



Full wwPDB EM Map Validation 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 Full wwPDB EM Map Validation Report for a publicly released PDB entry.

We welcome your comments at 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 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