



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:54 pm GMT

EMDB ID : EMD-6426
Title : Negative-stain electron microscopy of a full-length transmembrane receptor tyrosine kinase (PDGFR) in complex with PDGFB
Authors : , Chen.PH.; , Unger.VM.; , He.X.
Deposited on : 2015-08-12
Resolution : 27.00 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 | 4234 | Depositor |
| Resolution determination method | OTHER | Depositor |
| CTF correction method | Not provided | Depositor |
| Microscope | OTHER | Depositor |
| Voltage (kV) | 120 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | Not provided | Depositor |
| Minimum defocus (nm) | 0.5 | Depositor |
| Maximum defocus (nm) | 2.0 | Depositor |
| Magnification | 30000.0 | Depositor |
| Image detector | GENERIC CCD | Depositor |