



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:48 pm GMT

EMDB ID : EMD-6142
Title : Cryo-EM reconstructions of E. coli ribosomal 30S subunit assembly intermediates
Authors : , Sashital.DG.; , Greeman.CA.; , Lyumkis.D.; , Potter.CS.; , Carragher.B.; , Williamson.JR.
Deposited on : 2014-10-08
Resolution : 27.60 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 | Not Provided | Depositor |
| Number of images used | 3407 | Depositor |
| Resolution determination method | OTHER | Depositor |
| CTF correction method | Each micrograph | Depositor |
| Microscope | FEI TECNAI F20 | Depositor |
| Voltage (kV) | 200 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 33.67 | Depositor |
| Minimum defocus (nm) | 2.5 | Depositor |
| Maximum defocus (nm) | 5.0 | Depositor |
| Magnification | 29000.0 | Depositor |
| Image detector | GATAN K2 (4k x 4k) | Depositor |