



## Full wwPDB EM Validation Report ⓘ

Feb 24, 2025 – 12:19 pm GMT

EMDB ID : EMD-50027  
Title : Cryo-EM structure of the E. coli BrxX methyltransferase in complex with DNA  
Authors : Adams, M.C.; Ghilarov, D.  
Deposited on : 2024-04-05  
Resolution : 2.22 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](mailto: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>.

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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             | 216233                  | 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 ( $e^-/\text{\AA}^2$ ) | 50.5                    | Depositor |
| Minimum defocus (nm)                 | 0.7000000000000001      | Depositor |
| Maximum defocus (nm)                 | 2.4                     | Depositor |
| Magnification                        | Not provided            |           |
| Image detector                       | FEI FALCON IV (4k x 4k) | Depositor |