



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:55 pm GMT

EMDB ID : EMD-6169
Title : Electron cryo-microscopy of Rqc2 bound to yeast 60S ribosome, Rqc2-focused alignment
Authors : , Shen.PS.; , Park.J.; , Qin.Y.; , Li.X.; , Parsawar.K.; , Larson.M.; , Cox.J.; , Cheng.Y.; , Lambowitz.AM.; , Weissman.JS.; , Brandman.O.; , Frost.A.
Deposited on : 2014-11-04
Resolution : 6.70 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 | 9131 | Depositor |
| Resolution determination method | OTHER | Depositor |
| CTF correction method | each particle | Depositor |
| Microscope | FEI POLARA 300 | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 35 | Depositor |
| Minimum defocus (nm) | 0.8 | Depositor |
| Maximum defocus (nm) | 2.0 | Depositor |
| Magnification | 31000.0 | Depositor |
| Image detector | GATAN K2 (4k x 4k) | Depositor |