



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:33 pm GMT

EMDB ID : EMD-5365
Title : Structure of Endophilin N-BAR domain bound to bilayer
Authors : , Mim.C.; , Cui.H.; , Gawronski-Salerno.JA.; , Frost.A.; , Lyman.E.; ,
Voth.GA.; , Unger.VM.
Deposited on : 2011-12-09
Resolution : 11.00 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	helical	Depositor
Imposed symmetry	HELICAL, twist=67.55°, rise=20.08 Å, axial sym=C2	Depositor
Number of images used	Not provided	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	ACE,MATLAB	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	1.4	Depositor
Maximum defocus (nm)	2.0	Depositor
Magnification	30000.0	Depositor
Image detector	Not provided	Depositor