



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 02:44 pm GMT

EMDB ID : EMD-9865  
Title : The 1.54 Å resolution structure of apoferritin by CRYOARM300 with Cold-FEG  
Authors : , Kato.T.; , Nakane.T.; , Makino.F.; , Terahara.N.; , Yonekura.K.; , Namba.K.  
Deposited on : 2019-03-25  
Resolution : 1.54 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	POINT, O	Depositor
Number of images used	120295	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	88.0	Depositor
Minimum defocus (nm)	0.315	Depositor
Maximum defocus (nm)	2.167	Depositor
Magnification	101000.0	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor