



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 01:24 PM UTC

PDB ID : 9E0O / pdb_00009e0o
EMDB ID : EMD-47364
Title : CryoEM structure of inducible Lysine decarboxylase from *Hafnia alvei* L-hydrazino-Lysine analog at 2.04 Angstrom resolution
Authors : Duhoo, Y.; Desfosses, A.; Gutsche, I.; Doukov, T.I.; Berkowitz, D.B.
Deposited on : 2024-10-18
Resolution : 2.00 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
Mogul : **FAILED**
MolProbity : **FAILED**
Buster-report : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.8.1
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

PERCENTILES INFOmissingINFO

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

1 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D5	Depositor
Number of particles used	1300000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

2 Model quality [i](#)

2.1 Standard geometry [i](#)

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

2.2 Too-close contacts [i](#)

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

2.3 Torsion angles [i](#)

2.3.1 Protein backbone [i](#)

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

2.3.2 Protein sidechains [i](#)

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

2.3.3 RNA [i](#)

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

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

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

2.5 Carbohydrates [i](#)

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

2.6 Ligand geometry [i](#)

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

2.7 Other polymers [i](#)

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

2.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

3 Map visualisation

This section contains visualisations of the EMDB entry EMD-47364. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

3.1 Orthogonal projections

This section was not generated.

3.2 Central slices

This section was not generated.

3.3 Largest variance slices

This section was not generated.

3.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

3.5 Orthogonal surface views

This section was not generated.

3.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

4 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

4.1 Map-value distribution ⓘ

This section was not generated.

4.2 Volume estimate versus contour level ⓘ

This section was not generated.

4.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

5 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

6 Map-model fit

This section was not generated.