



Full wwPDB EM Validation Report ⓘ

Feb 24, 2025 – 12:08 pm GMT

EMDB ID : EMD-50038
Title : Cryo-EM structure of the Apo E. coli BrxX methyltransferase
Authors : Adams, M.C.; Ghilarov, D.
Deposited on : 2024-04-08
Resolution : 3.90 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/EMMapValidationReportHelp>

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 : **FAILED**
Validation Pipeline (wwPDB-VP) : 2.41

1 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	Not Provided	
Number of particles used	24284	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35.1	Depositor
Minimum defocus (nm)	0.9	Depositor
Maximum defocus (nm)	3.0	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor