



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:44 pm GMT

EMDB ID : EMD-5906  
Title : Cryo-EM structure of low salt treated immature 30S ribosomal subunit from rsga and rbfa deleted E.coli strain  
Authors : , Yang.Z.; , Guo.Q.; , Goto.S.; , Chen.Y.; , Li.N.; , Yan.K.; , Zhang.Y.; , Muto.A.; , Deng.H.; , Himeno.H.; , Lei.J.; , Gao.N.  
Deposited on : 2014-02-12  
Resolution : 17.80 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                | 50721               | Depositor |
| Resolution determination method      | OTHER               | Depositor |
| CTF correction method                | weiner filter       | Depositor |
| Microscope                           | FEI TITAN KRIOS     | Depositor |
| Voltage (kV)                         | 300                 | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 20                  | Depositor |
| Minimum defocus (nm)                 | 1.0                 | Depositor |
| Maximum defocus (nm)                 | 8.5                 | Depositor |
| Magnification                        | 59000.0             | Depositor |
| Image detector                       | FEI EAGLE (4k x 4k) | Depositor |