



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:43 pm GMT

EMDB ID : EMD-5568  
Title : Focused asymmetric reconstruction I (map 3/8): Visualization of Uncorrelated Tandem Symmetry Mismatches in the Internal Genome Packaging Apparatus of a dsDNA virus  
Authors : , Guo.F.; , Liu.Z.; , Vago.F.; , Ren.Y.; , Wu.W.; , Wright.E.; , Serwer.P.; , Jiang.W.  
Deposited on : 2013-01-09  
Resolution : 17.00 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](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.

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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                | 12360   | Depositor |
| Resolution determination method      | OTHER   | Depositor |
| CTF correction method                | phase flipping and amplitude weighted; per particle | Depositor |
| Microscope                           | FEI TITAN KRIOS                                     | Depositor |
| Voltage (kV)                         | 300   | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 25  | Depositor |
| Minimum defocus (nm)                 | 0.8   | Depositor |
| Maximum defocus (nm)                 | 4.5   | Depositor |
| Magnification                        | 57727.0   | Depositor |
| Image detector                       | KODAK SO-163 FILM                                   | Depositor |