



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 01:38 pm GMT

EMDB ID : EMD-8565  
Title : Cryo-EM structure of bacteriophage T7 replisome  
Authors : , Kulczyk.AW.  
Deposited on : 2017-01-20  
Resolution : 13.80 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](mailto: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                | 79519                       | Depositor |
| Resolution determination method      | FSC 0.5 CUT-OFF             | Depositor |
| CTF correction method                | CTFFIND4                    | Depositor |
| Microscope                           | FEI TITAN KRIOS             | Depositor |
| Voltage (kV)                         | 300                         | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 5.0                         | Depositor |
| Minimum defocus (nm)                 | 2.0                         | Depositor |
| Maximum defocus (nm)                 | 3.0                         | Depositor |
| Magnification                        | Not provided                | Depositor |
| Image detector                       | TVIPS TEMCAM-F416 (4k x 4k) | Depositor |