



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:38 pm GMT

EMDB ID : EMD-5614
Title : Yeast 20S proteasome with C-terminal peptide of yeast Rpt4
Authors : , Li.X.; , Kim.HM.; , Cheng.Y.
Deposited on : 2013-03-21
Resolution : 7.80 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 | 36303 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | Each particle | Depositor |
| Microscope | FEI TECNAI F20 | Depositor |
| Voltage (kV) | 200 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 25 | Depositor |
| Minimum defocus (nm) | 1.2 | Depositor |
| Maximum defocus (nm) | 2.1 | Depositor |
| Magnification | 100000.0 | Depositor |
| Image detector | TVIPS TEMCAM-F816 (8k x 8k) | Depositor |