



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:54 pm GMT

EMDB ID : EMD-6100
Title : CryoEM reveals different coronin binding modes for ADP- and ADP-BeFx-actin filaments
Authors : , Ge.P.; , Durer.ZAO.; , Kudryashov.D.; , Zhou.ZH.; , Reisler.E.
Deposited on : 2014-09-20
Resolution : 8.60 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=165.9°, rise=28.27 Å, axial sym=C1	Depositor
Number of images used	Not provided	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{Å}^2$)	25	Depositor
Minimum defocus (nm)	2.0	Depositor
Maximum defocus (nm)	4.0	Depositor
Magnification	104384.0	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor