



wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 01:38 pm GMT

EMDB ID : EMD-8772
Title : Core Factor local refinement from Pol I Initial Transcribing Complex at 4.2 angstrom
Authors : , Han.Y.; , He.Y.
Deposited on : 2017-06-16
Resolution : 4.20 Å(reported)

This is a wwPDB EM Map Validation Summary 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, C1 | Depositor |
| Number of images used | 124112 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | CTF amplitude correction was performed following 3D auto refinement in relion. | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 56.8 | Depositor |
| Minimum defocus (nm) | 1.5 | Depositor |
| Maximum defocus (nm) | 4.5 | Depositor |
| Magnification | 22500.0 | Depositor |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |