



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 01:03 pm GMT

EMDB ID : EMD-6840
Title : The first reconstruction of beta-galactosidase solved by cryoARM200
Authors : , Kato.T.; , Terahara.N.; , Namba.K.
Deposited on : 2017-10-26
Resolution : 2.60 Å(reported)

This is a Full wwPDB EM Map 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**
Validation Pipeline (wwPDB-VP) : 2.13

1 Experimental information

| Property | Value | Source |
|--------------------------------------|-----------------------|-----------|
| EM reconstruction method | singleParticle | Depositor |
| Imposed symmetry | POINT, D2 | Depositor |
| Number of images used | 93975 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | Not provided | Depositor |
| Microscope | JEOL CRYO ARM 200 | Depositor |
| Voltage (kV) | 200 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 70.0 | Depositor |
| Minimum defocus (nm) | 0.248 | Depositor |
| Maximum defocus (nm) | 2.167 | Depositor |
| Magnification | 56497. | Depositor |
| Image detector | GATAN K2 IS (4k x 4k) | Depositor |