



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:28 pm GMT

EMDB ID : EMD-5218
Title : Visualizing the structural changes of bacteriophage epsilon15 and its Salmonella host during infection
Authors : , Chang.JT.; , Schmid.MF.; , Haase-Pettingell.C.; , Weigele.PR.; , King.JA.; , Chiu.W.
Deposited on : 2010-07-22
Resolution : Not provided

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 | subtomogramAveraging | Depositor |
| Imposed symmetry | Not Provided | Depositor |
| Number of images used | Not provided | Depositor |
| Resolution determination method | Not provided | Depositor |
| CTF correction method | Not provided | Depositor |
| Microscope | JEOL 3200FSC | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 65 | Depositor |
| Minimum defocus (nm) | 6.0 | Depositor |
| Maximum defocus (nm) | 9.0 | Depositor |
| Magnification | 20000.0 | Depositor |
| Image detector | GENERIC CCD | Depositor |