0A0U0SI28	
A	146	LYS	-	expression tag	UNP A0A0U0SI28	
A	147	LEU	-	expression tag	UNP A0A0U0SI28	
A	148	ALA	-	expression tag	UNP A0A0U0SI28	
A	149	ALA	-	expression tag	UNP A0A0U0SI28	
A	150	ALA	-	expression tag	UNP A0A0U0SI28	
A	151	LEU	-	expression tag	UNP A0A0U0SI28	
A	152	GLU	-	expression tag	UNP A0A0U0SI28	
A	153	HIS	-	expression tag	UNP A0A0U0SI28	
A	154	HIS	-	expression tag	UNP A0A0U0SI28	
A	155	HIS	-	expression tag	UNP A0A0U0SI28	
A	156	HIS	-	expression tag	UNP A0A0U0SI28	
A	157	HIS	-	expression tag	UNP A0A0U0SI28	
A	158	HIS	-	expression tag	UNP A0A0U0SI28	

• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).





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

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
3	A	102	Total O 102 102	0	0	

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



3 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	38.14Å 63.35Å 68.31Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	40.00 - 2.30	Depositor	
% Data completeness	96.2 (40.00-2.30)	Depositor	
(in resolution range)	,		
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	23.33 (at 2.29Å)	Xtriage	
Refinement program	PHENIX	Depositor	
R, R_{free}	0.186 , 0.237	Depositor	
Wilson B-factor (\mathring{A}^2)	19.0	Xtriage	
Anisotropy	0.857	Xtriage	
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.33$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1299	wwPDB-VP	
Average B, all atoms (Å ²)	23.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.25% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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)

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

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

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

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 monosaccharides in this entry.

4.6 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	l Type	Chain	Res	Link	Bond lengths			Bond angles		
MIOI				Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACT	A	201	-	3,3,3	1.09	0	3,3,3	0.77	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.

No monomer is involved in short contacts.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

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)

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

5.4 Ligands (i)

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

5.5 Other polymers (i)

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

