



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 11:38 am GMT

EMDB ID : EMD-22350  
Title : CryoEM structure of human light chain apoferritin calculated from EER movies (intra-fraction motion correction experiment, 1.5x supersampling, particle motion corrected without B-spline interpolation)  
Authors : , Guo.H.; , Rubinstein.J.  
Deposited on : 2020-07-24  
Resolution : 2.10 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	POINT, O	Depositor
Number of images used	291408	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	41.0	Depositor
Minimum defocus (nm)	0.4	Depositor
Maximum defocus (nm)	1.6	Depositor
Magnification	75000.0	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor