



## wwPDB EM Validation Summary Report ⓘ

Mar 1, 2025 – 06:04 am GMT

EMDB ID : EMD-19757  
Title : CryoEM structure of Apo form of catalytic domain of human HMG-CoA reductase  
Authors : Manikandan, K.; Van Rooyen, J.  
Deposited on : 2024-02-27  
Resolution : 2.06 Å(reported)

This is a wwPDB EM 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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) : 2.41

# 1 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	1066707	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	54.8	Depositor
Minimum defocus (nm)	0.8	Depositor
Maximum defocus (nm)	2.0	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor