Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 02:56 pm GMT

EMDB ID	:	EMD-9296
Title	:	Cryo-EM structure of the HO BMC shell: Fully asymmetric reconstruction
Authors	:	, Greber.BJ.; , Sutter.M.; , Kerfeld.CA.
Deposited on	:	2018-11-04
Resolution	:	4.40 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, C1	Depositor
Number of images used	11107	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Initial CTF fitting using CTFFIND4, CTF correction applied within RELION.	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25.0	Depositor
Minimum defocus (nm)	1.0	Depositor
Maximum defocus (nm)	3.5	Depositor
Magnification	48543.	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor