



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:28 pm GMT

EMDB ID : EMD-5153  
Title : Model of human low density lipoprotein and bound receptor based on CryoEM  
Authors : , Ren.G.; , Rudenko.G.; , Ludtke.SJ.; , Deisenhofer.J.; , Chiu.W.; , Pownall.HJ.  
Deposited on : 2009-12-14  
Resolution : 28.00 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.

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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                | 8500            | Depositor |
| Resolution determination method      | FSC 0.5 CUT-OFF | Depositor |
| CTF correction method                | CTFIT           | Depositor |
| Microscope                           | JEOL 3000SFF    | Depositor |
| Voltage (kV)                         | 300             | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 25              | Depositor |
| Minimum defocus (nm)                 | Not provided    | Depositor |
| Maximum defocus (nm)                 | Not provided    | Depositor |
| Magnification                        | Not provided    | Depositor |
| Image detector                       | GENERIC CCD     | Depositor |