



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:52 pm GMT

EMDB ID : EMD-6225  
Title : CryoEM single particle reconstruction of anthrax toxin protective antigen pore (lacking the membrane-spanning beta barrel) at 3.6 Angstrom resolution  
Authors : , Jiang.J.; , Pentelute.BL.; , Collier.R.J.; , Zhou.ZH.  
Deposited on : 2014-12-25  
Resolution : 3.60 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                | 21632              | Depositor |
| Resolution determination method      | OTHER              | Depositor |
| CTF correction method                | Each particle      | Depositor |
| Microscope                           | FEI TITAN KRIOS    | Depositor |
| Voltage (kV)                         | 300                | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 30                 | Depositor |
| Minimum defocus (nm)                 | 1.8                | Depositor |
| Maximum defocus (nm)                 | 5.1                | Depositor |
| Magnification                        | 39062.0            | Depositor |
| Image detector                       | GATAN K2 (4k x 4k) | Depositor |